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(54) Title: SYSTEM AND USES FOR GENERATING DATABASES OF PROTEIN SECONDARY STRUCTURES INVOLVED IN INTER-CHAIN PROTEIN INTERACTIONS

(57) Abstract: The present invention relates to methods and systems for generating a database of protein secondary structures that are at an interface of a two-chain inter- protein interaction. Collections of secondary structures identified according to the methods disclosed herein, and their use in identifying therapeutic drug candidates potentially effective in modulating a two-chain inter-protein interaction having a secondary structure at its interface, are also disclosed.

SYSTEM AND USES FOR GENERATING DATABASES OF PROTEIN SECONDARY STRUCTURES INVOLVED IN INTER-CHAIN PROTEIN INTERACTIONS

[0001] This application claims the priority benefit of U.S. Provisional Patent Application Serial No. 61/166,211, filed April 2, 2009, which is hereby incorporated by reference in its entirety.

[0002] This invention was made with government support under grant number GM073943 awarded by the National Institutes of Health. The government has certain rights in this invention.

FIELD OF THE INVENTION

[0003] The present invention relates to methods and systems for generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction. Collections of the secondary structures that are at the interface of inter-protein interactions and methods of screening are also disclosed.

BACKGROUND OF THE INVENTION

[0004] A fundamental limitation of current drug development centers on the inability of traditional pharmaceuticals to target spatially extended protein interfaces. The majority of modern pharmaceuticals are small molecules that target enzymes or protein receptors with defined pockets. However, in general they cannot target protein–protein interactions involving large contact areas with the required specificity. Recent computational and experimental studies highlight the "hot-spots" on protein surfaces that contribute significantly to binding interactions (Clackson et al., "A Hot-Spot of Binding-Energy in a Hormone–Receptor Interface," *Science* 267:383-386 (1995); Guney et al., "HotSprint: Database of Computational Hot Spots in Protein Interfaces," *Nucleic Acids Res.* 36:D662-D666 (2008); Keskin et al., "Principles of Protein–Protein Interactions: What Are the Preferred Ways for Proteins to Interact?," *Chem. Rev.* 108:1225-1244 (2008); Wells et al., "Reaching for High-Hanging Fruit in Drug Discovery at Protein–Protein Interfaces," *Nature* 450:1001-1009 (2007)). Hot-spot residues are those residues at the protein interface that contribute to high affinity binding and are usually surrounded by energetically less important residues. Typically, the first step in developing a small molecule inhibitor to target a protein

interface is to identify hot-spot residues responsible for protein–complex recognition. Subsequently, the topography of these side chains is reproduced by similar peptidic or non-peptidic functionalities on a scaffold that positions the crucial recognition elements correctly. Thus, protein–protein recognition may be concentrated in a few key residues arranged in a particular three-dimensional shape.

[0005] Selective modulation of protein–protein interactions is a grand challenge for chemical biologists and medicinal chemists (Wells et al., "Reaching for High-Hanging Fruit in Drug Discovery at Protein–Protein Interfaces," *Nature* 450:1001-1009 (2007)). Protein interfaces are often composed of large shallow surfaces rendering them difficult targets for typical small molecule drugs (Argos, P., "An Investigation of Protein Subunit and Domain Interfaces," *Protein Eng.* 2:101-113 (1988); Miller, S., "The Structure of Interfaces Between Subunits of Dimeric and Tetrameric Proteins," *Protein Eng.* 3:77-83 (1989); Lo Conte et al., "The Atomic Structure of Protein–Protein Recognition Sites," *J. Mol. Biol.* 285:2177-2198 (1999)). A broad effort to develop new classes of protein–protein interaction inhibitors has focused on the fundamental role played by short folded domains, or protein secondary structures, at protein interfaces (Miller, S., "The Structure of Interfaces Between Subunits of Dimeric and Tetrameric Proteins," *Protein Eng.* 3:77-83 (1989)).

[0006] α-Helices constitute the largest class of protein secondary structures and mediate many protein interactions (Guharoy et al., "Secondary Structure Based Analysis and Classification of Biological Interfaces: Identification of Binding Motifs in Protein–Protein Interactions," *Bioinformatics* 23:1909-1918 (2007); Jones et al., "Protein–Protein Interactions: A Review of Protein Dimer Structures," *Prog. Biophys. Mol. Bio.* 63:31-65 (1995)). Helices located within the protein core are vital for the overall stability of protein tertiary structure, whereas exposed α-helices on protein surfaces constitute central bioactive regions for the recognition of numerous proteins, DNAs, and RNAs. Peptides composed of less than fifteen amino acid residues do not generally form α-helical structures at physiological conditions once excised from the protein environment; much of their ability to specifically bind their intended targets is lost because they adopt an ensemble of conformations rather than the biologically relevant one. Synthetic strategies that either stabilize short peptides (<15 residues) into α-helical conformations or mimic this domain with nonnatural scaffolds are

expected to be useful models for the design of bioactive molecules and for studying aspects of protein folding (Henchey et al., "Contemporary Strategies for the Stabilization of Peptides in the Alpha-Helical Conformation," *Curr. Opin. Chem. Biol.* 12:692-697 (2008); Garner et al., "Design and Synthesis of Alpha-Helical Peptides and Mimetics," *Org. Biomol. Chem.* 5:3577-3585 (2007); Davis et al., "Synthetic Non-Peptide Mimetics of Alpha-Helices," *Chem. Soc. Rev.* 36:326-334 (2007); Murray et al., "Targeting Protein–Protein Interactions: Lessons from p53/MDM2," *Biopolymers* 88:657-686 (2007)).

[0007] Several classes of helix mimetics have been described by the synthetic organic chemistry community (Henchey et al., "Contemporary Strategies for the Stabilization of Peptides in the Alpha-Helical Conformation," *Curr. Opin. Chem. Biol.* 12:692-697 (2008); Garner et al., "Design and Synthesis of Alpha-Helical Peptides and Mimetics," *Org. Biomol. Chem.* 5:3577-3585 (2007); Davis et al., "Synthetic Non-Peptide Mimetics of Alpha-Helices," *Chem. Soc. Rev.* 36:326-334 (2007); Murray et al., "Targeting Protein–Protein Interactions: Lessons from p53/MDM2," *Biopolymers* 88:657-686 (2007)), but progress in the use of these helix mimetics in biology has been limited to a set of model protein complexes. The restricted use of these mimetics can be attributed to the lack of a systematic method for identifying helical protein interfaces that may be targeted by the various classes of stabilized helices and synthetic helix mimetics. Therefore, what is needed is a comprehensive method for identifying inter-protein interactions that serve as potential targets for the development of helical and other secondary structure mimetics.

[0008] The present invention is directed to overcoming these and other deficiencies in the art.

SUMMARY OF THE INVENTION

[0009] A first aspect of the present invention relates to a method of generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction. This method involves retrieving, from a protein database, multi-entity protein structures having one or more inter-chain interactions; extracting, from the retrieved multi-entity protein structures, two-chain protein structures; distinguishing the extracted two-chain protein structures having inter-protein

interactions from the extracted two-chain protein structures having only intra-protein interactions; identifying the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface; and storing in a memory storage device the protein secondary structures at an interface of the identified two-chain inter-protein interactions.

[0010] Another aspect of the present invention relates to a computer readable medium that has stored thereon instructions that when executed by a processor generate a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction. This computer readable medium has residing thereon machine executable code that when executed by at least one processor, causes the processor to perform steps that include retrieving, from a protein database, multi-entity protein structures having one or more inter-chain interactions; extracting, from the retrieved multi-entity protein structures, two-chain protein structures. The machine executable code further contains instructions in a computer programming language for distinguishing the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions, and identifying the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface. The generated database of protein secondary structures that are at an interface of a two-chain inter-protein interaction are stored in a memory storage device in a format suitable for computer automated and/or manual data analysis, and/or for display/printing on a display or printing device linked to a computing system.

[0011] Another aspect of the present invention is directed to a system for generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction. The components of this system include a retrieval module that retrieves, from a protein database stored on a memory device, multi-entity protein structures having one or more inter-chain interactions; an extraction module that extracts, from the retrieved multi-entity protein structures, two-chain protein structures; a distinguishing module that distinguishes the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions; an identification module that identifies the distinguished two-chain inter-protein interactions that comprise a

protein secondary structure at their interface; and a storage module for storing to a memory storage device the protein secondary structures at an interface of the identified two-chain inter-protein interactions. The modules/sub-modules described herein can be hardware implemented, software implemented, or an appropriate combination of both, as can be contemplated by one skilled in the art, after reading this disclosure.

[0012] Another aspect of the present invention relates to a collection of isolated protein secondary structures that are at an interface of a two-chain inter-protein interaction. This collection preferably contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the isolated protein secondary structures of Table 2.

[0013] Another aspect of the present invention relates to a method of identifying a therapeutic drug candidate potentially effective in modulating a two-chain inter-protein interaction having a secondary structure at its interface. In one embodiment, this method involves providing a therapeutic drug candidate; selecting a protein secondary structure from a collection described herein; providing an agent that mimics the protein secondary structure; contacting the therapeutic drug candidate with the agent under conditions effective for the therapeutic drug candidate to bind to the agent; and detecting whether any binding occurs between the therapeutic drug candidate and the agent, where binding between the therapeutic drug candidate and the agent indicates that the therapeutic drug candidate is potentially effective in modulating a two-chain inter-protein interaction having the protein secondary structure at its interface.

[0014] In another embodiment, this method involves selecting a protein secondary structure from a collection of secondary structures described herein; providing a therapeutic drug candidate that mimics the protein secondary structure, and at least one protein of a two-chain inter-protein interaction having the secondary structure at its interface; contacting the therapeutic drug candidate with the at least one protein under conditions effective for the therapeutic drug candidate to bind to the at least one protein; and detecting whether any binding occurs between the therapeutic drug candidate and the at least one protein, where binding between the therapeutic

drug candidate and the at least one protein indicates that the therapeutic drug candidate is potentially effective in modulating the two-chain inter-protein interaction.

BRIEF DESCRIPTION OF THE DRAWINGS

[0015] Figures 1A–1B are block diagrams of a system and modules for generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction.

[0016] Figure 2 is a flow chart of a method of generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction.

[0017] Figure 3 shows an α-helix surrounded by various stabilized helices and nonnatural helix mimetics. Several of these mimetic strategies stabilize the R-helical conformation in peptides or mimic this domain with nonnatural scaffolds. These mimetic scaffolds include β-peptide helices, terphenyl helix mimetics, miniproteins, peptoid helices, side-chain crosslinked α-helices, and hydrogen-bond-surrogate ("HBS") backbone cross-linked α-helices.

[0018] Figure 4 is a flow chart illustrating a method of generating a database of helical secondary structures that are at an interface of a two-chain inter-protein interaction.

[0019] Figures 5A and 5B are pie charts showing the fraction of Protein Data Bank entries containing proteins involved in helical interfaces (Figure 5A) and the classification of these proteins by function (Figure 5B).

DETAILED DESCRIPTION OF THE INVENTION

[0020] A system **10** that generates a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction in accordance with other embodiments of the present invention is illustrated in Figure 1A. The system **10** includes a computing system **12**, a local database **32**, a server system **14**, a database **18**, and a communication network **16**, although the system **10** can include other types and numbers of components connected in other manners. The present invention provides a more effective method and system for generating a database of protein secondary structures that are at an interface of two-chain inter-protein interactions.

[0021] Referring more specifically to Figure 1A, the computing system **12** is used to generate a database of protein secondary structures that are at an interface of two-chain inter-protein interactions, although other types and numbers of systems could be used, such as a server **14** (*e.g.*, an application server), and other types and numbers of functions can be performed by the computing system **12**. The computing system **12** includes a central processing unit ("CPU") or processor **20**, a memory **22**, user input device **24**, a display **26**, and an interface system **28**, and which are coupled together by a bus **30** or other link, although the computing system **12** can include other numbers and types of components, parts, devices, systems, and elements in other configurations.

[0022] The processor **20** executes a computer program or code comprising stored instructions for one or more aspects of the present invention as described and illustrated herein, although the processor could execute other numbers and types of programmed instructions. Accordingly, the computer program or code when executed by the processor performs steps for generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction. The processor retrieves information from a database **18** connected to a remote server **14** via a communication network **16**, although server **14** may not be remotely connected. According to one embodiment, the database **18** is a protein database from which multi-entity protein structures having one or more inter-chain interactions are retrieved. By executing instructions/computer program code stored, for example, in memory **22**, the processor **20** extracts from the retrieved multi-entity protein structures, two-chain protein structures. The processor **20** further executes computer code that carries out the steps of distinguishing the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions, and identifying the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface. From the identified two-chain inter-protein interactions that comprise a protein secondary structure at their interface, the code executed by the processor **20** extracts information pertaining to the identified interactions either for display **26** or for storage in memory **22** for later retrieval, or both, for further manipulation by a user

of computing system **12**, or storage in a memory storage device which is a component of the computing system **12** or a local database **32**, or both.

[0023] The memory **22** stores the programmed instructions written in a computer programming language or software package for carrying out one or more aspects of the present invention as described and illustrated herein, although some or all of the programmed instructions could be stored and/or executed elsewhere. For example, instructions for executing the above-noted steps can be stored in a distributed storage environment where memory **22** is shared between one or more computing systems similar to computing system **12**. A local database **32** that is separate from the computing system **12** can optionally store the programmed instructions and the identified data sets of inter-protein interactions (or other extracted information) that are identified and stored in a database using the methods and systems of the present invention. Alternatively, instead of a single computing system **12**, a distributed computing system, controlled by one or more controller chips and comprising one or more computers, can also be used to execute computer program code instructions that perform various steps and methods, or control systems/modules that perform those steps of the present invention, can be contemplated by those skilled in the art, after reading this disclosure.

[0024] A variety of different types of memory storage devices, such as a random access memory (RAM) or a read only memory (ROM) in the system or a floppy disk, hard disk, CD ROM, or other computer readable medium which is read from and/or written to by a magnetic, optical, or other reading and/or writing system that is coupled to one or more processors, can be used for the memory **22**.

[0025] The user input device **24** in the computing system **12** is used to input information for a search query, although the user input device **24** could be used to input other types of data and interact with other elements. The user input device **24** can include a computer keyboard and a computer mouse, although other types and numbers of user input devices can be used.

[0026] The display **26** in the computing system **12** is used to show the extracted data or information from the identified two-chain inter-protein interactions containing a secondary structure at their interface. For example, the display can show the two-chain inter-protein interaction that contains a secondary structure at its

interface, the secondary structure that is at the interface of the identified two-chain inter-protein interaction, the interface residues of the secondary protein structure at the interface of the identified two-chain inter-protein interaction, or any combination of this extracted information. The display **26** can include a computer display screen, such as a CRT or LCD screen, although other types and numbers of displays could be used.

[0027] The interface system **28** is used to operatively couple and communicate between the computing system **12**, the server system **14**, and the database **18** over a communication network **16**, although other types and numbers of communication networks or systems with other types and numbers of connections and configurations to other types and numbers of systems, devices, and components can be used. By way of example only, the communication network **16** can use TCP/IP over Ethernet and industry-standard protocols, including SOAP, XML, LDAP, and SNMP, although other types and numbers of communication networks, such as a direct connection, a local area network, a wide area network, modems and phone lines, e-mail, optical and/or wireless communication technology, each having their own communications protocols, can be used.

[0028] The server system **14** is used to assist the computing system **10** retrieve and provide the requested data set of multi-chain inter-protein interactions although the server system **14** can perform other types and numbers of functions and the present invention can be executed in the computing system **12** without a network connection to the server system **14** or any other system. The interface system in server system **14** is used to operatively couple and communicate between the server system **14** and the computing system **12**, although other types of connections and other types and combinations of systems could be used. Alternatively, server system **14** can be a distributed server or a plurality of servers each handling respective one or more electronic queries from a user of computing system **12** or an automated querying code being executed at the computing system **12**.

[0029] Although embodiments of the computing system **12** and server system **14** are described and illustrated herein, the computing system and server can be implemented on any suitable computing system or computing device. It is to be understood that the devices and systems of the embodiments described herein are for

exemplary purposes, as many variations of the specific hardware and software used to implement the embodiments are possible, as will be appreciated by those skilled in the relevant art(s).

[0030] Furthermore, each of the systems of the embodiments may be conveniently implemented using one or more general purpose computer systems, microprocessors, digital signal processors, and micro-controllers, programmed according to the teachings of the embodiments, as described and illustrated herein, and as will be appreciated by those of ordinary skill in the art.

[0031] In addition, two or more computing systems or devices can be substituted for any one of the systems in any embodiment of the embodiments. Accordingly, principles and advantages of distributed processing, such as redundancy and replication, also can be implemented, as desired, to increase the robustness and performance of the devices and systems of the embodiments. The embodiments may also be implemented on computer system or systems that extend across any suitable network using any suitable interface mechanisms and communications technologies, including, by way of example only, telecommunications in any suitable form (*e.g.*, voice and modem), wireless communications media, wireless communications networks, cellular communications networks, G3 communications networks, Public Switched Telephone Networks (PSTNs), Packet Data Networks (PDNs), the Internet, intranets, and combinations thereof.

[0032] The embodiments may also be embodied as a computer readable medium having instructions stored thereon for one or more aspects of the present invention as described and illustrated by way of the embodiments herein, as described herein, which when executed by a processor, cause the processor to carry out the steps necessary to implement the methods of the embodiments, as described and illustrated herein. In a preferred embodiment, the computer readable code comprises a retrieval module, an extraction module, a distinguishing module, an identification module, and a storage module as shown in Figure 1B. Computer readable medium containing these modules can be executed by one or more processors to generate a database of protein secondary structures that are at an interface of a two-chain inter-protein in interaction.

[0033] The method for generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction in accordance with the exemplary embodiments will now be described with reference to Figure 2. Although in this particular example, the processing steps described herein are executed by the computing system **12**, some or all of these steps can be executed by other systems, devices, or components. Parts of the executable computer code can be fully automated scripts executed by CPU **20** requiring no human intervention, or alternatively can be manually executed in a step-by-step prompt manner.

[0034] In step **100**, using one or more search queries, the user of computing system **12** retrieves from a protein database (connected to a remote server or connected locally to the computing system **12**), multi-entity protein structures having one or more inter-chain interactions. A multi-entity protein structure encompasses any multi-protein macromolecule structure. Suitable multi-entity protein structures can be retrieved from protein databases like the Research Collaboratory for Structural Bioinformatics ("RCSB") Protein Data Bank or the World Wide Protein Data Bank, or from other public and private databases.

[0035] In step **102**, the computing system **12** executes code that extracts, from the retrieved multi-entity protein structures, two-chain protein structures. When multi-entity protein structures are retrieved from the Protein Data Bank, the format of a Protein Data Bank file allows for the retrieval of each protein chain from the file. For example, the first column of the file contains the word "ATOM" if that atom is part of a protein chain. Each chain is separated by the characters "TER". Additionally, the fifth row of every line that begins with the "ATOM" contains the single character representing the chain. Using these three variables, the computing system **12** first identifies all chains in the Protein Data Bank file. After all chains have been identified the computing system **12** creates all possible pairs of chains. If there are n chains in the Protein Data Bank file then there will be $\frac{n(n-1)}{2}$ pairs of chains. The computing system **12** then extracts the coordinates of each pair of chains to a new file. The extracted two-chain protein structures may include both inter-protein interactions (*i.e.*, interactions between two chains of different proteins) and intra-protein interactions (*i.e.*, interactions between two chains of the same protein).

[0036] In step **104**, the computing system **12** executes code that distinguishes the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions. The Protein Data Bank files list the chains of each separate entity. Using the list of chains in each protein entity, the computing system **12** creates a list of possible chain pairs subject to the condition that chain pairs are not created between chains that are within the same protein entity. Any chain pairs generated from step **102** are compared to this list. Those chain pairs which appear in the list are retained and those that do not are discarded. The retained chain pairs are referred to as "inter-protein" interactions and the discarded chain pairs are referred to as "intra-protein" interactions.

[0037] In step **106**, the computing system **12** executes code that identifies the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface. The protein secondary structure can be any secondary structure known in the art. Preferably, the protein secondary structure is a helical secondary structure, *e.g.*, an α-helical structure. Alternatively, the protein secondary structure is a β-strand structure (also called a β-extended strand), which comprises a single continuous stretch of amino acids (*e.g.*, 5-10 residues) that adopts an extended conformation. In another embodiment, the protein secondary structure is a β-turn structure, which comprises a short stretch of four amino acid residues in which the polypeptide chain folds back on itself by nearly 180-degrees. Methods of identifying these secondary structures are described below.

[0038] In accordance with this aspect of the present invention, identification of the distinguished two-chain inter-protein interactions that comprise a secondary structure at their interface (step **106**) is achieved by linking methods of identifying protein secondary structures with methods of identifying inter-protein interaction interface amino acid residues. Although various methods of identifying protein secondary structures and methods of identifying protein interaction interface amino acid residues are available in the art, using these methods or tools individually, or even sequentially, will not identify protein secondary structures that are at an interface of an inter-chain protein interaction and the corresponding amino acid residues comprising this interface. In other words, employing a computational method for predicting a secondary structure in a two-chain inter-protein structure will identify

secondary structures within the chains, but will not distinguish between secondary structures located within a protein core and secondary structures located at the interface of the inter-protein interaction. Likewise, methods of predicting amino acid residues involved in an inter-protein interaction of a two-chain protein structure will identify all interface residues without distinguishing between interface residues that are in a secondary structure and interface residues that are not in a secondary structure. The method of the present invention links these respective methods to simultaneously identify protein secondary structures at an interface and the corresponding interface amino acid residues.

[0039] The method of predicting secondary structures in step **106** can be any method known in the art. For example, as described *infra*, protein secondary structures can be identified by calculating the dihedral angles (ϕ and φ angles) of the protein backbone. Using this methodology, a helical secondary structure is identified as a protein chain segment containing at least four contiguous residues with ϕ and φ angles that are characteristic of an α-helix ($\varphi = -57° \pm 50°$, $\phi = -47° \pm 50°$). Alternatively, a β-strand structure is identified as a protein chain segment comprising a single continuous stretch of amino acids having characteristic dihedral angles of $\varphi = -180° \pm 50°$, $\phi = -180° \pm 50°$. A β-turn structure is identified as a short protein chain segment consisting of four amino acid residues (denoted by i, i+1, i+2, i+3) that fold back on themselves. There are nine classes of β-turns, each characterized by the ϕ and φ angles of residues i+1 and i+2 shown in Table 1.

Table 1. Dihedral Angles of β-Turn Structures

Type	Phi (i+1)	Psi (i+1)	Phi (i+2)	Psi (i+2)
I	-60	-30	-90	0
II	-60	120	80	0
VIII	-60	-30	-120	120
I′	60	30	90	0
II′	60	-120	-80	0
VIa1	-60	120	-90	0
VIa2	-120	120	-60	-0
VIb	-135	135	-75	160
IV	Turns excluded from all the above categories			

[0040] A variety of other methods for identifying or predicting protein secondary structures are known in the art and are suitable for use in step **106** of the method of the present invention. These methods include identifying secondary structures based on hydrogen bonding (Baker at al., "Hydrogen Bonding in Globular Proteins," *Prog. Biophys. Mol. Biol.* 44:97-179 (1984), which is hereby incorporated by reference in its entirety), hydrogen bond energy and statistically derived backbone torsion angle information (STRIDE) (Frishman et al., "Knowledge-Based Protein Secondary Structure Assignment," *Proteins: Structure, Function, and Genetics* 23:566-579 (1995), which is hereby incorporated by reference in its entirety), simplified distance criteria applied to donor and acceptor separation (Fan et al., "Three-Dimensional Structure of an Fv from a Human IgM Immunoglobulin," *J. Mol. Biol.* 228:188-207 (1992); Muller et al., "Structure of the Complex Between Adenylate Kinase from *Escherichia coli* and the Inhibitor Ap5A Refined at 1.9 Å Resolution," *J. Mol. Biol.* 224:159-177 (1992), which are hereby incorporated by reference in their entirety), distance and geometric criteria (Presta et al., "Helix Signals in Proteins," *Science* 240:1632-41 (1988), which is hereby incorporated by reference in its entirety), hydrogen bonding patterns in combination with main-chain dihedral angles (Benning et al., "Molecular Structure of Cytochrome c2 Isolated from *Rhodobacter capsulatis* Determined at 2.5 Å Resolution," *J. Mol. Biol.* 220:673-685 (1991) McPhalen et al., "X-ray Structure Refinement and Comparison of Three Forms of Mitochondrial Aspartate Aminotransferase," *J. Mol. Biol.* 225:495-517 (1992), which are hereby incorporated by reference in their entirety), the DSSP algorithm (Kabsch et al., "Dictionary of Protein Secondary Structure: Pattern Recognition of Hydrogen-Bonded and Geometrical Features," *Bioploymers* 22:2577-2637 (1983), which is hereby incorporated by reference in its entirety), visual criteria (Ofner et al., "Crystallographic Refinement and Structure of DNase I at 2 Å Resolution," *J. Mol. Biol.* 192:605-632 (1986), which is hereby incorporated by reference in its entirety), and a combination of several independent assignment methods (Weiss et al., "Structure of Porin Refined at 1.8 Å Resolution," *J. Mol. Biol.* 227:493-509 (1992), which is hereby incorporated by reference in its entirety).

[0041] The method employed for identifying the corresponding amino acid residues of the secondary structure that are at the interface of the two-chain inter-protein interaction of step **106** can be any method known in the art. For example, as described *infra*, an interface amino acid residue can be identified as a residue in one protein chain of an inter-protein interaction having at least one atom within a 5 Å radius of an atom in the other protein chain of the two-chain inter-protein interaction (Ofran et al., "Analysing Six Types of Protein Interfaces," *J. Mol. Biol.* 325:377-0387 (2003); Kortemme et al., "Computational Alanine Scanning of Protein–Protein Interfaces," *Sci. STKE* 2004(219):l2 (2004), which are hereby incorporated by reference in their entirety). Alternatively an interface amino acid residue is identified as a result of it becoming significantly buried upon interaction with residues of another protein. Accordingly, measuring the density of C_β atoms surrounding a C_β atom of an amino acid residue in one chain of an identified two-chain inter-protein interaction can identify interface amino acid residues (Ofran et al., "Analysing Six Types of Protein Interfaces," *J. Mol. Biol.* 325:377-0387 (2003); Kortemme et al., "Computational Alanine Scanning of Protein–Protein Interfaces," *Sci. STKE* 2004(219):l2 (2004), which are hereby incorporated by reference in their entirety).

[0042] An alternative method for identifying interface amino acid residues that is also suitable for use in step **106** of the claimed method involves calculating the solvent accessible surface area ("SASA") (Jones et al., "Principles of Protein–Protein Interactions," *Proc. Natl Acad. Sci. USA* 93:13–20 (1996), which is hereby incorporated by reference in its entirety). Various algorithms for calculating SASA are known in the art, each defining an interface residue based on its change in solvent accessible surface area when transitioning from an unbound state to a bound state.

[0043] Some two-chain inter-protein interactions may be present in more than one database (*e.g.*, PDB) entry. Following identification of the two-chain inter-protein interactions that contain a secondary structure at their interface in step **106**, it may be desirable to remove any redundant interactions from the identified two-chain inter-protein interactions before extracting and storing information regarding the identified interactions. As described herein, redundant interactions (*i.e.*, structures having greater than 95% sequence similarity) can be searched and removed using the CD-HIT algorithm (Li et al., "Clustering of Highly Homologous Sequences to

Reduce the Size of Large Protein Databases," *Bioinformatics* 17:282–283 (2001), which is hereby incorporated by reference in its entirety). Other sequence alignment programs known in the art are also suitable for removing redundant interactions. The CD-HIT algorithm searches the sequence information of each chain of an interaction from the PDB FASTA file. To ensure that only redundant two-chain interactions are removed (rather than redundant single chains), it is preferable to remove the chain identifier from the FASTA file before executing the CD-HIT algorithm search, so that the entire amino acid sequence of the protein–protein complex is searched rather than just the individual protein chains.

[0044] In step **108** the user computer executes code that extracts information from the identified two-chain inter-protein interactions that contain a secondary structure at their interface. This extracted information can be stored and/or displayed in any format suitable for the user viewing the information. The extracted information may contain a list of the two-chain inter-protein interactions that contain a secondary structure at their interface. In another embodiment, the extracted information may show the secondary structures that are at the interface of a two-chain inter-protein interaction. In another embodiment, the extracted information may name the interface residues within the protein secondary structures at the interface of a two-chain inter-protein interaction. The user computer can extract any of the above information alone or in combination. Suitable examples of extracted information include the information shown in Tables 2, 6, and 17 herein.

[0045] In step **110**, the extracted information is stored in a memory storage device. The stored extracted information can be readily retrieved by a user and used for any desired application. For example, as described below, the extracted information can be used to further identify hot-spot amino acid residues within the identified interface residues of a two-chain inter-protein interaction containing a secondary structure at its interface. Optionally, the extracted information can be forwarded to other computer systems and/or databases external to computing system **12** for further processing.

[0046] In step **112**, the database of secondary structures that are at an interface of a two-chain inter-protein interaction can be updated periodically by querying the protein database at various time intervals to identify one or more additional multi-

entity protein structures. Such updating can be manual or automated. Once a new multi-entity structure is identified (step **114**), it is retrieved, two-chain protein structures are extracted, two-chain protein structures containing inter-protein interactions are distinguished from two-chain protein structures containing only intra-protein interactions, and two-chain inter-protein interactions that have a protein secondary structure at their interface are identified and stored/displayed. Information (*e.g.*, the function and/or identity of the proteins involved in the two-chain inter-protein interactions, the secondary structures present at their interface, and/or the interface residues within the secondary structure) concerning the newly-identified two-chain inter-protein interactions is compared to the information present in the existing database to identify non-redundant information. Any non-redundant information can be added to the database by storing it in the memory storage device, or any of the databases shown in Figure 1A.

[0047] The present method identifies, *e.g.*, interface amino acid residues within a protein secondary structure at the interface of a two-chain inter-protein interaction. In a preferred embodiment of the present invention, the "hot spot" amino acid residues among the identified interface residues are also identified. As used herein, "hot spot" amino acid residues refers to those interface amino acid residues that are important mediators of the two-chain inter-protein binding interaction. More specifically, hot spot residues are the interface residues that contribute significantly to the binding free energy of the protein–protein complex. Hot spot residues and their corresponding binding sites can be identified, for example, using amino acid mutation or substitution technique. In a preferred embodiment, hot spot residues are identified using alanine mutagenesis techniques. Following substitution of an individual interface residue with an alanine residue, the free energy of the protein complex is computed. Hot-spot residues are identified as those residues in which alanine substitution has a destabilizing effect on the free energy of binding ($\Delta\Delta G_{bind}$) of more than 1kcal/mol (Bogan et al., "Anatomy of Hot Spots in Protein Interfaces," *J. Mol. Biol.* 280(1):1-9 (1998); Keskin et al., "Principles of Protein–Protein Interactions: What Are the Preferred Ways for Proteins to Interact?" *Chem. Rev.* 108(4): 1225-44 (2008), which are hereby incorporated by reference in their entirety).

[0048] Alanine mutagenesis can be carried out using experimental or theoretical approaches. Experimental approaches include systematic alanine mutagenesis of the identified interface residues by generating and purifying individual mutant proteins for analysis. However, because this is a time-consuming and laborious procedure, it is preferable to use an alternative, high through-put method such as a combinatorial library of alanine substitution or the method of "shotgun scanning." Shotgun scanning implements a simplified format for combinatorial alanine scanning and utilizes phage-display libraries of alanine-substituted proteins for analysis (Morrison et al., "Combinatorial Alanine-Scanning," *Curr. Opin. Chem. Biol.* 5:302-07 (2001), which is hereby incorporated by reference in its entirety). An alternative experimental approach suitable for use in the method of the present invention is covalent tethering, which is a process involving the use of equilibrium disulfide exchange to target potential binding partners within a specific region of the interface and calculate relative binding affinities (DeLano W., "Unraveling Hot Spots in Binding Interfaces: Progress and Challenges," *Curr. Opin. Struct. Biol.* 12:14-20 (2002), which is hereby incorporated by reference in its entirety).

[0049] In addition to the experimental approaches for determining hot spot amino acids through alanine mutagenesis, predictive computational approaches have been developed that reproduce the experimental values with less time, effort, and expense. A number of algorithms and methods have been developed to accurately calculate the binding free energies of known three-dimensional structures and the effect of mutations on these affinities. Suitable methods include empirical knowledge-based (statistical) scoring approaches in conjunction with simple physical models (Moreira et al., "Computational Determination of the Relative Free Energy of Binding—Application to Alanine Scanning Mutagenesis in Molecular Material with Specific Interactions," *in* MODELING AND DESIGN (Andrezej W. Sokalski ed., 2007), which is hereby incorporated by reference in its entirety), atomistic simulations including both the rigorous free energy perturbation and thermodynamic integration (Kollman PA, "Free Energy Calculations—Applications to Chemical and Biochemical Phenomena," *Chem. Rev.* 93:2395-2417 (1993); Gouda et al., "Free Energy Calculations for Theophylline Binding to an RNA Aptamer: Comparison of MM-PBSA and Thermodynamic Integration Methods," *Biopolymers* 68:16-34 (2002),

which are hereby incorporated by reference in their entirety), protein cleft analysis combined with physical properties (Burgoyne et al., "Predicting Protein Interaction Sites: Binding Hot-Spots in Protein–Protein and Protein–Ligand Interfaces," *Bioinformatics* 22(11):1335-1342 (2006), which is hereby incorporated by reference in its entirety). More approximate methods of identifying interface hot spot residues include MM-PBSA (Kollman et al., "Calculating Structures and Free Energies of Complex Molecules: Combining Molecular Mechanics and Continuum Models," *Acc. Chem. Res.* 33:889-897 (2000), which is hereby incorporated by reference in its entirety), λ-dynamics (Kong et al., "Lambda Dynamics—A New Approach to Free Energy Calculations," *J. Chem. Phys.* 105:2414-2423 (1996); Moreira et al., "Accuracy of the Numerical Solution of the Poisson–Boltzmann Equation," *J. Mol. Struct.* 729:11-18 (2005); Moreira et al., "Hot Spots Computational Identification—Application to the Complex Formed Between the Hen Egg-White Lysozyme (HEL) and the Antibody HyHEL-10," *Int. J. Quantum Chem.* 107:299-310 (2006), which are hereby incorporated by reference in their entirety), chemical Monte-Carlo/molecular mechanics (Moreira et al., "Accuracy of the Numerical Solution of the Poisson–Boltzmann Equation," *J. Mol. Struct.* 729:11-18 (2005), which is hereby incorporated by reference in its entirety), and ligand interaction scanning (Moreira et al., "Hot Spots Computational Identification—Application to the Complex Formed Between the Hen Egg-White Lysozyme (HEL) and the Antibody HyHEL-10," *Int. J. Quantum Chem.* 107:299-310 (2006), which is hereby incorporated by reference in its entirety).

[0050] The identity of interface hot spot residues can also be determined using other experimental approaches, including molecular biology based methods such as the yeast two-hybrid system, ubiquitin-based split-protein sensor, and Fluorescence Resonance Energy transfer; mass spectrometry methods; and protein microarrays.

[0051] In another embodiment of the present invention, the protein secondary structures at an interface of a two-chain inter-protein interaction are classified by the biological function(s) of the proteins involved in the respective interaction. This classification identifies new potential protein targets useful for targeted drug development and screening.

[0052] Another aspect of the present invention relates to a collection of isolated protein secondary structures that are at an interface of a two-chain inter-

protein interaction, where the collection contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the isolated protein secondary structures of Table 2. The representative collection of secondary structures at an interface of two-chain inter-protein interactions listed in Table 2 below was identified using the methods of the present invention. Redundant interactions have been removed from this collection to generate a non-redundant collection of two-chain inter-protein interactions having a secondary structure at their interface. In accordance with this aspect of the invention, the collection is a collection of helical protein secondary structures.

[0053] This collection of the present invention preferably contains *m* through *n* secondary structures, where *m* and *n* are integers and *n* is greater than *m*. Preferably, *m* is 2, 4, 8, 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, or 5000; and *n* is 10, 15, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, or 10000.

PDB CODE	PARTNER CHAINS	FUNCTION	CHAIN	DDG_{AVG} (KCAL/MOL)	DDG_{SUM} (KCAL/MOL)	# HOT SPOT RESIDUES	HELIX LENGTH	HELIX SEQUENCE	SEQ ID NO:
1O18	MZ	CONTRACTILE PROTEIN	Z	369.3	1477.1	4	12	SVWIGGSILASL	1
2VDC	FI	OXIDOREDUCTASE	I	682.1	1364.2	2	5	VIEQS	2
2VDC	BG	OXIDOREDUCTASE	G	682.1	1364.1	2	5	VIEQS	3
2VDC	DH	OXIDOREDUCTASE	H	681.9	1363.8	2	5	VIEQS	4
2VDC	EL	OXIDOREDUCTASE	L	617.6	1235.2	2	5	VIEQS	5
2VDC	AJ	OXIDOREDUCTASE	J	617.4	1234.7	2	5	VIEQS	6
2VDC	CK	OXIDOREDUCTASE	K	617.3	1234.6	2	5	VIEQS	7
1M8Q	D9	CONTRACTILE PROTEIN	9	288.4	1153.5	4	12	SVWIGGSILASL	8
2VDC	BG	OXIDOREDUCTASE	B	718.2	718.2	1	5	DKLRQ	9
2VDC	DH	OXIDOREDUCTASE	D	718.2	718.2	1	5	DKLRQ	10
2VDC	FI	OXIDOREDUCTASE	F	718.2	718.2	1	5	DKLRQ	11
1O18	MZ	CONTRACTILE PROTEIN	M	578.1	578.1	1	6	IFSILE	12
1M8Q	D9	CONTRACTILE PROTEIN	D	572.8	572.8	1	6	IFSILE	13
3DL8	HD	PROTEIN TRANSPORT	H	249.8	499.5	2	20	RQKFIFTLLMFVIYRLGSHI	14
2I2R	LP	TRANSPORT PROTEIN	L	181.3	362.5	2	8	WLPFARAA	15
1HDS	CD	OXYGEN TRANSPORT	D	122.3	244.6	2	12	PQNFRLLGNVLA	16
3A0B	ad	ELECTRON TRANSPORT	d	78.3	234.9	3	12	LGGALLCAIHGA	17
1IZL	JN	PHOTOSYNTHESIS	J	228.9	228.9	1	9	CVAYSAPLA	18
1IZL	AD	PHOTOSYNTHESIS	A	226.7	226.7	1	9	CVAYSAPLA	19
3FOE	AC	ISOMERASE/DNA	C	74.6	223.7	3	14	TDGAHIQTLLLTFF	20
1I84	VT	CONTRACTILE PROTEIN	T	108.9	217.7	2	11	YEELVRMVLSG	21
1DFK	AY	CONTRACTILE PROTEIN	Y	108.7	217.3	2	9	TMFLSIFSD	22
3DL8	AG	PROTEIN TRANSPORT	A	41.5	207.6	5	47	VSRAVESSQKRVEGNNFDSRKQLLQYDDVLRQQREVIYKQRFEVIDS	23
1HDS	CD	OXYGEN TRANSPORT	C	67.6	202.8	3	15	PAYGAQALQRMFLSF	24
1HDS	CD	OXYGEN TRANSPORT	C	95.3	190.6	2	8	HSLLVTLA	25
1O18	GI	CONTRACTILE PROTEIN	G	182.7	182.7	1	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	26
1YE9	LN	OXIDOREDUCTASE	L	44.3	177.2	4	12	FILREKITHFDH	27
2V1C	AC	RECOMBINATION	C	77.3	154.5	2	12	AHLMAEFADALF	28
1O18	MZ	CONTRACTILE PROTEIN	M	149.7	149.7	1	15	LALLFATYGGEAEGG	29
1O18	MZ	CONTRACTILE PROTEIN	M	146.5	146.5	1	9	SALFRENLN	30
1M8Q	D9	CONTRACTILE PROTEIN	D	144.3	144.3	1	9	SALFRENLN	31
3A0B	ad	ELECTRON TRANSPORT	a	137.2	137.2	1	16	WRVVGVWFAALGISTM	32

3A0B	ad	ELECTRON TRANSPORT	a	135.0	135.0	1	16	GGALFCAMHGSLVTSS	33
1IBT	ED	LYASE	D	32.3	129.1	4	17	GRRKAMAKSIAECGQDA	34
1DFK	AY	CONTRACTILE PROTEIN	A	28.8	115.0	4	9	IRKWLVLRN	35
1O18	JY	CONTRACTILE PROTEIN	J	56.5	113.0	2	5	YDEHL	36
1MVW	JY	CONTRACTILE PROTEIN	J	56.4	112.7	2	5	YDEHL	37
1O18	P1	CONTRACTILE PROTEIN	1	55.8	111.6	2	12	SVWIGGSILASL	38
1MVW	JW	CONTRACTILE PROTEIN	W	109.5	109.5	1	12	SVWIGGSILASL	39
1O18	JW	CONTRACTILE PROTEIN	W	109.5	109.5	1	12	SVWIGGSILASL	40
1MVW	D9	CONTRACTILE PROTEIN	9	108.1	108.1	1	12	SVWIGGSILASL	41
1O18	GX	CONTRACTILE PROTEIN	G	53.7	107.3	2	5	YDEHL	42
1M8Q	GX	CONTRACTILE PROTEIN	G	53.6	107.2	2	5	YDEHL	43
1MVW	GX	CONTRACTILE PROTEIN	G	53.6	107.1	2	5	YDEHL	44
3C91	GH	HYDROLASE	G	102.8	102.8	1	23	VADARVLVDFARISAQQEKVTYG	45
1CC0	AE	SIGNALING PROTEIN	A	99.9	99.9	1	9	DRLRPLSYP	46
1ZL8	AB	PROTEIN BINDING	B	98.7	98.7	1	16	DAVQRAKEVLEEISCY	47
2VOY	AF	HYDROLASE	A	89.9	89.9	1	12	VSDLKEAVDKLG	48
1MVW	GH	CONTRACTILE PROTEIN	H	87.8	87.8	1	11	KDDLRETFAAM	49
1W5C	AD	PHOTOSYNTHESIS	A	17.5	87.6	5	11	WADIINRANLG	50
1W5C	GJ	PHOTOSYNTHESIS	G	16.7	83.5	5	11	WADIINRANLG	51
1CC0	CF	SIGNALING PROTEIN	C	79.7	79.7	1	9	DRLRPLSYP	52
1IW7	DF	TRANSFERASE	F	25.9	77.8	3	27	TLEEEVELARKVEEGMEAIKKLSEITG	53
3HOY	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	19.4	77.4	4	11	DEFIAHRLGLI	54
1HVU	GH	TRANSFERASE/RNA	H	76.2	76.2	1	12	KETWETWWTEYW	55
1O18	MN	CONTRACTILE PROTEIN	N	75.8	75.8	1	15	ETEIEDFKEAFTVID	56
1OED	AB	ION CHANNEL/RECEPTOR	B	35.0	69.9	2	26	YLMFIMILVAFSVILSVVVLNLHHRS	57
2EKV	AC	CONTRACTILE PROTEIN	A	5.8	69.4	12	39	VLGMLEDMRDERLSKIISMFQAHIRGYLMRKAYKKLQDQ	58
1IW7	NP	TRANSFERASE	N	65.9	65.9	1	6	RFRQNL	59
2J37	W4	RIBOSOME	4	32.8	65.6	2	7	ALDVANK	60
1O18	PQ	CONTRACTILE PROTEIN	Q	64.6	64.6	1	15	ETEIEDFKEAFTVID	61
3FIN	4G	RIBOSOME	G	64.3	64.3	1	10	RMWIFLEKLL	62
1IW7	NP	TRANSFERASE	P	31.4	62.8	2	27	TLEEEVELARKVEEGMEAIKKLSEITG	63
1M8Q	AB	CONTRACTILE PROTEIN	A	31.3	62.6	2	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	64
1O18	MN	CONTRACTILE PROTEIN	M	15.3	61.2	4	19	ERRESIFCIQYNVRSFMNV	65
1IZL	AD	PHOTOSYNTHESIS	D	60.0	60.0	1	5	TKNLL	66
1YE9	LN	OXIDOREDUCTASE	N	29.5	58.9	2	18	PLLQGRLFSYTDTQISRL	67
2FUG	VW	OXIDOREDUCTASE	V	57.6	57.6	1	6	FEKTME	68
3FOE	BD	ISOMERASE/DNA	D	19.0	57.1	3	14	TDGAHIQTLLLTFF	69
2GUZ	OP	CHAPERONE, PROTEIN TRANSPORT	O	19.0	56.9	3	18	PFLATKINEAKDFLEKRG	70

1RF8	AB	BIOSYNTHETIC PROTEIN, TRANSLATION	A	28.3	56.5	2	11	VEEFWAIIQNI	71
2VOY	AJ	HYDROLASE	A	55.9	55.9	1	14	AACANRIEKRLNKI	72
1MVW	PQ	CONTRACTILE PROTEIN	Q	26.8	53.5	2	11	KDDLRETFAAM	73
2VOY	BF	HYDROLASE	F	52.4	52.4	1	8	IKKLVGLQ	74
3EDL	GD	STRUCTURAL PROTEIN	G	17.3	51.9	3	14	EFTEAESNMNDLVS	75
1OED	DE	ION CHANNEL/RECEPTOR	D	51.7	51.7	1	27	YFVVNVIIPCLLFSFLTGLVFYLPTDS	76
1VSA	DJ	RIBOSOME	D	49.8	49.8	1	6	PHLLWE	77
3DTP	BD	CONTRACTILE PROTEIN	D	16.5	49.5	3	11	GAEIRHVLVTL	78
1O18	DE	CONTRACTILE PROTEIN	D	11.9	47.6	4	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	79
2GJ7	AF	IMMUNE SYSTEM/VIRUS/VIRAL PROTEIN	A	47.5	47.5	1	6	HQDWLN	80
3FOE	BD	ISOMERASE/DNA	B	47.0	47.0	1	5	IMGER	81
1D9K	HQ	IMMUNE SYSTEM	H	46.3	46.3	1	7	ELGRPDA	82
1S5L	AC	PHOTOSYNTHESIS	C	11.6	46.3	4	33	PRSWLATSHFVLAFFFLVGHLWHAGRARAAAAG	83
1M8Q	AB	CONTRACTILE PROTEIN	B	45.3	45.3	1	11	KDDLRETFAAM	84
1XQ5	AB	OXYGEN STORAGE/TRANSPORT	B	44.9	44.9	1	16	YEAVGGATLARCLIVY	85
2GUZ	OP	CHAPERONE, PROTEIN TRANSPORT	P	14.5	43.6	3	8	LDESCKIL	86
1MVW	JL	CONTRACTILE PROTEIN	J	41.9	41.9	1	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	87
3EPC	R3	VIRAL PROTEIN	3	20.1	40.1	2	5	PRLSH	88
1O18	JL	CONTRACTILE PROTEIN	J	20.0	39.9	2	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	89
2J28	X9	RIBOSOME	X	39.9	39.9	1	7	LREQFNL	90
3DIN	BF	MEMBRANE PROTEIN, PROTEIN TRANSPORT	B	39.0	39.0	1	11	LEEVEHVKEAV	91
1MVW	PQ	CONTRACTILE PROTEIN	Q	38.8	38.8	1	9	NEELDAMIK	92
2HGI	IU	RIBOSOME	U	19.0	38.0	2	18	GKEQRILAKTIKRARILG	93
1S5L	AD	PHOTOSYNTHESIS	D	12.6	37.9	3	13	MVTANRFWSQIFG	94
3DL8	GE	PROTEIN TRANSPORT	E	37.2	37.2	1	27	FVIIAVVLIISTLLQKGRGDVGAAFGG	95
3DTP	AB	CONTRACTILE PROTEIN	A	1.5	37.2	25	110	ASMKEEFTRLKEALEKSEARRKELEEKMVSLLQEKNDLQLQVQAEQD NLADAEERCDQLIKNKIQLEAKVKEMNERLEDEEEMNAELTAKKRKLE DECSELKRDIDDLEL	96
2QOW	EH	RIBOSOME	E	12.3	36.9	3	8	PEMVAAKR	97
1WA8	AB	TUBERCULOSIS	A	12.1	36.2	3	34	AGTAAQAAVVRFQEAANKQKQELDEISTNIRQAG	98
1M8Q	PQ	CONTRACTILE PROTEIN	P	36.1	36.1	1	20	VERRESIFCIQYNVRSFMNV	99
3BZ1	Ky	ELECTRON TRANSPORT	K	18.0	35.9	2	25	DPLVDVLPVIPVLFLALAFVWQAAV	100
3DL8	HF	PROTEIN TRANSPORT	F	17.9	35.8	2	27	FVIIAVVLIISTLLQKGRGDVGAAFGG	101
2INN	BD	OXIDOREDUCTASE	B	17.7	35.3	2	14	AIDELRHSQTQQHA	102
1BCP	BD	TOXIN	D	17.4	34.8	2	12	PMEVMLRAVFMQ	103
3DL8	AG	PROTEIN TRANSPORT	G	34.6	34.6	1	33	DYGRYKINEYTKYLTLFVATVQSLGIAFWIRGQ	104
3DL8	BH	PROTEIN TRANSPORT	B	11.4	34.2	3	17	VALNHHINQALKAHVAM	105

2DFS	MQ	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	3.1	34.1	11	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRDATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	106
2BE6	CF	MEMBRANE PROTEIN	F	2.8	33.4	12	19	FYATFLIQEYFRKFKKRKE	107
2EC6	AC	CONTRACTILE PROTEIN	A	6.6	32.8	5	9	IISMFQAHI	108
2J28	79	RIBOSOME	7	31.8	31.8	1	15	GFPINFLTLYVTVQH	109
1ID3	AB	STRUCTURAL PROTEIN/DNA	B	4.5	31.3	7	29	GLIYEEVRAVLKSFLESVIRDSVTYTEHA	110
3DTP	AB	CONTRACTILE PROTEIN	B	1.8	30.9	17	97	SEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLADAEERCDQLIKNKIQLEAKVKEMNERLEDEEEMNAELTAKKRKLEDECSELKRDIDDLELTLA	111
1O18	PQ	CONTRACTILE PROTEIN	P	15.4	30.7	2	19	ERRESIFCIQYNVRSFMNV	112
1M1J	AB	BLOOD CLOTTING	B	1.9	29.9	16	100	KPVLRDLKDRVAKFSDTSTTMYQYVNMIDNKLVKTQKQRKDNDIILSEYNTEMELHYNYIKDNLDNNIPSSLRVLRAVIDSLHKKIQKLENAIATQTDYC	113
1O18	MN	CONTRACTILE PROTEIN	N	15.0	29.9	2	9	EIKNMWAAF	114
1WDC	AB	MUSCLE PROTEIN	A	3.0	29.8	10	49	DERLSKIISMFQAHIRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVLRN	115
1PTO	BD	TOXIN	D	14.7	29.4	2	12	PMEVMLRAVFMQ	116
2ZLE	KD	HYDROLASE	D	29.3	29.3	1	9	VVYDVTSWT	117
1MXE	BF	METAL BINDING PROTEIN	F	2.4	29.2	12	21	FAKSKWKQAFNATAVVRHMRK	118
1BCP	HJ	TOXIN	J	14.4	28.8	2	12	PMEVMLRAVFMQ	119
1YE9	CE	OXIDOREDUCTASE	C	9.6	28.8	3	12	FILREKITHFDH	120
1WDC	AC	MUSCLE PROTEIN	A	2.1	28.7	14	49	DERLSKIISMFQAHIRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVLRN	121
2EKV	AC	CONTRACTILE PROTEIN	C	9.6	28.7	3	11	EDQCNDIFTFC	122
1RCO	VP	LYASE	V	5.7	28.5	5	20	WRDRFLFCAEALYKAQAETG	123
2KA4	AB	TRANSCRIPTION REGULATOR	A	3.6	28.4	8	27	PEKRKLIQQQLVLLLHAHKCQRREQAN	124
3F1I	HS	PROTEIN BINDING	H	2.0	28.4	14	64	SAVLSLFQSINGMHPQLLELLNQLDERRLYYEGLQDKLAQIRDARGALSALREEHREKLRRAAE	125
1Y74	CB	TRANSPORT PROTEIN	C	14.1	28.2	2	19	LERDVSRAVELLERLQRSG	126
1I3R	AB	IMMUNE SYSTEM	A	4.6	27.7	6	22	AQGALANIAVNKANLDVMKERS	127
3FOE	BD	ISOMERASE/DNA	D	27.7	27.7	1	5	RAERR	128
2IX7	CB	CONTRACTILE PROTEIN/METAL BINDING	C	3.5	27.6	8	55	KLRAACIRIQKTIRGWLLRKRYLCMQRAAITVQRYVRGYQARCYAKFLRRTKAAT	129
1J1D	EF	CONTRACTILE PROTEIN	F	1.7	27.5	16	48	FAELQDLARQLHARVDKVDEERYDIEAKVTKNITEIADLTQKIFDLRG	130
1CAX	CF	SEED STORAGE PROTEIN	F	6.8	27.2	4	10	EEVEELLENQ	131
2O60	AB	METAL BINDING PROTEIN	B	2.5	27.1	11	15	FKKLAEAVKFSAKLM	132
1PTO	IK	TOXIN	K	13.4	26.8	2	12	PMEVMLRAVFMQ	133
3G43	BE	METAL BINDING PROTEIN	E	3.0	26.6	9	16	FYATFLIQEYFRKFKK	134

3B63	KL	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	L	13.3	26.5	2	15	KANREKMTQIMFETF	135
1J1E	EF	CONTRACTILE PROTEIN	F	2.0	26.4	13	47	FAELQDLARQLHARVDKVDEERYDIEAKVTKNITEIADLTQKIFDLR	136
1J1E	EF	CONTRACTILE PROTEIN	E	2.2	26.3	12	46	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN	137
1E1C	CD	ISOMERASE	D	3.3	26.2	8	24	YYVESLTRSLADAAWKEFQEVEKL	138
1IZN	AB	PROTEIN BINDING	B	2.4	26.0	11	36	HIANIGRLVEDMENKIRSTLNEIYFGKTKDIVNGLR	139
1BXR	GH	AMIDOTRANSFERASE	H	5.2	25.9	5	12	TRKLTRLLREKG	140
2CLY	AB	HYDROLASE	A	1.9	25.9	14	62	RHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMR QKEQEHMINWVEKRVV	141
3A0B	lm	ELECTRON TRANSPORT	m	25.9	25.9	1	8	ILYVQTES	142
1YE9	CE	OXIDOREDUCTASE	E	12.9	25.8	2	17	LLQGRLFSYTDTQISRL	143
3A0B	ad	ELECTRON TRANSPORT	d	12.9	25.8	2	8	VTANRFWS	144
1SUY	BD	CIRCADIAN CLOCK PROTEIN	B	12.9	25.7	2	22	VSQVLEIHVELMDTFSKQLKLE	145
1KF9	AC	HORMONE/GROWTH FACTOR	A	25.5	25.5	1	47	NVYDLLKDLEEGIQTLMGRLLLKNYGLLYCFNKDMSKVSTYLRTVQC	146
3EH3	AB	OXIDOREDUCTASE	A	25.4	25.4	1	25	YYQGLTLHGVLNAIVFTQLFAQAIM	147
1AYY	CD	HYDROLASE	C	12.7	25.3	2	16	NFGLHANVEAWKVLSK	148
2GHO	CD	TRANSFERASE	D	8.4	25.3	3	6	LTDILS	149
2CLY	DE	HYDROLASE	D	1.9	25.2	13	64	QKRHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNM MRQKEQEHMINWVEKRVV	150
1SUY	AC	CIRCADIAN CLOCK PROTEIN	A	24.9	24.9	1	22	VSQVLEIHVELMDTFSKQLKLE	151
1ZRT	CD	OXIDOREDUCTASE/METAL TRANSPORT	C	8.3	24.9	3	24	YFVIKDLFALALVLLGFFAVVAYM	152
1ZRT	PQ	OXIDOREDUCTASE/METAL TRANSPORT	P	24.9	24.9	1	26	MRYIHANGASLFFLAVYIHIFRGLYY	153
3CSY	MN	IMMUNE SYSTEM/VIRAL PROTEIN	N	2.8	24.9	9	23	LICGLRQLANETTQALQLFLRAT	154
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	A	5.0	24.8	5	17	AVPTGIKVFSWIATMWG	155
2BL0	AB	MUSCLE PROTEIN	A	1.9	24.8	13	45	RIGEIVKVVQAAARGWVERKHFRQAREKSVSARIIQDNIRAYLEF	156
2ONK	AC	MEMBRANE PROTEIN	C	12.3	24.6	2	10	VRLEHVARTL	157
2QOU	EH	RIBOSOME	E	8.2	24.6	3	8	PEMVAAKR	158
1BCP	CE	TOXIN	E	6.1	24.4	4	13	PMEVMLRAVFMQQ	159
3DD7	CD	RIBOSOME INHIBITOR	D	4.9	24.4	5	11	DAEFASLFDTL	160
2BYK	DC	DNA-BINDING PROTEIN	C	2.7	24.2	9	27	NEVLFLMTKCTELFVRHLAGAAYTEEF	161
3C1B	GH	STRUCTURAL PROTEIN/DNA	G	3.0	24.2	8	28	AGAPVYLAAVLEYLTAEILELAGNAARD	162
2P4N	KB	TRANSPORT PROTEIN	B	8.0	24.0	3	23	EMEFTEAESNMNDLVSEYQQYQD	163
2VAS	AB	MOTOR PROTEIN	A	2.0	24.0	12	31	NHWLICSRWKKVQWCSLSVIKLKNKIKYRAE	164

3A0B	AD	ELECTRON TRANSPORT	A	12.0	24.0	2	8	NLGMEVMH	165
3FWB	BC	CELL CYCLE, TRANSCRIPTION	B	2.2	23.9	11	52	EANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	166
1MXE	AE	METAL BINDING PROTEIN	E	2.4	23.8	10	21	FAKSKWKQAFNATAVVRHMRK	167
1I94	GK	RIBOSOME	K	23.6	23.6	1	8	PYAAQLAA	168
1G20	DG	OXIDOREDUCTASE	D	7.8	23.4	3	6	EDAAVF	169
1OED	AB	ION CHANNEL/RECEPTOR	B	7.8	23.3	3	28	SLSISALLAVTVFLLLLADKVPETSLSV	170
1RU7	GH	VIRAL PROTEIN	H	2.6	23.0	9	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	171
1FMH	AB	TRANSCRIPTION	A	4.6	22.8	5	30	VAQLEKEVAQAEAENYQLEQEVAQLEHECG	172
1S1H	JN	RIBOSOME	N	11.4	22.8	2	10	RQCFREKAND	173
1PTO	JH	TOXIN	J	22.7	22.7	1	12	PMEVMLRAVFMQ	174
1RU7	EF	VIRAL PROTEIN	F	2.5	22.6	9	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	175
1UCY	HE	COMPLEX (SERINE PROTEASE/COAGULATION)	H	22.6	22.6	1	5	AHCLL	176
1NZY	AB	LYASE	A	2.8	22.3	8	11	MRRAMELMLTN	177
2QJP	AB	ELECTRON TRANSPORT	A	3.7	22.3	6	24	YFIIKDVFALAVVLLVFFAIVGFM	178
1IZL	AD	PHOTOSYNTHESIS	D	22.2	22.2	1	7	PYNAIAF	179
2ZCY	OU	HYDROLASE	O	11.1	22.2	2	18	GPDYRVLVDKSRKVAHTS	180
1E1C	CD	ISOMERASE	D	3.2	22.1	7	22	QFLTIARLRALREAWARIGEVF	181
2F9Y	AB	LIGASE	B	2.8	22.0	8	21	LMSLMQMAKTSAALAKMQERG	182
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	C	2.8	22.0	8	21	PWKSARLMVHTVATFNSIKER	183
2JIZ	JK	HYDROLASE	J	4.4	21.9	5	15	MKLELAQYREVAAFA	184
1CDL	AE	CALCIUM-BINDING PROTEIN	E	2.4	21.8	9	17	RKWQKTGHAVRAIGRLS	185
2A1T	RS	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	7.3	21.8	3	15	AFGKNLLPRVAAKLE	186
1J1D	BC	CONTRACTILE PROTEIN	B	1.8	21.6	12	45	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRIND	187
3FWC	MN	CELL CYCLE, TRANSCRIPTION	N	2.4	21.6	9	82	KQVITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	188
3HKZ	CK	TRANSFERASE	K	7.2	21.5	3	14	RYEIARVISARALQ	189
3FWC	BC	CELL CYCLE, TRANSCRIPTION	B	2.4	21.3	9	80	VITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	190
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	B	2.6	21.1	8	16	RWKLDFSIVSLCNHLT	191
2GTL	MO	OXYGEN STORAGE/TRANSPORT	M	10.6	21.1	2	19	YLVKNQNLHIDYLAKKLHD	192
2JJ0	LM	PHOTOSYNTHESIS	M	3.5	21.1	6	14	TAAERWALFWRWTM	193
3FDL	AB	APOPTOSIS	B	2.6	21.0	8	20	EIWIAQELRRIGDEFNAYYA	194

1MVW	P1	CONTRACTILE PROTEIN	P	20.8	20.8	1	15	LALLFATYGGEAEGG	195
2E9X	BC	REPLICATION	B	2.6	20.8	8	22	LMEINTSGTFLTQALNHMYKLR	196
2QJK	MN	ELECTRON TRANSPORT	M	4.2	20.8	5	24	YFIIKDVFALAVVLLVFFAIVGFM	197
2ZCY	AG	HYDROLASE	A	6.9	20.7	3	18	GPDYRVLVDKSRKVAHTS	198
1W5C	AD	PHOTOSYNTHESIS	D	20.6	20.6	1	12	IFRFLLFFQGFH	199
2F66	AC	TRANSPORT PROTEIN	C	2.6	20.5	8	26	ADDLDQFIKNYLDIRTQYHLRREKLA	200
2H67	AB	HORMONE/GROWTH FACTOR	A	10.3	20.5	2	8	IVEQCCTS	201
3HD7	EF	EXOCYTOSIS	F	1.7	20.5	12	96	KQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG	202
1MVW	P1	CONTRACTILE PROTEIN	P	20.4	20.4	1	9	SALFRENLN	203
1PQ1	AB	APOPTOSIS	B	2.3	20.4	9	27	PEIRIAQELRRIGDEFNETYTRRVFAN	204
1S5L	AC	PHOTOSYNTHESIS	A	20.4	20.4	1	12	GVWFTALGISTM	205
1W5C	GJ	PHOTOSYNTHESIS	J	20.4	20.4	1	12	IFRFLLFFQGFH	206
1J1D	EF	CONTRACTILE PROTEIN	E	1.8	20.3	11	46	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN	207
1MVW	JW	CONTRACTILE PROTEIN	J	20.3	20.3	1	15	LALLFATYGGEAEGG	208
5CSC	AB	OXO-ACID-LYASE	A	10.1	20.2	2	24	KDVLAALIPKEQARIKTFRQQHGG	209
1QHH	BD	HYDROLASE	D	2.2	20.1	9	16	DDEMEEERRLAYVGIT	210
2DPP	AB	LYASE	A	2.5	20.1	8	18	QSFWEARAKALESLLIEK	211
1ZBB	cd	STRUCTURAL PROTEIN/DNA	c	2.5	20.0	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	212
2PQK	AB	APOPTOSIS	B	2.2	20.0	9	22	RPEIWIAQELRRIGDEFNAYYA	213
1AVO	EF	PROTEASOME ACTIVATOR	E	2.8	19.9	7	38	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	214
1M8Q	PR	CONTRACTILE PROTEIN	P	19.9	19.9	1	19	TATQARCRGFLMRVEYRAM	215
1MVW	JW	CONTRACTILE PROTEIN	J	19.9	19.9	1	9	SALFRENLN	216
2QJK	GH	ELECTRON TRANSPORT	G	5.0	19.9	4	24	YFIIKDVFALAVVLLVFFAIVGFM	217
3FWB	AB	CELL CYCLE, TRANSCRIPTION	B	3.3	19.9	6	52	EANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	218
1M8Q	P0	CONTRACTILE PROTEIN	P	19.8	19.8	1	9	SALFRENLN	219
2IBF	AB	CELL ADHESION, STRUCTURAL PROTEIN	B	3.3	19.8	6	18	AIYEKAKEVSSALSKVLS	220
1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.8	19.7	7	16	TWHLFYGYGYVVAQDR	221
2J37	WS	RIBOSOME	S	9.9	19.7	2	15	GFPINFLTLYVTVQH	222
2UVP	AB	UNKNOWN FUNCTION	A	3.3	19.7	6	19	FYDWIKEFIRDQGEFIAQQ	223
2GUZ	OP	CHAPERONE, PROTEIN TRANSPORT	P	19.6	19.6	1	15	MDKINNRFNYLFEVN	224
2GV5	DF	CELL CYCLE	F	1.8	19.6	11	50	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK	225
1M56	AC	OXIDOREDUCTASE	C	3.3	19.5	6	35	PVVRLGLRWGFILFIMSEVMFFSAWFWSFFKHALY	226
1NZY	CB	LYASE	B	3.9	19.5	5	11	MRRAMELMLTD	227
1R5W	AB	SIGNALING PROTEIN	A	19.5	19.5	1	23	AQGALANIAVDKANLDVMKERSN	228

1ZBB	CD	STRUCTURAL PROTEIN/DNA	C	2.4	19.5	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	229
3C1B	AB	STRUCTURAL PROTEIN/DNA	B	1.8	19.5	11	27	IYEETRGVLKVFLENVIRDAVTYTEHA	230
1ZBB	gh	STRUCTURAL PROTEIN/DNA	g	2.4	19.4	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	231
1ZBB	GH	STRUCTURAL PROTEIN/DNA	G	2.4	19.4	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	232
1OCC	CJ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	2.8	19.3	7	30	MTLLMIGLTTNMLTMYQWWRDVIRESTFQG	233
1SP4	AB	HYDROLASE	A	2.8	19.3	7	17	CWAFGAVEAISDRICIH	234
2G38	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	2.4	19.3	8	38	LVSEKAATFLVEYARKYRQTIAAAAVVLEEFAHALTTG	235
2JIY	LM	PHOTOSYNTHESIS	M	3.2	19.3	6	14	TAAERAALFWRWTM	236
2BG9	AB	ION CHANNEL/RECEPTOR	B	19.1	19.1	1	27	AVEAIKYIAEQLESASEFDDLKKDWQY	237
3DBH	HL	CELL CYCLE	H	9.6	19.1	2	13	IIARRWINGMLIS	238
3C1B	CD	STRUCTURAL PROTEIN/DNA	C	2.4	19.0	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	239
2VOY	GI	HYDROLASE	G	6.3	18.9	3	25	PLQQKLDEFGEQLSKVISLICVAVW	240
1Q16	AB	OXIDOREDUCTASE	A	3.1	18.8	6	11	DWEDGYRQRWQ	241
3F1I	HS	PROTEIN BINDING	S	1.9	18.8	10	50	PELLHLEAMCHQMGPLIDEKLEDIDRKHSELSELNVKVMEALSLYTKLMN	242
1AVO	IJ	PROTEASOME ACTIVATOR	I	2.7	18.7	7	38	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	243
1AVO	IJ	PROTEASOME ACTIVATOR	J	2.3	18.7	8	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	244
1R27	AB	OXIDOREDUCTASE	A	3.1	18.7	6	11	DWEDGYRQRWQ	245
2ONK	BD	MEMBRANE PROTEIN	D	9.4	18.7	2	10	VRLEHVARTL	246
3DHH	AE	OXIDOREDUCTASE	A	2.7	18.7	7	20	FKEFMYEWIIGQFERSLIDL	247
1V54	NY	OXIDOREDUCTASE	Y	1.7	18.6	11	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	248
1BMV	12	VIRUS/RNA	1	9.3	18.5	2	9	PISNLLRVA	249
2AXT	ad	ELECTRON TRANSPORT	a	9.3	18.5	2	26	PFHQLGVAGVFGGALFCAMHGSLVTS	250
2VJH	AB	PHOTOSYNTHESIS	A	3.1	18.5	6	25	AEKVAKCYRDIDHYMRLINYCLVVG	251
2NQB	GH	STRUCTURAL PROTEIN/DNA	G	2.3	18.4	8	29	AGAPVYLAAVMEYLAAEVLELAGNAARDN	252
1IHF	AB	TRANSCRIPTION/DNA	A	2.0	18.3	9	21	KRDAKELVELFFEEIRRALEN	253
1IZL	AD	PHOTOSYNTHESIS	D	9.2	18.3	2	7	FQGFHNW	254
1N4M	BD	CELL CYCLE	B	18.3	18.3	1	30	VAIGSQRYKLGVRLYYRVMESMLKSEEERL	255
2BYP	CH	RECEPTOR	H	18.3	18.3	1	6	PRCAWR	256
3EAB	FL	CELL CYCLE	F	4.6	18.3	4	28	SMEAERVRVFHKQAFEYISIALRIDEDE	257
1AVO	MN	PROTEASOME ACTIVATOR	M	2.3	18.2	8	38	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	258
1B0N	AB	TRANSCRIPTION REGULATOR	A	4.6	18.2	4	17	KKQFREFLDYQKWRKSQ	259
1E3D	AB	HYDROGENASE	A	9.1	18.2	2	9	IDTLILDTI	260
2H4C	EF	HYDROLASE	E	4.6	18.2	4	11	FFQFAEMIVKM	261
2NQB	EF	STRUCTURAL PROTEIN/DNA	F	2.3	18.2	8	27	IYEETRGVLKVFLENVIRDAVTYTEHA	262
3FOE	BD	ISOMERASE/DNA	D	18.2	18.2	1	5	NVLMG	263
1R27	CD	OXIDOREDUCTASE	C	3.0	18.1	6	11	DWEDGYRQRWQ	264
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	D	6.0	18.1	3	12	AIYVYKVLKQVH	265

3BVH	AB	BLOOD CLOTTING	A	1.6	18.1	11	22	NVRAQLVDMKRLEVDIDIKIRS	266
3DVE	AB	MEMBRANE PROTEIN	B	2.6	18.1	7	17	MGKVYAALMIFDFYKQN	267
2FUG	JL	OXIDOREDUCTASE	J	9.0	18.0	2	19	TPCREGVAGFMVNLFAKIG	268
2QAC	AT	MEMBRANE PROTEIN	T	2.3	18.0	8	13	MRVQAHIRKRMVA	269
3FWC	NO	CELL CYCLE, TRANSCRIPTION	N	1.8	18.0	10	82	KQVITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	270
1EQZ	EF	STRUCTURAL PROTEIN/DNA	E	2.6	17.9	7	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	271
1FRT	AC	COMPLEX (RECEPTOR/IMMUNOGLOBULIN)	A	17.9	17.9	1	12	PETDIVGNLWMK	272
1M1J	AB	BLOOD CLOTTING	A	1.6	17.9	11	74	IVETINILKPGLEGAQQLDENYGHVSTELRRRIVTLKQRVATQVNRIKALQNSIQEQVVEMKRLEVDIDIKIRA	273
3A0B	ef	ELECTRON TRANSPORT	e	4.5	17.9	4	12	LFIAGWLFVSTG	274
3DL8	GC	PROTEIN TRANSPORT	C	17.9	17.9	1	34	ATISVIIFSLAIGVYLWILDLTFTKIISFILSLR	275
3GE8	DF	OXIDOREDUCTASE	F	2.2	17.9	8	25	YRTYNLMQDGQESYVQSLFDQFNER	276
1CI6	AB	TRANSCRIPTION	B	2.0	17.8	9	44	RDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRNLFK	277
1RP3	GH	TRANSCRIPTION	H	2.0	17.8	9	13	DEKVVKGLIEFFT	278
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	E	2.5	17.8	7	23	EGNTYFWHAFWFAIGVAWIGYWS	279
2V7Q	DJ	HYDROLASE	J	2.0	17.8	9	30	AFGKREQAEEERYFRARAKEQLAALKKHHE	280
1ID3	GH	STRUCTURAL PROTEIN/DNA	G	2.0	17.7	9	29	SGAPVYLTAVLEYLAAEILELAGNAARDN	281
1RP3	AB	TRANSCRIPTION	B	2.2	17.7	8	13	DEKVVKGLIEFFT	282
1Y76	CB	TRANSPORT PROTEIN	C	5.9	17.7	3	15	TQNEKLSAFYETLKS	283
3G43	DF	METAL BINDING PROTEIN	F	2.0	17.7	9	42	TLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLD	284
1DPJ	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.8	17.6	10	28	DQQKVSEIFQSSKEKLQGDAKVVSDAFK	285
1PMA	ES	PROTEASE	E	17.6	17.6	1	23	VADARVLVDFARISAQQEKVTYG	286
2F8X	CM	TRANSCRIPTION/DNA	M	2.0	17.6	9	54	SAVMERLRRRIELCRRHHSTCEARYEAVSPERLELERQHTFALHQRCIQAKAKR	287
1SQB	CD	OXIDOREDUCTASE	D	1.9	17.5	9	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	288
1YL3	S5	RIBOSOME	S	17.5	17.5	1	12	PRKVRLVVDLIR	289
2DXB	HI	HYDROLASE	H	1.9	17.5	9	16	IWELNTFATCECLAWR	290
3FH6	FG	TRANSPORT PROTEIN	F	5.8	17.5	3	12	SFISILIFKGLF	291
1HDS	AD	OXYGEN TRANSPORT	D	17.4	17.4	1	12	PQNFRLLGNVLA	292
1V54	AL	OXIDOREDUCTASE	L	1.6	17.4	11	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	293
2E 74	AB	PHOTOSYNTHESIS	A	5.8	17.4	3	8	QVGYWAVK	294
2HVY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	C	3.5	17.4	5	13	GEYRRRWKREVLG	295
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	3.5	17.4	5	17	PQEFFFHAMGGREGLID	296
1N1J	AB	DNA BINDING PROTEIN	A	4.3	17.3	4	15	DSYVEPLKLYLQKFR	297

2VOF	CD	APOPTOSIS	D	2.5	17.3	7	20	WAREIGAQLRRIADDLNAQY	298
3FWC	BD	CELL CYCLE, TRANSCRIPTION	B	1.7	17.3	10	80	VITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	299
1EQZ	AB	STRUCTURAL PROTEIN/DNA	A	2.2	17.2	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	300
1MTY	EC	MONOOXYGENASE	E	8.6	17.2	2	6	SDGFIS	301
1N1J	AB	DNA BINDING PROTEIN	B	2.5	17.2	7	29	AEAPVLFAKAAQIFITELTLRAWIHTEDN	302
1Q7L	AB	HYDROLASE	B	1.9	17.2	9	19	EAVFLRGVDIYTRLLPALA	303
2HUE	BC	DNA BINDING PROTEIN	C	2.5	17.2	7	27	IYEETRGVLKVFLENVIRDAVTYTEHA	304
3BO0	AC	RIBOSOME	A	8.6	17.2	2	27	PLLAFLVIIQIAFGSIILIYLDEIVSK	305
1BPL	AB	GLYCOSYLTRANSFERASE	B	2.9	17.1	6	18	PDVAAEIKRWGTWYANEL	306
1MHY	BD	OXIDOREDUCTASE	B	1.6	17.1	11	32	DTIRQTAVFAALDKVDNAQMIQMERLFIAKLV	307
2FYN	GH	OXIDOREDUCTASE	G	2.9	17.1	6	24	YFIIKDVFALAVVLLVFFAIVGFM	308
2QFA	AB	CELL CYCLE/CELL CYCLE/CELL CYCLE	B	1.9	17.1	9	46	LRRRKLASFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	309
3D7V	AB	APOPTOSIS	B	2.4	17.1	7	22	PEIWIAQEARRIGDEANAYYAR	310
3DL8	BH	PROTEIN TRANSPORT	H	17.1	17.1	1	33	DYGRYKINEYTKYLTLFVATVQSLGIAFWIRGQ	311
1BGY	CD	ELECTRON TRANSPORT	D	3.4	17.0	5	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	312
1S5L	CV	PHOTOSYNTHESIS	V	17.0	17.0	1	6	PKMRNL	313
3C4M	BD	MEMBRANE PROTEIN	D	2.8	17.0	6	19	NSMERVEWLRKKLQDVHNF	314
1QVI	AZ	CONTRACTILE PROTEIN	A	2.1	16.9	8	32	VLGNLEEMRDERLSKIISMFQAHIRGYLIRKA	315
1U35	GH	STRUCTURAL PROTEIN/DNA	G	1.7	16.9	10	29	VGAPVYMAAVLEYLTAEILELAVNAARDN	316
1URQ	BC	TRANSPORT PROTEIN	B	1.7	16.9	10	61	TRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY	317
1URQ	CD	TRANSPORT PROTEIN	C	1.7	16.9	10	65	RADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDL	318
1V54	NP	OXIDOREDUCTASE	P	2.4	16.9	7	35	PAVQKGLRYGMILFIISEVLFFTGFFWAFYHSSLA	319
2INP	BD	OXIDOREDUCTASE	D	2.1	16.9	8	29	TTVSQMHIYTGMDRLGIGQYLSRIALMID	320
3C72	AB	TRANSFERASE	A	16.9	16.9	1	14	YGTWHHRCWLLSRL	321
1IRE	AB	LYASE	A	2.1	16.8	8	23	DEEIQKEITARVKALESMLIEQG	322
1RP3	EF	TRANSCRIPTION	F	2.1	16.8	8	13	DEKVVKGLIEFFT	323
1V54	AC	OXIDOREDUCTASE	C	2.4	16.8	7	35	PAVQKGLRYGMILFIISEVLFFTGFFWAFYHSSLA	324
1ZBB	AB	STRUCTURAL PROTEIN/DNA	B	2.4	16.8	7	27	IYEETRGVLKVFLENVIRDAVTYTEHA	325
1ZBB	ef	STRUCTURAL PROTEIN/DNA	f	2.1	16.8	8	27	IYEETRGVLKVFLENVIRDAVTYTEHA	326
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	2.1	16.8	8	24	PVEYLLVALSGCLTTSLVAHAAAR	327
2P5T	AB	TRANSCRIPTION REGULATOR	A	1.5	16.8	11	31	PVEDYELTLKIEIVKERGANLLSRLYRYQDS	328
3EYM	CD	VIRAL PROTEIN	D	1.9	16.8	9	52	RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLR	329
1IW7	CD	TRANSFERASE	C	16.7	16.7	1	14	AHTLQEMLTLKSDD	330
2NZD	GH	STRUCTURAL PROTEIN/DNA	G	2.1	16.7	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	331

3FWC	IJ	CELL CYCLE, TRANSCRIPTION	J	2.1	16.7	8	77	QIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERL YLIYMDSRAELKRNSTLKKKFFEKWQAS	332
3H87	AD	TOXIN/ANTITOXIN	D	2.8	16.7	6	11	AADLRRLRGAV	333
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	B	5.5	16.6	3	34	PLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVR	334
1YDI	AB	CELL ADHESION, STRUCTURAL PROTEIN	B	2.4	16.6	7	22	WEQLLTTIARTINEVENQILTR	335
2QFA	AB	CELL CYCLE/CELL CYCLE/CELL CYCLE	A	2.4	16.6	7	43	LGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA	336
3B5N	CD	MEMBRANE PROTEIN	D	1.7	16.6	10	61	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRLAG	337
3EZJ	CD	PROTEIN TRANSPORT	C	3.3	16.6	5	15	ERQYYQLFLNLLEAQ	338
2VE7	BD	CELL CYCLE	D	2.8	16.5	6	38	AKRTSRFLSGIINFIHFREACRETYMEFLWQYKSSADK	339
3FOE	BD	ISOMERASE/DNA	B	5.5	16.5	3	10	FGRYSKYIIQ	340
1M56	GI	OXIDOREDUCTASE	I	16.4	16.4	1	33	IYGANFFMATGFHGFHVIVGTIFLLVCLIRVQR	341
2C2V	BC	CHAPERONE	C	5.5	16.4	3	14	RNFRLLEELEEGQK	342
1KTD	AB	IMMUNE SYSTEM	A	2.3	16.3	7	22	AQGALANIAVDKANLDVMKERS	343
1OQS	CD	HYDROLASE	C	5.4	16.3	3	13	LFQFGEMILQKTG	344
2P2C	DQ	HYDROLASE	D	8.2	16.3	2	13	WYIEALAQVFSER	345
3HD7	BC	EXOCYTOSIS	B	1.6	16.3	10	95	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH AVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG	346
1CDL	DH	CALCIUM-BINDING PROTEIN	H	1.8	16.2	9	17	KWQKTGHAVRAIGRLSS	347
1KVD	AB	TOXIN	A	2.3	16.2	7	22	IVGCIAAGILAILQGFEVNWHN	348
1MHY	DG	OXIDOREDUCTASE	D	4.1	16.2	4	10	DWGERQWLIE	349
1NLW	AB	TRANSCRIPTION/DNA	A	1.8	16.2	9	41	LSLLTKAKLHIKKLEDSDRKAVHQIDQLQREQRHLKRQLEK	350
1RP3	CD	TRANSCRIPTION	D	2.0	16.2	8	13	DEKVVKGLIEFFT	351
1UZD	HW	LYASE	H	4.1	16.2	4	20	WRDRFLFVAEAIYKAQAETG	352
1YEW	JK	OXIDOREDUCTASE, MEMBRANE PROTEIN	K	1.8	16.2	9	32	FTHLVWLVAYAWAIYWGASYFTEQDGTWHQTI	353
2DD4	BC	HYDROLASE	B	2.0	16.2	8	16	IWELNTFATCECLAWR	354
2GHO	CD	TRANSFERASE	C	4.1	16.2	4	10	EMEVWALEAY	355
3EXG	MN	OXIDOREDUCTASE	M	5.4	16.2	3	15	VPLGAGIALACKYNG	356
1BCP	IK	TOXIN	K	2.7	16.1	6	13	PMEVMLRAVFMQQ	357
1I3Q	CK	TRANSCRIPTION	K	1.8	16.1	9	29	PKDALKNACNSIINKLGALKTNFETEWNL	358
1N86	DE	BLOOD CLOTTING	D	2.3	16.1	7	18	LVDMKRLEVDIDIKIRSC	359
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	A	2.3	16.1	7	22	VFTWSLPFVGEKVTEMLVNVLN	360
3DL8	BH	PROTEIN TRANSPORT	B	16.1	16.1	1	10	EEGMTKAEKA	361
3FWC	FH	CELL CYCLE, TRANSCRIPTION	F	1.8	16.1	9	76	KQVITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAF LHERLYLIYMDSRAELKRNSTLKKKF	362
1DP5	AB	HYDROLASE/HYDROLASE INHIBITOR	B	2.0	16.0	8	29	TDQQKVSEIFQSSKEKLQGDAKVVSDAFM	363

1K6L	LM	PHOTOSYNTHESIS	M	2.7	16.0	6	14	TAAERAALFWRWTM	364
1M1J	DE	BLOOD CLOTTING	E	2.0	16.0	8	34	NIPSSLRVLRAVIDSLHKKIQKLENAIATQTDYC	365
3CK4	IJ	PROTEIN BINDING	I	2.0	16.0	8	30	KVKQLVDKVEELLSKNYHLVNEVARLVKLV	366
1AOI	GH	DNA BINDING PROTEIN/DNA	G	2.0	15.9	8	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	367
2DFS	MP	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	2.3	15.9	7	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRD ATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	368
3GBN	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.8	15.9	9	53	RRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYEKV KSQLK	369
1JNR	AB	OXIDOREDUCTASE	A	3.2	15.8	5	17	FSGCGAAYEAAYWAKLG	370
1URQ	BC	TRANSPORT PROTEIN	C	2.0	15.8	8	65	RADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGM NHINQDMKEAEKNLKDL	371
2NZD	CD	STRUCTURAL PROTEIN/DNA	C	2.0	15.8	8	28	AGAPVYLAAVLEYLTAEILELAGNAARD	372
2V36	CD	TRANSFERASE	C	2.6	15.8	6	22	WEKYQLLAETMHLSYADRASYA	373
3CXH	CD	OXIDOREDUCTASE	C	2.3	15.8	7	24	YFIFKDLVTVFLFMLILALFVFYS	374
1N2D	AC	CELL CYCLE	C	2.0	15.7	8	46	SQAIKYLQNNIKGFIIRQRVNDEMKVNCATLLQAAYRGHSIRANVF	375
1RZO	AB	HYDROLASE	A	7.9	15.7	2	6	VSILIP	376
1W2W	IJ	ISOMERASE	J	3.1	15.7	5	14	QGSRLTAYELVYDK	377
2P80	CD	OXIDOREDUCTASE	D	15.7	15.7	1	13	KIVQERLEKVIAS	378
3DL8	BH	PROTEIN TRANSPORT	H	15.7	15.7	1	33	QDTVKYLERIINRLIFFGALFLSVIALIPILIS	379
1AVO	EF	PROTEASOME ACTIVATOR	F	2.6	15.6	6	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	380
1SFC	JK	TRANSPORT PROTEIN	J	1.7	15.6	9	65	EIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVD YVERAVSDTKKAVKYQ	381
2NQB	CD	STRUCTURAL PROTEIN/DNA	C	2.2	15.6	7	29	AGAPVYLAAVMEYLAAEVLELAGNAARDN	382
2V6Q	AB	APOPTOSIS	B	2.2	15.6	7	19	RPEIWIAQELRRIGDEFNA	383
3DL8	BH	PROTEIN TRANSPORT	H	15.6	15.6	1	10	LINPVELAEN	384
1JMX	AG	OXIDOREDUCTASE	A	15.5	15.5	1	15	PEGWLMSIARMQVMH	385
1M1J	AC	BLOOD CLOTTING	A	1.7	15.5	9	74	IVETINILKPGLEGAQQLDENYGHVSTELRRRIVTLKQRVATQVNRIKAL QNSIQEQVVEMKRLEVDIDIKIRA	386
1QLS	AD	METAL BINDING PROTEIN/INHIBITOR	D	7.8	15.5	2	9	MVSAFLKQA	387
1W2W	AB	ISOMERASE	B	3.1	15.5	5	13	QGSRLTAYELVYD	388
2D1P	GI	TRANSLATION	I	2.6	15.5	6	11	YTDFVRLTVKH	389
2GUZ	CD	CHAPERONE, PROTEIN TRANSPORT	D	3.1	15.5	5	23	FYLQSKVYRAAERLKWELAQREK	390
2NQB	AB	STRUCTURAL PROTEIN/DNA	B	1.9	15.5	8	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	391
2VGL	BM	PROTEIN TRANSPORT	M	3.9	15.5	4	17	AAMVFEFLYKMCDVMAA	392
2VYN	DA	OXIDOREDUCTASE	A	5.2	15.5	3	10	ADYMAYMLKY	393
3FWC	AB	CELL CYCLE, TRANSCRIPTION	B	1.9	15.5	8	80	VITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLH ERLYLIYMDSRAELKRNSTLKKKFFEKWQA	394
3HKZ	IM	TRANSFERASE	I	3.9	15.5	4	8	YMQRRLIN	395
1AHJ	EF	LYASE	F	2.2	15.4	7	18	EWEHLPYSLMFAGVAELG	396

1KX4	EF	STRUCTURAL PROTEIN/DNA	F	1.9	15.4	8	27	IYEETRGVLKVFLENVIRDAVTYTEHA	397
2DD4	KL	HYDROLASE	K	1.9	15.4	8	16	IWELNTFATCECLAWR	398
3FWC	NP	CELL CYCLE, TRANSCRIPTION	N	1.7	15.4	9	82	KQVITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAF LHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	399
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	3.1	15.3	5	26	HAPYVKDKAEEWRYTDRFLQGYSADG	400
1XME	BC	OXIDOREDUCTASE	C	1.9	15.3	8	28	KGALAVILVLTLTILVFWLGVYAVFFAR	401
2DXB	HI	HYDROLASE	I	1.9	15.3	8	16	DFEILEMAVRELAIEK	402
2GTL	BC	OXYGEN STORAGE/TRANSPORT	C	5.1	15.3	3	19	PKFSAHALRILNGLDLAIN	403
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.9	15.3	8	24	PVEYLLVALSGCLTTSLVAHAAAR	404
2RAW	AB	CELL CYCLE	A	1.9	15.3	8	43	LGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA	405
3DHH	AB	OXIDOREDUCTASE	B	2.6	15.3	6	25	YRTYNLMQDGQESYVQSLFDQFNER	406
3GE8	AE	OXIDOREDUCTASE	A	1.9	15.3	8	20	FKEFMYEWIIGQFERSLIDL	407
3HOY	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	2.2	15.3	7	29	PKDALKNACNSIINKLGALKTNFETEWNL	408
1CDL	BF	CALCIUM-BINDING PROTEIN	F	2.5	15.2	6	17	RKWQKTGHAVRAIGRLS	409
1JNR	CD	OXIDOREDUCTASE	C	3.0	15.2	5	17	FSGCGAAYEAAYWAKLG	410
1QGW	BD	PHOTOSYNTHESIS	D	1.7	15.2	9	25	NRRMAACLRDGEIILRYVSYALLSG	411
1URQ	CD	TRANSPORT PROTEIN	D	1.9	15.2	8	60	SRENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSN KTRIDEANQRAT	412
2HLD	KX	HYDROLASE	X	15.2	15.2	1	13	IEDVVAKAEKLAA	413
2JBL	LM	ELECTRON TRANSPORT	M	3.0	15.2	5	14	TAVERAALFWRWTI	414
3CXH	DI	OXIDOREDUCTASE	I	2.5	15.2	6	27	VGTIFAGAFVFQTVFDTAITSWYENHN	415
1B33	EF	PHOTOSYNTHESIS	E	3.8	15.1	4	25	QEMTATCLRDLDYYLRLITYGIVAG	416
1NKP	DE	TRANSCRIPTION/DNA	D	1.7	15.1	9	43	KVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQL	417
1O18	MN	CONTRACTILE PROTEIN	N	15.1	15.1	1	10	KSFLEELLTT	418
2BCX	AB	CALCIUM BINDING PROTEIN	B	2.2	15.1	7	23	KAVWHKLLSKQRRRAVVACFRMT	419
2F66	DE	TRANSPORT PROTEIN	D	2.2	15.1	7	27	LDTFVKQGRELARQQFLVRWHIQRITS	420
2OBH	BD	CELL CYCLE	D	3.8	15.1	4	15	WKLLAKGLLIRERLK	421
2Q9Q	EH	REPLICATION	E	2.5	15.1	6	22	LMEINTSGTFLTQALNHMYKLR	422
3BL2	BD	VIRAL PROTEIN/APOPTOSIS	D	2.2	15.1	7	17	MENLSRRLKVTGDLFDI	423
3FWC	JK	CELL CYCLE, TRANSCRIPTION	J	2.2	15.1	7	77	QIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERL YLIYMDSRAELKRNSTLKKKFFEKWQAS	424
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	2.5	15.0	6	32	DVTRVSLAFWGFDKIDIAQMIQLERGFLAKIV	425
2BR2	EF	HYDROLASE	F	1.9	15.0	8	18	RREIELSKVIREALESAV	426
2EC6	AC	CONTRACTILE PROTEIN	C	7.5	15.0	2	8	FADYMEAF	427
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	A	1.9	15.0	8	30	AGAPVYLAAVLEYLTAEILELAGNAARDNK	428

2NZD	AB	STRUCTURAL PROTEIN/DNA	B	1.7	15.0	9	27	IYEETRGVLKVFLENVIRDAVTYTEHA	429
3EZB	AB	TRANSFERASE	B	7.5	15.0	2	7	LFKLQTL	430
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	3.8	15.0	4	13	YAAKLLFQELMAM	431
1B8D	AB	PHOTOSYNTHESIS	A	2.5	14.9	6	25	PEKINKCYRDIDHYMRLINYSLVVG	432
1G20	DG	OXIDOREDUCTASE	G	7.5	14.9	2	8	IMEMAAEA	433
1M45	AB	CELL CYCLE PROTEIN	B	1.9	14.9	8	24	ISQAIKYLQNNIKGFIIRQRVNDE	434
1NKP	AB	TRANSCRIPTION/DNA	B	1.9	14.9	8	42	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRA	435
1S5L	cv	PHOTOSYNTHESIS	v	14.9	14.9	1	6	PKMRNL	436
1SFC	AB	TRANSPORT PROTEIN	B	1.7	14.9	9	68	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH AVDYVERAVSDTKKAVKY	437
1W2W	EF	ISOMERASE	F	3.0	14.9	5	13	QGSRLTAYELVYD	438
2BE6	BE	MEMBRANE PROTEIN	E	2.1	14.9	7	13	VTVGKFYATFLIQ	439
2E1M	AC	OXIDOREDUCTASE	C	2.1	14.9	7	17	IEGAVETAVRAAIAVNE	440
2G38	CD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	C	2.5	14.9	6	38	LVSEKAATFLVEYARKYRQTIAAAAVVLEEFAHALTTG	441
2HQS	AH	TRANSPORT PROTEIN/LIPOPROTEIN	H	2.1	14.9	7	22	PEYNISLGERRANAVKMYLQGK	442
3CXH	CG	OXIDOREDUCTASE	C	2.5	14.9	6	35	PYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	443
1BXN	AI	LYASE	A	4.9	14.8	3	22	IQAGATANRVALEAMVLARNEG	444
1EQZ	CD	STRUCTURAL PROTEIN/DNA	D	2.1	14.8	7	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	445
1J1E	BC	CONTRACTILE PROTEIN	B	1.6	14.8	9	46	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN	446
2BE6	AD	MEMBRANE PROTEIN	D	2.5	14.8	6	25	VTVGKFYATFLIQEYFRKFKKRKEQ	447
2DXB	KL	HYDROLASE	K	1.9	14.8	8	16	IWELNTFATCECLAWR	448
2DXB	WX	HYDROLASE	W	1.9	14.8	8	16	IWELNTFATCECLAWR	449
3HD7	EF	EXOCYTOSIS	E	1.6	14.8	9	41	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIII	450
1AHJ	CD	LYASE	D	2.1	14.7	7	18	EWEHLPYSLMFAGVAELG	451
1BGY	DH	ELECTRON TRANSPORT	H	3.7	14.7	4	6	CTEELL	452
1GOT	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	B	3.7	14.7	4	23	ELDQLRQEAEQLKNQIRDARKAC	453
1JTH	AD	ENDOCYTOSIS/EXOCYTOSIS	A	1.5	14.7	10	61	EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLER IEEGMDQINKDMK	454
1T0J	BC	SIGNALING PROTEIN	C	2.9	14.7	5	15	QLEEDLKGYLDWITQ	455
1XK4	BD	METAL BINDING PROTEIN	B	2.5	14.7	6	20	ELEKALNSIIDVYHKYSLIK	456
2HVY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	3.7	14.7	4	15	LHDLVDYYYFWKEDG	457
3GLH	NO	TRANSFERASE	O	14.7	14.7	1	21	PSRLQAILGDVCHIREQLMSV	458
1IRU	FG	HYDROLASE	F	14.6	14.6	1	5	QIPTQ	459
1IWP	LM	LYASE	M	3.7	14.6	4	16	HAVARNFRRAAELIAI	460
1ZBB	ab	STRUCTURAL PROTEIN/DNA	b	2.4	14.6	6	27	IYEETRGVLKVFLENVIRDAVTYTEHA	461

2QJK	AB	ELECTRON TRANSPORT	B	2.9	14.6	5	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	462
2VOH	AB	APOPTOSIS	B	1.8	14.6	8	20	ILGQVGRQLALIGDDINRRY	463
3DTP	BD	CONTRACTILE PROTEIN	B	14.6	14.6	1	6	FQEFRQ	464
3FDZ	AB	ISOMERASE	A	2.4	14.6	6	14	KRAIRTLWHVQDQM	465
1H4J	GH	OXIDOREDUCTASE	H	2.1	14.5	7	24	KQADSIKQMEERNKKRVENFKKTG	466
1VYT	AE	TRANSPORT PROTEIN	E	2.9	14.5	5	22	LREKQQLEEDLKGYLDWITQAE	467
1XK4	JL	METAL BINDING PROTEIN	J	2.4	14.5	6	18	ELEKALNSIIDVYHKYSL	468
1YV0	IC	CONTRACTILE PROTEIN	I	2.1	14.5	7	23	RAATARRQHLKSAMLQLAVTEIE	469
1SFC	KL	TRANSPORT PROTEIN	L	1.6	14.4	9	61	NEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLG	470
1WYU	CD	OXIDOREDUCTASE	C	2.4	14.4	6	18	QGVLQATFEYQTMIAELA	471
2DXB	TU	HYDROLASE	U	1.8	14.4	8	16	DFEILEMAVRELAIEK	472
2F8N	HG	STRUCTURAL PROTEIN/DNA	G	2.1	14.4	7	29	VGAPVYMAAVLEYLTAEILELAVNAARDN	473
2HQW	AB	METAL BINDING PROTEIN	B	2.9	14.4	5	16	KATFRAITSTLASSFK	474
2J5G	FD	HYDROLASE	D	3.6	14.4	4	9	YRGRYFLFT	475
2OBH	AC	CELL CYCLE	C	3.6	14.4	4	15	WKLLAKGLLIRERLK	476
3DTP	AC	CONTRACTILE PROTEIN	A	3.6	14.4	4	13	IAFQAQCRGYLAR	477
1IR2	FO	LYASE	F	2.9	14.3	5	20	WRDRFLFVAEAIYKAQAETG	478
1M1J	DE	BLOOD CLOTTING	D	1.6	14.3	9	59	QQLDENYGHVSTELRRRIVTLKQRVATQVNRIKALQNSIQEQVVEMKRLEVDIDIKIRA	479
1NKP	DE	TRANSCRIPTION/DNA	E	1.8	14.3	8	42	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRA	480
2HZS	HL	TRANSCRIPTION	L	2.0	14.3	7	11	VDDVLKFTFTG	481
2NZD	EF	STRUCTURAL PROTEIN/DNA	F	1.8	14.3	8	28	IYEETRGVLKVFLENVIRDAVTYTEHAK	482
2ZBK	AB	ISOMERASE	B	2.0	14.3	7	21	KKLLAYLKYIPEVSRSLATFL	483
3B63	IJ	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	I	14.3	14.3	1	12	NERFRAPEALFH	484
3HKZ	IJ	TRANSFERASE	I	4.8	14.3	3	11	EEAIAEAKEIM	485
1AVO	KL	PROTEASOME ACTIVATOR	K	1.8	14.2	8	38	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	486
1E6Y	DF	OXIDOREDUCTASE	F	2.0	14.2	7	20	AEVVEWVHRIFDQRTKFGFQ	487
1Y74	AD	TRANSPORT PROTEIN	A	4.7	14.2	3	19	LERDVSRAVELLERLQRSG	488
2E9X	BC	REPLICATION	C	2.4	14.2	6	22	EMERGLFQTGQKGLNDFQCWEK	489
2IX7	CA	CONTRACTILE PROTEIN/METAL BINDING	C	2.0	14.2	7	55	KLRAACIRIQKTIRGWLLRKRYLCMQRAAITVQRYVRGYQARCYAKFLRRTKAAT	490
2PON	AB	APOPTOSIS INHIBITOR	A	14.2	14.2	1	16	TMENLSRRLKVTGDLF	491
2QXV	AB	GENE REGULATION	B	2.4	14.2	6	23	MFSSNRQKILERTETLNQEWKQR	492
3CXH	NO	OXIDOREDUCTASE	N	1.8	14.2	8	24	YFIFKDLVTVFLFMLILALFVFYS	493
3EYM	AB	VIRAL PROTEIN	B	1.6	14.2	9	52	RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLR	494
1NKP	AB	TRANSCRIPTION/DNA	A	1.6	14.1	9	44	KVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQLG	495
1SYQ	AB	CELL ADHESION	B	2.0	14.1	7	20	LLQAAKGLAGAVSELLRSAQ	496

2AHM	CG	VIRAL PROTEIN, REPLICATION	G	2.4	14.1	6	68	EVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMADQAMTQMYKQARS EDKRAKVTSAMQTMLFTMLRKLD	497
2DD4	HI	HYDROLASE	I	2.0	14.1	7	16	DFEILEMAVRELAIEK	498
2IBX	EF	VIRAL PROTEIN	F	2.0	14.1	7	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQL	499
2J8S	AE	MEMBRANE PROTEIN	E	14.1	14.1	1	8	PLHLAAYW	500
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	A	1.4	14.1	10	61	LGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMVNLKEKI KELHQQYKEASEV	501
1F99	MN	PHOTOSYNTHESIS	N	3.5	14.0	4	14	GNKRLDVVNKITNN	502
1V54	NQ	OXIDOREDUCTASE	Q	2.3	14.0	6	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	503
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	I	2.0	14.0	7	23	EGNTYFWHAFWFAIGVAWIGYWS	504
2BL0	AC	MUSCLE PROTEIN	A	1.8	14.0	8	45	RIGEIVKVVQAAARGWVERKHFRQAREKSVSARIIQDNIRAYLEF	505
2FJ7	CD	STRUCTURAL PROTEIN/DNA	D	7.0	14.0	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	506
2QFA	AC	CELL CYCLE/CELL CYCLE/CELL CYCLE	C	1.8	14.0	8	39	PIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFT	507
3CXH	OT	OXIDOREDUCTASE	T	2.3	14.0	6	27	VGTIFAGAFVFQTVFDTAITSWYENHN	508
1AVO	GH	PROTEASOME ACTIVATOR	G	2.3	13.9	6	38	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	509
1F66	GH	STRUCTURAL PROTEIN/DNA	G	2.3	13.9	6	26	AAVYSAAILEYLTAEVLELAGNASKD	510
1F99	MN	PHOTOSYNTHESIS	M	3.5	13.9	4	12	PLTEAIAAADSQ	511
1H4J	CD	OXIDOREDUCTASE	D	1.7	13.9	8	24	KQADSIKQMEERNKKRVENFKKTG	512
1IAO	AB	MHC II	A	1.7	13.9	8	22	PQGGLQNIAAEKHNLGILTKRS	513
1M1J	DF	BLOOD CLOTTING	D	2.0	13.9	7	59	QQLDENYGHVSTELRRRIVTLKQRVATQVNRIKALQNSIQEQVVEMKR LEVDIDIKIRA	514
1YE9	KO	OXIDOREDUCTASE	O	3.5	13.9	4	17	PFEQRHIVDGFSFELSK	515
1YHU	QS	OXYGEN STORAGE/TRANSPORT	S	2.8	13.9	5	20	PEFQGHVVRVMGGLDILINA	516
2GUZ	KL	CHAPERONE, PROTEIN TRANSPORT	L	2.3	13.9	6	23	FYLQSKVYRAAERLKWELAQREK	517
3HKZ	IJ	TRANSFERASE	I	4.6	13.9	3	8	QDYISGAY	518
1KIL	AD	MEMBRANE PROTEIN	D	1.4	13.8	10	62	ARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSN KTRIDEANQRATKM	519
1N2D	BC	CELL CYCLE	C	2.0	13.8	7	46	SQAIKYLQNNIKGFIIRQRVNDEMKVNCATLLQAAYRGHSIRANVF	520
1QVI	AY	CONTRACTILE PROTEIN	A	2.0	13.8	7	26	YKKLQDQRIGLSVIQRNIRKWLVLRN	521
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	3.5	13.8	4	9	IADIQGYNY	522
2QL2	CD	TRANSCRIPTION/DNA	D	1.7	13.8	8	20	KIETLRLAKNYIWALSEILR	523
3GE8	DH	OXIDOREDUCTASE	D	2.3	13.8	6	20	FKEFMYEWIIGQFERSLIDL	524
1P4Q	AB	TRANSCRIPTION/TRANSFERASE	B	13.7	13.7	1	26	PEKRKLIQQQLVLLLHAHKCQRREQA	525
1W2W	MN	ISOMERASE	N	2.7	13.7	5	13	QGSRLTAYELVYD	526
1XFU	FT	LYASE/METAL BINDING PROTEIN	F	1.7	13.7	8	15	SLEKQKGVTNLLIKY	527

2C4O	AD	LIGASE	D	13.7	13.7	1	14	ISKVLLSICSLLCD	528
2DOQ	BD	CELL CYCLE	D	3.4	13.7	4	41	NDEAESFRNTWLLFRSFQQWITLTQTFKEQSRLADQAFLNK	529
2E9X	FG	REPLICATION	F	2.3	13.7	6	23	LMEINTSGTFLTQALNHMYKLRT	530
2GUZ	OP	CHAPERONE, PROTEIN TRANSPORT	P	2.3	13.7	6	23	FYLQSKVYRAAERLKWELAQREK	531
2GV5	AC	CELL CYCLE	C	2.0	13.7	7	50	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK	532
2NPS	AD	TRANSPORT PROTEIN	D	1.4	13.7	10	58	LELVSGSIGVLKNMSQRIGGELEEQAVMLEDFSHELESTQSRLDNVMKKLAKVSHMTS	533
2NQB	GH	STRUCTURAL PROTEIN/DNA	H	2.3	13.7	6	29	SKAMSIMNSFVNDIFERIAAEASRLAHYN	534
2P1L	GH	APOPTOSIS	H	2.7	13.7	5	21	SGTMENLSRRLKVTGDLFDIM	535
2PMZ	QR	TRANSLATION, TRANSFERASE	R	2.7	13.7	5	13	YAFKLLIQELMSM	536
2QJY	MN	OXIDOREDUCTASE	N	2.3	13.7	6	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	537
3A0B	ad	ELECTRON TRANSPORT	d	6.9	13.7	2	29	GLWTFIALHGAFGLIGFMLRQFEIARLVG	538
3DA7	GH	PROTEIN BINDING	H	2.7	13.7	5	12	LDALWDCLTGWV	539
3E1R	AC	CELL CYCLE/TRANSPORT PROTEIN	A	2.7	13.7	5	45	NIHEMEIQLKDALEKNQQWLVYDQQREVYVKGLLAKIFELEKKTE	540
3HKZ	IM	TRANSFERASE	M	3.4	13.7	4	14	IGIVAAQSVGEPGT	541
1J1E	DF	CONTRACTILE PROTEIN	D	13.6	13.6	1	8	YDEFLEFM	542
1M1J	BC	BLOOD CLOTTING	B	1.5	13.6	9	100	KPVLRDLKDRVAKFSDTSTTMYQYVNMIDNKLVKTQKQRKDNDIILSEYNTEMELHYNYIKDNLDNNIPSSLRVLRAVIDSLHKKIQKLENAIATQTDYC	543
1MDU	AB	STRUCTURAL PROTEIN	B	13.6	13.6	1	5	STFQQ	544
1U35	GH	STRUCTURAL PROTEIN/DNA	H	1.7	13.6	8	29	SKAMGIMNSFVNDIFERIASEASRLAHYN	545
2J5G	ED	HYDROLASE	E	3.4	13.6	4	9	YRGRYFLFT	546
2ZXE	AB	HYDROLASE/TRANSPORT PROTEIN	B	1.9	13.6	7	31	SSWFKIFLFYLIFYGCLAGIFIGTIQVLLLT	547
3B63	JL	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	L	6.8	13.6	2	6	RKDLYA	548
3EYM	EF	VIRAL PROTEIN	F	1.9	13.6	7	52	RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLR	549
1AOI	CD	DNA BINDING PROTEIN/DNA	C	1.9	13.5	7	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	550
1E6Y	AC	OXIDOREDUCTASE	C	2.3	13.5	6	20	AEVVEWVHRIFDQRTKFGFQ	551
1FYZ	BD	OXIDOREDUCTASE	D	1.9	13.5	7	31	DVTRVSLAFWGFDKIDIAQMIQLERGFLAKI	552
1ID5	LH	HYDROLASE	L	2.7	13.5	5	9	EKELFESYI	553
1KX4	GH	STRUCTURAL PROTEIN/DNA	G	2.3	13.5	6	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	554
1RU7	AB	VIRAL PROTEIN	B	1.9	13.5	7	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	555
1RUZ	HI	VIRAL PROTEIN	I	1.9	13.5	7	46	RRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYE	556
1SFC	BC	TRANSPORT PROTEIN	B	1.5	13.5	9	68	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY	557

1XK4	IK	METAL BINDING PROTEIN	I	2.3	13.5	6	18	ELEKALNSIIDVYHKYSL	558
2DD4	HI	HYDROLASE	H	1.7	13.5	8	16	IWELNTFATCECLAWR	559
2DPP	AB	LYASE	B	3.4	13.5	4	14	EKELDERTEVFLKK	560
2IBZ	CD	OXIDOREDUCTASE	C	1.7	13.5	8	24	YFIFKDLVTVFLFMLILALFVFYS	561
2PSM	BC	CYTOKINE	B	2.7	13.5	5	19	KVTAMNCFLLELQVILHEY	562
3A0B	ad	ELECTRON TRANSPORT	d	6.8	13.5	2	11	KRWLHFFMLFV	563
3B5N	FG	MEMBRANE PROTEIN	F	1.4	13.5	10	67	LAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVEDAQLDVEQGVGHTDKAVKSA	564
1B0N	AB	TRANSCRIPTION REGULATOR	A	2.7	13.4	5	12	SEWEKLVRDAMT	565
1EQZ	CD	STRUCTURAL PROTEIN/DNA	C	1.9	13.4	7	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	566
1G2C	EB	VIRAL PROTEIN	B	1.9	13.4	7	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	567
1J1E	AC	CONTRACTILE PROTEIN	C	2.7	13.4	5	38	ASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRA	568
1KIL	AD	MEMBRANE PROTEIN	A	1.5	13.4	9	50	VDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKY	569
1KX4	CD	STRUCTURAL PROTEIN/DNA	C	1.9	13.4	7	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	570
1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	2.2	13.4	6	35	PAVQKGLRYGMILFIISEVLFFTGFFWAFYHSSLA	571
1YE9	BF	OXIDOREDUCTASE	B	2.2	13.4	6	12	PETLHNVMWAMS	572
1ZGL	BP	IMMUNE SYSTEM	B	13.4	13.4	1	10	GRPDAEYWNS	573
2DD4	KL	HYDROLASE	L	1.9	13.4	7	16	DFEILEMAVRELAIEK	574
2VE7	AC	CELL CYCLE	C	2.7	13.4	5	29	AKRTSRFLSGIINFIHFREACRETYMEFL	575
3DBO	AB	TOXIN/ANTITOXIN	A	2.7	13.4	5	9	KTEFLSRLR	576
1GX7	AD	OXIDOREDUCTASE	D	2.2	13.3	6	18	IKDYMLDRINGVYGADAK	577
1J1E	BC	CONTRACTILE PROTEIN	C	1.5	13.3	9	47	FAELQDLARQLHARVDKVDEERYDIEAKVTKNITEIADLTQKIFDLR	578
1WYU	AB	OXIDOREDUCTASE	B	2.7	13.3	5	14	ELTLVRHYTGLSRR	579
2WEL	AD	TRANSFERASE	A	1.7	13.3	8	16	ARRKLKGAILTTMLAT	580
3CXH	NR	OXIDOREDUCTASE	N	2.2	13.3	6	36	VPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	581
1B8D	KL	PHOTOSYNTHESIS	K	2.6	13.2	5	25	PEKINKCYRDIDHYMRLINYSLVVG	582
1G73	AC	APOPTOSIS/APOPTOSIS INHIBITOR	A	3.3	13.2	4	48	EEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQT	583
1KDD	DC	DE NOVO PROTEIN	C	1.5	13.2	9	32	VKQLEAEVEELESEIWHLENEVARLEKENAEC	584
1M56	GI	OXIDOREDUCTASE	G	2.6	13.2	5	22	PRMNNLSYWLYVAGTSLAVASL	585
1O18	PR	CONTRACTILE PROTEIN	R	13.2	13.2	1	10	GAELRHVLAT	586
1SFC	IL	TRANSPORT PROTEIN	L	1.5	13.2	9	61	NEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLG	587
1YTZ	TI	CONTRACTILE PROTEIN	T	1.5	13.2	9	46	EDKLRDKAKELWDWLYQLQTEKYDFAEQIKRKKYEIVTLRNRIDQA	588
1ZBB	ab	STRUCTURAL PROTEIN/DNA	b	3.3	13.2	4	11	KPAIRRLARRG	589
1ZBB	AB	STRUCTURAL PROTEIN/DNA	B	3.3	13.2	4	11	KPAIRRLARRG	590

2DXB	NO	HYDROLASE	N	1.9	13.2	7	16	IWELNTFATCECLAWR	591
2F8N	EF	STRUCTURAL PROTEIN/DNA	F	2.6	13.2	5	27	IYEETRGVLKVFLENVIRDAVTYTEHA	592
2HZS	BI	TRANSCRIPTION	I	2.2	13.2	6	11	VDDVLKFTFTG	593
2PJR	AB	HYDROLASE/DNA	B	1.9	13.2	7	16	DDEMEEERRLAYVGIT	594
2QJY	PQ	OXIDOREDUCTASE	Q	2.2	13.2	6	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	595
3BXK	CD	MEMBRANE PROTEIN, SIGNALING PROTEIN	D	1.9	13.2	7	18	IYAAMMIMEYYRQSKAKK	596
3C1B	AB	STRUCTURAL PROTEIN/DNA	B	3.3	13.2	4	11	KPAIRRLARRG	597
3HOU	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	1.7	13.2	8	29	PKDALKNACNSIINKLGALKTNFETEWNL	598
1CI6	AB	TRANSCRIPTION	A	1.6	13.1	8	55	QNKTAATRYRQKKRAEQEALTGECKELEKKNEALKERADSLAKEIQYLKDLIEEV	599
1I7Q	CD	LYASE	C	2.6	13.1	5	21	HKELAEHLMLVDLARNDLARI	600
1J1D	BC	CONTRACTILE PROTEIN	C	1.6	13.1	8	47	FAELQDLARQLHARVDKVDEERYDIEAKVTKNITEIADLTQKIFDLR	601
1KDD	EF	DE NOVO PROTEIN	E	1.5	13.1	9	33	VKQLKAKVEELKSKLWHLKNKVARLKKKNAECK	602
1KX4	AB	STRUCTURAL PROTEIN/DNA	A	2.2	13.1	6	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	603
1LVC	CF	LYASE	C	1.9	13.1	7	15	SLEKQKGVTNLLIKY	604
1RUY	HI	VIRAL PROTEIN	I	2.2	13.1	6	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	605
1SFC	AB	TRANSPORT PROTEIN	A	1.5	13.1	9	63	RRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN	606
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	B	1.9	13.1	7	29	IVSQTRNKELLDKKIRSEIEAIKKIIAEF	607
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	A	2.2	13.1	6	23	EGNTYFWHAFWFAIGVAWIGYWS	608
2D0V	AB	OXIDOREDUCTASE	B	2.2	13.1	6	24	KQVESRKGEEERNANRAEHFKKTG	609
2F66	AB	TRANSPORT PROTEIN	A	2.2	13.1	6	26	LDTFVKQGRELARQQFLVRWHIQRIT	610
2NPS	CD	TRANSPORT PROTEIN	D	1.5	13.1	9	58	LELVSGSIGVLKNMSQRIGGELEEQAVMLEDFSHELESTQSRLDNVMKKLAKVSHMTS	611
2QJP	JK	ELECTRON TRANSPORT	J	2.6	13.1	5	24	YFIIKDVFALAVVLLVFFAIVGFM	612
2QRV	AB	TRANSFERASE/TRANSFERASE REGULATOR	B	2.2	13.1	6	16	PSWYLFQFHRLLQYAR	613
2VOY	IK	HYDROLASE	K	13.1	13.1	1	31	GRAIYNNMKQFIRYLISSNVGEVVCIFLTAA	614
3CRP	AB	PROTEIN BINDING	A	1.9	13.1	7	29	KVKQLADKVEELLSKNYHLANEVARLAKL	615
3FWC	FG	CELL CYCLE, TRANSCRIPTION	F	1.9	13.1	7	76	KQVITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKF	616
1GXS	CD	LYASE	D	3.3	13.0	4	14	PAQAFLLFKQFLKG	617
1I3R	AB	IMMUNE SYSTEM	B	13.0	13.0	1	9	RPDAENWNS	618
1JTH	AD	ENDOCYTOSIS/EXOCYTOSIS	D	1.9	13.0	7	44	ETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH	619
1KG0	BD	VIRAL PROTEIN/IMMUNE SYSTEM	B	6.5	13.0	2	9	KDLLEQRRA	620

1KYO	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.6	13.0	8	24	YFIFKDLVTVFLFMLILALFVFYS	621
1LWU	JK	BLOOD CLOTTING	J	3.3	13.0	4	37	NMQLQQLTLLQHNIKTQVSQILRVEVDIDVALRACKG	622
1OCC	AC	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	2.2	13.0	6	35	PAVQKGLRYGMILFIISEVLFFTGFFWAFYHSSLA	623
1OO0	AB	SIGNALING PROTEIN	A	2.2	13.0	6	26	PEGLRCFYYLVQDLKCLVFSLIGLHF	624
1RF8	AB	BIOSYNTHETIC PROTEIN, TRANSLATION	B	3.3	13.0	4	12	PTFLLQFKDKLN	625
1U35	AB	STRUCTURAL PROTEIN/DNA	A	3.3	13.0	4	14	KLPFQRLVREIAQD	626
1U35	CD	STRUCTURAL PROTEIN/DNA	C	1.6	13.0	8	29	VGAPVYMAAVLEYLTAEILELAVNAARDN	627
1U35	EF	STRUCTURAL PROTEIN/DNA	F	2.2	13.0	6	27	IYEETRGVLKVFLENVIRDAVTYTEHA	628
1UKL	AC	PROTEIN TRANSPORT/DNA BINDING PROTEIN	A	13.0	13.0	1	24	VDYLNELRESCLEAYTGIVQGLKG	629
1YE9	BH	OXIDOREDUCTASE	B	4.3	13.0	3	12	FILREKITHFDH	630
2DYM	EF	PROTEIN TURNOVER/PROTEIN TURNOVER	F	2.2	13.0	6	18	MDDLLIRRLTDRNDKEAH	631
2QJK	GH	ELECTRON TRANSPORT	H	2.6	13.0	5	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	632
2VOF	AB	APOPTOSIS	B	1.9	13.0	7	21	EWAREIGAQLRRIADDLNAQY	633
3BC1	EF	SIGNALING PROTEIN/TRANSPORT PROTEIN	F	1.9	13.0	7	29	PEFEEQEAIMKVLQRDAALKRAEEERVRH	634
3GBM	AB	VIRAL PROTEIN / IMMUNE SYSTEM	B	1.9	13.0	7	53	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLR	635
1H4J	EF	OXIDOREDUCTASE	F	1.8	12.9	7	24	KQADSIKQMEERNKKRVENFKKTG	636
1NIW	EF	SIGNALING PROTEIN/OXIDOREDUCTASE	F	1.8	12.9	7	13	FKEVANAVKISAS	637
1T0Q	AB	OXIDOREDUCTASE	B	6.5	12.9	2	12	PMQTWYKKYCFD	638
1TQY	CD	TRANSFERASE	D	2.6	12.9	5	15	FDFTHREFRKLWSEG	639
1WYU	EF	OXIDOREDUCTASE	E	2.2	12.9	6	18	QGVLQATFEYQTMIAELA	640
1XLS	DH	TRANSCRIPTION	D	12.9	12.9	1	29	RFAKLLLRLPALRSIGLKCLEHLFFFKLI	641
1Z56	AC	LIGASE	A	4.3	12.9	3	6	RAMMVT	642
2AST	BC	CELL CYCLE/LIGASE/PROTEIN TURNOVER	C	2.6	12.9	5	8	ESEWRNLG	643
2BR2	EF	HYDROLASE	E	2.6	12.9	5	17	NAIELARVVDRSLRDSK	644
2D10	DH	CELL ADHESION	H	4.3	12.9	3	11	WSKKNELFSNL	645
2DFS	MO	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	1.8	12.9	7	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRDATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	646
2DXB	TU	HYDROLASE	T	1.8	12.9	7	16	IWELNTFATCECLAWR	647
2NZD	AB	STRUCTURAL PROTEIN/DNA	A	1.8	12.9	7	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	648
2VJM	AB	TRANSFERASE	B	6.5	12.9	2	5	LYFTM	649
3BPQ	AB	TOXIN	A	2.2	12.9	6	22	RKEYEKIEEILDIGLAKAMEET	650

3CWB	PQ	OXIDOREDUCTASE	Q	2.2	12.9	6	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	651
3HOY	DG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	6.5	12.9	2	9	PFEVAQLGS	652
1AOI	AB	DNA BINDING PROTEIN/DNA	B	2.1	12.8	6	27	IYEETRGVLKVFLENVIRDAVTYTEHA	653
1B0N	AB	TRANSCRIPTION REGULATOR	B	2.6	12.8	5	13	QEWVELMVEAKEA	654
1E1H	AB	HYDROLASE	B	2.6	12.8	5	8	FEELRTFG	655
1F99	MN	PHOTOSYNTHESIS	M	2.6	12.8	5	27	NTELQVVNGRYNRATSSLEAAKALTAN	656
1JTH	CB	ENDOCYTOSIS/EXOCYTOSIS	B	1.6	12.8	8	66	LSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAV DYVERAVSDTKKAVKY	657
1NIK	CK	TRANSCRIPTION	K	2.1	12.8	6	29	PKDALKNACNSIINKLGALKTNFETEWNL	658
1V29	AB	LYASE	A	1.8	12.8	7	18	QSFWEARAKALESLLIEK	659
1YMM	AB	IMMUNE SYSTEM	B	6.4	12.8	2	9	YCRHNYGVV	660
2DYM	AB	PROTEIN TURNOVER/PROTEIN TURNOVER	B	1.8	12.8	7	18	MDDLLIRRLTDRNDKEAH	661
2I2P	CN	RIBOSOME	C	2.1	12.8	6	22	TKEFADNLDSDFKVRQYLTKEL	662
2IBZ	CF	OXIDOREDUCTASE	C	2.1	12.8	6	36	VPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	663
2P22	AC	TRANSPORT PROTEIN	A	3.2	12.8	4	30	DGLNQLYNLVAQDYALTDTIECLSRMLHRG	664
2QJK	JK	ELECTRON TRANSPORT	K	2.1	12.8	6	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	665
3DVU	AC	VIRAL PROTEIN/APOPTOSIS	C	1.8	12.8	7	20	GTMENLSRRLKVTGDLFDIM	666
3GE8	DF	OXIDOREDUCTASE	D	3.2	12.8	4	22	YPEYVSIQREKDAGAYSVKAAL	667
1JFI	AB	TRANSCRIPTION/DNA	A	1.8	12.7	7	27	AAVPVIISRALELFLESLLKKACQVTQ	668
1KYO	DF	OXIDOREDUCTASE/ELECTRON TRANSPORT	F	3.2	12.7	4	22	VEEFFHLQHYLDTATAPRLFDK	669
1MTY	DG	MONOOXYGENASE	G	3.2	12.7	4	9	LEELRKQRG	670
1NIK	CK	TRANSCRIPTION	C	1.8	12.7	7	25	VDQVVVRGIDTLQKKVASILLALTQ	671
1OQP	AB	PROTEIN BINDING	B	2.5	12.7	5	14	KRELIESKWHRLLF	672
1SQX	CD	OXIDOREDUCTASE	C	2.1	12.7	6	24	YYTIKDILGALLLILALMLLVLFA	673
1T3L	AB	TRANSPORT PROTEIN	B	3.2	12.7	4	15	LEEDLRGYMSWITQG	674
2DFS	AE	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	A	1.6	12.7	8	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRD ATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	675
2F8N	HG	STRUCTURAL PROTEIN/DNA	H	2.1	12.7	6	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	676
2W0C	ER	VIRUS	R	12.7	12.7	1	23	TGLDALISGWARVEQIKAAKAST	677
2ZU0	AC	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	A	3.2	12.7	4	10	DEQIFYLRSR	678
3B5N	IL	MEMBRANE PROTEIN	I	1.8	12.7	7	57	AELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFKRG ANRVRKAMW	679
3C1B	EF	STRUCTURAL PROTEIN/DNA	F	1.8	12.7	7	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	680
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	B	6.3	12.6	2	6	PIEVIW	681

1OCC	AL	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	L	1.8	12.6	7	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	682
1OCC	NY	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Y	1.8	12.6	7	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	683
1OR0	CD	HYDROLASE	C	6.3	12.6	2	5	PGRTL	684
1UM9	AB	OXIDOREDUCTASE	B	6.3	12.6	2	5	LRYRS	685
1WA8	AB	TUBERCULOSIS	A	4.2	12.6	3	34	AATLAQEAGNFERISGDLKTQIDQVESTAGSLQG	686
1XL3	BD	CELL INVASION	B	4.2	12.6	3	6	FWQFFS	687
2FJ7	BD	STRUCTURAL PROTEIN/DNA	D	6.3	12.6	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	688
2GGM	BD	CELL CYCLE	D	3.2	12.6	4	11	WKLLAKGLLIR	689
2PQR	AC	APOPTOSIS	C	3.2	12.6	4	15	LFEGFKATVSIIQQR	690
2VOY	GI	HYDROLASE	I	12.6	12.6	1	7	ALEVAEK	691
2WJV	BE	HYDROLASE	E	2.1	12.6	6	20	DEDFIQALDKMMLENLQQRS	692
3B5N	EF	MEMBRANE PROTEIN	E	1.8	12.6	7	57	AELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFKRGANRVRKAMW	693
3CJH	IL	PROTEIN TRANSPORT	L	2.1	12.6	6	28	SQEEQCLSNCVNRFLDTNIRIVNGLQNT	694
3G43	CE	METAL BINDING PROTEIN	E	2.5	12.6	5	44	TLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLDQV	695
3GE8	DF	OXIDOREDUCTASE	F	2.5	12.6	5	19	LRYLFHCLQMSSAYVQQMA	696
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.1	12.6	6	35	PQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKA	697
1FS2	AD	LIGASE	A	4.2	12.5	3	8	DPIVNTLA	698
1GXS	AB	LYASE	B	3.1	12.5	4	10	AVFNSINYLN	699
1HBM	BC	METHANOGENESIS	B	1.8	12.5	7	17	VSSTLLYYNDLIEFETG	700
1KD8	CD	DE NOVO PROTEIN	C	1.3	12.5	10	34	VKQLEAEVEEIESEVWHLENEVARLEKENAECEA	701
1M56	AB	OXIDOREDUCTASE	A	2.1	12.5	6	30	LTQQSYFMMATMVIAVPTGIKIFSWIATMW	702
1XME	BC	OXIDOREDUCTASE	B	2.5	12.5	5	35	HKAHKAILAYEKGWLAFSLAMLFVFIALIAYTLAT	703
1YE9	JN	OXIDOREDUCTASE	J	2.1	12.5	6	12	PETLHNVMWAMS	704
1YTZ	TI	CONTRACTILE PROTEIN	I	1.8	12.5	7	41	SMQELQELSKKLHAKIDSVDEERYDTEVKLQKTNKELEDLS	705
1ZBB	GH	STRUCTURAL PROTEIN/DNA	H	1.8	12.5	7	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	706
2DD4	BC	HYDROLASE	C	1.8	12.5	7	16	DFEILEMAVRELAIEK	707
2Q9Q	CD	REPLICATION	C	4.2	12.5	3	38	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	708
2QJP	JK	ELECTRON TRANSPORT	K	2.5	12.5	5	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	709
2V36	AB	TRANSFERASE	A	2.5	12.5	5	21	WEKYQLLAETMHLSYADRASY	710
3B5N	AB	MEMBRANE PROTEIN	A	1.8	12.5	7	60	SRTAELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFKRGANRVRKAMW	711
3CK4	EF	PROTEIN BINDING	E	1.8	12.5	7	29	VKQLVDKVEELLSKNYHLVNEVARLVKLV	712
1AOI	EF	DNA BINDING PROTEIN/DNA	F	2.1	12.4	6	27	IYEETRGVLKVFLENVIRDAVTYTEHA	713
1XK4	FH	METAL BINDING PROTEIN	F	2.1	12.4	6	18	ELEKALNSIIDVYHKYSL	714
1ZBB	ef	STRUCTURAL PROTEIN/DNA	e	2.1	12.4	6	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	715
2BA1	DG	RNA BINDING PROTEIN	D	4.1	12.4	3	35	RDEVKQAIELAKKGALQIYEMQREAILRRYIEVGE	716

2BEX	AC	HYDROLASE/INHIBITOR	C	6.2	12.4	2	9	WAQWFETQH	717
2DXB	EF	HYDROLASE	F	1.8	12.4	7	16	DFEILEMAVRELAIEK	718
2F9I	AB	TRANSFERASE	B	1.8	12.4	7	20	IISLMQMGKTSVSLKRHSDA	719
2QJY	JK	OXIDOREDUCTASE	K	2.1	12.4	6	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	720
2ROD	AB	APOPTOSIS	B	2.5	12.4	5	19	EFAAQLRKIGDKVYCTWSA	721
2ZJS	YE	PROTEIN TRANSPORT/IMMUNE SYSTEM	E	1.8	12.4	7	27	QVVEGTQAILLFTLAFMVILGLYDTVF	722
3CK4	HG	PROTEIN BINDING	H	2.1	12.4	6	29	VKQLVDKVEELLSKNYHLVNEVARLVKLV	723
1AHJ	AB	LYASE	B	2.5	12.3	5	18	EWEHLPYSLMFAGVAELG	724
1BCC	CD	OXIDOREDUCTASE	C	2.5	12.3	5	27	FHPYYSFKDILGLTLMLTPFLTLALFS	725
1E6Y	EF	OXIDOREDUCTASE	F	2.1	12.3	6	20	AEVVEWVHRIFDQRTKFGFQ	726
1FYZ	BF	OXIDOREDUCTASE	B	2.1	12.3	6	10	QWGERMWLAE	727
1G72	CD	OXIDOREDUCTASE	D	1.5	12.3	8	19	KQEESIKAMDARNAKRIAN	728
1IZN	CD	PROTEIN BINDING	C	2.5	12.3	5	37	DVQTAKEFIKIIENAENEYQTAISENYQTMSDTTFKA	729
1IZN	CD	PROTEIN BINDING	D	2.1	12.3	6	25	HIANIGRLVEDMENKIRSTLNEIYF	730
1KX4	AB	STRUCTURAL PROTEIN/DNA	A	2.5	12.3	5	16	KLPFQRLVREIAQDFK	731
2BC4	CD	IMMUNE SYSTEM	C	2.1	12.3	6	20	GDAPAILFDKEFCEWMIQQI	732
2EC6	AC	CONTRACTILE PROTEIN	C	12.3	12.3	1	6	NEDVFA	733
2GUZ	EF	CHAPERONE, PROTEIN TRANSPORT	F	2.1	12.3	6	23	FYLQSKVYRAAERLKWELAQREK	734
3A0B	ef	ELECTRON TRANSPORT	f	6.2	12.3	2	17	TLAVPTIFFLGAIAAMQ	735
3BXK	AB	MEMBRANE PROTEIN, SIGNALING PROTEIN	B	2.1	12.3	6	16	IYAAMMIMEYYRQSKA	736
3CXH	CD	OXIDOREDUCTASE	D	2.5	12.3	5	36	EHDERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	737
1E6Y	BC	OXIDOREDUCTASE	C	2.0	12.2	6	20	AEVVEWVHRIFDQRTKFGFQ	738
1G72	AB	OXIDOREDUCTASE	B	1.7	12.2	7	19	KQEESIKAMDARNAKRIAN	739
1ZBB	gh	STRUCTURAL PROTEIN/DNA	h	1.7	12.2	7	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	740
2BZW	AB	TRANSCRIPTION	B	2.4	12.2	5	20	WAAQRYGRELRRMSDEFEGS	741
2DXB	QR	HYDROLASE	Q	2.4	12.2	5	16	IWELNTFATCECLAWR	742
2F9I	CD	TRANSFERASE	D	2.0	12.2	6	20	IISLMQMGKTSVSLKRHSDA	743
2GGM	AC	CELL CYCLE	C	3.1	12.2	4	16	WKLLAKGLLIRERLKR	744
2GV5	EF	CELL CYCLE	F	2.0	12.2	6	16	LKKFRERLLEIVKSEE	745
2PQN	AB	APOPTOSIS	B	2.4	12.2	5	16	LFQGFKSYLPIAELAI	746
2VJM	AB	TRANSFERASE	A	1.7	12.2	7	14	RIKLRDQQRLERTG	747
2VJM	AB	TRANSFERASE	B	1.7	12.2	7	14	RIKLRDQQRLERTG	748
2Z2T	AD	VIRAL PROTEIN/INHIBITOR	D	2.0	12.2	6	31	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK	749
3B5N	BC	MEMBRANE PROTEIN	B	1.4	12.2	9	68	LAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVED AQLDVEQGVGHTDKAVKSAR	750
3C1B	EF	STRUCTURAL PROTEIN/DNA	E	2.0	12.2	6	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	751
3C1B	EF	STRUCTURAL PROTEIN/DNA	F	3.1	12.2	4	11	KPAIRRLARRG	752
3C7B	DE	OXIDOREDUCTASE	E	1.7	12.2	7	15	IYTVRELCDIADKYS	753

1E6V	AC	OXIDOREDUCTASE	C	1.7	12.1	7	20	EELLQVVQRIHELRTLAGYR	754
1LRW	AB	OXIDOREDUCTASE	B	2.0	12.1	6	29	PAELSKQGESLAVMDARNEWRVWNMKKTG	755
1OR0	CD	HYDROLASE	C	2.4	12.1	5	16	APSAFYGYGWAQARSH	756
2IY1	AB	HYDROLASE/NUCLEAR PROTEIN	A	4.0	12.1	3	15	DEIINFYMNMLMERS	757
2QJK	MN	ELECTRON TRANSPORT	N	2.4	12.1	5	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	758
2QM6	AB	TRANSFERASE	A	2.4	12.1	5	22	SKNIHIAAEAMRQAYADRSVYM	759
2ROC	AB	APOPTOSIS	B	2.4	12.1	5	25	EEWAREIGAQLRRIADDLNAQYERR	760
3BL2	AC	VIRAL PROTEIN/APOPTOSIS	C	2.4	12.1	5	17	MENLSRRLKVTGDLFDI	761
3DTU	AB	OXIDOREDUCTASE	B	2.0	12.1	6	35	PVATQIHWLDGFILVIIAAITIFVTLLILYAVWRF	762
3EAB	FL	CELL CYCLE	L	2.0	12.1	6	20	SVGTSVASAEQDELSQRLAR	763
3EX7	AB	HYDROLASE/RNA BINDING PROTEIN/RNA	A	2.4	12.1	5	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	764
3GTM	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	1.7	12.1	7	30	PKDALKNACNSIINKLGALKTNFETEWNLQ	765
3H0L	AC	LIGASE	A	2.0	12.1	6	19	YLKAQKVRRLITNDFLKAF	766
1AHJ	GH	LYASE	H	2.4	12.0	5	14	LPYSLMFAGVAELG	767
1BCC	CD	OXIDOREDUCTASE	D	2.0	12.0	6	35	DHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLKSR	768
1DML	GH	DNA BINDING PROTEIN/TRANSFERASE	H	1.7	12.0	7	15	AEETRRMLHRAFDTL	769
1F99	MN	PHOTOSYNTHESIS	N	4.0	12.0	3	25	SRRMAACLRDMEIVLRYVSYAMIAG	770
1FYZ	AC	OXIDOREDUCTASE	C	1.7	12.0	7	31	DVTRVSLAFWGFDKIDIAQMIQLERGFLAKI	771
1FYZ	AE	OXIDOREDUCTASE	A	3.0	12.0	4	10	QWGERMWLAE	772
1GK0	CD	HYDROLASE	C	2.0	12.0	6	16	APSAFYGYGWAQARSH	773
1JM7	AB	ANTITUMOR	A	3.0	12.0	4	19	SQLVEELLKIICAFQLDTG	774
1LIA	AB	LIGHT HARVESTING PROTEIN	A	2.0	12.0	6	25	QEKINKCYRDIDHYMRLINYTLVVG	775
1N5W	DE	OXIDOREDUCTASE	E	4.0	12.0	3	11	RYVAADAIELV	776
1RUY	LM	VIRAL PROTEIN	M	2.4	12.0	5	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	777
1RUZ	JK	VIRAL PROTEIN	K	2.0	12.0	6	46	RRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYE	778
1WYU	AB	OXIDOREDUCTASE	A	2.4	12.0	5	19	QGVLQATFEYQTMIAELAG	779
1XL3	AC	CELL INVASION	A	4.0	12.0	3	6	FWQFFS	780
2A6Q	CF	TOXIN INHIBITOR/TOXIN	C	2.0	12.0	6	16	PANARRLMDSIDSLKS	781
2BL0	AC	MUSCLE PROTEIN	A	3.0	12.0	4	12	AWWKLFAKARPL	782
2C52	AB	TRANSFERASE	B	12.0	12.0	1	7	ELDRALG	783
2DF4	AC	LIGASE	A	1.7	12.0	7	26	YYDAYYKKSQKVRTLIKNDFDKVFEN	784
2EC6	AB	CONTRACTILE PROTEIN	A	3.0	12.0	4	9	VIQRNIRKW	785
2P24	AB	IMMUNE SYSTEM	A	1.7	12.0	7	22	PQGGLQNIATGKHNLGVLTKRS	786
2PI2	BF	REPLICATION, DNA BINDING PROTEIN	B	1.7	12.0	7	23	MNEFTTHILEVINAHMVLSKANS	787
2QL2	AB	TRANSCRIPTION/DNA	B	2.0	12.0	6	19	KIETLRLAKNYIWALSEIL	788
3A0B	lt	ELECTRON TRANSPORT	t	12.0	12.0	1	9	CIIALFFFA	789

3CXH	CH	OXIDOREDUCTASE	H	2.4	12.0	5	29	KSQFLYVLIPAGIYWYWWKNGNEYNEFLY	790
3EQS	AB	LIGASE	B	3.0	12.0	4	9	FAEYWNLLS	791
3GE8	AB	OXIDOREDUCTASE	B	3.0	12.0	4	11	QGLRELMEKQL	792
1DCE	CD	TRANSFERASE	C	4.0	11.9	3	15	YSSWHYRSCLLPQLH	793
1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.4	11.9	5	15	EIDNLALLTALKDKY	794
1FOE	CD	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	C	4.0	11.9	3	8	KVASHINE	795
1FYZ	AC	OXIDOREDUCTASE	A	3.0	11.9	4	32	PKWNETMKVVSNFLEVGEYNAIAATGMLWDSA	796
1FYZ	BD	OXIDOREDUCTASE	B	2.0	11.9	6	31	AEQKNGYLAQVLDEIRHTHQCAYVNYYFAKN	797
1H4J	AB	OXIDOREDUCTASE	B	2.0	11.9	6	24	KQADSIKQMEERNKKRVENFKKTG	798
1HL6	AB	SIGNAL PROTEIN	B	3.0	11.9	4	27	PEGLRCFYYLVQDLKCLVFSLIGLHFK	799
1IHF	AB	TRANSCRIPTION/DNA	B	2.4	11.9	5	21	AKTVEDAVKEMLEHMASTLAQ	800
1L9B	LM	PHOTOSYNTHESIS	M	2.4	11.9	5	14	TAAERAALFWRWTM	801
1N86	EF	BLOOD CLOTTING	F	4.0	11.9	3	14	SSIRYLQEIYNSNN	802
1U35	AB	STRUCTURAL PROTEIN/DNA	A	2.0	11.9	6	29	SSAVMALQEACEAYLVGLFEDTNLCAIHA	803
1XK4	EG	METAL BINDING PROTEIN	E	2.4	11.9	5	18	ELEKALNSIIDVYHKYSL	804
1YR5	AB	METAL BINDING PROTEIN/TRANSFERASE	B	1.7	11.9	7	16	KWKQSVRLISLCQRLS	805
1ZBB	EF	STRUCTURAL PROTEIN/DNA	E	2.0	11.9	6	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	806
1ZBB	EF	STRUCTURAL PROTEIN/DNA	F	3.0	11.9	4	11	KPAIRRLARRG	807
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	G	2.0	11.9	6	29	AGAPVYLAAVLEYLTAEILELAGNWERDN	808
2AFF	AB	CELL CYCLE	B	3.0	11.9	4	14	PTFLERRKSQVAEL	809
2DXB	EF	HYDROLASE	E	2.4	11.9	5	16	IWELNTFATCECLAWR	810
2F66	DF	TRANSPORT PROTEIN	D	2.4	11.9	5	29	DGLNQLYNLVAQDYALTDTIEALSRMLHR	811
2JE6	AB	HYDROLASE	A	2.0	11.9	6	18	ENAIELARVVDRSLRDSK	812
2NQB	EF	STRUCTURAL PROTEIN/DNA	E	2.0	11.9	6	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	813
2NQB	EF	STRUCTURAL PROTEIN/DNA	F	3.0	11.9	4	11	KPAIRRLARRG	814
3B5N	AB	MEMBRANE PROTEIN	B	2.4	11.9	5	68	LAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVED AQLDVEQGVGHTDKAVKSAR	815
3B5N	EF	MEMBRANE PROTEIN	F	2.0	11.9	6	67	LAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVED AQLDVEQGVGHTDKAVKSA	816
3B5N	FG	MEMBRANE PROTEIN	G	1.3	11.9	9	68	SIKFTKQSSVASTRNTLKMAQDAERAGMNTLGMLGHQSEQLNNVEGN LDLMKVQNKVADEKVAELKKL	817
3CK4	DC	PROTEIN BINDING	D	1.5	11.9	8	32	VKQLVDKVEELLSKNYHLVNEVARLVKLVGER	818
1E6V	DF	OXIDOREDUCTASE	F	1.7	11.8	7	20	EELLQVVQRIHELRTLAGYR	819
1F66	CD	STRUCTURAL PROTEIN/DNA	C	2.0	11.8	6	26	AAVYSAAILEYLTAEVLELAGNASKD	820
1L9J	RS	PHOTOSYNTHESIS	S	3.0	11.8	4	29	GLWLIASFFMFVAVWSWWGRTYLRAQALG	821
1SXJ	DE	REPLICATION	D	5.9	11.8	2	15	EHIQLLNLLVKISQL	822
3CXH	DF	OXIDOREDUCTASE	F	3.0	11.8	4	17	VEEFFHLQHYLDTATAP	823

1FOE	EF	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	E	5.9	11.7	2	8	IKPIQRVL	824
1G2C	OR	VIRAL PROTEIN	R	2.0	11.7	6	32	SDEFDASISQVNEKINQSLAFIRKSDELLHNV	825
1GXS	AB	LYASE	B	2.9	11.7	4	14	PAQAFLLFKQFLKG	826
1LTX	AB	TRANSFERASE/PROTEIN BINDING	A	11.7	11.7	1	11	YGTWHHRCWLL	827
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	2.3	11.7	5	14	TAVERAALFWRWTI	828
1Q7L	CD	HYDROLASE	D	2.0	11.7	6	19	EAVFLRGVDIYTRLLPALA	829
1XK4	AC	METAL BINDING PROTEIN	A	2.3	11.7	5	18	ELEKALNSIIDVYHKYSL	830
2BBA	AP	SIGNALING PROTEIN	P	3.9	11.7	3	6	PIARAW	831
2FYN	DE	OXIDOREDUCTASE	D	2.0	11.7	6	24	YFIIKDVFALAVVLLVFFAIVGFM	832
2GUZ	GH	CHAPERONE, PROTEIN TRANSPORT	H	2.3	11.7	5	23	FYLQSKVYRAAERLKWELAQREK	833
2GUZ	IJ	CHAPERONE, PROTEIN TRANSPORT	J	2.3	11.7	5	23	FYLQSKVYRAAERLKWELAQREK	834
2PQR	BD	APOPTOSIS	D	2.9	11.7	4	13	LFEGFKATVSIIQ	835
3FKU	IJ	VIRAL PROTEIN/IMMUNE SYSTEM	J	2.3	11.7	5	40	GFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	836
1AOI	AB	DNA BINDING PROTEIN/DNA	A	1.9	11.6	6	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	837
1F66	EF	STRUCTURAL PROTEIN/DNA	F	1.9	11.6	6	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	838
1FOS	EF	TRANSCRIPTION/DNA	F	1.9	11.6	6	56	KRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQV AQLKQKVM	839
1SFC	IL	TRANSPORT PROTEIN	I	1.3	11.6	9	63	RRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGAS QFETSAAKLKRKYWWKN	840
1TBG	BF	COMPLEX (GTP-BINDING/TRANSDUCER)	F	2.3	11.6	5	14	VSKCCEEFRDYVEE	841
1UZD	VC	LYASE	V	3.9	11.6	3	20	WRDRFLFVAEAIYKAQAETG	842
1VOQ	MS	RIBOSOME	M	11.6	11.6	1	5	YRGLR	843
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	E	1.9	11.6	6	21	DRKVAMGFLAATILIVVMAMS	844
1ZBB	ef	STRUCTURAL PROTEIN/DNA	f	2.9	11.6	4	11	KPAIRRLARRG	845
2DXB	NO	HYDROLASE	O	1.9	11.6	6	16	DFEILEMAVRELAIEK	846
2DXB	QR	HYDROLASE	R	1.7	11.6	7	16	DFEILEMAVRELAIEK	847
2FFD	AB	BLOOD CLOTTING	A	1.5	11.6	8	33	EKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRS	848
2GUZ	AB	CHAPERONE, PROTEIN TRANSPORT	B	2.3	11.6	5	23	FYLQSKVYRAAERLKWELAQREK	849
2NP0	AB	HYDROLASE	B	1.9	11.6	6	13	FAKLKEKFFNEIN	850
2NPS	AB	TRANSPORT PROTEIN	B	1.7	11.6	7	63	RETAIQQLEADILDVNQIFKDLAMMIHDQGDLIDSIEANVESSEVHVER ASDQLQRAAYYQKK	851
2Q9Q	FG	REPLICATION	F	2.3	11.6	5	31	LKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	852
2QJK	JK	ELECTRON TRANSPORT	J	2.3	11.6	5	24	YFIIKDVFALAVVLLVFFAIVGFM	853
3D5O	CF	IMMUNE SYSTEM	C	3.9	11.6	3	10	PENILSAYQG	854
3EAB	EK	CELL CYCLE	K	1.9	11.6	6	20	GSVGTSVASAEQDELSQRLA	855
3EQY	BD	ONCOPROTEIN	D	3.9	11.6	3	8	FAEYWNLL	856
3GFK	AB	TRANSCRIPTION/TRANSFERASE	B	1.9	11.6	6	10	VRSYNCLKRA	857

3HOU	PS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	P	5.8	11.6	2	13	KDLKNTMQYLTNF	858
1AHJ	CD	LYASE	C	2.3	11.5	5	15	VSDRAWALFRALDGK	859
1BIQ	AB	OXIDOREDUCTASE	B	2.3	11.5	5	27	PELETWVETWAFSETIHSRSFTHIIRN	860
1CP9	AB	HYDROLASE	A	2.9	11.5	4	16	TYSLFYGYGYAVAQDR	861
1E9Y	AB	HYDROLASE	B	3.8	11.5	3	6	RKEYVS	862
1KX4	AB	STRUCTURAL PROTEIN/DNA	B	2.9	11.5	4	11	KPAIRRLARRG	863
1MTY	EC	MONOOXYGENASE	E	2.3	11.5	5	31	AEQKNGYLAQVLDEIRHTHQCAYVNYYFAKN	864
1MZN	AB	TRANSCRIPTION	B	1.9	11.5	6	9	KILHRLLQD	865
1SFC	EF	TRANSPORT PROTEIN	E	1.4	11.5	8	64	LQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFE TSAAKLKRKYWWKNLKM	866
1ZBB	ab	STRUCTURAL PROTEIN/DNA	a	2.3	11.5	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	867
1ZBB	AB	STRUCTURAL PROTEIN/DNA	A	2.3	11.5	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	868
2DFS	MS	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	1.6	11.5	7	29	LARVHYHRTLKAIVYLQCCYRRMMAKREL	869
2DXB	BC	HYDROLASE	B	1.6	11.5	7	16	IWELNTFATCECLAWR	870
2PJR	AB	HYDROLASE/DNA	A	2.9	11.5	4	12	KRILQAANEVIE	871
2Q9Q	AB	REPLICATION	B	2.9	11.5	4	18	PAELIERLEQAWMNEKFA	872
2QFA	BC	CELL CYCLE/CELL CYCLE/CELL CYCLE	C	2.3	11.5	5	39	PIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFT	873
3BS5	AB	SIGNALING PROTEIN/MEMBRANE PROTEIN	B	2.3	11.5	5	19	IGHQELILEAVDLLCALNY	874
3CK4	LK	PROTEIN BINDING	L	1.6	11.5	7	30	KVKQLVDKVEELLSKNYHLVNEVARLVKLV	875
3DTU	CD	OXIDOREDUCTASE	D	1.9	11.5	6	35	PVATQIHWLDGFILVIIAAITIFVTLLILYAVWRF	876
3EAB	DJ	CELL CYCLE	D	2.3	11.5	5	28	SMEAERVRVFHKQAFEYISIALRIDEDE	877
3H32	DE	BLOOD CLOTTING	D	1.6	11.5	7	41	VLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSC	878
1BCC	CD	OXIDOREDUCTASE	C	11.4	11.4	1	13	LAFSSVAHTCRNV	879
1F66	AB	STRUCTURAL PROTEIN/DNA	B	2.9	11.4	4	11	KPAIRRLARRG	880
1H3O	AB	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	A	1.6	11.4	7	22	VVSYVSHATQQRLQNLVEKISE	881
1IRE	AB	LYASE	B	2.3	11.4	5	16	EWEKVAFAMFPATFRA	882
1JB7	AB	DNA-BINDING PROTEIN/DNA	B	1.9	11.4	6	23	DEFKTTIQHFRHTALQAAINKTV	883
1OED	AB	ION CHANNEL/RECEPTOR	A	3.8	11.4	3	27	YFVVNVIIPCLLFSFLTGLVFYLPTDS	884
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	B	1.9	11.4	6	14	KTGHAVRAIGRLSS	885
1XDK	AB	HORMONE/GROWTH FACTOR RECEPTOR	B	2.9	11.4	4	7	MFPKILM	886
1Y3A	BF	SIGNALING PROTEIN	F	2.9	11.4	4	7	WYDFLME	887
1YV0	IC	CONTRACTILE PROTEIN	C	5.7	11.4	2	8	IEELGEIL	888
1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	E	1.9	11.4	6	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	889
2IBZ	CF	OXIDOREDUCTASE	F	5.7	11.4	2	19	PVLSKLCVPVANQFINLAG	890
2NQB	CD	STRUCTURAL PROTEIN/DNA	D	2.3	11.4	5	29	SKAMSIMNSFVNDIFERIAAEASRLAHYN	891

3B5N	BC	MEMBRANE PROTEIN	C	1.4	11.4	8	68	SIKFTKQSSVASTRNTLKMAQDAERAGMNTLGMLGHQSEQLNNVEGN LDLMKVQNKVADEKVAELKKL	892
3C1B	AB	STRUCTURAL PROTEIN/DNA	A	2.3	11.4	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	893
3EQY	AC	ONCOPROTEIN	C	3.8	11.4	3	8	FAEYWNLL	894
3GE8	DF	OXIDOREDUCTASE	F	1.9	11.4	6	32	STISNCCILQTADSLRWLTHTAYRTHELSLTY	895
3H0L	AC	LIGASE	C	2.3	11.4	5	18	EEEIEVFQKQLSDILDFI	896
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.9	11.4	6	35	PQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKA	897
1ALL	AB	LIGHT HARVESTING PROTEIN	A	2.8	11.3	4	25	ADMTATCLRDLDYYLRLITYGIVAG	898
1AVO	MN	PROTEASOME ACTIVATOR	N	2.3	11.3	5	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	899
1CM1	AB	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	B	1.6	11.3	7	16	ARRKLKGAILTTMLAT	900
1JY2	NP	BLOOD CLOTTING	N	2.8	11.3	4	27	GCRMKGLIDEVDQDFTSRINKLRDSLF	901
1JY2	QS	BLOOD CLOTTING	S	1.9	11.3	6	27	TCGIADFLNNYQTSVDKDLRTLEGILY	902
1KX4	AB	STRUCTURAL PROTEIN/DNA	B	2.3	11.3	5	27	IYEETRGVLKVFLENVIRDAVTYTEHA	903
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	1.9	11.3	6	31	AEQKNGYLAQVLDEIRHTHQCAYVNYYFAKN	904
1QHH	BC	HYDROLASE	B	1.9	11.3	6	15	KEIKDILAYLRVIAN	905
1RF8	AB	BIOSYNTHETIC PROTEIN, TRANSLATION	A	11.3	11.3	1	15	IDELWLCTLLAVIGE	906
1U35	EF	STRUCTURAL PROTEIN/DNA	E	2.3	11.3	5	29	SSAVMALQEACEAYLVGLFEDTNLCAIHA	907
1V54	PW	OXIDOREDUCTASE	P	1.9	11.3	6	29	TLLMIGLTTNMLTMYQWWRDVIRESTFQG	908
1VZJ	CI	HYDROLASE	C	2.8	11.3	4	19	TLDEAERQWKAEFHRWSSY	909
1WYU	GH	OXIDOREDUCTASE	H	2.3	11.3	5	25	LEGLKKAAALAVLNARYLKELLKEK	910
2AZE	AB	CELL CYCLE, TRANSCRIPTION	B	1.6	11.3	7	35	RLEGLTQDLRQLQESEQQLDHLMNICTTQLRLLSE	911
2BG9	DE	ION CHANNEL/RECEPTOR	E	11.3	11.3	1	28	SCVEACNFIAKSTKEQNDSGSENENWVL	912
2DXB	KL	HYDROLASE	L	1.9	11.3	6	16	DFEILEMAVRELAIEK	913
2DXB	WX	HYDROLASE	X	1.9	11.3	6	16	DFEILEMAVRELAIEK	914
2F8N	DK	STRUCTURAL PROTEIN/DNA	K	2.3	11.3	5	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	915
2JBL	LM	ELECTRON TRANSPORT	L	1.9	11.3	6	29	PGHMSSVSFLFVNAMALGLHGGLILSVAN	916
2PI2	CG	REPLICATION, DNA BINDING PROTEIN	C	1.6	11.3	7	22	MNEFTTHILEVINAHMVLSKAN	917
2RAW	AB	CELL CYCLE	B	2.8	11.3	4	6	WLDYFA	918
2UVP	AB	UNKNOWN FUNCTION	B	2.3	11.3	5	19	FYDWIKEFVRDQGEFIAQQ	919
2VJH	AB	PHOTOSYNTHESIS	B	2.8	11.3	4	12	AFSKAVVSADQK	920
2Z2T	BE	VIRAL PROTEIN/INHIBITOR	E	1.6	11.3	7	31	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK	921
3BTP	AB	DNA BINDING PROTEIN, CHAPERONE	B	1.9	11.3	6	15	SLDLEMIELENFVLH	922
3C4M	AC	MEMBRANE PROTEIN	C	2.8	11.3	4	19	NSMERVEWLRKKLQDVHNF	923
3CFI	JK	PROTEIN TRANSPORT/IMMUNE SYSTEM	J	2.3	11.3	5	22	YLEQKMFAAMVADNQMAMVMLN	924

3ECH	AC	TRANSCRIPTION, TRANSCRIPTION REGULATION	C	5.7	11.3	2	7	AWDLYGE	925
3H0L	GI	LIGASE	I	1.9	11.3	6	18	EEEIEVFQKQLSDILDFI	926
3H0L	SU	LIGASE	U	2.8	11.3	4	18	EEEIEVFQKQLSDILDFI	927
3HD7	BC	EXOCYTOSIS	C	1.6	11.3	7	61	ADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNL	928
1EO8	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.9	11.2	6	51	RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQL	929
1G2C	UX	VIRAL PROTEIN	X	1.9	11.2	6	31	SDEFDASISQVNEKINQSLAFIRKSDELLHN	930
1KQF	BC	OXIDOREDUCTASE	C	2.2	11.2	5	32	MQVVRYSLLIHAAAGIILIHAILIHMYMAFWV	931
1KYO	CH	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	2.2	11.2	5	23	VLSKFFFFIFVFNFVLLGQIGAC	932
1RIW	BC	HYDROLASE/BLOOD CLOTTING	C	2.8	11.2	4	10	KKWIQKVIDQ	933
1Y3A	DH	SIGNALING PROTEIN	H	2.8	11.2	4	6	WYDFLM	934
2EHO	FH	REPLICATION	F	1.9	11.2	6	37	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY	935
2IBX	CD	VIRAL PROTEIN	D	1.9	11.2	6	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	936
2JIZ	JK	HYDROLASE	K	5.6	11.2	2	14	LTVSRARKIQRFLS	937
2NPS	CD	TRANSPORT PROTEIN	C	1.6	11.2	7	57	RLEAGYQIAVETEQIGQEMLENLSHDRERIQRARERLRETDANLGKSSRILTGMLRR	938
2VOG	AB	APOPTOSIS	B	1.9	11.2	6	20	AEVQIARKLQCIADQFHRLH	939
3DHH	AB	OXIDOREDUCTASE	B	1.9	11.2	6	32	STISNCCILQTADSLRWLTHTAYRTHELSLTY	940
3E 95	BC	LIGASE	C	2.2	11.2	5	15	RSFRLLDELERGQKG	941
3FSG	BD	HYDROLASE	D	2.8	11.2	4	16	REAVGFHFDLFLDELN	942
3G5O	AB	TOXIN/ANTITOXIN	A	2.2	11.2	5	15	ADEWESLQETLYWLA	943
3HJW	BC	ISOMERASE/RNA	B	2.8	11.2	4	12	GEYRRRWKREVL	944
1CA0	GH	COMPLEX (SERINE PROTEASE/INHIBITOR)	H	2.2	11.1	5	12	LVNWVQQTLAAN	945
1CHO	FG	COMPLEX (SERINE PROTEINASE-INHIBITOR)	G	2.2	11.1	5	11	VNWVQQTLAAN	946
1E6Y	DF	OXIDOREDUCTASE	D	1.9	11.1	6	22	LEVVKDIATESTLYGIETYEKF	947
1G0U	KL	HYDROLASE	K	2.8	11.1	4	22	AADCQFWETWLGSQCRLHELRE	948
1ICF	AB	HYDROLASE	A	3.7	11.1	3	12	EKALMKAVATVG	949
1O18	PQ	CONTRACTILE PROTEIN	Q	11.1	11.1	1	12	FTVFLTMFGEKL	950
1OR7	AC	TRANSCRIPTION	C	2.2	11.1	5	18	PEMQKTWESYHLIRDSMR	951
1SFC	IJ	TRANSPORT PROTEIN	J	1.9	11.1	6	65	EIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQ	952
1WYU	EF	OXIDOREDUCTASE	F	2.2	11.1	5	25	LEGLKKAAALAVLNARYLKELLKEK	953
1Y3A	CG	SIGNALING PROTEIN	G	2.8	11.1	4	6	WYDFLM	954

1YCR	AB	COMPLEX (ONCOGENE PROTEIN/PEPTIDE)	B	3.7	11.1	3	6	FSDLWK	955
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	D	2.2	11.1	5	27	GLIYEETRGVLKVFLENVIRDAVTYTE	956
2NZD	AB	STRUCTURAL PROTEIN/DNA	B	2.8	11.1	4	11	KPAIRRLARRG	957
2WAQ	AB	TRANSCRIPTION	A	3.7	11.1	3	12	AQDYISGAYLLT	958
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	B	2.8	11.1	4	7	AFDIISG	959
3BC1	EB	SIGNALING PROTEIN/TRANSPORT PROTEIN	B	1.9	11.1	6	29	PEFEEQEAIMKVLQRDAALKRAEEERVRH	960
3BVH	AB	BLOOD CLOTTING	B	2.2	11.1	5	23	ILENLRSKIQKLESDVSAQMEYC	961
3H32	EF	BLOOD CLOTTING	F	1.6	11.1	7	30	SIRYLQEIYNSNNQKIVNLKEKVAQLEAQC	962
3HJW	AB	ISOMERASE/RNA	A	2.8	11.1	4	15	LHDLVDYYYFWKEDG	963
1AHJ	EF	LYASE	E	2.8	11.0	4	13	YVEGWKKTFEEDF	964
1BCC	DH	OXIDOREDUCTASE	H	5.5	11.0	2	23	TEELFDFLHARDHCVAHKLFNSL	965
1CUL	AB	LYASE/LYASE/SIGNALING PROTEIN	B	1.8	11.0	6	19	LECLRLLNEIIADFDDLLS	966
1FLC	AB	HYDROLASE	B	2.2	11.0	5	43	LEIENARSEALLGELGIIRALLVGNISIGLQESLWELASEITN	967
1GH0	QR	PHOTOSYNTHESIS	R	3.7	11.0	3	25	SRRMAACLRDMEIILRYVTYAVFAG	968
1I3R	GH	IMMUNE SYSTEM	G	2.2	11.0	5	22	AQGALANIAVNKANLDVMKERS	969
1M1J	AC	BLOOD CLOTTING	C	1.6	11.0	7	56	IEQLTQKSKKIIEEIIRYENTILAHENTIQQLTDMHIMNSNKITQLKQKIAQLESH	970
1M93	AB	VIRAL PROTEIN	A	1.8	11.0	6	14	PPSISSVLTILYYG	971
1RU7	GH	VIRAL PROTEIN	H	5.5	11.0	2	9	NECMESVRN	972
1RYP	CJ	MULTICATALYTIC PROTEINASE	J	2.8	11.0	4	23	ATDVTTLNEMFRYKTNLYKLKEE	973
1SQB	CG	OXIDOREDUCTASE	C	2.2	11.0	5	22	PLSQCLFWALVADLLTLTWIGG	974
1XG2	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.8	11.0	6	22	YNSLNIYASAAFDGAGTCEDSF	975
1YTZ	IC	CONTRACTILE PROTEIN	I	1.8	11.0	6	43	KKRRAATARRQHLKSAMLQLAVTEIEKEAAAKEVEKQNYLAEH	976
1ZBB	EF	STRUCTURAL PROTEIN/DNA	F	2.2	11.0	5	27	IYEETRGVLKVFLENVIRDAVTYTEHA	977
2AL2	AB	LYASE	B	2.2	11.0	5	17	ERLAKLNQLLRIEEELG	978
2DXB	WX	HYDROLASE	X	2.2	11.0	5	14	AEDHRVWKDYVHTL	979
2IO5	BC	CHAPERONE/STRUCTURAL PROTEIN	C	1.8	11.0	6	27	IYEETRGVLKVFLENVIRDAVTYTEHA	980
2JIY	LM	PHOTOSYNTHESIS	L	2.2	11.0	5	12	PDHEDTFFRDLV	981
2NZ0	AB	MEMBRANE PROTEIN	B	3.7	11.0	3	8	WLPFARAA	982
2NZD	EF	STRUCTURAL PROTEIN/DNA	F	2.8	11.0	4	11	KPAIRRLARRG	983
2P1L	CD	APOPTOSIS	D	1.8	11.0	6	21	SGTMENLSRRLKVTGDLFDIM	984
2VJM	AB	TRANSFERASE	A	1.8	11.0	6	25	LGDSNSGMHLMIGILAALEIRHKTG	985
2ZAE	AB	HYDROLASE	B	1.6	11.0	7	26	KKEKKKIAIERIDTLFTLAERVARYS	986
3G03	AB	CELL CYCLE	B	2.8	11.0	4	9	FEHYWAQLT	987
3GE8	AB	OXIDOREDUCTASE	B	1.8	11.0	6	32	STISNCCILQTADSLRWLTHTAYRTHELSLTY	988

3HAX	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	C	2.8	11.0	4	13	GEYRRRWKREVLG	989
1AVO	IJ	PROTEASOME ACTIVATOR	J	1.6	10.9	7	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	990
1E1H	CD	HYDROLASE	D	3.6	10.9	3	9	EDNFVNFFK	991
1EYS	LM	ELECTRON TRANSPORT	M	2.7	10.9	4	28	GWWLIAGLFLTLSILLWWVRTYKRAEAL	992
1GH0	GH	PHOTOSYNTHESIS	H	3.6	10.9	3	25	SRRMAACLRDMEIILRYVTYAVFAG	993
1I3R	EF	IMMUNE SYSTEM	E	2.7	10.9	4	22	AQGALANIAVNKANLDVMKERS	994
1I3R	GH	IMMUNE SYSTEM	H	2.7	10.9	4	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	995
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	B	1.8	10.9	6	13	LDTLILVKAMGHR	996
1KYO	NO	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	1.8	10.9	6	23	FIFKDLVTVFLFMLILALFVFYS	997
1KYO	OT	OXIDOREDUCTASE/ELECTRON TRANSPORT	T	2.2	10.9	5	27	VGTIFAGAFVFQTVFDTAITSWYENHN	998
1MTY	EC	MONOOXYGENASE	C	2.2	10.9	5	25	HAPYVKDKAEEWRYTDRFLQGYSAD	999
1N73	DE	BLOOD CLOTTING	E	1.4	10.9	8	42	EVKIRIESTVAGSLRSMKSVLEHLRAKMQRMEEAIKTQKELC	1000
1OAO	BC	OXIDOREDUCTASE	B	1.8	10.9	6	29	PQVAARKILDALEYRTWKLGVHKEVAERY	1001
1SFC	KL	TRANSPORT PROTEIN	K	1.4	10.9	8	48	LVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG	1002
1TBG	AE	COMPLEX (GTP-BINDING/TRANSDUCER)	E	2.7	10.9	4	14	VSKCCEEFRDYVEE	1003
1V54	AM	OXIDOREDUCTASE	M	2.7	10.9	4	25	PKEQAIGLSVTFLSFLLPAGWVLYH	1004
1WYU	EF	OXIDOREDUCTASE	F	1.8	10.9	6	13	ELTLVRHYTGLSR	1005
1YE9	KO	OXIDOREDUCTASE	K	1.8	10.9	6	12	PETLHNVMWAMS	1006
2HDN	KL	TRANSLATION	K	2.2	10.9	5	16	KTTLTAAITTVLAKTY	1007
2JF9	BQ	TRANSCRIPTION	Q	2.2	10.9	5	9	REWFKDMLS	1008
2QJP	AB	ELECTRON TRANSPORT	B	2.7	10.9	4	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	1009
2Z2S	EF	TRANSCRIPTION	E	2.2	10.9	5	19	EAAFAELFQHFAPKVKGFL	1010
3CK4	DC	PROTEIN BINDING	C	1.6	10.9	7	30	KVKQLEDVVEELLSVNYHLENVVARLKKLV	1011
3CUE	OW	PROTEIN TRANSPORT	W	3.6	10.9	3	19	TELFTLTYGSIVAQLCQDY	1012
3FWC	JL	CELL CYCLE, TRANSCRIPTION	J	1.8	10.9	6	77	QIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQAS	1013
1DFL	AZ	CONTRACTILE PROTEIN	A	2.2	10.8	5	32	VLGNLEEMRDERLSKIISMFQAHIRGYLIRKA	1014
1DFL	BX	CONTRACTILE PROTEIN	B	2.2	10.8	5	32	VLGNLEEMRDERLSKIISMFQAHIRGYLIRKA	1015
1FOE	AB	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	A	5.4	10.8	2	8	IKPIQRVL	1016
1G0U	YZ	HYDROLASE	Y	2.7	10.8	4	22	AADCQFWETWLGSQCRLHELRE	1017
1J1D	DF	CONTRACTILE PROTEIN	F	1.8	10.8	6	37	SRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRA	1018
1KTD	CD	IMMUNE SYSTEM	C	2.2	10.8	5	22	AQGALANIAVDKANLDVMKERS	1019
1MHY	BD	OXIDOREDUCTASE	D	3.6	10.8	3	32	PRWGETMKVISNFLEVGEYNAIAASAMLWDSA	1020

1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	1.8	10.8	6	31	AEQKNGYLAQVLDEIRHTHQCAYVNYYFAKN	1021
1N86	EF	BLOOD CLOTTING	E	3.6	10.8	3	6	LRVLRS	1022
1OR0	AB	HYDROLASE	A	2.2	10.8	5	16	APSAFYGYGWAQARSH	1023
1V54	AD	OXIDOREDUCTASE	D	1.8	10.8	6	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	1024
1XK4	JL	METAL BINDING PROTEIN	J	2.2	10.8	5	20	FQEFLILVIKMGVAAHKKSH	1025
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	C	1.8	10.8	6	29	AGAPVYLAAVLEYLTAEILELAGNWERDN	1026
2B5I	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.8	10.8	6	23	TKKTQLQLEHLLLDLQMILNGIN	1027
2BR2	OP	HYDROLASE	O	1.8	10.8	6	17	NAIELARVVDRSLRDSK	1028
2G4D	AB	HYDROLASE/PROTEIN BINDING	A	3.6	10.8	3	17	DEIINFYMNMLMERSKE	1029
2P1L	EF	APOPTOSIS	F	2.2	10.8	5	21	SGTMENLSRRLKVTGDLFDIM	1030
2RAW	AB	CELL CYCLE	B	2.2	10.8	5	37	FLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILR	1031
2VE7	BD	CELL CYCLE	B	1.8	10.8	6	16	NKLFLDYTIKCYESFM	1032
2VGO	BC	TRANSFERASE	C	2.7	10.8	4	14	GNLLTQAIRQQYYK	1033
3B5N	KL	MEMBRANE PROTEIN	L	1.4	10.8	8	59	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRL	1034
3FDZ	AB	ISOMERASE	B	2.7	10.8	4	14	KRAIRTLWHVQDQM	1035
1AKH	AB	DNA BINDING PROTEIN/DNA	A	3.6	10.7	3	12	SKEKEEVAKKCG	1036
1B33	EF	PHOTOSYNTHESIS	F	3.6	10.7	3	25	TRRYAACIRDLDYYLRYATYAMLAG	1037
1D8D	AB	TRANSFERASE	A	2.1	10.7	5	13	NSVWNQRHFVISN	1038
1E6Y	AC	OXIDOREDUCTASE	A	1.8	10.7	6	22	LEVVKDIATESTLYGIETYEKF	1039
1IR2	DK	LYASE	D	3.6	10.7	3	20	WRDRFLFVAEAIYKAQAETG	1040
1KIL	CD	MEMBRANE PROTEIN	D	1.3	10.7	8	62	ARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSN KTRIDEANQRATKM	1041
1KYO	DI	OXIDOREDUCTASE/ELECTRON TRANSPORT	I	2.1	10.7	5	27	VGTIFAGAFVFQTVFDTAITSWYENHN	1042
1KYO	NO	OXIDOREDUCTASE/ELECTRON TRANSPORT	O	2.1	10.7	5	34	DERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	1043
1KYO	NR	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	2.1	10.7	5	35	PYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	1044
1MTY	EC	MONOOXYGENASE	C	1.8	10.7	6	31	DVTRVSLAFWGFDKIDIAQMIQLERGFLAKI	1045
1NLW	DE	TRANSCRIPTION/DNA	D	1.8	10.7	6	40	TLSLLTKAKLHIKKLEDSDRKAVHQIDQLQREQRHLKRQL	1046
1R8U	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	B	1.8	10.7	6	27	EKRKLIQQQLVLLLHAHKCQRREQANG	1047
1RYP	Z1	MULTICATALYTIC PROTEINASE	Z	2.7	10.7	4	22	AADCQFWETWLGSQCRLHELRE	1048
1SQX	CD	OXIDOREDUCTASE	C	5.4	10.7	2	29	GWIIRYMHANGASMFFICLYMHVGRGLYY	1049
1URQ	AD	TRANSPORT PROTEIN	D	1.5	10.7	7	60	SRENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSN KTRIDEANQRAT	1050
1V54	NP	OXIDOREDUCTASE	N	2.7	10.7	4	24	PRMNNMSFWLLPPSFLLLLASSMV	1051
1V54	YZ	OXIDOREDUCTASE	Y	1.8	10.7	6	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	1052

1YKE	CD	GENE REGULATION	C	1.8	10.7	6	39	YRPHQSRESLIMLLEEQLEYKRGEIREIEQVCKQVHDKL	1053
1YRT	AB	LAYSE, TOXIN	A	2.7	10.7	4	19	RERIDLLWKIARAGARSAV	1054
1ZBB	ef	STRUCTURAL PROTEIN/DNA	e	2.1	10.7	5	16	KLPFQRLVREIAQDFK	1055
1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	F	2.1	10.7	5	27	IYEETRGVLKVFLENVIRDAVTYTEHA	1056
2BEQ	BE	VIRAL PROTEIN	B	1.5	10.7	7	35	QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	1057
2EHO	BD	REPLICATION	B	3.6	10.7	3	35	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW	1058
2FJ7	CD	STRUCTURAL PROTEIN/DNA	C	2.7	10.7	4	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	1059
2HDN	IJ	TRANSLATION	I	1.8	10.7	6	16	KTTLTAAITTVLAKTY	1060
2NPS	BC	TRANSPORT PROTEIN	C	1.8	10.7	6	57	RLEAGYQIAVETEQIGQEMLENLSHDRERIQRARERLRETDANLGKSSRILTGMLRR	1061
2PBI	AB	SIGNALING PROTEIN	A	2.7	10.7	4	17	VTAVRKEIMYYQQALMR	1062
3B5N	GH	MEMBRANE PROTEIN	G	1.3	10.7	8	68	SIKFTKQSSVASTRNTLKMAQDAERAGMNTLGMLGHQSEQLNNVEGNLDLMKVQNKVADEKVAELKKL	1063
3CXH	NS	OXIDOREDUCTASE	S	2.7	10.7	4	28	SQFLYVLIPAGIYWYWWKNGNEYNEFLY	1064
3EAB	CI	CELL CYCLE	I	1.8	10.7	6	22	SVGTSVASAEQDELSQRLARLR	1065
3FLO	AB	TRANSFERASE	B	1.5	10.7	7	20	PLQLTSQIEHSIRAHISLYY	1066
3GHG	GI	BLOOD CLOTTING	G	2.1	10.7	5	85	QKNNKDSHSLTTNIMEILRGDFSSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSC	1067
3GZU	BJ	VIRUS	B	10.7	10.7	1	10	QLMEALMQLS	1068
3HD7	EF	EXOCYTOSIS	E	1.8	10.7	6	41	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA	1069
1NOV	BE	VIRUS	E	2.7	10.6	4	12	FWERVRSILKSG	1070
1AVO	AB	PROTEASOME ACTIVATOR	B	2.1	10.6	5	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	1071
1DE4	GI	METAL TRANSPORT INHIBITOR/RECEPTOR	G	2.7	10.6	4	28	SQMWLQLSQSLKGWDHMFTVDFWTIMEN	1072
1E1H	AB	HYDROLASE	B	3.5	10.6	3	9	EDNFVNFFK	1073
1F66	AB	STRUCTURAL PROTEIN/DNA	B	2.1	10.6	5	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	1074
1FOE	CD	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	C	3.5	10.6	3	12	KYPLLLRELFAL	1075
1KDD	BA	DE NOVO PROTEIN	A	1.5	10.6	7	34	VKQLEAEVEELESEIWHLENEVARLEKENAECEA	1076
1KIL	AB	MEMBRANE PROTEIN	A	1.5	10.6	7	50	VDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKY	1077
1KYO	CG	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	2.1	10.6	5	36	VPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	1078
1NFD	CD	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)	D	5.3	10.6	2	8	KAEIANKQ	1079
1V54	NZ	OXIDOREDUCTASE	N	1.8	10.6	6	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	1080
1WYU	AB	OXIDOREDUCTASE	B	2.1	10.6	5	25	LEGLKKAAALAVLNARYLKELLKEK	1081
2BH1	BY	TRANSPORT PROTEIN	Y	2.7	10.6	4	12	MEALVETKRVVK	1082
2HZS	DJ	TRANSCRIPTION	J	1.8	10.6	6	10	VDDVLKFTFT	1083

2NZD	EF	STRUCTURAL PROTEIN/DNA	E	2.1	10.6	5	16	KLPFQRLVREIAQDFK	1084
2OS8	AC	CONTRACTILE PROTEIN	A	2.1	10.6	5	36	IRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVLRNW	1085
2PI2	AE	REPLICATION, DNA BINDING PROTEIN	A	1.8	10.6	6	21	NEFTTHILEVINAHMVLSKAN	1086
3B5N	EH	MEMBRANE PROTEIN	E	1.5	10.6	7	57	AELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFKRG ANRVRKAMW	1087
3BC1	AB	SIGNALING PROTEIN/TRANSPORT PROTEIN	B	2.1	10.6	5	29	PEFEEQEAIMKVLQRDAALKRAEEERVRH	1088
3C60	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	C	2.1	10.6	5	22	PQGGLQNIAVVKHNLGVLTKRS	1089
3C7B	AB	OXIDOREDUCTASE	B	2.1	10.6	5	15	IYTVRELCDIADKYS	1090
3CRP	DC	PROTEIN BINDING	D	1.8	10.6	6	31	KVKQLADKVEELLSKNYHLANEVARLAKLVG	1091
3EAB	DJ	CELL CYCLE	J	2.1	10.6	5	19	GSVGTSVASAEQDELSQRL	1092
3EX7	AC	HYDROLASE/RNA BINDING PROTEIN/RNA	C	2.7	10.6	4	12	DIRILRDIEQYY	1093
3GTU	CD	TRANSFERASE	D	3.5	10.6	3	27	EEEKIRVDIIENQVMDFRTQLIRLCYS	1094
1AOI	EF	DNA BINDING PROTEIN/DNA	E	2.1	10.5	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1095
1AVO	AB	PROTEASOME ACTIVATOR	A	1.8	10.5	6	15	SYFPKKISELDAFLK	1096
1AVO	GH	PROTEASOME ACTIVATOR	H	2.1	10.5	5	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	1097
1IRE	AB	LYASE	A	2.1	10.5	5	11	TSMIDRMAEIY	1098
1IZN	AB	PROTEIN BINDING	A	2.1	10.5	5	32	DVQTAKEFIKIIENAENEYQTAISENYQTMSD	1099
1KD8	CD	DE NOVO PROTEIN	D	1.5	10.5	7	34	VKQLKAKVEELKSKLWHLKNKVARLKKKNAECKA	1100
1KX4	EF	STRUCTURAL PROTEIN/DNA	E	2.1	10.5	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1101
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	3.5	10.5	3	32	PKWNETMKVVSNFLEVGEYNAIAATGMLWDSA	1102
1NVP	BD	TRANSCRIPTION/DNA	B	2.1	10.5	5	16	EQVLMELKTLWENKLM	1103
1P27	CD	RNA BINDING PROTEIN	C	2.1	10.5	5	26	PEGLRVFYYLVQDLKCLVFSLIGLHF	1104
1V54	NZ	OXIDOREDUCTASE	Z	2.6	10.5	4	25	PKEQAIGLSVTFLSFLLPAGWVLYH	1105
1WCM	AB	TRANSCRIPTION	B	3.5	10.5	3	9	ASFLKERLM	1106
1Z6O	AM	METAL BINDING PROTEIN	A	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1107
1Z6O	BN	METAL BINDING PROTEIN	B	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1108
1Z6O	CO	METAL BINDING PROTEIN	C	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1109
1Z6O	EQ	METAL BINDING PROTEIN	E	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1110
1Z6O	FR	METAL BINDING PROTEIN	F	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1111
1Z6O	GS	METAL BINDING PROTEIN	G	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1112
1Z6O	HT	METAL BINDING PROTEIN	H	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1113
1Z6O	IU	METAL BINDING PROTEIN	I	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1114
1Z6O	JV	METAL BINDING PROTEIN	J	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1115
1Z6O	KW	METAL BINDING PROTEIN	K	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1116
1Z6O	LX	METAL BINDING PROTEIN	L	2.1	10.5	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1117
2BSK	CD	PROTEIN TRANSPORT	C	2.1	10.5	5	25	PEETTCSEHCLQKYLKMTQRISMRF	1118

2HDN	EF	TRANSLATION	E	1.8	10.5	6	16	KTTLTAAITTVLAKTY	1119
2J5G	AD	HYDROLASE	A	3.5	10.5	3	17	GKTHREFPDAFYDISRD	1120
2JIY	LM	PHOTOSYNTHESIS	L	2.6	10.5	4	29	PAHMIAISFFFTNALALALHGALVLSAAN	1121
2KA6	AB	TRANSCRIPTION REGULATOR	B	2.6	10.5	4	12	PEEFDEVSRIVG	1122
2ODY	CD	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	C	2.6	10.5	4	9	EKELFESYI	1123
2ONL	BD	TRANSFERASE	B	2.6	10.5	4	21	DDHVQFLIYQILRGLKYIHSA	1124
2QJK	DE	ELECTRON TRANSPORT	D	1.8	10.5	6	24	YFIIKDVFALAVVLLVFFAIVGFM	1125
2QJY	AB	OXIDOREDUCTASE	A	1.8	10.5	6	24	YFIIKDVFALAVVLLVFFAIVGFM	1126
2QJY	PQ	OXIDOREDUCTASE	P	2.1	10.5	5	24	YFIIKDVFALAVVLLVFFAIVGFM	1127
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	A	1.3	10.5	8	59	LGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMVNLKEKIKELHQQYKEAS	1128
3CJH	KH	PROTEIN TRANSPORT	H	1.8	10.5	6	28	SQEEQCLSNCVNRFLDTNIRIVNGLQNT	1129
1A02	FJ	TRANSCRIPTION/DNA	J	1.5	10.4	7	50	KRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQ	1130
1AOI	EF	DNA BINDING PROTEIN/DNA	F	2.6	10.4	4	11	KPAIRRLARRG	1131
1FBV	AC	LIGASE	C	1.7	10.4	6	12	RLMKELEEIRKC	1132
1IW7	NP	TRANSFERASE	N	2.6	10.4	4	23	DLNDLYRRLINRNNRLKKLLAQG	1133
1IWP	AB	LYASE	B	2.1	10.4	5	19	VRPKFMAKAALFHIKETKH	1134
1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	B	3.5	10.4	3	8	FKLSGFSF	1135
1JSM	AB	VIRAL PROTEIN	B	2.1	10.4	5	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	1136
1KFU	LS	HYDROLASE	S	2.1	10.4	5	10	IQEWLQLTMY	1137
1MF8	AB	HYDROLASE, LIGASE	A	2.1	10.4	5	12	EKVTEMLVNVLN	1138
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	B	2.1	10.4	5	32	DVTRVSLAFWGFDKIDIAQMIQLERGFLAKIV	1139
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	2.1	10.4	5	29	PAHMIAISFFFTNALALALHGALVLSAAN	1140
1RCO	BW	LYASE	B	2.6	10.4	4	20	WRDRFLFCAEALYKAQAETG	1141
1TBG	CG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	2.1	10.4	5	14	VSKCCEEFRDYVEE	1142
1V54	AM	OXIDOREDUCTASE	A	1.7	10.4	6	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	1143
1VF6	AC	PROTEIN BINDING/PROTEIN TRANSPORT	C	5.2	10.4	2	16	SQSQEDISLLLQLVQN	1144
1WCM	BC	TRANSCRIPTION	C	3.5	10.4	3	11	DEFIAHRLGLI	1145
1XEW	XY	CELL CYCLE	X	3.5	10.4	3	12	PLERRLLIDDIS	1146
1Z6O	DP	METAL BINDING PROTEIN	D	2.1	10.4	5	28	AGFSKLFKKLSDEAWSKTIDIIKHVTKR	1147
1ZLA	AB	PROTEIN BINDING/VIRUS/DNA	A	2.1	10.4	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1148
2AHM	AE	VIRAL PROTEIN, REPLICATION	E	1.7	10.4	6	23	EDKRAKVTSAMQTMLFTMLRKLD	1149
2CMR	HA	IMMUNE SYSTEM	A	3.5	10.4	3	38	LLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	1150

2DD4	BC	HYDROLASE	C	2.6	10.4	4	13	AEDHRVWKDYVHT	1151
2DFS	AG	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	A	2.6	10.4	4	29	LARVHYHRTLKAIVYLQCCYRRMMAKREL	1152
2DXB	HI	HYDROLASE	I	2.6	10.4	4	13	AEDHRVWKDYVHT	1153
2E9X	AD	REPLICATION	D	2.6	10.4	4	24	PEELAFAREFMANTESYLKNVALK	1154
2E9X	EG	REPLICATION	E	1.5	10.4	7	38	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	1155
2E9X	FH	REPLICATION	H	1.7	10.4	6	31	LKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	1156
2FK0	CD	VIRAL PROTEIN	D	1.3	10.4	8	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	1157
2NQB	GH	STRUCTURAL PROTEIN/DNA	H	1.7	10.4	6	19	ELAKHAVSEGTKAVTKYTS	1158
2PV2	DF	ISOMERASE	F	2.1	10.4	5	9	TLKFWDIFR	1159
2QJK	DE	ELECTRON TRANSPORT	E	2.6	10.4	4	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	1160
2UUN	AB	ELECTRON TRANSPORT	B	3.5	10.4	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1161
2ZJQ	GN	RIBOSOME	N	10.4	10.4	1	19	DRRNKKRDFRRLWIQRINA	1162
3C60	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	G	2.1	10.4	5	22	PQGGLQNIAVVKHNLGVLTKRS	1163
3E6P	LH	HYDROLASE	L	2.1	10.4	5	10	ERELLESYID	1164
3HRD	EF	OXIDOREDUCTASE	F	3.5	10.4	3	14	SGTAMAQIAAEELG	1165
1EJR	CA	HYDROLASE	A	2.1	10.3	5	23	PREKDKLLLFTAALVAERRLARG	1166
1EQZ	GH	STRUCTURAL PROTEIN/DNA	G	2.1	10.3	5	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	1167
1FCD	BD	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	B	2.1	10.3	5	23	DWVLEREVQYAYSWYNNIVHDTF	1168
1G2C	IL	VIRAL PROTEIN	L	1.7	10.3	6	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	1169
1GOT	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	2.6	10.3	4	15	VSKCCEEFRDYVEER	1170
1RU7	KL	VIRAL PROTEIN	L	1.7	10.3	6	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	1171
1RYP	LM	MULTICATALYTIC PROTEINASE	L	3.4	10.3	3	22	AADCQFWETWLGSQCRLHELRE	1172
1SFC	IJ	TRANSPORT PROTEIN	I	1.5	10.3	7	63	RRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN	1173
1WYU	CD	OXIDOREDUCTASE	D	2.1	10.3	5	25	LEGLKKAAALAVLNARYLKELLKEK	1174
1XK4	BD	METAL BINDING PROTEIN	B	1.7	10.3	6	20	FQEFLILVIKMGVAAHKKSH	1175
2HUE	BC	DNA BINDING PROTEIN	B	2.1	10.3	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1176
2QJY	GH	OXIDOREDUCTASE	G	2.1	10.3	5	24	YFIIKDVFALAVVLLVFFAIVGFM	1177
2QJY	GH	OXIDOREDUCTASE	H	1.7	10.3	6	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	1178
2UW1	AB	OXIDOREDUCTASE	A	2.1	10.3	5	15	MRKIEKTIQYLIGSG	1179
2V7Q	HI	HYDROLASE	I	2.1	10.3	5	14	YIRYSQICAKAVRD	1180
2Z2S	GH	TRANSCRIPTION	G	2.1	10.3	5	19	EAAFAELFQHFAPKVKGFL	1181
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	B	5.2	10.3	2	7	IEYNVEH	1182
3EAB	EK	CELL CYCLE	E	2.6	10.3	4	26	EAERVRVFHKQAFEYISIALRIDEDE	1183

3FOE	BD	ISOMERASE/DNA	D	10.3	10.3	1	7	RPLVEAG	1184
1E1C	CD	ISOMERASE	D	2.0	10.2	5	19	PYVNILRGSIATFSASVGG	1185
1EQZ	GH	STRUCTURAL PROTEIN/DNA	H	1.7	10.2	6	27	IYEETRGVLKVFLENVIRDAVTYTEHA	1186
1JTH	CD	ENDOCYTOSIS/EXOCYTOSIS	D	1.5	10.2	7	44	ETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH	1187
1VZJ	GJ	HYDROLASE	G	3.4	10.2	3	19	TLDEAERQWKAEFHRWSSY	1188
1YE9	LP	OXIDOREDUCTASE	L	3.4	10.2	3	12	PETLHNVMWAMS	1189
1Z7Q	Za	HYDROLASE/HYDROLASE ACTIVATOR	Z	2.0	10.2	5	23	AADCQFWETWLGSQCRLHELREK	1190
1ZLA	BD	PROTEIN BINDING/VIRUS/DNA	B	5.1	10.2	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	1191
2B8K	AB	TRANSFERASE	B	2.6	10.2	4	9	ASFLKERLM	1192
2BSK	AB	PROTEIN TRANSPORT	A	1.7	10.2	6	27	PEETTCSEHCLQKYLKMTQRISMRFQE	1193
2F66	AC	TRANSPORT PROTEIN	A	3.4	10.2	3	29	DGLNQLYNLVAQDYALTDTIEALSRMLHR	1194
2F8N	EF	STRUCTURAL PROTEIN/DNA	E	2.0	10.2	5	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	1195
2FJ7	GH	STRUCTURAL PROTEIN/DNA	G	2.0	10.2	5	29	AGAPVYLAAVLEYLTAEILELAGNAARDN	1196
2FUG	13	OXIDOREDUCTASE	1	5.1	10.2	2	19	TPCREGVAGFMVNLFAKIG	1197
2IAN	LM	IMMUNE SYSTEM	L	5.1	10.2	2	14	AVDTYCRHNYGVGE	1198
2J0S	CD	HYDROLASE	C	2.6	10.2	4	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	1199
2NNU	AB	TRANSCRIPTION	B	2.6	10.2	4	11	IDMNFQSDLLS	1200
2NQB	AB	STRUCTURAL PROTEIN/DNA	B	2.6	10.2	4	11	KPAIRRLARRG	1201
2P1L	AB	APOPTOSIS	B	2.0	10.2	5	21	SGTMENLSRRLKVTGDLFDIM	1202
2P22	AB	TRANSPORT PROTEIN	A	1.7	10.2	6	28	LDTFVKQGRELARQQFLVRWHIQRITSP	1203
2P22	AC	TRANSPORT PROTEIN	A	1.7	10.2	6	35	TNHHEMLQNLQTVVNELYREDVDYVADKILTRQTV	1204
2PBI	CD	SIGNALING PROTEIN	C	2.6	10.2	4	16	VTAVRKEIMYYQQALM	1205
2QJP	GH	ELECTRON TRANSPORT	G	3.4	10.2	3	24	YFIIKDVFALAVVLLVFFAIVGFM	1206
2QJY	DE	OXIDOREDUCTASE	E	2.6	10.2	4	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	1207
2SIV	AB	ENVELOPE GLYCOPROTEIN	A	2.0	10.2	5	35	GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT	1208
3B5N	AD	MEMBRANE PROTEIN	A	1.5	10.2	7	60	SRTAELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFK RGANRVRKAMW	1209
3CUE	SX	PROTEIN TRANSPORT	S	2.6	10.2	4	21	SNEYLILASTLHGVFAIASQL	1210
3DL8	BH	PROTEIN TRANSPORT	B	10.2	10.2	1	12	EGLHQAIEAKEG	1211
3G43	DE	METAL BINDING PROTEIN	E	1.7	10.2	6	44	TLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLDQV	1212
1AHJ	GH	LYASE	G	3.4	10.1	3	15	VSDRAWALFRALDGK	1213
1AHJ	GH	LYASE	G	2.5	10.1	4	13	YVEGWKKTFEEDF	1214
1AOI	AB	DNA BINDING PROTEIN/DNA	B	2.5	10.1	4	11	KPAIRRLARRG	1215
1AVO	CD	PROTEASOME ACTIVATOR	C	2.0	10.1	5	38	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	1216
1EYS	LM	ELECTRON TRANSPORT	M	2.5	10.1	4	13	AAEGAALFWRWTM	1217
1F66	GH	STRUCTURAL PROTEIN/DNA	H	2.0	10.1	5	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1218
1IR2	Y7	LYASE	7	2.5	10.1	4	14	DEQIAAQVDYIVAN	1219
1IWP	AG	LYASE	A	3.4	10.1	3	14	PWSKAFLASAYASR	1220
1KAT	WX	CELL CYCLE, HORMONE/GROWTH FACTOR	W	2.5	10.1	4	9	FMDVYQRSY	1221

1MTY	EH	MONOOXYGENASE	H	2.5	10.1	4	9	LEELRKQRG	1222
1P4E	BD	DNA BINDING PROTEIN/RECOMBINATION/DNA	D	2.0	10.1	5	14	ITDIVSSLQLQFES	1223
1QZ7	AB	CELL ADHESION	B	2.0	10.1	5	12	ESILDEHVQRVM	1224
1RU7	CD	VIRAL PROTEIN	D	2.0	10.1	5	52	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEK VKSQL	1225
1RUZ	LM	VIRAL PROTEIN	M	2.0	10.1	5	46	RRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYE	1226
1SFC	BC	TRANSPORT PROTEIN	C	1.4	10.1	7	73	ELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQL DRVEEGMNHINQDMKEAEKNLKDLG	1227
1TUE	AB	REPLICATION	A	2.0	10.1	5	11	WRPIVQFLRYQ	1228
1YL3	12	RIBOSOME	1	10.1	10.1	1	21	RNAFQTLLNAATYEYRDRRNK	1229
2BR2	UV	HYDROLASE	V	1.7	10.1	6	18	RREIELSKVIREALESAV	1230
2BYK	DC	DNA-BINDING PROTEIN	D	2.5	10.1	4	19	ESFVPSLTQDLEVYRKVVK	1231
2DFS	MQ	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	Q	2.5	10.1	4	8	DEEVDEMI	1232
2FK0	EF	VIRAL PROTEIN	F	1.7	10.1	6	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQL	1233
2INP	BL	OXIDOREDUCTASE	B	5.1	10.1	2	22	QSDEARHMTLGLEVIKFILEQH	1234
2JE6	AB	HYDROLASE	B	2.0	10.1	5	18	RREIELSKVIREALESAV	1235
2NUP	BC	PROTEIN TRANSPORT	C	2.5	10.1	4	10	DTFIQKTKKL	1236
2QJY	AB	OXIDOREDUCTASE	B	2.0	10.1	5	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	1237
2QJY	JK	OXIDOREDUCTASE	J	2.0	10.1	5	24	YFIIKDVFALAVVLLVFFAIVGFM	1238
2UUN	IJ	ELECTRON TRANSPORT	J	3.4	10.1	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1239
3B5N	IJ	MEMBRANE PROTEIN	J	2.0	10.1	5	62	EVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVEDAQ LDVEQGVGHTDKAV	1240
3CK4	AB	PROTEIN BINDING	A	1.7	10.1	6	30	KVKQLVDKVEELLSKNYHLVNEVARLVKLV	1241
3FDO	AB	CELL CYCLE	B	3.4	10.1	3	8	FEHYWAQL	1242
3H0L	JL	LIGASE	L	2.0	10.1	5	18	EEEIEVFQKQLSDILDFI	1243
3HOU	CJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	10.1	10.1	1	7	LIEKFLR	1244
1E1C	AB	ISOMERASE	B	2.5	10.0	4	24	YYVESLTRSLADAAWKEFQEVEKL	1245
1F66	AB	STRUCTURAL PROTEIN/DNA	A	2.0	10.0	5	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1246
1FQV	EF	LIGASE	E	3.3	10.0	3	9	LPELLKVSG	1247
1GH0	QR	PHOTOSYNTHESIS	Q	3.3	10.0	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	1248
1KDD	EF	DE NOVO PROTEIN	F	1.7	10.0	6	33	VKQLEAEVEELESEIWHLENEVARLEKENAECE	1249
1NH2	BD	TRANSCRIPTION/DNA	B	2.5	10.0	4	18	AEASRVYEIIVESVVNEV	1250
1R8Q	AE	PROTEIN TRANSPORT/EXCHANGE FACTOR	E	1.7	10.0	6	19	TDTCYVLSYSVIMLNTDLH	1251
1RK8	AB	TRANSLATION	B	2.5	10.0	4	26	PEGLRCFYYLVQDLKCLVFSLIGLHF	1252

1RP3	EF	TRANSCRIPTION	E	2.0	10.0	5	13	EREKLVIQLIFYE	1253
1TUE	HJ	REPLICATION	J	3.3	10.0	3	22	KETLSERLSALQDKIIDHYEND	1254
1WCM	AB	TRANSCRIPTION	A	3.3	10.0	3	19	PQEFFFHAMGGREGLIDTA	1255
1ZSZ	BC	DE NOVO PROTEIN	C	2.5	10.0	4	16	KRPYYLRGFYDWLVDN	1256
2DXB	BC	HYDROLASE	C	1.7	10.0	6	16	DFEILEMAVRELAIEK	1257
2F8N	EF	STRUCTURAL PROTEIN/DNA	F	2.5	10.0	4	11	KPAIRRLARRG	1258
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	C	2.0	10.0	5	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	1259
2NPS	AD	TRANSPORT PROTEIN	A	1.7	10.0	6	52	QVDEVIDVMQENITKVIERGERLDELQDKSESLSDNATAFSNRSKQLRRQMW	1260
2PF4	AF	HYDROLASE REGULATOR/VIRAL PROTEIN	A	10.0	10.0	1	9	QHVKSALAS	1261
2Q9Q	BC	REPLICATION	B	1.7	10.0	6	32	DLKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	1262
2Q9Q	BC	REPLICATION	C	3.3	10.0	3	22	AEEMEWFNNYKRSLATYMRSLG	1263
3CK4	IJ	PROTEIN BINDING	J	1.4	10.0	7	30	KVKQLEDVVEELLSVNYHLENVVARLKKLV	1264
3CWB	PQ	OXIDOREDUCTASE	P	2.5	10.0	4	21	YYSFKDILGLTLMLTPFLTLA	1265
3DTU	CD	OXIDOREDUCTASE	C	2.0	10.0	5	30	LTQQSYFMMATMVIAVPTGIKIFSWIATMW	1266
3DWL	IK	STRUCTURAL PROTEIN	I	2.0	10.0	5	16	MRKRVADFQKVLNRAK	1267
1A02	FJ	TRANSCRIPTION/DNA	F	1.7	9.9	6	52	RIRRERNKMAAAKSRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEK	1268
1CPC	KL	LIGHT HARVESTING PROTEIN	L	3.3	9.9	3	25	SRRMAACLRDMEIILRYVTYAIFAG	1269
1EQZ	GH	STRUCTURAL PROTEIN/DNA	H	2.5	9.9	4	11	KPAIRRLARRG	1270
1F45	AB	CYTOKINE/CYTPKINE	B	2.0	9.9	5	47	FLDQNMLAVIDELMQALYKTKIKLCILLHAFRIRAVTIDRVMSYLNA	1271
1I84	ST	CONTRACTILE PROTEIN	S	2.0	9.9	5	16	AFQAQCRGYLARKAFA	1272
1K5D	DF	SIGNALING PROTEIN/SIGNALING ACTIVATOR	D	3.3	9.9	3	11	RVTYKNVPNWH	1273
1M56	GI	OXIDOREDUCTASE	I	2.0	9.9	5	21	IWPFMASVGAFVMLFGAVLWM	1274
1M56	GI	OXIDOREDUCTASE	I	2.0	9.9	5	35	PVVRLGLRWGFILFIMSEVMFFSAWFWSFFKHALY	1275
1M63	AB	HYDROLASE/ISOMERASE	A	2.0	9.9	5	15	VFTWSLPFVGEKVTE	1276
1RU7	IJ	VIRAL PROTEIN	J	1.7	9.9	6	52	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQL	1277
1SQB	CG	OXIDOREDUCTASE	G	2.0	9.9	5	40	YFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQEFEK	1278
1TI8	AB	VIRAL PROTEIN	B	1.4	9.9	7	52	KQIGNVINWTRDSMTEVWSYNAELLVAMENQHTIDLTDSEMNKLYERVKRQL	1279
1UZD	KI	LYASE	K	2.0	9.9	5	20	WRDRFLFVAEAIYKAQAETG	1280
1V54	AB	OXIDOREDUCTASE	A	2.5	9.9	4	25	PAMMWALGFIFLFTVGGLTGIVLAN	1281
1V54	AB	OXIDOREDUCTASE	B	1.4	9.9	7	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	1282
1ZLA	AB	PROTEIN BINDING/VIRUS/DNA	B	2.5	9.9	4	11	KPAIRRLARRG	1283
1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	F	2.5	9.9	4	11	KPAIRRLARRG	1284

2BR2	QR	HYDROLASE	Q	2.5	9.9	4	17	NAIELARVVDRSLRDSK	1285
2BV8	OP	PHOTOSYNTHESIS	O	3.3	9.9	3	24	ATGKAKCARDIGYYLRMVTYCLVV	1286
2F66	DF	TRANSPORT PROTEIN	F	2.0	9.9	5	26	DDLDQFIKNYLDIRTQYHLRREKLAT	1287
2FYN	JK	OXIDOREDUCTASE	J	1.7	9.9	6	24	YFIIKDVFALAVVLLVFFAIVGFM	1288
2FYN	PQ	OXIDOREDUCTASE	P	2.0	9.9	5	24	YFIIKDVFALAVVLLVFFAIVGFM	1289
2GJE	AD	TRANSLATION/RNA	D	3.3	9.9	3	6	FRQHYA	1290
2I2X	IJ	TRANSFERASE	I	5.0	9.9	2	17	RFETKALADAKAALEAL	1291
2IAN	GH	IMMUNE SYSTEM	G	2.5	9.9	4	22	KDLLEQRRAAVDTYCRHNYGVG	1292
2IBF	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	2.5	9.9	4	25	TAPVAAVQAAVSNLVRVGKETVQTT	1293
2INP	BD	OXIDOREDUCTASE	B	2.5	9.9	4	31	AGARVACQMQAIDELRHSQTQQHAMSHYNKH	1294
2ISS	AD	LYASE, TRANSFERASE	D	2.0	9.9	5	11	STTMIRILKEM	1295
2NPS	BC	TRANSPORT PROTEIN	B	1.2	9.9	8	63	RETAIQQLEADILDVNQIFKDLAMMIHDQGDLIDSIEANVESSEVHVERASDQLQRAAYYQKK	1296
2ONK	GI	MEMBRANE PROTEIN	I	5.0	9.9	2	10	VRLEHVARTL	1297
2P22	CD	TRANSPORT PROTEIN	C	2.0	9.9	5	38	TDFAGKIHAFRDQFKQLEENFEDLHEQKDKVQALLENA	1298
2PA8	DL	TRANSFERASE	D	1.4	9.9	7	27	PERILLEAGKSIIRKIEELEKKLVEVV	1299
2PJR	FG	HYDROLASE/DNA	G	2.5	9.9	4	16	DDEMEEERRLAYVGIT	1300
2QRV	AB	TRANSFERASE/TRANSFERASE REGULATOR	A	2.5	9.9	4	16	TGRLFFEFYRLLHDAR	1301
2UUN	WX	ELECTRON TRANSPORT	X	3.3	9.9	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1302
3BVH	DE	BLOOD CLOTTING	E	1.7	9.9	6	25	RSILENLRSKIQKLESDVSAQMEYC	1303
3EXG	ST	OXIDOREDUCTASE	T	2.5	9.9	4	15	IDQVINSAAKTYYMS	1304
1BH8	AB	TRANSCRIPTION REGULATION COMPLEX	B	2.0	9.8	5	29	QNVVIAMSGISKVFVGEVVEEALDVCEKW	1305
1EQZ	AB	STRUCTURAL PROTEIN/DNA	B	1.6	9.8	6	29	SKAMGIMNSFVNDIFERIAGEASRLAHYN	1306
1FCD	AC	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	A	2.5	9.8	4	19	DWVLEREVQYAYSWYNNIV	1307
1G20	CH	OXIDOREDUCTASE	C	2.5	9.8	4	7	EKDIVFG	1308
1ID3	AB	STRUCTURAL PROTEIN/DNA	A	2.0	9.8	5	29	SSAIGALQESVEAYLVSLFEDTNLAAIHA	1309
1IR2	X7	LYASE	X	3.3	9.8	3	20	WRDRFLFVAEAIYKAQAETG	1310
1JTH	CB	ENDOCYTOSIS/EXOCYTOSIS	C	1.6	9.8	6	68	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMKEAEKNL	1311
1KD8	FE	DE NOVO PROTEIN	F	1.4	9.8	7	34	VKQLEAEVEEIESEVWHLENEVARLEKENAECEA	1312
1MTY	DB	MONOOXYGENASE	B	2.0	9.8	5	32	DVTRVSLAFWGFDKIDIAQMIQLERGFLAKIV	1313
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	3.3	9.8	3	25	PFHGLSIAFLYGSALLFAMHGATIL	1314
1RM1	BC	TRANSCRIPTION/DNA	B	2.0	9.8	5	22	ASLAMRVLETFDKVVAETLKDN	1315
1TBG	DH	COMPLEX (GTP-BINDING/TRANSDUCER)	H	2.0	9.8	5	14	VSKCCEEFRDYVEE	1316
1U35	EF	STRUCTURAL PROTEIN/DNA	F	2.5	9.8	4	11	KPAIRRLARRG	1317

1UCY	HE	COMPLEX (SERINE PROTEASE/COAGULATION)	E	2.5	9.8	4	9	KKWIQKVID	1318
1V54	DE	OXIDOREDUCTASE	E	3.3	9.8	3	16	FASAVRILEVVKDKAG	1319
2BR2	OP	HYDROLASE	P	2.5	9.8	4	18	RREIELSKVIREALESAV	1320
2DXB	BC	HYDROLASE	C	2.5	9.8	4	14	AEDHRVWKDYVHTL	1321
2JIY	MH	PHOTOSYNTHESIS	H	2.0	9.8	5	24	LASLAIYSFWIFLAGLIYYLQTEN	1322
2NQB	AB	STRUCTURAL PROTEIN/DNA	A	2.5	9.8	4	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	1323
2QJP	DE	ELECTRON TRANSPORT	D	2.5	9.8	4	24	YFIIKDVFALAVVLLVFFAIVGFM	1324
2QKM	EF	HYDROLASE	E	1.6	9.8	6	18	DENILRNAVNLQVLKFHY	1325
2ZBK	GH	ISOMERASE	H	2.0	9.8	5	29	KRKEQEAKKKLLAYLKYIPEVSRSLATFL	1326
3D3C	BK	TRANSCRIPTION	B	3.3	9.8	3	21	AARRRARECAVQALYSWQLSQ	1327
3DBH	AB	CELL CYCLE	A	4.9	9.8	2	32	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS	1328
3HE6	AD	IMMUNE SYSTEM	A	4.9	9.8	2	29	NQQWEKLQHMFQVYRVSFTRDIQELVKMM	1329
1E1H	AB	HYDROLASE	A	1.9	9.7	5	17	PAVTLAHELIHAEHRLY	1330
1E1H	AB	HYDROLASE	B	1.9	9.7	5	25	SLQENEFRLYYYNKFKDVASTLNKA	1331
1FYZ	AC	OXIDOREDUCTASE	C	1.9	9.7	5	25	HAPYVKDKAEEWRYTDRFLQGYSAD	1332
1HBM	BC	METHANOGENESIS	B	3.2	9.7	3	24	LAMWNAYAAAGLMAATMVNQGAAR	1333
1HTL	AC	ENTEROTOXIN	C	2.4	9.7	4	30	DTCNEETQNLSTIYLREYQSKVKRQIFSDY	1334
1JY2	NO	BLOOD CLOTTING	N	1.6	9.7	6	27	GCRMKGLIDEVDQDFTSRINKLRDSLF	1335
1K5D	GI	SIGNALING PROTEIN/SIGNALING ACTIVATOR	G	3.2	9.7	3	11	RVTYKNVPNWH	1336
1LWU	GH	BLOOD CLOTTING	G	1.9	9.7	5	37	NMQLQQLTLLQHNIKTQVSQILRVEVDIDVALRACKG	1337
1OR0	CD	HYDROLASE	C	3.2	9.7	3	10	EQTTVWLLTN	1338
1RCO	RT	LYASE	R	1.9	9.7	5	21	NAPGAVANRVALEACVQARNE	1339
2I3S	EF	CELL CYCLE	F	2.4	9.7	4	9	TEEILAMIK	1340
2JTT	AD	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	A	2.4	9.7	4	16	FQEYITFLGALAMIYN	1341
2NQB	EF	STRUCTURAL PROTEIN/DNA	E	1.9	9.7	5	16	KLPFQRLVREIAQDFK	1342
2PA8	DL	TRANSFERASE	L	1.4	9.7	7	27	PKDALLKAIENIRGMTSHYIDEIKGLT	1343
2PMZ	DL	TRANSLATION, TRANSFERASE	D	1.9	9.7	5	24	PERILLEAGKSIIRKIEELEKKLV	1344
2QAG	BC	CELL CYCLE, STRUCTURAL PROTEIN	B	9.7	9.7	1	25	MEDLREQTHTRHYELYRRCKLEEMG	1345
2QM6	CD	TRANSFERASE	C	2.4	9.7	4	21	SKNIHIAAEAMRQAYADRSVY	1346
2UUN	UV	ELECTRON TRANSPORT	V	3.2	9.7	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1347
2UVP	AB	UNKNOWN FUNCTION	A	1.9	9.7	5	21	LDYKLLQLFKLFENALFSVLY	1348
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	A	2.4	9.7	4	40	ITAEFLVKSKHRDLTALCKEYDELAETQGKLEEKLQELEA	1349
2UZ6	EO	RECEPTOR	O	3.2	9.7	3	7	PPCILNN	1350
3B5N	EH	MEMBRANE PROTEIN	H	1.4	9.7	7	61	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRLAG	1351
3CK4	AB	PROTEIN BINDING	B	1.4	9.7	7	30	VKQLEDVVEELLSVNYHLENVVARLKKLVG	1352

3DI2	AB	CYTOKINE/CYTOKINE RECEPTOR	A	2.4	9.7	4	18	GKQYESVLMVSIDQLLDS	1353
3DWL	DF	STRUCTURAL PROTEIN	D	2.4	9.7	4	16	MRKRVADFQKVLNRAK	1354
3DWL	IK	STRUCTURAL PROTEIN	I	1.9	9.7	5	15	TDRIFGKVFLQEFVD	1355
3FWB	AB	CELL CYCLE, TRANSCRIPTION	A	1.9	9.7	5	11	IKNLRRVAKEL	1356
3H0L	MO	LIGASE	O	1.9	9.7	5	18	EEEIEVFQKQLSDILDFI	1357
1AHJ	GH	LYASE	G	1.9	9.6	5	10	FEYRARVVRE	1358
1DE4	GI	METAL TRANSPORT INHIBITOR/RECEPTOR	I	1.9	9.6	5	23	QWLYSARGDFFRATSRLTTDFGN	1359
1DX5	CO	SERINE PROTEINASE	C	2.4	9.6	4	9	ERELLESYI	1360
1E6V	AE	OXIDOREDUCTASE	A	9.6	9.6	1	6	FGVLAD	1361
1EQZ	CD	STRUCTURAL PROTEIN/DNA	D	2.4	9.6	4	11	KPAIRRLARRG	1362
1GG2	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	B	1.6	9.6	6	24	ELDQLRQEAEQLKNQIRDARKACA	1363
1KYO	OQ	OXIDOREDUCTASE/ELECTRON TRANSPORT	Q	3.2	9.6	3	17	VEEFFHLQHYLDTATAP	1364
1N86	EF	BLOOD CLOTTING	F	3.2	9.6	3	16	QKIVNLKEKVAQLEAQ	1365
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	2.4	9.6	4	12	PDHEDTFFRDLV	1366
1SFC	CD	TRANSPORT PROTEIN	C	1.4	9.6	7	73	ELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG	1367
1SXJ	CD	REPLICATION	D	1.9	9.6	5	19	TNFKNQISWLLFTTDSRLN	1368
1V54	CJ	OXIDOREDUCTASE	C	1.6	9.6	6	29	TLLMIGLTTNMLTMYQWWRDVIRESTFQG	1369
1YE9	LP	OXIDOREDUCTASE	P	2.4	9.6	4	13	FHRRELWEAIEAG	1370
1ZBB	EF	STRUCTURAL PROTEIN/DNA	E	1.9	9.6	5	16	KLPFQRLVREIAQDFK	1371
2BBM	AB	CALCIUM-BINDING PROTEIN	B	1.6	9.6	6	17	KKNFIAVSAANRFKKIS	1372
2BBV	BE	VIRUS/RNA	E	2.4	9.6	4	12	MWERVKSIIKSS	1373
2D0V	IJ	OXIDOREDUCTASE	J	1.9	9.6	5	24	KQVESRKGEEERNANRAEHFKKTG	1374
2DFS	MQ	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	Q	3.2	9.6	3	10	YEEFVQMMTA	1375
2E9X	FG	REPLICATION	G	3.2	9.6	3	23	EMERGLFQTGQKGLNDFQCWEKG	1376
2F8N	DK	STRUCTURAL PROTEIN/DNA	D	1.9	9.6	5	29	SKAMGIMNSFVNDIFERIASEASRLAHYN	1377
2FK0	OP	VIRAL PROTEIN	P	1.9	9.6	5	34	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTL	1378
2GEZ	GH	HYDROLASE	G	1.9	9.6	5	15	PLDVVELVVRELENI	1379
2JJ0	LM	PHOTOSYNTHESIS	L	1.9	9.6	5	12	PDHEDTFFRDLV	1380
2Q9Q	EH	REPLICATION	H	1.9	9.6	5	22	EMERGLFQTGQKGLNDFQCWEK	1381
2UUN	GH	ELECTRON TRANSPORT	H	3.2	9.6	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1382
2W0C	GP	VIRUS	G	9.6	9.6	1	8	DLVQQRMF	1383
2WAX	AB	HYDROLASE	A	1.9	9.6	5	12	RFNLKSIEEQLG	1384
3CXH	CH	OXIDOREDUCTASE	C	1.9	9.6	5	22	VLSKFFFFIFVFNFVLLGQIGA	1385
3CXH	NO	OXIDOREDUCTASE	O	1.9	9.6	5	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	1386
3DHH	AB	OXIDOREDUCTASE	A	2.4	9.6	4	22	YPEYVSIQREKDAGAYSVKAAL	1387

3E0J	GH	TRANSFERASE	G	2.4	9.6	4	26	TKKTQAASVEAVKMLDEILLQLSASV	1388
3H32	EF	BLOOD CLOTTING	E	1.4	9.6	7	40	DETVNSNIPTNLRVLRSILENLRSKIQKLESDVSAQMEYC	1389
3HD7	AB	EXOCYTOSIS	B	1.6	9.6	6	95	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH AVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG	1390
3HKJ	AB	HYDROLASE	A	2.4	9.6	4	10	ERELLESYID	1391
1NOV	AD	VIRUS	D	3.2	9.5	3	12	FWERVRSILKSG	1392
1BGY	PT	ELECTRON TRANSPORT	T	4.8	9.5	2	22	CTEELLDFLHARDHCVAHKLFN	1393
1DD4	BD	RIBOSOME	D	1.9	9.5	5	12	TIDEIIEAIEKL	1394
1F80	AE	TRANSFERASE	E	1.9	9.5	5	13	DVVELVMELEDEF	1395
1F8V	AD	VIRUS/RNA	D	3.2	9.5	3	13	KFWEGVLRVLNQI	1396
1GH0	KL	PHOTOSYNTHESIS	L	3.2	9.5	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1397
1GH0	ST	PHOTOSYNTHESIS	T	3.2	9.5	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1398
1GK0	AB	HYDROLASE	A	1.9	9.5	5	16	APSAFYGYGWAQARSH	1399
1IR2	GP	LYASE	G	4.8	9.5	2	20	WRDRFLFVAEAIYKAQAETG	1400
1KBH	AB	TRANSCRIPTION	B	1.9	9.5	5	17	PQLMAAFIKQRTAKYVA	1401
1KFY	CD	OXIDOREDUCTASE	C	2.4	9.5	4	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	1402
1LRW	CD	OXIDOREDUCTASE	D	1.6	9.5	6	24	KQGESLAVMDARNEWRVWNMKKTG	1403
1MMO	EH	OXIDOREDUCTASE (MONOOXYGENASE)	H	2.4	9.5	4	9	LEELRKQRG	1404
1N73	BC	BLOOD CLOTTING	C	3.2	9.5	3	47	ILEEVRILEQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	1405
1NTK	CD	OXIDOREDUCTASE	D	1.9	9.5	5	24	PEHDHRKRMGLKMLLMMGLLLPLV	1406
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	3.2	9.5	3	29	TLGIIHRLGLLLSLSAVFFSALCMIITGTI	1407
1RCO	EM	LYASE	E	2.4	9.5	4	20	WRDRFLFCAEALYKAQAETG	1408
1RP3	GH	TRANSCRIPTION	G	1.9	9.5	5	14	EREKLVIQLIFYEE	1409
1SQX	CD	OXIDOREDUCTASE	D	1.9	9.5	5	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	1410
1TUE	HJ	REPLICATION	H	1.9	9.5	5	11	WRPIVQFLRYQ	1411
1V29	AB	LYASE	B	2.4	9.5	4	16	DWERLTFGLVAGCMAQ	1412
1V54	AB	OXIDOREDUCTASE	A	1.6	9.5	6	30	VDTRAYFTSATMIIAIPTGVKVFSWLATLH	1413
1VF5	EF	PHOTOSYNTHESIS	F	9.5	9.5	1	26	EMLYAALLSFGLIFVGWGLGVLLLKI	1414
1YE9	IM	OXIDOREDUCTASE	I	2.4	9.5	4	12	PETLHNVMWAMS	1415
2A6Q	AE	TOXIN INHIBITOR/TOXIN	A	2.4	9.5	4	16	PANARRLMDSIDSLKS	1416
2AL2	AB	LYASE	A	1.6	9.5	6	17	ERLAKLNQLLRIEEELG	1417
2DD4	EF	HYDROLASE	F	1.9	9.5	5	16	DFEILEMAVRELAIEK	1418
2IBX	AB	VIRAL PROTEIN	B	1.9	9.5	5	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQL	1419
2P5T	EF	TRANSCRIPTION REGULATOR	E	1.6	9.5	6	32	PVEDYELTLKIEIVKERGANLLSRLYRYQDSQ	1420
2VML	KL	PHOTOSYNTHESIS	K	3.2	9.5	3	25	DTNQAKCARDISHYLRFITYSLVAG	1421

3B5N	IJ	MEMBRANE PROTEIN	I	1.6	9.5	6	57	AELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFKRG ANRVRKAMW	1422
3DD2	LH	HYDROLASE/RNA	L	2.4	9.5	4	10	ERELLESYID	1423
3DXR	AB	PROTEIN TRANSPORT	A	1.9	9.5	5	31	NKEQTCIMKCSEKFLKHSERVGQRFQEQNAA	1424
3E7S	AB	OXIDOREDUCTASE	A	4.8	9.5	2	19	HHAATVSFMKHLDNEQKAR	1425
3GBM	CD	VIRAL PROTEIN / IMMUNE SYSTEM	D	1.9	9.5	5	53	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQLR	1426
1BIQ	AB	OXIDOREDUCTASE	A	1.9	9.4	5	27	PELETWVETWAFSETIHSRSFTHIIRN	1427
1E1C	AB	ISOMERASE	B	1.9	9.4	5	19	DFPLRIARNTGIVLAEEVN	1428
1EQZ	GH	STRUCTURAL PROTEIN/DNA	G	1.9	9.4	5	16	KLPFQRLVREIAQDFK	1429
1G2C	ST	VIRAL PROTEIN	S	2.4	9.4	4	48	LEGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	1430
1HX1	AB	CHAPERONE/CHAPERONE INHIBITOR	A	3.1	9.4	3	18	KRAVRRLRTACERAKRTL	1431
1IAK	AP	HISTOCOMPATIBILITY ANTIGEN I-AK	A	1.9	9.4	5	22	PQGGLQNIATGKHNLEILTKRS	1432
1JTH	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.3	9.4	7	61	EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLER IEEGMDQINKDMK	1433
1JY2	QR	BLOOD CLOTTING	Q	1.6	9.4	6	27	GCRMKGLIDEVDQDFTSRINKLRDSLF	1434
1KF6	CD	OXIDOREDUCTASE	C	1.9	9.4	5	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	1435
1MHY	DG	OXIDOREDUCTASE	G	2.4	9.4	4	9	LEGLRKERG	1436
1MTY	DB	MONOOXYGENASE	D	4.7	9.4	2	8	ARRTRTIG	1437
1MVW	JK	CONTRACTILE PROTEIN	J	3.1	9.4	3	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	1438
1N8O	BC	HYDROLASE	C	1.9	9.4	5	11	VNWVQQTLAAN	1439
1NZY	CB	LYASE	C	2.4	9.4	4	16	THLQVMAKERFHAGWM	1440
1RYP	J1	MULTICATALYTIC PROTEINASE	1	1.9	9.4	5	13	ASLIMPFLDNQVN	1441
1XLS	HP	TRANSCRIPTION	P	1.9	9.4	5	9	ALLRYLLDK	1442
2D1P	AC	TRANSLATION	C	1.9	9.4	5	11	YTDFVRLTVKH	1443
2DD4	EF	HYDROLASE	E	1.9	9.4	5	16	IWELNTFATCECLAWR	1444
2DPP	AB	LYASE	A	2.4	9.4	4	15	SDAIERVIKHYEHEL	1445
2FFD	AB	BLOOD CLOTTING	B	1.9	9.4	5	36	NSNIPTNLRVLRSILENLRSKIQKLESDVSAQMEYC	1446
2HDN	AB	TRANSLATION	A	1.9	9.4	5	16	KTTLTAAITTVLAKTY	1447
2HYI	AB	HYDROLASE/RNA BINDING PROTEIN/RNA	A	1.9	9.4	5	25	GLRVFYYLVQDLKCLVFSLIGLHFK	1448
2JBL	HM	ELECTRON TRANSPORT	H	1.6	9.4	6	26	IAQLVWYAQWLVIWTVVLLYLRREDR	1449
2NNW	CD	TRANSFERASE	C	2.4	9.4	4	17	WFEEYYKVGVALTRMRI	1450
2PJR	FG	HYDROLASE/DNA	F	3.1	9.4	3	12	KRILQAANEVIE	1451
2Q0O	AC	TRANSCRIPTION	C	2.4	9.4	4	33	KSELEALAVSAIREHRRLLWADQAVYEEWLRAS	1452
2RAX	AB	CELL CYCLE	B	1.9	9.4	5	39	SFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	1453
2RAX	EF	CELL CYCLE	E	2.4	9.4	4	22	LGEFLKLDRERAKNKIAKETNN	1454
2UUN	EF	ELECTRON TRANSPORT	F	3.1	9.4	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1455
2WB1	AB	TRANSCRIPTION	B	3.1	9.4	3	17	LGQIMEGIAGKYAALSG	1456

2Z2T	AD	VIRAL PROTEIN/INHIBITOR	A	2.4	9.4	4	35	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	1457
3B5N	IL	MEMBRANE PROTEIN	L	1.6	9.4	6	59	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRL	1458
3CJT	IJ	TRANSFERASE/RIBOSOMAL PROTEIN	I	3.1	9.4	3	8	WLEAWRRD	1459
3CUE	TV	PROTEIN TRANSPORT	T	1.9	9.4	5	19	LSAMAFLFQEMISQLHRTC	1460
3DS3	AC	VIRAL PROTEIN	C	2.4	9.4	4	9	FEDLLDYYG	1461
3HOU	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.6	9.4	6	22	VVRGIDTLQKKVASILLALTQM	1462
1BGY	DJ	ELECTRON TRANSPORT	J	1.9	9.3	5	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	1463
1F66	EF	STRUCTURAL PROTEIN/DNA	F	2.3	9.3	4	11	KPAIRRLARRG	1464
1FYZ	AC	OXIDOREDUCTASE	A	1.9	9.3	5	31	AEQKNGYLAQVLDEIRHTHQCAYVNYYFAKN	1465
1G2C	CF	VIRAL PROTEIN	F	1.9	9.3	5	31	SDEFDASISQVNEKINQSLAFIRKSDELLHN	1466
1GH0	IJ	PHOTOSYNTHESIS	J	3.1	9.3	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1467
1IW7	CD	TRANSFERASE	D	3.1	9.3	3	24	VLEYFISSHGARKGGADTALRTAD	1468
1JB0	AB	PHOTOSYNTHESIS	A	3.1	9.3	3	23	SAYGLLFLGAHFIWAFSLMFLFS	1469
1JYO	CF	CHAPERONE	F	2.3	9.3	4	15	QKILQTFLHALTEKY	1470
1N86	DE	BLOOD CLOTTING	E	3.1	9.3	3	8	ILENLRSK	1471
1NIW	CD	SIGNALING PROTEIN/OXIDOREDUCTASE	D	1.9	9.3	5	14	FKEVANAVKISASL	1472
1NTK	AI	OXIDOREDUCTASE	A	9.3	9.3	1	14	MRDVVFNYLHATAF	1473
1PTO	CE	TOXIN	E	9.3	9.3	1	13	PMEVMLRAVFMQQ	1474
1RM1	BC	TRANSCRIPTION/DNA	C	1.9	9.3	5	18	AEASRVYEIIVESVVNEV	1475
1U35	AB	STRUCTURAL PROTEIN/DNA	B	1.6	9.3	6	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	1476
1U35	CD	STRUCTURAL PROTEIN/DNA	D	2.3	9.3	4	29	SKAMGIMNSFVNDIFERIASEASRLAHYN	1477
1WYU	GH	OXIDOREDUCTASE	G	1.6	9.3	6	19	QGVLQATFEYQTMIAELAG	1478
1Y3A	AE	SIGNALING PROTEIN	E	3.1	9.3	3	6	WYDFLM	1479
2D7D	AB	HYDROLASE/DNA	B	3.1	9.3	3	16	FERAAELRDLLLELKA	1480
2G9H	AB	IMMUNE SYSTEM	A	2.3	9.3	4	22	AQGALANIAVDKANLEIMTKRS	1481
2GOO	DE	TRANSFERASE	D	4.7	9.3	2	13	NHAIVQTLVNSVN	1482
2HDN	GH	TRANSLATION	G	1.9	9.3	5	16	KTTLTAAITTVLAKTY	1483
2HUE	BC	DNA BINDING PROTEIN	B	3.1	9.3	3	16	KLPFQRLVREIAQDFK	1484
2JGD	AB	OXIDOREDUCTASE	A	2.3	9.3	4	15	QVVIDQFISSGEQKW	1485
2ZBK	EF	ISOMERASE	F	2.3	9.3	4	21	KKLLAYLKYIPEVSRSLATFL	1486
3C1B	EF	STRUCTURAL PROTEIN/DNA	E	1.9	9.3	5	16	KLPFQRLVREIAQDFK	1487
3EJB	GH	OXIDOREDUCTASE/LIPID TRANSPORT	G	2.3	9.3	4	14	LDTVELVMALEEEF	1488
3H0L	PR	LIGASE	R	1.9	9.3	5	18	EEEIEVFQKQLSDILDFI	1489
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.9	9.3	5	19	PQEFFFHAMGGREGLIDTA	1490
1DML	AB	DNA BINDING PROTEIN/TRANSFERASE	B	3.1	9.2	3	16	AEETRRMLHRAFDTLA	1491
1DX5	BN	SERINE PROTEINASE	B	2.3	9.2	4	9	ERELLESYI	1492

1EYS	MH	ELECTRON TRANSPORT	H	1.8	9.2	5	25	AAQITIWAFWLFFFGLIIYLRREDK	1493
1F80	AE	TRANSFERASE	A	2.3	9.2	4	10	RQKRFAERIL	1494
1GH0	MN	PHOTOSYNTHESIS	N	3.1	9.2	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1495
1GH0	OP	PHOTOSYNTHESIS	O	3.1	9.2	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	1496
1II8	AB	REPLICATION	A	1.5	9.2	6	32	DKFETAYKKLSELKKTINNRIKEYRDILARTE	1497
1KF6	OP	OXIDOREDUCTASE	O	2.3	9.2	4	27	PVIVIINLITLAAALLHTKTWFELAPK	1498
1KIL	AB	MEMBRANE PROTEIN	B	1.8	9.2	5	39	SEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID	1499
1LWU	EF	BLOOD CLOTTING	F	1.3	9.2	7	46	LEEVRILEQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	1500
1NIK	AK	TRANSCRIPTION	A	4.6	9.2	2	10	DQVLNMLYWV	1501
1RCO	BW	LYASE	B	2.3	9.2	4	14	AKNYGRAVYECLRG	1502
1SFC	EH	TRANSPORT PROTEIN	E	1.5	9.2	6	64	LQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFE TSAAKLKRKYWWKNLKM	1503
1UCY	JK	COMPLEX (SERINE PROTEASE/COAGULATION)	J	2.3	9.2	4	11	EKELFESYIEG	1504
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	1.8	9.2	5	14	LVPGAIILDTVLML	1505
1YHU	MO	OXYGEN STORAGE/TRANSPORT	O	2.3	9.2	4	20	PEFQGHVVRVMGGLDILINA	1506
1ZLA	BD	PROTEIN BINDING/VIRUS/DNA	D	3.1	9.2	3	12	SREIQTAVRLLL	1507
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	H	1.5	9.2	6	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1508
1ZV8	AF	VIRAL PROTEIN	A	1.8	9.2	5	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	1509
2FFD	BC	BLOOD CLOTTING	B	1.5	9.2	6	36	NSNIPTNLRVLRSILENLRSKIQKLESDVSAQMEYC	1510
2FYN	AB	OXIDOREDUCTASE	A	2.3	9.2	4	24	YFIIKDVFALAVVLLVFFAIVGFM	1511
2HNT	EF	SERINE PROTEASE	F	3.1	9.2	3	9	KKWIQKVID	1512
2IBZ	DH	OXIDOREDUCTASE	H	3.1	9.2	3	17	VEEFFHLQHYLDTATAP	1513
2JFA	AB	TRANSCRIPTION	B	1.3	9.2	7	32	LQQQHQRLAQLLLILSHIRHMSNKGMEHLYSM	1514
2K2I	AB	CELL CYCLE	B	4.6	9.2	2	10	LHRALQAWVT	1515
2NZD	GH	STRUCTURAL PROTEIN/DNA	H	1.8	9.2	5	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1516
2O26	BY	CYTOKINE/SIGNALING PROTEIN	B	1.8	9.2	5	19	NYSIIDKLGKIVDDLVLCM	1517
2ODY	AB	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	A	1.8	9.2	5	11	EKELFESYIEG	1518
2P22	CD	TRANSPORT PROTEIN	D	1.5	9.2	6	27	LQPTRDLLCPWYEECDNITKVCQLHDS	1519
2PQA	CD	REPLICATION	C	1.5	9.2	6	19	MNEFTTHILEVINAHMVLS	1520
2QOU	JN	RIBOSOME	N	9.2	9.2	1	11	RIKVREAAMRG	1521
2RII	BX	OXIDOREDUCTASE COMPLEX	B	3.1	9.2	3	17	VDETLRLVQAFQFTDKH	1522
2VJM	AB	TRANSFERASE	B	1.8	9.2	5	21	NSGMHLMIGILAALEIRHKTG	1523
3DTP	BF	CONTRACTILE PROTEIN	B	2.3	9.2	4	15	QQLTAMKVIQRNCAA	1524
3EXG	AB	OXIDOREDUCTASE	A	3.1	9.2	3	16	AQVPLGAGIALACKYN	1525
3G5O	DC	TOXIN/ANTITOXIN	D	3.1	9.2	3	16	ADEWESLQETLYWLAQ	1526

3HKZ	DL	TRANSFERASE	D	1.3	9.2	7	24	PERILLEAGKSIIRKIEELEKKLV	1527
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	B	3.0	9.1	3	23	TLVPVLILVAIGAFSLPILFRSQ	1528
1CDL	CG	CALCIUM-BINDING PROTEIN	G	2.3	9.1	4	17	RRKWQKTGHAVRAIGRL	1529
1FYZ	BD	OXIDOREDUCTASE	B	3.0	9.1	3	32	PKWNETMKVVSNFLEVGEYNAIAATGMLWDSA	1530
1G0U	YZ	HYDROLASE	Z	4.6	9.1	2	15	INSAARNIQHLLYGK	1531
1G2C	SV	VIRAL PROTEIN	V	1.8	9.1	5	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	1532
1H1L	CD	OXIDOREDUCTASE	C	1.8	9.1	5	15	DKKLSKLIEEMELLF	1533
1JRO	CD	OXIDOREDUCTASE	C	3.0	9.1	3	20	AAYRMNAAQAMALRYVRELS	1534
1JY2	QS	BLOOD CLOTTING	Q	3.0	9.1	3	27	GCRMKGLIDEVDQDFTSRINKLRDSLF	1535
1NLW	DE	TRANSCRIPTION/DNA	E	1.5	9.1	6	40	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQV	1536
1OQP	AB	PROTEIN BINDING	A	9.1	9.1	1	11	EDEFIRIMKKT	1537
1PSB	BD	METAL BINDING PROTEIN	D	1.8	9.1	5	16	KETEFLRLKRTRLGLE	1538
1SQX	CG	OXIDOREDUCTASE	C	2.3	9.1	4	23	PLSQCLFWALVADLLTLTWIGGQ	1539
1XK4	JL	METAL BINDING PROTEIN	L	1.8	9.1	5	20	FEEFIMLMARLTWASHEKMH	1540
2B9S	AB	ISOMERASE/DNA	A	1.5	9.1	6	20	TADKLAYFNKANTEVAILCN	1541
2D2M	AD	OXYGEN STORAGE/TRANSPORT	A	3.0	9.1	3	15	QATINADLAHLAGQH	1542
2DD4	KL	HYDROLASE	L	2.3	9.1	4	14	AEDHRVWKDYVHTL	1543
2DYM	GH	PROTEIN TURNOVER/PROTEIN TURNOVER	H	1.8	9.1	5	18	MDDLLIRRLTDRNDKEAH	1544
2E 74	AD	PHOTOSYNTHESIS	D	3.0	9.1	3	31	MGRRQFMNLLAFGTVTGVALGALYPLVKYFI	1545
2E 74	EH	PHOTOSYNTHESIS	H	2.3	9.1	4	24	IDVLGWVALLVVFTWSIAMVVWGR	1546
2FHH	DE	HYDROLASE	E	1.5	9.1	6	23	AAVAVEFARLYAVELEHYEKLEG	1547
2H61	HG	METAL BINDING PROTEIN, SIGNALING PROTEIN	H	2.3	9.1	4	18	ELEKAMVALIDVFHQYSG	1548
2HDN	CD	TRANSLATION	C	1.8	9.1	5	16	KTTLTAAITTVLAKTY	1549
2HGP	FQ	RIBOSOME	F	9.1	9.1	1	11	YRHLLLEDQRI	1550
2HQS	BC	TRANSPORT PROTEIN/LIPOPROTEIN	C	2.3	9.1	4	22	PEYNISLGERRANAVKMYLQGK	1551
2JBL	HM	ELECTRON TRANSPORT	M	2.3	9.1	4	26	IESVHRWGWFFSLMVMVSASVGILLT	1552
2KA4	AB	TRANSCRIPTION REGULATOR	A	3.0	9.1	3	16	AHCASSRQIISHWKNC	1553
2Q9Q	AD	REPLICATION	D	2.3	9.1	4	24	NADISQSLLQTFIGRFRRIMDSSQ	1554
2RGN	BC	SIGNALING PROTEIN COMPLEX	B	4.6	9.1	2	35	EEEQKKKALERSMYVLSELVETEKMYVDDLGQIVE	1555
2UUN	ST	ELECTRON TRANSPORT	T	3.0	9.1	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1556
2Z2S	CD	TRANSCRIPTION	C	1.8	9.1	5	19	EAAFAELFQHFAPKVKGFL	1557
2ZCY	KL	HYDROLASE	K	2.3	9.1	4	22	AADCQFWETWLGSQCRLHELRE	1558
2ZXE	AG	HYDROLASE/TRANSPORT PROTEIN	G	1.8	9.1	5	24	YYRLRVVGLIVAAVLCVIGIIILL	1559
3CXH	NS	OXIDOREDUCTASE	N	2.3	9.1	4	36	VPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	1560
3EG5	CD	SIGNALING PROTEIN	C	3.0	9.1	3	9	DRLRPLSYP	1561
3GE8	AB	OXIDOREDUCTASE	B	2.3	9.1	4	25	YRTYNLMQDGQESYVQSLFDQFNER	1562
3H32	AB	BLOOD CLOTTING	A	1.5	9.1	6	44	EVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRG	1563

3H6P	BC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.8	9.1	5	63	HTAFAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVA AAAKVNTLLDIAQANLG	1564
3HAX	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	3.0	9.1	3	15	LHDLVDYYYFWKEDG	1565
3HKZ	DL	TRANSFERASE	L	1.8	9.1	5	21	PKDALLKAIENIRGMTSHYID	1566
1NOV	CF	VIRUS	F	2.3	9.0	4	12	FWERVRSILKSG	1567
1AHJ	CD	LYASE	C	2.3	9.0	4	13	YVEGWKKTFEEDF	1568
1BGY	OP	ELECTRON TRANSPORT	P	1.8	9.0	5	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	1569
1E6Y	BC	OXIDOREDUCTASE	B	2.3	9.0	4	20	AQNVSSTLLYFNDILEKETG	1570
1F6F	AB	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR	A	2.3	9.0	4	34	ENVRRVAFYRLFHCLHRDSSKIYTYLRILKCRLT	1571
1FLC	AF	HYDROLASE	F	4.5	9.0	2	24	KGFEKIGNDIQILKSSINIAIEKL	1572
1G2C	WT	VIRAL PROTEIN	T	1.8	9.0	5	32	SDEFDASISQVNEKINQSLAFIRKSDELLHNV	1573
1GH0	EF	PHOTOSYNTHESIS	F	3.0	9.0	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1574
1JFI	AB	TRANSCRIPTION/DNA	B	2.3	9.0	4	29	NDARELVVNCCTEFIHLISSEANEICNKS	1575
1LQB	AB	GENE REGULATION	B	2.3	9.0	4	17	SHVLSKVCMYFTYKVRY	1576
1M1J	DF	BLOOD CLOTTING	F	3.0	9.0	3	37	NTILAHENTIQQLTDMHIMNSNKITQLKQKIAQLESH	1577
1N73	DF	BLOOD CLOTTING	D	1.5	9.0	6	45	IIHLQRRINMQLQQLTLLQHNIKTQVSQILRVEVDIDVALRACKG	1578
1NTK	CG	OXIDOREDUCTASE	G	2.3	9.0	4	24	ILRVAPPFVAFYLVYTWGTQEFEK	1579
1OCC	CJ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	J	2.3	9.0	4	10	VAEKQKLFQE	1580
1T0Q	AB	OXIDOREDUCTASE	B	1.5	9.0	6	32	STITNCATYETADHLRWLTHTAYRTRELANCY	1581
1UKV	GY	PROTEIN TRANSPORT	G	2.3	9.0	4	15	LGELPQGFARLSAIY	1582
1V54	NP	OXIDOREDUCTASE	P	1.5	9.0	6	23	PWPLTGALSALLMTSGLTMWFHF	1583
1WCM	AB	TRANSCRIPTION	B	1.8	9.0	5	13	YAAKLLFQELMAM	1584
1WYU	GH	OXIDOREDUCTASE	H	2.3	9.0	4	13	ELTLVRHYTGLSR	1585
1ZLA	AB	PROTEIN BINDING/VIRUS/DNA	B	2.3	9.0	4	27	IYEETRGVLKVFLENVIRDAVTYTEHA	1586
1ZSZ	BC	DE NOVO PROTEIN	B	2.3	9.0	4	16	KRPYLLRSLYDWLVDN	1587
2AHM	CG	VIRAL PROTEIN, REPLICATION	C	1.8	9.0	5	18	TTEAFEKMVSLLSVLLSM	1588
2BBV	CF	VIRUS/RNA	F	1.8	9.0	5	14	MWERVKSIIKSSLA	1589
2D10	BF	CELL ADHESION	F	4.5	9.0	2	10	WSKKNELFSN	1590
2DPP	AB	LYASE	B	2.3	9.0	4	16	DWERLAFGLVAGCMAQ	1591
2DXB	KL	HYDROLASE	L	2.3	9.0	4	13	AEDHRVWKDYVHT	1592
2EY4	BF	ISOMERASE/BIOSYNTHETIC PROTEIN	B	1.8	9.0	5	14	LHDLVDYYYFWKED	1593
2FRV	SL	OXIDOREDUCTASE	L	3.0	9.0	3	10	PRDAQHFTQR	1594
2HOD	KL	BLOOD CLOTTING	L	1.5	9.0	6	33	THDSSIRYLQEIYNSNNQKIVNLKEKVAQLEAQ	1595
2J3R	AB	TRANSPORT	B	1.5	9.0	6	18	VSAFALLFSEMVQYCQSR	1596
2P22	AC	TRANSPORT PROTEIN	C	1.8	9.0	5	38	TDFAGKIHAFRDQFKQLEENFEDLHEQKDKVQALLENA	1597
2QB0	AD	HYDROLASE REGULATOR	A	3.0	9.0	3	8	KEDFRYRS	1598
2UUN	QR	ELECTRON TRANSPORT	R	3.0	9.0	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1599

2Z2T	CF	VIRAL PROTEIN/INHIBITOR	F	1.5	9.0	6	31	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK	1600
3B9F	LH	HYDROLASE/HYDROLASE INHIBITOR	L	2.3	9.0	4	9	ERELLESYI	1601
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.8	9.0	5	11	IQEWLQLTMYS	1602
3BZ1	AC	ELECTRON TRANSPORT	C	2.3	9.0	4	33	PRSWLATSHFVLAFFFLVGHLWHAGRARAAAAG	1603
3CJT	MN	TRANSFERASE/RIBOSOMAL PROTEIN	M	3.0	9.0	3	9	WLEAWRRDL	1604
3CVH	AL	IMMUNE SYSTEM	A	3.0	9.0	3	11	EAERLRAYLEG	1605
3D36	AC	TRANSFERASE/TRANSFERASE INHIBITOR	A	4.5	9.0	2	26	ADKRRQYARIAIEELDRAEAIITDYL	1606
3GE8	DF	OXIDOREDUCTASE	D	1.5	9.0	6	21	PGNRNMATFGMMDELRHGQLQ	1607
3H0L	VX	LIGASE	X	1.8	9.0	5	18	EEEIEVFQKQLSDILDFI	1608
1E3A	AB	ANTIBIOTIC RESISTANCE	B	1.5	8.9	6	13	EVASLLAWTHQMK	1609
1E6Y	EF	OXIDOREDUCTASE	E	2.2	8.9	4	20	AQNVSSTLLYFNDILEKETG	1610
1F3J	BP	IMMUNE SYSTEM	B	1.8	8.9	5	34	RHSAEYYNKQYLERTRAELDTACRHNYEETEVPT	1611
1F51	DH	TRANSFERASE	D	2.2	8.9	4	23	ELIHLLGHSRHDWMNKLQLIKGN	1612
1GX7	AD	OXIDOREDUCTASE	D	3.0	8.9	3	9	TQVKALYKS	1613
1KD8	AB	DE NOVO PROTEIN	B	1.5	8.9	6	34	VKQLKAKVEELKSKLWHLKNKVARLKKKNAECKA	1614
1KD8	FE	DE NOVO PROTEIN	E	1.5	8.9	6	33	VKQLKAKVEELKSKLWHLKNKVARLKKKNAECK	1615
1KVD	CD	TOXIN	C	1.8	8.9	5	16	IVGCIAAGILAILQGF	1616
1L9B	LM	PHOTOSYNTHESIS	L	1.8	8.9	5	29	PAHMIAISFFFTNALALALHGALVLSAAN	1617
1MHY	BD	OXIDOREDUCTASE	D	2.2	8.9	4	32	AEQKNGYLAQVLDEIRHTHQCAFINHYYSKHY	1618
1N73	EF	BLOOD CLOTTING	E	1.5	8.9	6	42	EVKIRIESTVAGSLRSMKSVLEHLRAKMQRMEEAIKTQKELC	1619
1NIW	GH	SIGNALING PROTEIN/OXIDOREDUCTASE	H	2.2	8.9	4	14	FKEVANAVKISASL	1620
1NZY	AB	LYASE	B	3.0	8.9	3	16	THLQVMAKERFHAGWM	1621
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	4.5	8.9	2	12	IDEKVELYRLKF	1622
1RD8	AB	VIRAL PROTEIN	B	1.8	8.9	5	24	NERTLDFHDSNVRNLYEKVKSQLK	1623
1TQY	CD	TRANSFERASE	C	2.2	8.9	4	12	ATSLEREYLLLS	1624
1YOV	CD	SIGNALING PROTEIN	D	1.5	8.9	6	21	ASTNAVIAAVCATEVFKIATS	1625
1Z6O	AM	METAL BINDING PROTEIN	M	2.2	8.9	4	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	1626
1Z6O	CO	METAL BINDING PROTEIN	O	2.2	8.9	4	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	1627
1Z6O	EQ	METAL BINDING PROTEIN	Q	2.2	8.9	4	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	1628
1Z6O	IU	METAL BINDING PROTEIN	U	2.2	8.9	4	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	1629
2ADV	AC	HYDROLASE	A	2.2	8.9	4	16	APSAFYGYGWAQARSH	1630
2E9X	EH	REPLICATION	H	2.2	8.9	4	31	LKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	1631
2EHB	AD	SIGNALLING PROTEIN/TRANSFERASE	D	3.0	8.9	3	6	AFEMIT	1632
2IBF	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	8.9	8.9	1	26	DMPPAFIKVENACTKLVQAAQMLQSD	1633
2JIZ	CD	HYDROLASE	C	2.2	8.9	4	15	MKLELAQYREVAAFA	1634
2JJ0	LM	PHOTOSYNTHESIS	L	2.2	8.9	4	29	PAHMIAISFFFTNALALALHGALVLSAAN	1635

2NZD	AB	STRUCTURAL PROTEIN/DNA	A	2.2	8.9	4	16	KLPFQRLVREIAQDFK	1636
2NZD	EF	STRUCTURAL PROTEIN/DNA	E	2.2	8.9	4	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1637
2QAR	DE	HYDROLASE REGULATOR	D	2.2	8.9	4	8	KEDFRYRS	1638
2QJY	MN	OXIDOREDUCTASE	M	2.2	8.9	4	24	YFIIKDVFALAVVLLVFFAIVGFM	1639
2QKL	AB	HYDROLASE	B	3.0	8.9	3	15	FSQVLDDLSARFILN	1640
3C1B	AB	STRUCTURAL PROTEIN/DNA	A	2.2	8.9	4	16	KLPFQRLVREIAQDFK	1641
3CRP	AB	PROTEIN BINDING	B	1.5	8.9	6	31	KVKQLEDAVEELLSANYHLENAVARLKKLVG	1642
3H0L	DF	LIGASE	F	2.2	8.9	4	18	EEEIEVFQKQLSDILDFI	1643
3H0L	JL	LIGASE	J	1.8	8.9	5	15	PEVKRRIMLGTFALS	1644
1A0H	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	A	2.2	8.8	4	10	EKELFESYIE	1645
1AHJ	EF	LYASE	E	2.2	8.8	4	15	VSDRAWALFRALDGK	1646
1AOI	GH	DNA BINDING PROTEIN/DNA	H	1.3	8.8	7	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1647
1B33	LM	PHOTOSYNTHESIS	L	2.2	8.8	4	25	QEMTATCLRDLDYYLRLITYGIVAG	1648
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	2.9	8.8	3	9	TERYSTAYY	1649
1EFU	CD	COMPLEX (TWO ELONGATION FACTORS)	D	2.9	8.8	3	9	FAAEVAAMS	1650
1F66	EF	STRUCTURAL PROTEIN/DNA	E	2.2	8.8	4	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	1651
1F99	KL	PHOTOSYNTHESIS	K	2.2	8.8	4	25	AIGKAKCARDIGYYLRMVTYCLVVG	1652
1FOS	EF	TRANSCRIPTION/DNA	E	1.3	8.8	7	58	RRIRRERNKMAAAKSRNRRRELTDTLQAETDQLEDEKSALQTEIANLL KEKEKLEFIL	1653
1ID3	AB	STRUCTURAL PROTEIN/DNA	B	2.2	8.8	4	12	KPAIRRLARRGG	1654
1IR2	AI	LYASE	I	2.9	8.8	3	14	DEQIAAQVDYIVAN	1655
1JPW	CF	CELL ADHESION	F	2.9	8.8	3	7	LADVKSS	1656
1KDD	DC	DE NOVO PROTEIN	D	1.5	8.8	6	32	VKQLKAKVEELKSKLWHLKNKVARLKKKNAEC	1657
1KYO	CH	OXIDOREDUCTASE/ELECTRON TRANSPORT	H	2.2	8.8	4	29	KSQFLYVLIPAGIYWYWWKNGNEYNEFLY	1658
1MHY	BD	OXIDOREDUCTASE	B	2.2	8.8	4	26	PYWRDEILNKYFGALLYSEYGLFNAH	1659
1N73	DE	BLOOD CLOTTING	D	1.3	8.8	7	45	IIHLQRRINMQLQQLTLLQHNIKTQVSQILRVEVDIDVALRACKG	1660
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.8	8.8	5	29	PGHMSSVSFLFVNAMALGLHGGLILSVAN	1661
1Q5R	DK	HYDROLASE	K	1.8	8.8	5	23	AGIAIELVRLFAVELEHYEKIEG	1662
1RCO	HC	LYASE	H	2.2	8.8	4	20	WRDRFLFCAEALYKAQAETG	1663
1TQY	AB	TRANSFERASE	B	2.2	8.8	4	15	FDFTHREFRKLWSEG	1664
1U3H	DP	IMMUNE SYSTEM	D	1.8	8.8	5	34	DAEYYNKQYLERTRAELDTVCRYNYEETEVPTSL	1665
1V54	QR	OXIDOREDUCTASE	R	2.9	8.8	3	16	FASAVRILEVVKDKAG	1666
1VZJ	HJ	HYDROLASE	H	4.4	8.8	2	19	TLDEAERQWKAEFHRWSSY	1667
1XIU	AE	TRANSCRIPTION/TRANSFERASE	E	2.2	8.8	4	10	KILHRLLQEG	1668
2BA1	DG	RNA BINDING PROTEIN	G	1.5	8.8	6	19	DENSIELARVVDRGIRESE	1669
2DS2	AB	PLANT PROTEIN	A	2.2	8.8	4	13	RACQRFIHRRAQF	1670

2DXB	NO	HYDROLASE	O	2.2	8.8	4	14	AEDHRVWKDYVHTL	1671
2FFD	DE	BLOOD CLOTTING	E	1.5	8.8	6	28	RVLRSILENLRSKIQKLESDVSAQMEYC	1672
2FUG	UV	OXIDOREDUCTASE	V	1.8	8.8	5	10	VIYHFKHYTE	1673
2HV8	CF	PROTEIN TRANSPORT	F	2.2	8.8	4	31	RDELMEAIQKQEEINFRLQDYIDRIIVAIME	1674
2P1N	AB	SIGNALING PROTEIN	A	1.8	8.8	5	16	KNLLDLTCQTVADMIK	1675
2PBI	CD	SIGNALING PROTEIN	C	1.8	8.8	5	15	SSVSLGGIVKYSEQF	1676
2QFA	BC	CELL CYCLE/CELL CYCLE/CELL CYCLE	B	1.8	8.8	5	46	LRRRKLASFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	1677
2QNA	AB	TRANSPORT PROTEIN	B	1.8	8.8	5	27	LEQSERRRRLLELQKSKRLDYVNHARR	1678
2Z2Y	CD	HYDROLASE	C	2.2	8.8	4	14	YSDIAIGIEQAILG	1679
3BXK	CD	MEMBRANE PROTEIN, SIGNALING PROTEIN	C	2.9	8.8	3	12	FPEFLTMMARKM	1680
3C1B	GH	STRUCTURAL PROTEIN/DNA	H	1.8	8.8	5	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1681
3CJH	EB	PROTEIN TRANSPORT	B	1.8	8.8	5	28	SQEEQCLSNCVNRFLDTNIRIVNGLQNT	1682
3DHH	AB	OXIDOREDUCTASE	A	2.2	8.8	4	11	RQFDWAWRAYH	1683
3DTU	CD	OXIDOREDUCTASE	D	1.5	8.8	6	24	TIVPIVILVAIGAFSLPVLFNQQE	1684
3H87	BC	TOXIN/ANTITOXIN	C	2.9	8.8	3	11	AADLRRLRGAV	1685
1CPC	KL	LIGHT HARVESTING PROTEIN	K	2.9	8.7	3	25	QTGKDKCVRDIGYYLRMVTYCLVVG	1686
1DX5	AM	SERINE PROTEINASE	A	2.2	8.7	4	9	ERELLESYI	1687
1EQZ	CD	STRUCTURAL PROTEIN/DNA	C	2.2	8.7	4	16	KLPFQRLVREIAQDFK	1688
1G2C	EB	VIRAL PROTEIN	E	1.7	8.7	5	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	1689
1I3Q	AB	TRANSCRIPTION	A	2.2	8.7	4	36	PQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKAL	1690
1I3Q	CK	TRANSCRIPTION	C	1.7	8.7	5	27	VDQVVVRGIDTLQKKVASILLALTQMD	1691
1IR2	Y8	LYASE	Y	2.9	8.7	3	20	WRDRFLFVAEAIYKAQAETG	1692
1JSD	AB	VIRAL PROTEIN	B	2.2	8.7	4	53	TRLNMINNKIDDQIQDIWTYNAELLVLLENQKTLDEHDANVNNLYNKV KRALG	1693
1MTY	DB	MONOOXYGENASE	D	2.2	8.7	4	31	AEQKNGYLAQVLDEIRHTHQCAYVNYYFAKN	1694
1MTY	DB	MONOOXYGENASE	D	2.2	8.7	4	21	AKEYARMEAVKDERQFGSLQV	1695
1MTY	DB	MONOOXYGENASE	D	2.9	8.7	3	32	PKWNETMKVVSNFLEVGEYNAIAATGMLWDSA	1696
1MTY	EC	MONOOXYGENASE	E	2.2	8.7	4	21	AKEYARMEAVKDERQFGSLQV	1697
1NH2	BD	TRANSCRIPTION/DNA	B	2.2	8.7	4	17	EQTLQDLKNIWQKKLTE	1698
1NTK	BI	OXIDOREDUCTASE	B	8.7	8.7	1	19	NPDVQAAKNKLKAGYLMSV	1699
1O96	QZ	ELECTRON TRANSFER	Q	1.7	8.7	5	14	ISEQAAKIIQIINE	1700
1OED	AB	ION CHANNEL/RECEPTOR	A	8.7	8.7	1	29	MTLSISVLLSLTVFLLVIVELIPSTSSAV	1701
1PZL	AB	TRANSCRIPTION	B	2.2	8.7	4	11	KILHRLLQEGS	1702
1R20	AD	HORMONE/GROWTH FACTOR RECEPTOR	D	2.2	8.7	4	33	PRSAVIFGKILGILTEIRTLGMQNSNMCISLKL	1703
1R5V	AB	SIGNALING PROTEIN	B	2.9	8.7	3	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	1704
1SFC	AD	TRANSPORT PROTEIN	D	1.5	8.7	6	59	NEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRI DEANQRATKM	1705

1T0Q	AB	OXIDOREDUCTASE	B	1.7	8.7	5	25	YRTYNLLQDGQESYVQGLFDQLNDR	1706
1UCY	MN	COMPLEX (SERINE PROTEASE/COAGULATION)	M	1.7	8.7	5	10	EKELFESYIE	1707
1V54	NO	OXIDOREDUCTASE	N	2.2	8.7	4	30	VDTRAYFTSATMIIAIPTGVKVFSWLATLH	1708
1WA8	AB	TUBERCULOSIS	B	4.4	8.7	2	34	GIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAW	1709
1XK4	AC	METAL BINDING PROTEIN	C	2.2	8.7	4	17	FEEFIMLMARLTWASHE	1710
1XME	AB	OXIDOREDUCTASE	A	2.2	8.7	4	36	PTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLR	1711
1YKE	CD	GENE REGULATION	D	2.9	8.7	3	22	RLTQLQICLDQMTEQFCATLNY	1712
2AGH	AB	TRANSCRIPTION	A	1.7	8.7	5	19	EKRIKELELLLMSTENELK	1713
2BCJ	AQ	TRANSFERASE/HYDROLASE	A	1.7	8.7	5	22	EEERLVCSREIFDTYIMKELLA	1714
2BG9	DE	ION CHANNEL/RECEPTOR	D	2.2	8.7	4	27	YFVVNVIIPCLLFSFLTVLVFYLPTDS	1715
2DXB	EF	HYDROLASE	F	2.2	8.7	4	13	AEDHRVWKDYVHT	1716
2OCY	AC	ENDOCYTOSIS/EXOCYTOSIS	A	1.7	8.7	5	22	EADKLNKEVEDLTASLFDEANN	1717
2ONL	AC	TRANSFERASE	A	2.9	8.7	3	8	LNNIVKCQ	1718
2VGL	AB	PROTEIN TRANSPORT	B	2.9	8.7	3	12	PDLRDRGYIYWR	1719
3BYH	AB	STRUCTURAL PROTEIN	A	8.7	8.7	1	17	WDDMEKIWHHTFYNELR	1720
3C91	EL	HYDROLASE	E	2.2	8.7	4	23	VADARVLVDFARISAQQEKVTYG	1721
3CIP	AG	STRUCTURAL PROTEIN	G	2.2	8.7	4	18	QDESGAAAIFTVQLDDYL	1722
3DWL	AD	STRUCTURAL PROTEIN	D	2.2	8.7	4	19	FRNTLHFHIKASKAYMHQR	1723
3G43	CF	METAL BINDING PROTEIN	F	1.7	8.7	5	42	TLFALVRTALRIKTEGNLEQANEELRAIIKKIWKRTSMKLLD	1724
3H6P	BD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	1.7	8.7	5	20	YAGTLQSLGADIASEQAVLS	1725
3HJW	BC	ISOMERASE/RNA	C	2.2	8.7	4	10	AHLPPLCEEK	1726
1BGY	CG	ELECTRON TRANSPORT	G	2.2	8.6	4	29	CILRVAPPFVAFYLVYTWGTQEFEKSKRK	1727
1BR1	EF	MUSCLE PROTEIN	E	1.7	8.6	5	21	TDVIIAFQAQCRGYLARKAFA	1728
1DS6	AB	SIGNALING PROTEIN	B	1.7	8.6	5	12	ESLIKYKKTLLG	1729
1E1C	CD	ISOMERASE	C	2.9	8.6	3	19	DFSARIARNTQLFLQQESG	1730
1EQZ	EF	STRUCTURAL PROTEIN/DNA	F	1.7	8.6	5	29	SKAMGIMNSFVNDIFERIAGEASRLAHYN	1731
1FOE	CD	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	C	2.9	8.6	3	8	IKPIQRVL	1732
1GH0	CD	PHOTOSYNTHESIS	D	2.9	8.6	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1733
1GH0	ST	PHOTOSYNTHESIS	S	2.9	8.6	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	1734
1H8B	AB	STRUCTURAL PROTEIN	A	2.9	8.6	3	12	AEQVIASFRILA	1735
1HBM	DB	METHANOGENESIS	B	2.2	8.6	4	12	MYDANMVKAAVL	1736
1IWP	LM	LYASE	L	2.9	8.6	3	14	PWSKAFLASAYASR	1737
1J1E	DF	CONTRACTILE PROTEIN	F	2.2	8.6	4	39	ASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRAQ	1738
1JEK	AB	VIRAL PROTEIN	B	2.2	8.6	4	33	QQWEEEIEQHEGNLSLLLREAALQVHIAQRDAR	1739
1JTH	AB	ENDOCYTOSIS/EXOCYTOSIS	B	1.4	8.6	6	66	LSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY	1740

1KIL	BC	MEMBRANE PROTEIN	C	1.7	8.6	5	70	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKD	1741
1MF8	AB	HYDROLASE, LIGASE	A	2.9	8.6	3	10	VFTWSLPFVG	1742
1MHY	BG	OXIDOREDUCTASE	G	2.2	8.6	4	20	VNVFLRTDAALGTVLMEIRN	1743
1MTY	DB	MONOOXYGENASE	B	2.2	8.6	4	25	HAPYVKDKAEEWRYTDRFLQGYSAD	1744
1NIK	AB	TRANSCRIPTION	A	2.2	8.6	4	21	PQEFFFHAMGGREGLIDTAVK	1745
1OCC	AC	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	1.4	8.6	6	23	PWPLTGALSALLMTSGLTMWFHF	1746
1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	1.4	8.6	6	23	PWPLTGALSALLMTSGLTMWFHF	1747
1QGW	AC	PHOTOSYNTHESIS	C	1.7	8.6	5	25	NRRMAACLRDGEIILRYVSYALLSG	1748
1QUQ	AB	DNA-BINDING PROTEIN	A	1.7	8.6	5	13	MNEFTTHILEVIN	1749
1RCO	LF	LYASE	L	2.2	8.6	4	20	WRDRFLFCAEALYKAQAETG	1750
1SQX	DG	OXIDOREDUCTASE	D	2.2	8.6	4	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	1751
1TI2	IJ	OXIDOREDUCTASE	J	1.7	8.6	5	12	NCFMGCMDEHEL	1752
1V54	DI	OXIDOREDUCTASE	I	2.2	8.6	4	17	FAVAEKRKKAYADFYRN	1753
1YE9	BH	OXIDOREDUCTASE	H	4.3	8.6	2	8	TDTQISRL	1754
1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	E	1.7	8.6	5	16	KLPFQRLVREIAQDFK	1755
1ZW3	AB	PROTEIN BINDING	B	2.2	8.6	4	19	SVLAGHSRTVSDSIKKLIT	1756
2AUS	CD	ISOMERASE/STRUCTURAL PROTEIN	C	2.2	8.6	4	14	LHDLVDYYHFWKED	1757
2AZE	AB	CELL CYCLE, TRANSCRIPTION	A	1.7	8.6	5	48	AQECQNLEVERQRRLERIKQKQSQLQELILQQIAFKNLVQRNRHAEQQ	1758
2B8K	AB	TRANSFERASE	A	1.7	8.6	5	19	PQEFFFHAMGGREGLIDTA	1759
2D10	AE	CELL ADHESION	E	2.9	8.6	3	10	WSKKNELFSN	1760
2DD4	EF	HYDROLASE	F	2.9	8.6	3	10	PNYRRRLVRW	1761
2EKV	AB	CONTRACTILE PROTEIN	A	2.9	8.6	3	5	WWRLF	1762
2HQS	FG	TRANSPORT PROTEIN/LIPOPROTEIN	G	2.2	8.6	4	22	PEYNISLGERRANAVKMYLQGK	1763
2IDO	CD	TRANSFERASE	C	2.9	8.6	3	6	DEFLLD	1764
2NLA	AB	APOPTOSIS	B	2.2	8.6	4	15	QLRRIGDKVNLRQKL	1765
2NQB	AB	STRUCTURAL PROTEIN/DNA	A	2.2	8.6	4	16	KLPFQRLVREIAQDFK	1766
2NQB	CD	STRUCTURAL PROTEIN/DNA	D	2.2	8.6	4	20	ELAKHAVSEGTKAVTKYTSS	1767
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	B	2.9	8.6	3	8	RYWRILAE	1768
2PK9	AB	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	A	1.7	8.6	5	12	STAIREISLMKE	1769
2PT7	AG	HYDROLASE/PROTEIN BINDING	A	1.7	8.6	5	30	SAEDKKFLEVERALKEAALNPLRHATEELF	1770
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	G	2.2	8.6	4	26	WGDFAAAAVMSALPITIVFLLAQRWL	1771
2V36	CD	TRANSFERASE	D	1.4	8.6	6	17	ATIISSVLQTILYHIEY	1772
2Z3R	GH	CYTOKINE/CYTOKINE RECEPTOR	G	4.3	8.6	2	20	KVTAMKCFLLELQVISLESG	1773
3C01	DH	MEMBRANE PROTEIN, PROTEIN TRANSPORT	H	4.3	8.6	2	13	QRALAVRAYAEKV	1774

3FGC	AB	OXIDOREDUCTASE	B	2.2	8.6	4	15	PVRVAEEACLLDQMS	1775
3GE8	AB	OXIDOREDUCTASE	A	1.4	8.6	6	21	PGNRNMATFGMMDELRHGQLQ	1776
3H0L	AC	LIGASE	A	1.7	8.6	5	13	IFEMYARTRDEGF	1777
3H0L	DF	LIGASE	D	1.7	8.6	5	15	PEVKRRIMLGTFALS	1778
3MON	CD	SWEET-TASTING PROTEIN	D	2.2	8.6	4	18	PFTQNLGKFAVDEENKIG	1779
1BGY	DJ	ELECTRON TRANSPORT	D	1.7	8.5	5	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	1780
1CPC	AB	LIGHT HARVESTING PROTEIN	A	2.8	8.5	3	24	QTGKDKCVRDIGYYLRMVTYCLVV	1781
1E3D	CD	HYDROGENASE	D	4.3	8.5	2	32	ANATYIRNLVLGNQFMHDHLVHFYHLHALDFV	1782
1GH0	QR	PHOTOSYNTHESIS	Q	1.7	8.5	5	27	STEIQVAFGRFRQAKAGLEAAKALTSK	1783
1GX7	AD	OXIDOREDUCTASE	A	2.8	8.5	3	20	EFTADVTIWEEGSEFVERLT	1784
1I3Q	AK	TRANSCRIPTION	A	2.8	8.5	3	11	LDQVLNMLYWV	1785
1LNU	AB	SUGAR BINDING PROTEIN	A	1.7	8.5	5	21	PQGGLQNIAVVKHNLGVLTKR	1786
1LWU	DE	BLOOD CLOTTING	E	2.1	8.5	4	23	SVLEHLRAKMQRMEEAIKTQKEL	1787
1M63	AB	HYDROLASE/ISOMERASE	B	1.4	8.5	6	16	DTQLQQIVDKTIINAD	1788
1N73	EF	BLOOD CLOTTING	F	1.7	8.5	5	39	EQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	1789
1NZY	CB	LYASE	C	1.4	8.5	6	16	VEECTEFEIQNVIASV	1790
1QUQ	CD	DNA-BINDING PROTEIN	C	1.7	8.5	5	15	MNEFTTHILEVINAH	1791
1RM1	BC	TRANSCRIPTION/DNA	B	2.1	8.5	4	16	TIGNSLVDALDTLISD	1792
1S9K	DE	TRANSCRIPTION/DNA	E	1.7	8.5	5	48	RMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVA	1793
1V54	DK	OXIDOREDUCTASE	K	1.7	8.5	5	22	GNAVLASGATFCVAVWVYMATQ	1794
1V54	LM	OXIDOREDUCTASE	L	1.7	8.5	5	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	1795
1W2W	IJ	ISOMERASE	I	2.1	8.5	4	15	TALGVIRSLWKDSLA	1796
1XK4	AC	METAL BINDING PROTEIN	A	1.7	8.5	5	20	FQEFLILVIKMGVAAHKKSH	1797
1XK4	BD	METAL BINDING PROTEIN	D	2.1	8.5	4	19	FEEFIMLMARLTWASHEKM	1798
1XKP	BC	MEMBRANE PROTEIN/CHAPERON	C	2.1	8.5	4	14	VTLLRSLMQQALAW	1799
1XLS	CG	TRANSCRIPTION	C	2.8	8.5	3	29	RFAKLLLRLPALRSIGLKCLEHLFFFKLI	1800
1YE9	CG	OXIDOREDUCTASE	C	1.7	8.5	5	12	PETLHNVMWAMS	1801
1YNJ	JK	TRANSFERASE	K	2.8	8.5	3	16	YRLTVVVAKRAQQLLR	1802
2A4J	AB	STRUCTURAL PROTEIN	B	8.5	8.5	1	5	LIRER	1803
2A6Q	AE	TOXIN INHIBITOR/TOXIN	A	2.1	8.5	4	16	LEEYNSLEETAYLLRS	1804
2DS2	CD	PLANT PROTEIN	C	2.1	8.5	4	13	RACQRFIHRRAQF	1805
2DXB	HI	HYDROLASE	H	1.7	8.5	5	18	LTELHNKIVEMRERVASG	1806
2FFD	BC	BLOOD CLOTTING	C	2.1	8.5	4	36	ILTHDSSIRYLQEIYNSNNQKIVNLKEKVAQLEAQC	1807
2FSE	BE	IMMUNE SYSTEM, STRUCTURAL PROTEIN	B	2.1	8.5	4	11	ELGRPDAEYWN	1808
2I2X	KL	TRANSFERASE	K	4.3	8.5	2	16	RFETKALADAKAALEA	1809
2IY0	AB	HYDROLASE/HYDROLASE ACTIVATOR	A	4.3	8.5	2	15	DEIINFYMNMLMERS	1810
2JGD	AB	OXIDOREDUCTASE	A	4.3	8.5	2	8	LERYLQLC	1811
2JJ0	LM	PHOTOSYNTHESIS	M	2.1	8.5	4	27	PFHGLSIAFLYGSALLFAMHGATILAV	1812

2PV2	BE	ISOMERASE	E	2.8	8.5	3	8	TLKFWDIF	1813
2PV2	CF	ISOMERASE	F	2.8	8.5	3	9	TLKFWDIFR	1814
2Q9Q	EF	REPLICATION	F	2.1	8.5	4	31	LKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	1815
2QJK	AB	ELECTRON TRANSPORT	A	2.1	8.5	4	24	YFIIKDVFALAVVLLVFFAIVGFM	1816
2UUN	KL	ELECTRON TRANSPORT	K	2.8	8.5	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	1817
3BUA	BF	DNA BINDING PROTEIN	B	1.7	8.5	5	16	VSRLLRVMQCLSRIEE	1818
3BZ1	AD	ELECTRON TRANSPORT	D	2.1	8.5	4	19	FYTKNLLLNEGIRAWMAPQ	1819
3EDL	GF	STRUCTURAL PROTEIN	F	2.8	8.5	3	8	VHWYVGEG	1820
3GHG	GH	BLOOD CLOTTING	G	1.2	8.5	7	85	QKNNKDSHSLTTNIMEILRGDFSSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSC	1821
3H6P	AD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.7	8.5	5	58	FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQAN	1822
3HKZ	OW	TRANSFERASE	W	4.3	8.5	2	6	INEVIH	1823
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.7	8.5	5	11	EMERDCMIAHG	1824
1CPC	AB	LIGHT HARVESTING PROTEIN	B	2.8	8.4	3	25	SRRMAACLRDMEIILRYVTYAIFAG	1825
1DIO	AG	LYASE	G	1.7	8.4	5	16	DRLAMNFERAAELTAV	1826
1E 08	AD	HYDROGENASE	D	2.1	8.4	4	9	TQVKALYKS	1827
1E1C	CD	ISOMERASE	C	2.1	8.4	4	19	VYNNVVRTCIEAMAATQGH	1828
1EFU	CD	COMPLEX (TWO ELONGATION FACTORS)	D	4.2	8.4	2	6	DFVAKD	1829
1GOT	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	2.8	8.4	3	5	PLVKG	1830
1I3R	CD	IMMUNE SYSTEM	C	2.1	8.4	4	22	AQGALANIAVNKANLDVMKERS	1831
1KQF	BC	OXIDOREDUCTASE	B	1.7	8.4	5	25	ALKPLAAAGFIATFAGLIFHYIGIG	1832
1L9J	LM	PHOTOSYNTHESIS	M	2.8	8.4	3	11	ERAALFWRWTM	1833
1M8Q	PR	CONTRACTILE PROTEIN	R	8.4	8.4	1	7	EEEVEEL	1834
1NIW	AB	SIGNALING PROTEIN/OXIDOREDUCTASE	B	1.7	8.4	5	12	FKEVANAVKISA	1835
1NZY	AB	LYASE	B	1.7	8.4	5	18	VEECTEFEIQNVIASVTH	1836
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	2.1	8.4	4	12	AERAALFWRWTM	1837
1RCO	RS	LYASE	R	2.1	8.4	4	20	WRDRFLFCAEALYKAQAETG	1838
1TBG	CG	COMPLEX (GTP-BINDING/TRANSDUCER)	C	1.7	8.4	5	20	QLRQEAEQLKNQIRDARKAC	1839
1TIL	AB	TRANSCRIPTION	B	4.2	8.4	2	17	HHTAEELREQVTDVLEN	1840
1TY4	AC	APOPTOSIS	C	2.1	8.4	4	11	IGYEIGSKLAA	1841
1V54	NY	OXIDOREDUCTASE	N	2.1	8.4	4	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	1842
1VKT	AB	HORMONE	A	8.4	8.4	1	5	LYQLE	1843
1WE3	CQ	CHAPERONE	C	8.4	8.4	1	15	VRELLPILEQVAQTG	1844
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	B	1.4	8.4	6	19	EERKLYDSALSKIEKLIET	1845

1YEW	BC	OXIDOREDUCTASE, MEMBRANE PROTEIN	C	1.4	8.4	6	32	FTHLVWLVAYAWAIYWGASYFTEQDGTWHQTI	1846
2BA1	DG	RNA BINDING PROTEIN	D	2.1	8.4	4	16	RRSIEISKVSKEAFEA	1847
2BDN	AL	IMMUNE SYSTEM	A	8.4	8.4	1	13	KWVQDSMDHLDKQ	1848
2E9X	EH	REPLICATION	H	1.7	8.4	5	25	PEELAFAREFMANTESYLKNVALKH	1849
2F8N	AB	STRUCTURAL PROTEIN/DNA	B	2.1	8.4	4	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	1850
2FHH	ST	HYDROLASE	S	2.1	8.4	4	22	FNEFDNLRRGGIQFADTRGYAY	1851
2FJ7	EF	STRUCTURAL PROTEIN/DNA	E	2.8	8.4	3	14	KLPFQRLVREIAQD	1852
2I3S	CD	CELL CYCLE	D	2.8	8.4	3	9	TEEILAMIK	1853
2IBZ	CD	OXIDOREDUCTASE	D	1.7	8.4	5	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	1854
2IDO	AB	TRANSFERASE	A	2.8	8.4	3	6	DEFLLD	1855
2JBL	LM	ELECTRON TRANSPORT	L	1.7	8.4	5	12	AEHENQYFRDVV	1856
2Q9Q	AD	REPLICATION	D	2.8	8.4	3	22	EMERGLFQTGQKGLNDFQCWEK	1857
2QM6	AB	TRANSFERASE	B	1.7	8.4	5	15	IITTVLQVISNVIDY	1858
2UUN	MN	ELECTRON TRANSPORT	N	2.8	8.4	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1859
2V4J	DE	OXIDOREDUCTASE	E	2.8	8.4	3	15	ITHIREMCDIADKYC	1860
2VML	GH	PHOTOSYNTHESIS	H	2.8	8.4	3	25	NRRMAACLRDMEIILRYVSYALLAG	1861
2WAQ	BN	TRANSCRIPTION	N	2.8	8.4	3	8	YCCRRMLL	1862
2WB1	AC	TRANSCRIPTION	C	2.8	8.4	3	12	MRHILLVADVMT	1863
2Z2T	CE	VIRAL PROTEIN/INHIBITOR	C	1.7	8.4	5	35	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	1864
3A0B	AC	ELECTRON TRANSPORT	C	8.4	8.4	1	8	ATCFVWFN	1865
3BG0	HG	PROTEIN TRANSPORT, HYDROLASE	G	2.8	8.4	3	17	SQLIFNAQALKDRYEGN	1866
3BZ1	LT	ELECTRON TRANSPORT	L	2.1	8.4	4	24	RTSLYLGLLLILVLALLFSSYFFN	1867
3DA7	EF	PROTEIN BINDING	F	4.2	8.4	2	10	LDALWDCLTG	1868
3DF0	AB	HYDROLASE	A	2.8	8.4	3	8	LISWLSFS	1869
3DTU	AB	OXIDOREDUCTASE	A	1.7	8.4	5	30	LTQQSYFMMATMVIAVPTGIKIFSWIATMW	1870
3EXG	CD	OXIDOREDUCTASE	C	2.1	8.4	4	17	AQVPLGAGIALACKYNG	1871
3H0L	JL	LIGASE	J	1.7	8.4	5	19	YLKAQKVRRLITNDFLKAF	1872
1AHJ	AB	LYASE	A	2.1	8.3	4	13	YVEGWKKTFEEDF	1873
1AOI	AB	DNA BINDING PROTEIN/DNA	A	2.1	8.3	4	16	KLPFQRLVREIAQDFK	1874
1B33	AB	PHOTOSYNTHESIS	A	2.1	8.3	4	25	QEMTATCLRDLDYYLRLITYGIVAG	1875
1B33	AB	PHOTOSYNTHESIS	B	2.8	8.3	3	25	TRRYAACIRDLDYYLRYATYAMLAG	1876
1EYX	KL	PHOTOSYNTHESIS	K	2.1	8.3	4	25	QEKINKCYRDIDHYMRLVNYSLVIG	1877
1FYZ	CE	OXIDOREDUCTASE	E	2.1	8.3	4	20	VNYFLDGERQLGTRLMELRN	1878
1GH0	UV	PHOTOSYNTHESIS	V	2.8	8.3	3	25	SRRMAACLRDMEIILRYVTYAVFAG	1879
1JEY	AB	DNA BINDING PROTEIN/DNA	A	1.7	8.3	5	15	SSTLFSALLIKCLEK	1880
1KIL	BC	MEMBRANE PROTEIN	B	1.4	8.3	6	39	SEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID	1881
1L9J	MH	PHOTOSYNTHESIS	M	4.2	8.3	2	27	PFHGLSIAFLYGSALLFAMHGATILAV	1882
1MMO	DG	OXIDOREDUCTASE (MONOOXYGENASE)	G	2.8	8.3	3	20	VNYFLDGERQLGTRLMELRN	1883

1PNB	AB	SEED STORAGE PROTEIN	A	2.8	8.3	3	12	RACQQWIRQQLA	1884
1PRC	CM	PHOTOSYNTHETIC REACTION CENTER	C	2.8	8.3	3	19	PQRAIAWWGIRMVRDLNMN	1885
1Q7L	AB	HYDROLASE	B	2.8	8.3	3	8	DNRYIRAV	1886
1SPB	PS	COMPLEX (SERINE PROTEINASE/PROSEGMENT)	S	2.8	8.3	3	14	YSWIINGIEWAIAN	1887
1T0J	BC	SIGNALING PROTEIN	B	2.8	8.3	3	12	PKVLQRLIKSRH	1888
1UM9	CD	OXIDOREDUCTASE	D	2.8	8.3	3	5	LRYRS	1889
1V54	NO	OXIDOREDUCTASE	O	1.7	8.3	5	24	TILPAIILILIALPSLRILYMMDE	1890
1VZJ	BI	HYDROLASE	B	4.2	8.3	2	19	TLDEAERQWKAEFHRWSSY	1891
1W2W	EF	ISOMERASE	E	1.7	8.3	5	19	TALGVIRSLWKDSLAKTDK	1892
1WDC	AC	MUSCLE PROTEIN	C	2.8	8.3	3	18	QDEIDDLKDVFELFDFWD	1893
1YE9	KO	OXIDOREDUCTASE	K	2.1	8.3	4	9	DTFWDYVSL	1894
1YOK	AB	TRANSCRIPTION	B	2.8	8.3	3	9	ALLRYLLDK	1895
2E9X	BC	REPLICATION	C	4.2	8.3	2	9	FRRIMDSSQ	1896
2F8N	EF	STRUCTURAL PROTEIN/DNA	E	2.1	8.3	4	14	KLPFQRLVREIAQD	1897
2I3S	AB	CELL CYCLE	B	2.1	8.3	4	9	TEEILAMIK	1898
2JIY	LM	PHOTOSYNTHESIS	M	2.1	8.3	4	27	PFHGLSIAFLYGSALLFAMHGATILAV	1899
2Q0O	BD	TRANSCRIPTION	D	2.1	8.3	4	34	KSELEALAVSAIREHRRLLWADQAVYEEWLRASD	1900
2QJY	DE	OXIDOREDUCTASE	D	2.1	8.3	4	24	YFIIKDVFALAVVLLVFFAIVGFM	1901
2QKH	BA	SIGNALING PROTEIN/HORMONE	B	1.7	8.3	5	27	FISDYSIAMDKIHQQDFVNWLLAQKGK	1902
2QMB	CB	TRANSPORT PROTEIN	B	4.2	8.3	2	7	PWTQRFF	1903
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	G	2.8	8.3	3	17	VPILAVVFILSFIAAIT	1904
2RAX	AB	CELL CYCLE	A	2.1	8.3	4	19	LGEFLKLDRERAKNKIAKE	1905
2W0C	AP	VIRUS	A	8.3	8.3	1	8	DLVQQRMF	1906
2WB1	AB	TRANSCRIPTION	A	4.2	8.3	2	5	LEDVS	1907
2Z2Y	AB	HYDROLASE	A	2.8	8.3	3	14	YSDIAIGIEQAILG	1908
2Z3R	CD	CYTOKINE/CYTOKINE RECEPTOR	C	2.8	8.3	3	20	KVTAMKCFLLELQVISLESG	1909
2Z3R	KL	CYTOKINE/CYTOKINE RECEPTOR	K	2.8	8.3	3	20	KVTAMKCFLLELQVISLESG	1910
3CHX	AB	MEMBRANE PROTEIN	B	4.2	8.3	2	8	LADLVGFH	1911
3CJH	GJ	PROTEIN TRANSPORT	J	1.7	8.3	5	26	SQEEQCLSNCVNRFLDTNIRIVNGLQ	1912
3CJH	IJ	PROTEIN TRANSPORT	J	2.8	8.3	3	20	KQKVQMSIHQFTNICFKKCV	1913
3CUE	OW	PROTEIN TRANSPORT	O	8.3	8.3	1	17	TQVLQYIYSHIYVKYVS	1914
3EAB	BH	CELL CYCLE	B	2.8	8.3	3	28	SMEAERVRVFHKQAFEYISIALRIDEDE	1915
3GHG	JL	BLOOD CLOTTING	J	1.4	8.3	6	113	GCRMKGLIDEVNQDFTNRINKLKNSLFEYQKNNKDSHSLTTNIMEILRG DFSSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQL VDMKRLEVDIDIKIRS	1916
3GJX	BA	PROTEIN TRANSPORT	B	2.1	8.3	4	11	SMEELSQALAS	1917
3H32	DE	BLOOD CLOTTING	E	2.1	8.3	4	40	DETVNSNIPTNLRVLRSILENLRSKIQKLESDVSAQMEYC	1918
3H6P	AD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	1.7	8.3	5	23	YQGWQTQWNQALEDLVRAYQSMS	1919

3HHR	AC	HORMONE/RECEPTOR	A	2.1	8.3	4	28	LSRLFDNAMLRAHRLHQLAFDTYQEFEE	1920
3HJW	AB	ISOMERASE/RNA	B	2.1	8.3	4	12	GEYRRRWKREVL	1921
3KIN	AB	MOTOR PROTEIN	B	1.7	8.3	5	16	EAETKSTLMFGQRAKT	1922
1DIO	AG	LYASE	A	8.2	8.2	1	14	TDVAQDMLNIQKAK	1923
1E6V	DF	OXIDOREDUCTASE	D	1.6	8.2	5	22	MDVVKDVATEVTLYGLEQYERY	1924
1EUC	AB	LIGASE	B	2.7	8.2	3	14	AGLAMATCDIIFLN	1925
1EYX	KL	PHOTOSYNTHESIS	L	2.1	8.2	4	25	NRRMAACLRDGEIILRYISYALLAG	1926
1H2A	SL	OXIDOREDUCTASE	L	2.1	8.2	4	29	PETNLIATAHYLEALRLQVKAARAMAVFG	1927
1HDM	AB	IMMUNE SYSTEM	A	2.1	8.2	4	15	ILFDKEFCEWMIQQI	1928
1I2M	CD	CELL CYCLE	C	2.1	8.2	4	13	VPNWHRDLVRVCE	1929
1IWP	LE	LYASE	E	2.1	8.2	4	19	VRPKFMAKAALFHIKETKH	1930
1J3I	BC	OXIDOREDUCTASE, TRANSFERASE	C	2.1	8.2	4	11	DEEEDDFVYFN	1931
1JEY	AB	DNA BINDING PROTEIN/DNA	B	1.6	8.2	5	14	EAQLNAVDALIDSM	1932
1K6L	LM	PHOTOSYNTHESIS	L	2.1	8.2	4	29	PAHMIAISFFFTNALALALHGALVLSAAN	1933
1KDD	BA	DE NOVO PROTEIN	B	1.4	8.2	6	33	VKQLKAKVEELKSKLWHLKNKVARLKKKNAECK	1934
1KYO	NS	OXIDOREDUCTASE/ELECTRON TRANSPORT	S	2.7	8.2	3	29	KSQFLYVLIPAGIYWYWWKNGNEYNEFLY	1935
1L4A	BC	ENDOCYTOSIS/EXOCYTOSIS	B	1.4	8.2	6	42	TQQAKQTLADIEARHADIMKLETSIRELHDMFMDMAMLVESQ	1936
1M46	AB	CELL CYCLE PROTEIN	B	1.6	8.2	5	24	VLRTITNLQKKIRKELKQRQLKQE	1937
1MJG	BN	OXIDOREDUCTASE	B	2.1	8.2	4	29	PQVAARKILDALEYRTWKLGVHKEVAERY	1938
1NLW	AB	TRANSCRIPTION/DNA	B	1.6	8.2	5	40	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQV	1939
1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	2.1	8.2	4	30	VDTRAYFTSATMIIAIPTGVKVFSWLATLH	1940
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.1	8.2	4	30	VDTRAYFTSATMIIAIPTGVKVFSWLATLH	1941
1OXK	AB	SIGNALING PROTEIN	B	2.7	8.2	3	14	HVNQEVIKRMLNLE	1942
1R4M	EF	CELL CYCLE	E	2.1	8.2	4	21	HTIAAFLGGAAAQEVIKIITK	1943
1RH5	AB	PROTEIN TRANSPORT	B	1.4	8.2	6	37	KDEYLAVAKVTALGISLLGIIGYIIHVPATYIKGILK	1944
1SFC	AD	TRANSPORT PROTEIN	A	1.4	8.2	6	63	RRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGAS QFETSAAKLKRKYWWKN	1945
1T0Q	AB	OXIDOREDUCTASE	A	1.6	8.2	5	32	PGWVSTMQLHFGAIALEEYAASTAEARMARFA	1946
1TQY	GH	TRANSFERASE	H	2.1	8.2	4	15	FDFTHREFRKLWSEG	1947
1VRA	AB	TRANSFERASE	B	2.1	8.2	4	22	WANFYKALQLACEDLAKQIARD	1948
1VZJ	EJ	HYDROLASE	E	4.1	8.2	2	14	ERQWKAEFHRWSSY	1949
1W2W	AB	ISOMERASE	A	1.6	8.2	5	19	TALGVIRSLWKDSLAKTDK	1950
1XLS	EM	TRANSCRIPTION	M	2.1	8.2	4	9	ALLRYLLDK	1951
1YEW	FG	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	1.4	8.2	6	34	HAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT	1952
2FYN	MN	OXIDOREDUCTASE	M	2.1	8.2	4	24	YFIIKDVFALAVVLLVFFAIVGFM	1953

2H61	HG	METAL BINDING PROTEIN, SIGNALING PROTEIN	G	2.1	8.2	4	18	ELEKAMVALIDVFHQYSG	1954
2IAE	DF	HYDROLASE	D	2.7	8.2	3	9	VDVKYFAQE	1955
2NZ0	CD	MEMBRANE PROTEIN	D	4.1	8.2	2	9	AWLPFARAA	1956
2PBI	AB	SIGNALING PROTEIN	A	2.1	8.2	4	15	SSVSLGGIVKYSEQF	1957
2PL9	AD	SIGNALING PROTIEN	D	1.6	8.2	5	11	QDQVDDLLDSL	1958
2Q9Q	FG	REPLICATION	F	2.1	8.2	4	25	PEELAFAREFMANTESYLKNVALKH	1959
2SIV	CD	ENVELOPE GLYCOPROTEIN	C	2.1	8.2	4	35	GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT	1960
2UUN	CD	ELECTRON TRANSPORT	D	2.7	8.2	3	25	SDRMAACLRDMEIILRYVTYAVFAG	1961
2UW1	AB	OXIDOREDUCTASE	B	1.6	8.2	5	15	MRKIEKTIQYLIGSG	1962
2VOI	AB	APOPTOSIS	B	2.1	8.2	4	21	QEEIIHNIARHLAQIGDEMDH	1963
3B5N	GH	MEMBRANE PROTEIN	H	1.6	8.2	5	61	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRLAG	1964
3B5N	JK	MEMBRANE PROTEIN	J	1.4	8.2	6	62	EVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVEDAQ LDVEQGVGHTDKAV	1965
3CUE	IK	PROTEIN TRANSPORT	K	4.1	8.2	2	28	FNKVNDHLYSMGYNIGCRLIEDFLARTA	1966
3EZQ	MN	APOPTOSIS	M	1.6	8.2	5	32	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDI	1967
3FLO	CD	TRANSFERASE	D	1.6	8.2	5	20	PLQLTSQIEHSIRAHISLYY	1968
3GM1	AF	TRANSFERASE	A	1.6	8.2	5	28	PEGYVVVVKNVGLTLRKLIGSVDDLLPS	1969
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	4.1	8.2	2	6	IRARLK	1970
1E1H	CD	HYDROLASE	C	1.6	8.1	5	17	PAVTLAHELIHAEHRLY	1971
1FQV	AB	LIGASE	A	2.0	8.1	4	8	KRWYRLAS	1972
1GXS	AB	LYASE	B	2.7	8.1	3	6	NTIFDQ	1973
1JB0	AB	PHOTOSYNTHESIS	B	2.0	8.1	4	23	SVWAWMFLFGHLVWATGFMFLIS	1974
1JFI	BC	TRANSCRIPTION/DNA	B	2.7	8.1	3	28	EEELLRQQQELFAKARQQQAELAQQEWL	1975
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	B	2.7	8.1	3	25	APYVKDKAEEWRYTDRFLQGYSADG	1976
1Q7L	CD	HYDROLASE	D	2.7	8.1	3	8	DNRYIRAV	1977
1QHH	BC	HYDROLASE	C	2.0	8.1	4	21	IEAQSRLENLDEFLSVTKHFE	1978
1RUY	JK	VIRAL PROTEIN	K	1.6	8.1	5	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKV RS	1979
1RYP	BI	MULTICATALYTIC PROTEINASE	B	2.7	8.1	3	18	GPDYRVLVDKSRKVAHTS	1980
1TUE	AB	REPLICATION	B	2.7	8.1	3	23	PKETLSERLSALQDKIIDHYEND	1981
1VZJ	DI	HYDROLASE	D	4.1	8.1	2	19	TLDEAERQWKAEFHRWSSY	1982
1XK4	EG	METAL BINDING PROTEIN	G	2.0	8.1	4	20	FEEFIMLMARLTWASHEKMH	1983
1YHU	UW	OXYGEN STORAGE/TRANSPORT	W	2.0	8.1	4	20	PEFQGHVVRVMGGLDILINA	1984
1ZBB	AB	STRUCTURAL PROTEIN/DNA	A	2.0	8.1	4	16	KLPFQRLVREIAQDFK	1985
1ZBB	cd	STRUCTURAL PROTEIN/DNA	d	2.0	8.1	4	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1986
1ZBB	CD	STRUCTURAL PROTEIN/DNA	D	2.0	8.1	4	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	1987

1ZDT	AP	TRANSCRIPTION	P	2.0	8.1	4	9	ALLRYLLDK	1988
2B9S	AB	ISOMERASE/DNA	B	2.0	8.1	4	10	PRIICSWAKA	1989
2DXB	TU	HYDROLASE	U	2.7	8.1	3	14	AEDHRVWKDYVHTL	1990
2FHH	YZ	HYDROLASE	Y	2.0	8.1	4	22	FNEFDNLRRGGIQFADTRGYAY	1991
2FJ7	AB	STRUCTURAL PROTEIN/DNA	A	2.0	8.1	4	13	LPFQRLVREIAQD	1992
2IBZ	CG	OXIDOREDUCTASE	G	2.0	8.1	4	30	FKSQFLYVLIPAGIYWYWWKNGNEYNEFLY	1993
2IDO	CD	TRANSFERASE	D	2.7	8.1	3	22	QEERDKVNVDLAASGVAYKERL	1994
2IVF	AB	OXIDOREDUCTASE	A	2.0	8.1	4	11	YHFLSEARYKG	1995
2NZD	CD	STRUCTURAL PROTEIN/DNA	D	2.0	8.1	4	19	ELAKHAVSEGTKAVTKYTS	1996
2P1N	AB	SIGNALING PROTEIN	B	1.6	8.1	5	9	DKDRNSVSL	1997
2PRG	AC	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	C	2.0	8.1	4	8	HKLVQLLT	1998
2QL2	AB	TRANSCRIPTION/DNA	A	1.6	8.1	5	19	KLLILQQAVQVILGLEQQV	1999
2QSH	AX	DNA BINDING PROTEIN/DNA	A	1.4	8.1	6	30	NEERKRRKYFHMLYLVCLMVHGFIRNEWIN	2000
2UUN	QR	ELECTRON TRANSPORT	Q	2.7	8.1	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2001
2W84	AB	PROTEIN TRANSPORT	B	4.1	8.1	2	17	VADLALSENWAQEFLAA	2002
2WAQ	DL	TRANSCRIPTION	L	1.6	8.1	5	22	PKDALLKAIETVRVMASHYIDE	2003
2Z3R	EF	CYTOKINE/CYTOKINE RECEPTOR	E	2.7	8.1	3	20	KVTAMKCFLLELQVISLESG	2004
3BPL	AB	CYTOKINE/CYTOKINE RECEPTOR	A	2.0	8.1	4	26	AQQFHRHKQLIRFLKRLDRNLWGLAG	2005
3CFI	DE	PROTEIN TRANSPORT/IMMUNE SYSTEM	D	2.0	8.1	4	22	YLEQKMFAAMVADNQMAMVMLN	2006
3DCO	NB	MOTOR PROTEIN	B	4.1	8.1	2	23	EMEFTEAESNMNDLVSEYQQYQD	2007
3FKU	CD	VIRAL PROTEIN/IMMUNE SYSTEM	D	1.6	8.1	5	50	IENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	2008
3FKU	KL	VIRAL PROTEIN/IMMUNE SYSTEM	L	2.7	8.1	3	49	ENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	2009
3FWC	EF	CELL CYCLE, TRANSCRIPTION	F	4.1	8.1	2	6	FEKWQA	2010
1AVO	EF	PROTEASOME ACTIVATOR	F	2.0	8.0	4	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	2011
1B33	CD	PHOTOSYNTHESIS	C	2.0	8.0	4	25	QEMTATCLRDLDYYLRLITYGIVAG	2012
1E 44	BA	RIBONUCLEASE	B	4.0	8.0	2	6	FKDYGH	2013
1E1H	CD	HYDROLASE	D	1.6	8.0	5	25	SLQENEFRLYYYNKFKDVASTLNKA	2014
1FYZ	AE	OXIDOREDUCTASE	E	2.0	8.0	4	9	LEELRKQRG	2015
1G2C	GJ	VIRAL PROTEIN	J	2.0	8.0	4	31	SDEFDASISQVNEKINQSLAFIRKSDELLHN	2016
1GH0	MN	PHOTOSYNTHESIS	M	2.7	8.0	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2017
1H2R	SL	OXIDOREDUCTASE	L	2.0	8.0	4	10	PRDAQHFTQR	2018
1HL6	CD	SIGNAL PROTEIN	D	2.7	8.0	3	27	PEGLRCFYYLVQDLKCLVFSLIGLHFK	2019
1HVU	JK	TRANSFERASE/RNA	K	8.0	8.0	1	21	DVKQLTEAVQKITTESIVIWG	2020
1I3Q	AB	TRANSCRIPTION	B	1.6	8.0	5	11	EMERDCMIAHG	2021
1I5K	AC	BLOOD CLOTTING	C	2.7	8.0	3	22	ADAELQRLKNERHEEAELERLK	2022
1ICF	CD	HYDROLASE	C	2.7	8.0	3	12	EKALMKAVATVG	2023

1M63	EF	HYDROLASE/ISOMERASE	E	2.0	8.0	4	12	VFTWSLPFVGEK	2024
1MJG	AM	OXIDOREDUCTASE	A	2.0	8.0	4	29	PQVAARKILDALEYRTWKLGVHKEVAERY	2025
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	B	2.0	8.0	4	26	PTWRTSSCNRYWGAFLFNEYGLFNAH	2026
1MTY	DG	MONOOXYGENASE	G	2.7	8.0	3	20	VNYFLDGERQLGTRLMELRN	2027
1O18	JK	CONTRACTILE PROTEIN	J	2.7	8.0	3	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	2028
1OAO	AD	OXIDOREDUCTASE	A	2.0	8.0	4	16	DLIYSILTQIASDVYG	2029
1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	B	2.0	8.0	4	23	TILPAIILILIALPSLRILYMMD	2030
1OCC	BI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	B	1.3	8.0	6	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	2031
1OCC	OV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	O	1.3	8.0	6	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	2032
1P4E	BC	DNA BINDING PROTEIN/RECOMBINATION/DNA	B	1.6	8.0	5	14	ITDIVSSLQLQFES	2033
1Q5Q	AH	HYDROLASE	H	1.6	8.0	5	23	AGIAIELVRLFAVELEHYEKIEG	2034
1SQX	CG	OXIDOREDUCTASE	G	2.7	8.0	3	42	YFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQEFEKSK	2035
1U35	CD	STRUCTURAL PROTEIN/DNA	D	2.0	8.0	4	18	ELAKHAVSEGTKAVTKYT	2036
1VRQ	AB	OXIDOREDUCTASE	A	4.0	8.0	2	9	VEHIKRYTS	2037
1W1I	BE	HYDROLASE	E	1.6	8.0	5	19	PDEVVSLVNQGLQEGERDF	2038
1XLS	BF	TRANSCRIPTION	B	2.7	8.0	3	29	RFAKLLLRLPALRSIGLKCLEHLFFFKLI	2039
1Z8U	CD	ELECTRON TRANSPORT	C	2.0	8.0	4	21	EEDMVTVVEDWMNFYINYYRQ	2040
1ZLA	BD	PROTEIN BINDING/VIRUS/DNA	D	2.7	8.0	3	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	2041
2BC4	AB	IMMUNE SYSTEM	A	2.0	8.0	4	18	APAILFDKEFCEWMIQQI	2042
2BR2	QR	HYDROLASE	R	2.0	8.0	4	18	RREIELSKVIREALESAV	2043
2DSQ	AC	PROTEIN BINDING/HORMONE/GROWTH FACTOR	A	2.7	8.0	3	7	PLHTLMH	2044
2E 74	BC	PHOTOSYNTHESIS	B	1.6	8.0	5	26	PNDLLYVFPVVIMGTFACIVALSVLD	2045
2E9X	AC	REPLICATION	A	2.0	8.0	4	37	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY	2046
2E9X	FG	REPLICATION	G	2.0	8.0	4	24	NADISQSLLQTFIGRFRRIMDSSQ	2047
2EFC	AB	TRANSPORT PROTEIN	A	2.7	8.0	3	18	EAAYFFTNILSAESFISN	2048
2FJ7	EF	STRUCTURAL PROTEIN/DNA	F	2.0	8.0	4	16	VLKVFLENVIRDAVTY	2049
2HNT	LE	SERINE PROTEASE	L	2.7	8.0	3	8	ERELLESY	2050
2P22	AC	TRANSPORT PROTEIN	C	2.0	8.0	4	25	DIALKKKLEQNTKKLDEESSQLETT	2051
2Q9Q	BC	REPLICATION	B	2.0	8.0	4	25	PEELAFAREFMANTESYLKNVALKH	2052
2RFT	AB	VIRAL PROTEIN	B	1.3	8.0	6	53	NEILELDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLKKMLG	2053
2UZ1	DC	LYASE	D	2.0	8.0	4	10	DTIFQACLDH	2054
2VML	EF	PHOTOSYNTHESIS	E	2.7	8.0	3	25	DTNQAKCARDISHYLRFITYSLVAG	2055

2VML	EF	PHOTOSYNTHESIS	F	2.7	8.0	3	25	NRRMAACLRDMEIILRYVSYALLAG	2056
2ZCY	YZ	HYDROLASE	Y	2.7	8.0	3	22	AADCQFWETWLGSQCRLHELRE	2057
2ZNV	DE	HYDROLASE/SIGNALING PROTEIN	D	2.0	8.0	4	14	SVDLHTHCSYQLML	2058
3B4V	FH	HORMONE REGULATOR COMPLEX	H	2.0	8.0	4	9	KINLLGFLG	2059
3BRV	AB	TRANSFERASE/TRANSCRIPTION	B	2.0	8.0	4	60	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQ EARKLVERLGL	2060
3BVH	DE	BLOOD CLOTTING	D	1.6	8.0	5	30	QHIQLLQKNVRAQLVDMKRLEVDIDIKIRS	2061
3CJT	AB	TRANSFERASE/RIBOSOMAL PROTEIN	A	4.0	8.0	2	8	WLEAWRRD	2062
3CK4	LK	PROTEIN BINDING	K	1.6	8.0	5	29	VKQLEDVVEELLSVNYHLENVVARLKKLV	2063
3DHH	AB	OXIDOREDUCTASE	A	2.7	8.0	3	31	PGWISTLKSHYGAIAVGEYAAVTGEGRMARF	2064
3H0L	MO	LIGASE	M	1.6	8.0	5	15	PEVKRRIMLGTFALS	2065
3HD7	FG	EXOCYTOSIS	F	1.3	8.0	6	96	KQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVE HAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG	2066
3HKZ	OV	TRANSFERASE	O	1.6	8.0	5	24	PERILLEAGKSIIRKIEELEKKLV	2067
1A93	AB	LEUCINE ZIPPER	B	2.0	7.9	4	29	MRRKNDTHQQDIDDLKRQNALLEQQVRAL	2068
1ALL	AB	LIGHT HARVESTING PROTEIN	A	2.6	7.9	3	12	IVTKSIVNADAE	2069
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	A	2.0	7.9	4	14	DYHDYVGTFEFWWN	2070
1BGY	DG	ELECTRON TRANSPORT	D	4.0	7.9	2	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	2071
1BIQ	AB	OXIDOREDUCTASE	A	2.6	7.9	3	31	EHEKHIFISNLKYQTLLDSIQGRSPNVALLP	2072
1BP3	AB	HORMONE/GROWTH FACTOR	A	1.6	7.9	5	31	ALLKNYGLLYCFRKDMDKVETFLRIVQCRSV	2073
1BR1	CD	MUSCLE PROTEIN	C	1.6	7.9	5	21	TDVIIAFQAQCRGYLARKAFA	2074
1BR1	GH	MUSCLE PROTEIN	G	2.0	7.9	4	21	TDVIIAFQAQCRGYLARKAFA	2075
1DIO	LE	LYASE	E	1.6	7.9	5	19	ARPKYQAKSAILHIKETKY	2076
1FNT	OP	HYDROLASE/HYDROLASE ACTIVATOR	P	7.9	7.9	1	6	QIDYAL	2077
1G2C	QR	VIRAL PROTEIN	R	1.6	7.9	5	32	SDEFDASISQVNEKINQSLAFIRKSDELLHNV	2078
1G2C	UV	VIRAL PROTEIN	U	2.0	7.9	4	48	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVN	2079
1GH0	WX	PHOTOSYNTHESIS	W	2.6	7.9	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2080
1HBM	BC	METHANOGENESIS	C	2.6	7.9	3	6	AIREMV	2081
1HVU	GH	TRANSFERASE/RNA	H	7.9	7.9	1	21	DVKQLTEAVQKITTESIVIWG	2082
1I3R	EF	IMMUNE SYSTEM	F	4.0	7.9	2	6	NFLVPR	2083
1IW7	NP	TRANSFERASE	N	2.0	7.9	4	20	EIIIRNEKRMLQEAVDALLD	2084
1LUJ	AB	STRUCTURAL PROTEIN	A	2.0	7.9	4	14	EGVATYAAAVLFRM	2085
1MMO	EH	OXIDOREDUCTASE (MONOOXYGENASE)	E	2.6	7.9	3	10	QWGERMWLAE	2086
1MTY	DG	MONOOXYGENASE	D	2.6	7.9	3	10	QWGERMWLAE	2087
1N4Q	EF	TRANSFERASE	F	2.0	7.9	4	13	EKELNRIKRWCIM	2088
1O18	DE	CONTRACTILE PROTEIN	E	7.9	7.9	1	9	EIKNMWAAF	2089

1O18	MN	CONTRACTILE PROTEIN	N	7.9	7.9	1	12	FTVFLTMFGEKL	2090
1OR0	AB	HYDROLASE	A	4.0	7.9	2	21	PDFRANLDAFAAGINAYAQQN	2091
1Q16	AB	OXIDOREDUCTASE	A	2.6	7.9	3	13	TPDAHFFTEVRYK	2092
1QD6	BD	MEMBRANE PROTEIN	B	2.0	7.9	4	7	IIANMLQ	2093
1R5V	CD	SIGNALING PROTEIN	D	2.0	7.9	4	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	2094
1SFC	CD	TRANSPORT PROTEIN	D	1.3	7.9	6	59	NEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKM	2095
1TI2	CD	OXIDOREDUCTASE	D	1.6	7.9	5	12	NCFMGCMDEHEL	2096
1UM9	AB	OXIDOREDUCTASE	A	2.6	7.9	3	14	VPPAAGAAISMKLL	2097
1UVQ	AC	IMMUNOLOGY	A	2.6	7.9	3	22	PQGALRNMAVAKHNLNIMIKRY	2098
1V29	AB	LYASE	B	1.6	7.9	5	14	EKELEDRTQAFMEK	2099
1XK4	IK	METAL BINDING PROTEIN	K	2.0	7.9	4	20	FEEFIMLMARLTWASHEKMH	2100
1YE9	LP	OXIDOREDUCTASE	P	2.0	7.9	4	11	YYSHPRLFWLS	2101
1Z6O	BN	METAL BINDING PROTEIN	N	2.6	7.9	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2102
1Z6O	FR	METAL BINDING PROTEIN	R	2.6	7.9	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2103
1Z6O	GS	METAL BINDING PROTEIN	S	2.6	7.9	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2104
1Z6O	HT	METAL BINDING PROTEIN	T	2.6	7.9	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2105
1Z6O	KW	METAL BINDING PROTEIN	W	2.6	7.9	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2106
1Z6O	LX	METAL BINDING PROTEIN	X	2.6	7.9	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2107
2A6Q	CF	TOXIN INHIBITOR/TOXIN	C	2.0	7.9	4	14	LEEYNSLEETAYLL	2108
2ACL	AB	TRANSCRIPTION	B	1.6	7.9	5	29	PLMFPRMLMKLVSLRTLSSVHSEQVFALR	2109
2BRU	BC	OXIDOREDUCTASE	B	2.6	7.9	3	10	PEVKEQVQSM	2110
2CLY	AC	HYDROLASE	A	1.6	7.9	5	62	RHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMRQKEQEHMINWVEKRVV	2111
2E1M	BC	OXIDOREDUCTASE	C	2.6	7.9	3	7	RRIEVFY	2112
2GBW	CD	OXIDOREDUCTASE	C	2.6	7.9	3	15	PATKSMIQREAIRTF	2113
2GMI	AB	LIGASE, HUMAN PROTEIN	B	2.6	7.9	3	14	RNFRLLEELEKGEK	2114
2HQS	DE	TRANSPORT PROTEIN/LIPOPROTEIN	E	2.0	7.9	4	22	PEYNISLGERRANAVKMYLQGK	2115
2I2R	JN	TRANSPORT PROTEIN	J	4.0	7.9	2	8	WLPFARAA	2116
2JDQ	BD	PROTEIN TRANSPORT	B	4.0	7.9	2	17	FRTRKEAAWAITNATSG	2117
2NOJ	GH	IMMUNE SYSTEM	H	2.0	7.9	4	13	VATHRKAQRAVNL	2118
2NU9	AB	LIGASE	B	2.0	7.9	4	14	AGLAMGTMDIVKLH	2119
2QE7	AE	HYDROLASE	E	7.9	7.9	1	11	TREGNDLYHEM	2120
2V1S	DK	OXIDOREDUCTASE	D	4.0	7.9	2	25	DLKDAEAVQKFFLEEIQLGEELLAQ	2121
2VE7	BD	CELL CYCLE	B	2.6	7.9	3	23	TWPHIVAALVWLIDCIKIHTAMK	2122
2Z2S	AB	TRANSCRIPTION	A	1.3	7.9	6	18	LGTIKSRIRLALDRLRQH	2123
3CJH	CD	PROTEIN TRANSPORT	D	2.6	7.9	3	20	KQKVQMSIHQFTNICFKKCV	2124
3CXH	NS	OXIDOREDUCTASE	N	1.6	7.9	5	22	VLSKFFFFIFVFNFVLLGQIGA	2125
3DVU	BD	VIRAL PROTEIN/APOPTOSIS	D	2.0	7.9	4	18	TMENLSRRLKVTGDLFDI	2126
3G5O	AB	TOXIN/ANTITOXIN	A	2.0	7.9	4	8	EDEIRAEF	2127

3HRD	AB	OXIDOREDUCTASE	A	2.0	7.9	4	16	LIETLEKAREKAVEVM	2128
1A2X	AB	COMPLEX (SKELETAL MUSCLE/MUSCLE PROTEIN)	B	1.6	7.8	5	28	KRNRAITARRQHLKSVMLQIAATELEKE	2129
1A6A	BC	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)	B	1.6	7.8	5	16	RVDNYCRHNYGVVESF	2130
1ALL	AB	LIGHT HARVESTING PROTEIN	B	2.6	7.8	3	25	TRRYAACIRDLDYYLRYATYAMLAG	2131
1AVO	CD	PROTEASOME ACTIVATOR	D	2.0	7.8	4	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	2132
1B33	HI	PHOTOSYNTHESIS	I	2.6	7.8	3	25	TRRYAACIRDLDYYLRYATYAMLAG	2133
1BGY	PS	ELECTRON TRANSPORT	P	3.9	7.8	2	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	2134
1E7P	HI	OXIDOREDUCTASE	H	2.6	7.8	3	8	DEDYYELI	2135
1FYZ	BD	OXIDOREDUCTASE	D	2.0	7.8	4	25	HAPYVKDKAEEWRYTDRFLQGYSAD	2136
1GH0	OP	PHOTOSYNTHESIS	P	2.6	7.8	3	25	SRRMAACLRDMEIILRYVTYAVFAG	2137
1GK0	AB	HYDROLASE	A	3.9	7.8	2	21	PDFRANLDAFAAGINAYAQQN	2138
1IR2	HM	LYASE	H	2.6	7.8	3	20	WRDRFLFVAEAIYKAQAETG	2139
1IW7	DE	TRANSFERASE	E	2.6	7.8	3	18	KYRLTVVVAKRAQQLLRH	2140
1IZN	CD	PROTEIN BINDING	C	2.6	7.8	3	6	WNKILS	2141
1JD2	EL	HYDROLASE	L	3.9	7.8	2	21	AADGDALVKRFKNSVKWYHFD	2142
1JD2	KL	HYDROLASE	K	2.6	7.8	3	7	AADCQFW	2143
1LIA	KL	LIGHT HARVESTING PROTEIN	K	2.6	7.8	3	25	QEKINKCYRDIDHYMRLINYTLVVG	2144
1N9G	FE	HYDROLASE	F	2.6	7.8	3	7	TSLYIFK	2145
1NBW	CD	HYDROLASE	D	2.6	7.8	3	14	AGAINELCWGLEEQ	2146
1R4M	GH	CELL CYCLE	H	1.6	7.8	5	21	ASTNAVIAAVCATEVFKIATS	2147
1S5L	ad	PHOTOSYNTHESIS	a	2.6	7.8	3	12	IVAAHGYFGRLI	2148
1SA0	CD	CELL CYCLE	C	2.6	7.8	3	8	VHWYVGEG	2149
1SQX	CE	OXIDOREDUCTASE	E	3.9	7.8	2	35	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMS	2150
1TN6	AB	TRANSFERASE	A	3.9	7.8	2	14	YTVWHFRRVLLKSL	2151
1V54	BI	OXIDOREDUCTASE	B	1.6	7.8	5	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	2152
1VCB	KL	TRANSCRIPTION	L	2.0	7.8	4	13	LKERCLQVVRSLV	2153
1Z6O	DP	METAL BINDING PROTEIN	P	2.6	7.8	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2154
1Z6O	JV	METAL BINDING PROTEIN	V	2.6	7.8	3	28	PGFAQLFFDAASEEREHAMKLIEYLLMR	2155
1ZAV	AU	STRUCTURAL PROTEIN	A	1.6	7.8	5	41	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK	2156
2B5I	AC	CYTOKINE/CYTOKINE RECEPTOR	A	3.9	7.8	2	20	IVEFLNRWITFCQSIISTLT	2157
2DD4	KL	HYDROLASE	L	2.0	7.8	4	10	PNYRRRLVRW	2158
2E9X	BD	REPLICATION	D	2.6	7.8	3	32	DLKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	2159
2EY4	AE	ISOMERASE/BIOSYNTHETIC PROTEIN	A	2.6	7.8	3	14	LHDLVDYYYFWKED	2160
2EY4	AE	ISOMERASE/BIOSYNTHETIC PROTEIN	E	2.0	7.8	4	13	GEYRRRWKREVLG	2161
2FHH	BC	HYDROLASE	B	2.0	7.8	4	22	FNEFDNLRRGGIQFADTRGYAY	2162
2FHH	OP	HYDROLASE	O	2.0	7.8	4	22	FNEFDNLRRGGIQFADTRGYAY	2163
2GBW	AB	OXIDOREDUCTASE	B	2.6	7.8	3	11	FGELKQRVERL	2164
2I2X	EF	TRANSFERASE	E	3.9	7.8	2	16	RFETKALADAKAALEA	2165

2IBZ	CG	OXIDOREDUCTASE	C	2.0	7.8	4	22	VLSKFFFFIFVFNFVLLGQIGA	2166
2IO5	BC	CHAPERONE/STRUCTURAL PROTEIN	B	2.0	7.8	4	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	2167
2NXX	AE	HORMONE/GROWTH FACTOR	E	1.1	7.8	7	32	PGTIFAKLLSVLTELRTLGNQNSEMCFSLKLK	2168
2Q9Q	EH	REPLICATION	H	2.0	7.8	4	24	NADISQSLLQTFIGRFRRIMDSSQ	2169
2QM6	CD	TRANSFERASE	D	2.0	7.8	4	15	IITTVLQVISNVIDY	2170
2UUN	KL	ELECTRON TRANSPORT	L	2.6	7.8	3	25	SDRMAACLRDMEIILRYVTYAVFAG	2171
2UVP	AB	UNKNOWN FUNCTION	B	2.0	7.8	4	21	LDYKLLQLFKLFENALFSVLY	2172
2VML	IJ	PHOTOSYNTHESIS	I	2.6	7.8	3	25	DTNQAKCARDISHYLRFITYSLVAG	2173
2WAQ	DL	TRANSCRIPTION	D	1.6	7.8	5	24	RILLEAGKSIIRKIEELEKKLVEV	2174
2Z2T	BE	VIRAL PROTEIN/INHIBITOR	B	2.0	7.8	4	34	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARI	2175
3A0B	bd	ELECTRON TRANSPORT	d	7.8	7.8	1	10	SAPIAVFVSV	2176
3BMC	AC	OXIDOREDUCTASE	A	1.6	7.8	5	21	SLYNMGKHALVGLTQSAALEL	2177
3BZ1	EF	ELECTRON TRANSPORT	E	2.0	7.8	4	24	VRYWVIHSITIPALFIAGWLFVST	2178
3C01	CG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	G	3.9	7.8	2	13	QRALAVRAYAEKV	2179
3C91	PX	HYDROLASE	X	3.9	7.8	2	22	VGDAQVLVRYMKAELELYRLQR	2180
3CFA	SH	FLUORESCENT PROTEIN	S	3.9	7.8	2	6	FDILST	2181
3CJH	CD	PROTEIN TRANSPORT	C	2.0	7.8	4	24	DACIDQCLAKYMRSWNVISKAYIS	2182
3CUE	BD	PROTEIN TRANSPORT	B	2.0	7.8	4	19	LSAMAFLFQEMISQLHRTC	2183
3CXH	DI	OXIDOREDUCTASE	D	2.0	7.8	4	36	EHDERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	2184
3EG5	AB	SIGNALING PROTEIN	A	2.6	7.8	3	9	DRLRPLSYP	2185
3EZQ	OP	APOPTOSIS	O	2.0	7.8	4	33	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	2186
3GE8	DF	OXIDOREDUCTASE	D	2.6	7.8	3	31	PGWISTLKSHYGAIAVGEYAAVTGEGRMARF	2187
3H0L	PR	LIGASE	P	1.3	7.8	6	19	YLKAQKVRRLITNDFLKAF	2188
1BIQ	AB	OXIDOREDUCTASE	B	1.9	7.7	4	19	ISSYYDELIEMTSYWHLLG	2189
1DX5	DP	SERINE PROTEINASE	D	2.6	7.7	3	9	ERELLESYI	2190
1EUC	AB	LIGASE	A	1.9	7.7	4	13	QQDMVRVKHRLLR	2191
1F66	CD	STRUCTURAL PROTEIN/DNA	D	1.9	7.7	4	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	2192
1G0U	AG	HYDROLASE	A	1.9	7.7	4	18	GPDYRVLVDKSRKVAHTS	2193
1GK0	CD	HYDROLASE	C	3.9	7.7	2	21	PDFRANLDAFAAGINAYAQQN	2194
1HBM	AC	METHANOGENESIS	C	1.9	7.7	4	20	VEAVEIMQRIHVLRSQGGFN	2195
1I2M	AB	CELL CYCLE	A	1.9	7.7	4	13	VPNWHRDLVRVCE	2196
1IWP	AG	LYASE	G	2.6	7.7	3	12	DERILAIYNALR	2197
1JH4	AB	RNA BINDING PROTEIN	A	3.9	7.7	2	9	NSELLHMLE	2198
1JTH	CD	ENDOCYTOSIS/EXOCYTOSIS	C	1.3	7.7	6	68	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMKEAEKNL	2199
1K3B	BC	HYDROLASE	B	1.9	7.7	4	18	CYSFASMGMLEARIRILT	2200
1KJY	CD	SIGNALING PROTEIN	D	1.3	7.7	6	12	IEGLVELLNRVQ	2201
1L8C	AB	GENE REGULATION	A	1.5	7.7	5	27	PEKRKLIQQQLVLLLHAHKCQRREQAN	2202
1MDY	AB	TRANSCRIPTION/DNA	B	2.6	7.7	3	18	KVEILRNAIRYIEGLQAL	2203

1MTY	BG	MONOOXYGENASE	G	1.9	7.7	4	20	VNYFLDGERQLGTRLMELRN	2204
1MU2	AB	TRANSFERASE	A	1.9	7.7	4	22	KGSPAIFQHTMRQVLEPFRKAN	2205
1MZN	EF	TRANSCRIPTION	F	1.9	7.7	4	9	KILHRLLQD	2206
1N4Q	CD	TRANSFERASE	D	1.9	7.7	4	15	EKELNRIKRWCIMRQ	2207
1N95	AB	TRANSFERASE	A	2.6	7.7	3	13	NSVWNQRHFVISN	2208
1OCC	NZ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.6	7.7	3	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	2209
1R8Q	BF	PROTEIN TRANSPORT/EXCHANGE FACTOR	F	1.5	7.7	5	19	TDTCYVLSYSVIMLNTDLH	2210
1RYP	J1	MULTICATALYTIC PROTEINASE	J	1.9	7.7	4	17	PEDLFETISQALLNAAD	2211
1T2K	CD	TRANSCRIPTION/DNA	C	1.3	7.7	6	61	KAERKRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANML REQVAQLKQKVMN	2212
1UZH	AT	LYASE	A	1.9	7.7	4	14	AKNYGRAVYECLRG	2213
1W63	BM	ENDOCYTOSIS	B	7.7	7.7	1	11	PYVRKTAAVCV	2214
1YE9	LP	OXIDOREDUCTASE	P	1.9	7.7	4	18	PLLQGRLFSYTDTQISRL	2215
2ADV	AC	HYDROLASE	A	3.9	7.7	2	21	PDFRANLDAFAAGINAYAQQN	2216
2AVU	BE	TRANSCRIPTION ACTIVATOR	B	1.9	7.7	4	22	DDLQQIHTGIMLSTRLLNDVNQ	2217
2BV8	AB	PHOTOSYNTHESIS	A	2.6	7.7	3	24	ATGKAKCARDIGYYLRMVTYCLVV	2218
2E 30	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	B	2.6	7.7	3	21	INEEIHTQFLDHLLTGIEDIC	2219
2E 74	AB	PHOTOSYNTHESIS	A	1.9	7.7	4	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	2220
2E9X	CD	REPLICATION	D	3.9	7.7	2	32	DLKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	2221
2FHH	YZ	HYDROLASE	Z	1.9	7.7	4	23	AAVAVEFARLYAVELEHYEKLEG	2222
2FUG	JL	OXIDOREDUCTASE	L	3.9	7.7	2	17	DVVREAQAGMVEFTLLN	2223
2HL5	AC	STRUCTURAL PROTEIN	A	1.9	7.7	4	37	ELMQQVNVLKLTVEDLEKERDFYFGKLRNIELICQEN	2224
2HOD	GH	BLOOD CLOTTING	G	1.5	7.7	5	12	RLEVDIDIKIRS	2225
2I2R	LO	TRANSPORT PROTEIN	O	1.9	7.7	4	15	KRELQVLYRGFKNEC	2226
2I3T	GH	CELL CYCLE	H	2.6	7.7	3	9	LEEVLAISR	2227
2IDO	AB	TRANSFERASE	B	2.6	7.7	3	22	QEERDKVNVDLAASGVAYKERL	2228
2J3R	AB	TRANSPORT	A	1.5	7.7	5	19	SELFTLTYGALVTQLCKDY	2229
2KA4	AB	TRANSCRIPTION REGULATOR	A	2.6	7.7	3	10	PVCLPLKNAS	2230
2NU9	HI	LIGASE	I	2.6	7.7	3	14	AGLAMGTMDIVKLH	2231
2PMZ	SX	TRANSLATION, TRANSFERASE	S	1.5	7.7	5	24	PERILLEAGKSIIRKIEELEKKLV	2232
2UUN	OP	ELECTRON TRANSPORT	P	2.6	7.7	3	25	SDRMAACLRDMEIILRYVTYAVFAG	2233
2VML	GH	PHOTOSYNTHESIS	G	3.9	7.7	2	25	DTNQAKCARDISHYLRFITYSLVAG	2234
3B63	IJ	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	J	7.7	7.7	1	16	KANREKMTQIMFETFN	2235
3CF4	AG	OXIDOREDUCTASE	G	2.6	7.7	3	9	AHMLGFYLT	2236
3DAC	MP	CELL CYCLE	P	3.9	7.7	2	7	FSDLWKL	2237
3DXC	AB	PROTEIN BINDING	B	1.9	7.7	4	9	PTYKFFEQM	2238

3EZQ	KL	APOPTOSIS	K	2.6	7.7	3	32	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDI	2239
3EZQ	OP	APOPTOSIS	P	1.5	7.7	5	16	NLVADLVQEVQQARDL	2240
3FAL	AB	SIGNALING PROTEIN	A	1.9	7.7	4	12	RLPALRSIGLKC	2241
3GM1	BD	TRANSFERASE	B	2.6	7.7	3	24	PEGYVVVVKNVGLTLRKLIGSVDD	2242
3GTM	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.9	7.7	4	20	VRGIDTLQKKVASILLALTQ	2243
3HRD	EF	OXIDOREDUCTASE	E	3.9	7.7	2	18	VPQASVCHEGQMNALAKA	2244
1APY	CD	HYDROLASE	C	7.6	7.6	1	13	KNATEAAWRALAS	2245
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.9	7.6	4	14	PRQALVLFQYFLQG	2246
1BH8	AB	TRANSCRIPTION REGULATION COMPLEX	A	1.5	7.6	5	25	TESVDILEDLVIEFITEMTHKAMSI	2247
1DML	CD	DNA BINDING PROTEIN/TRANSFERASE	D	3.8	7.6	2	16	AEETRRMLHRAFDTLA	2248
1E1C	AB	ISOMERASE	A	1.9	7.6	4	19	VYNNVVRTCIEAMAATQGH	2249
1E8O	AB	ALU RIBONUCLEOPROTEIN PARTICLE	A	1.9	7.6	4	19	AQDVKKIEKFHSQLMRLMV	2250
1F3J	EQ	IMMUNE SYSTEM	E	1.5	7.6	5	36	ELGRHSAEYYNKQYLERTRAELDTACRHNYEETEVP	2251
1FCC	AC	COMPLEX (ANTIBODY/ANTIGEN)	C	7.6	7.6	1	12	AEKVFKQYANDN	2252
1FOE	GH	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	G	3.8	7.6	2	8	IKPIQRVL	2253
1G2C	AD	VIRAL PROTEIN	D	1.9	7.6	4	30	DEFDASISQVNEKINQSLAFIRKSDELLHN	2254
1HBM	BC	METHANOGENESIS	C	1.9	7.6	4	20	VEAVEIMQRIHVLRSQGGFN	2255
1I7Y	AB	PHOTOSYNTHESIS	A	3.8	7.6	2	25	PEGKAKCARDIGYYLRMITYCLVAG	2256
1ID3	GH	STRUCTURAL PROTEIN/DNA	H	1.9	7.6	4	29	QKSMSILNSFVNDIFERIATEASKLAAYN	2257
1IR2	HM	LYASE	H	1.5	7.6	5	15	AKNYGRAVYECLRGG	2258
1LQB	BC	GENE REGULATION	C	2.5	7.6	3	11	LKERCLQVVRS	2259
1LWU	BC	BLOOD CLOTTING	C	1.5	7.6	5	46	LEEVRILEQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	2260
1RP3	AB	TRANSCRIPTION	A	1.9	7.6	4	14	EREKLVIQLIFYEE	2261
1TUE	KL	REPLICATION	K	1.9	7.6	4	11	WRPIVQFLRYQ	2262
1ULI	EF	OXIDOREDUCTASE	E	1.5	7.6	5	17	VFEQDDGENWVEIQQVL	2263
1UVQ	AB	IMMUNOLOGY	A	1.9	7.6	4	22	PQGALRNMAVAKHNLNIMIKRY	2264
1UW4	DC	RNA BINDING PROTEIN	D	1.5	7.6	5	22	EDVGIHVVDGVLEDIRLGMEVN	2265
1V54	AT	OXIDOREDUCTASE	A	1.9	7.6	4	16	YMGMVWAMMSIGFLGF	2266
1V54	NQ	OXIDOREDUCTASE	N	1.9	7.6	4	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	2267
1VQP	AZ	RIBOSOME	Z	2.5	7.6	3	11	RRVAEIESEMN	2268
1VZJ	FJ	HYDROLASE	F	3.8	7.6	2	19	TLDEAERQWKAEFHRWSSY	2269
1X3Z	AB	HYDROLASE	A	1.9	7.6	4	20	FDSIAKMLLIKYKDFILSKF	2270
1YE9	BF	OXIDOREDUCTASE	F	2.5	7.6	3	17	PFEQRHIVDGFSFELSK	2271
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	A	1.9	7.6	4	10	IFIPRLLMVD	2272

2D0V	DE	OXIDOREDUCTASE	E	2.5	7.6	3	23	KQVESRKGEEERNANRAEHFKKT	2273
2D7D	AB	HYDROLASE/DNA	A	2.5	7.6	3	11	FERAAELRDLL	2274
2DOQ	AD	CELL CYCLE	D	2.5	7.6	3	26	FANQAKLRVQEAVFYIWSDKTLKYSQ	2275
2EHO	AC	REPLICATION	A	3.8	7.6	2	12	PAELIERLEQAW	2276
2FHH	KL	HYDROLASE	K	1.5	7.6	5	22	FNEFDNLRRGGIQFADTRGYAY	2277
2HYI	GH	HYDROLASE/RNA BINDING PROTEIN/RNA	G	2.5	7.6	3	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	2278
2IZV	AC	TRANSCRIPTION	A	1.9	7.6	4	13	LQHICRTVICNCT	2279
2NQB	BD	STRUCTURAL PROTEIN/DNA	D	1.9	7.6	4	12	SREIQTAVRLLL	2280
2NU9	AB	LIGASE	A	1.5	7.6	5	14	TLDMLTVKVKLDEA	2281
2OS8	AB	CONTRACTILE PROTEIN	A	1.9	7.6	4	36	IRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVLRNW	2282
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	A	3.8	7.6	2	15	QGTLFELILAANYLD	2283
2PHE	AC	TRANSCRIPTION	C	2.5	7.6	3	6	FEQMFT	2284
2PMS	BD	METAL TRANSPORT, HYDROLASE	D	1.9	7.6	4	19	PQAKIAELENQVHRLEQEL	2285
2PT7	DH	HYDROLASE/PROTEIN BINDING	D	1.9	7.6	4	30	SAEDKKFLEVERALKEAALNPLRHATEELF	2286
2UUN	WX	ELECTRON TRANSPORT	W	2.5	7.6	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2287
2ZBK	CD	ISOMERASE	D	2.5	7.6	3	29	KRKEQEAKKKLLAYLKYIPEVSRSLATFL	2288
3DBH	EF	CELL CYCLE	E	3.8	7.6	2	9	ATGTEILKN	2289
3DIN	CE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	E	2.5	7.6	3	23	TIISVALIYMVQVQMSKFSELGG	2290
3DTU	AB	OXIDOREDUCTASE	A	1.9	7.6	4	8	ASVDRYYH	2291
3EDL	GF	STRUCTURAL PROTEIN	G	2.5	7.6	3	8	RKLAVNMV	2292
3GBN	BH	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.9	7.6	4	22	QKSTQNAIDGITNKVNSVIEKM	2293
3GHG	DF	BLOOD CLOTTING	F	7.6	7.6	1	21	SRKMLEEIMKYEASILTHDSS	2294
3HKZ	DN	TRANSFERASE	N	3.8	7.6	2	6	INEVIH	2295
1AHJ	AB	LYASE	A	1.9	7.5	4	10	FEYRARVVRE	2296
1B6C	AB	COMPLEX (ISOMERASE/PROTEIN KINASE)	B	1.9	7.5	4	10	LLVQRTIART	2297
1F99	MN	PHOTOSYNTHESIS	M	3.8	7.5	2	24	AIGKAKCARDIGYYLRMVTYCLVV	2298
1GH0	EF	PHOTOSYNTHESIS	E	1.5	7.5	5	27	STEIQVAFGRFRQAKAGLEAAKALTSK	2299
1HBM	AC	METHANOGENESIS	A	1.5	7.5	5	22	MDTVLDVATEVTFYGLEQYEEY	2300
1HBM	AE	METHANOGENESIS	E	2.5	7.5	3	12	MYDANMVKAAVL	2301
1KEN	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	2.5	7.5	3	12	LLVALENQHTID	2302
1KX4	GH	STRUCTURAL PROTEIN/DNA	H	1.9	7.5	4	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	2303
1LDK	AB	LIGASE	A	3.8	7.5	2	23	PKMYVQTVLDVHKKYNALVMSAF	2304
1MTY	EC	MONOOXYGENASE	E	2.5	7.5	3	32	PKWNETMKVVSNFLEVGEYNAIAATGMLWDSA	2305
1N4Q	GH	TRANSFERASE	H	1.9	7.5	4	13	EKELNRIKRWCIM	2306
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	O	1.9	7.5	4	23	TILPAIILILIALPSLRILYMMD	2307

1OCC	NZ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Z	1.9	7.5	4	25	PKEQAIGLSVTFLSFLLPAGWVLYH	2308
1OR0	CD	HYDROLASE	C	3.8	7.5	2	21	PDFRANLDAFAAGINAYAQQN	2309
1Q16	AB	OXIDOREDUCTASE	B	2.5	7.5	3	6	YQNLHT	2310
1QD6	AC	MEMBRANE PROTEIN	A	1.9	7.5	4	7	IIANMLQ	2311
1R5W	AB	SIGNALING PROTEIN	B	2.5	7.5	3	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	2312
1R5W	CD	SIGNALING PROTEIN	D	2.5	7.5	3	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	2313
1RSO	CD	NEUROPEPTIDE/MEMBRANE PROTEIN	D	1.5	7.5	5	17	QHLHTLLDLYDKINTKS	2314
1U6H	AB	CELL ADHESION	B	1.9	7.5	4	21	RKLLSAAKILADATAKMVEAA	2315
1VF5	AB	PHOTOSYNTHESIS	A	1.5	7.5	5	29	GWLIRSIHRWSASMMVLMMILHVFRVYLT	2316
1W63	BM	ENDOCYTOSIS	B	7.5	7.5	1	10	WAQIFILDCL	2317
1XK4	FH	METAL BINDING PROTEIN	F	1.5	7.5	5	19	FQEFLILVIKMGVAAHKKS	2318
1YE9	DH	OXIDOREDUCTASE	H	2.5	7.5	3	13	FHRRELWEAIEAG	2319
1YEW	BC	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.5	7.5	5	34	HAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT	2320
1YHU	AC	OXYGEN STORAGE/TRANSPORT	C	1.5	7.5	5	20	PEFQGHVVRVMGGLDILINA	2321
1YNJ	DK	TRANSFERASE	K	3.8	7.5	2	10	AVTWAMKELL	2322
1ZBB	CD	STRUCTURAL PROTEIN/DNA	D	1.9	7.5	4	18	ELAKHAVSEGTKAVTKYT	2323
2AGH	AB	TRANSCRIPTION	B	1.5	7.5	5	23	RDEYYHLLAEKIYKIQKELEEKR	2324
2AVU	DF	TRANSCRIPTION ACTIVATOR	D	1.5	7.5	5	21	DDLQQIHTGIMLSTRLLNDVN	2325
2B8K	AE	TRANSFERASE	A	7.5	7.5	1	10	LFCCLLRSRL	2326
2BC4	AB	IMMUNE SYSTEM	B	1.9	7.5	4	19	GLQNCATHTQPFWGSLTNR	2327
2BSK	EF	PROTEIN TRANSPORT	E	1.5	7.5	5	27	PEETTCSEHCLQKYLKMTQRISMRFQE	2328
2C9W	AC	TRANSCRIPTION REGULATION	A	1.9	7.5	4	13	LQHLCRLTINKCT	2329
2CKF	EF	OXIDOREDUCTASE	F	1.9	7.5	4	12	FEELKQRVERLY	2330
2DD4	JB	HYDROLASE	B	2.5	7.5	3	18	LTELHNKIVEMRERVASG	2331
2DT7	AB	RNA BINDING PROTEIN	A	1.9	7.5	4	18	EFAEFYNRLKQIKEFHRK	2332
2E9X	BD	REPLICATION	D	1.5	7.5	5	18	PAELIERLEQAWMNEKFA	2333
2E9X	EH	REPLICATION	E	2.5	7.5	3	20	AEEMEWFNNYKRSLATYMRS	2334
2GEZ	CD	HYDROLASE	C	1.9	7.5	4	24	PERRKPREEGLRHCLQIGVEALKA	2335
2GID	AD	TRANSLATION	D	3.8	7.5	2	5	FRQHY	2336
2JIZ	JM	HYDROLASE	J	1.5	7.5	5	14	RSTVAQLVKRLTDA	2337
2QL2	CD	TRANSCRIPTION/DNA	C	1.9	7.5	4	21	KLLILQQAVQVILGLEQQVRE	2338
2UUN	MN	ELECTRON TRANSPORT	M	1.9	7.5	4	27	STEIQVAFGRFRQAAAGLSAATALTSA	2339
2UUN	OP	ELECTRON TRANSPORT	O	2.5	7.5	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2340
2V8F	BC	PROTEIN BINDING	B	3.8	7.5	2	11	WQSYVDNLMCD	2341
2V8Q	AB	TRANSFERASE	A	2.5	7.5	3	15	HTIEFFEMCANLIKI	2342
3CWB	RW	OXIDOREDUCTASE	R	1.9	7.5	4	32	SEDRKGFSYLVTATACVATAYAAKNVVTQFIS	2343
3D3C	AJ	TRANSCRIPTION	A	2.5	7.5	3	21	AARRRARECAVQALYSWQLSQ	2344
3DBJ	GH	PHOTOSYNTHESIS	H	3.8	7.5	2	25	TRRYAACIRDLDYYLRYATYAMLAG	2345

3DCG	BF	LIGASE/VIRAL PROTEIN	F	1.9	7.5	4	11	LQYLALAALIK	2346
3DD7	AB	RIBOSOME INHIBITOR	A	2.5	7.5	3	16	PEELIALHDANISRYG	2347
3EXG	EF	OXIDOREDUCTASE	E	3.8	7.5	2	16	AQVPLGAGIALACKYN	2348
3EZJ	GH	PROTEIN TRANSPORT	G	2.5	7.5	3	15	ERQYYQLFLNLLEAQ	2349
3FBI	AB	TRANSCRIPTION	B	2.5	7.5	3	10	NFKNYLKYLE	2350
3FH6	FG	TRANSPORT PROTEIN	F	2.5	7.5	3	23	VYPGMAGMGLFVLFPLVCTIAIA	2351
3FH6	HI	TRANSPORT PROTEIN	H	2.5	7.5	3	23	VYPGMAGMGLFVLFPLVCTIAIA	2352
3HOY	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.9	7.5	4	23	VDQVVVRGIDTLQKKVASILLAL	2353
1AVO	GH	PROTEASOME ACTIVATOR	H	1.5	7.4	5	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	2354
1AVO	KL	PROTEASOME ACTIVATOR	L	1.9	7.4	4	39	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	2355
1B33	LM	PHOTOSYNTHESIS	M	2.5	7.4	3	25	TRRYAACIRDLDYYLRYATYAMLAG	2356
1C0G	SA	CONTRACTILE PROTEIN	S	1.9	7.4	4	18	QDESGAAAIFTVQLDDYL	2357
1E6V	AC	OXIDOREDUCTASE	A	1.5	7.4	5	22	MDVVKDVATEVTLYGLEQYERY	2358
1EF1	BD	MEMBRANE PROTEIN	D	1.9	7.4	4	18	ERVQKHLKALTSELANAR	2359
1FYZ	CE	OXIDOREDUCTASE	C	1.9	7.4	4	15	SDYNRTVMRNWTGKW	2360
1GH0	EF	PHOTOSYNTHESIS	E	2.5	7.4	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2361
1H1L	CD	OXIDOREDUCTASE	C	3.7	7.4	2	13	DAWASRILLEEMG	2362
1IR2	S4	LYASE	S	1.9	7.4	4	14	AKNYGRAVYECLRG	2363
1IR2	V3	LYASE	V	2.5	7.4	3	20	WRDRFLFVAEAIYKAQAETG	2364
1J1E	AC	CONTRACTILE PROTEIN	A	1.9	7.4	4	12	EEELSDLFRMFD	2365
1JB0	BM	PHOTOSYNTHESIS	B	1.9	7.4	4	25	NGDLYQGAIFLLILASLALFAGWLH	2366
1JB0	BM	PHOTOSYNTHESIS	M	1.5	7.4	5	26	DTQVYVALVIALLPAVLAFRLSTELY	2367
1KX4	EF	STRUCTURAL PROTEIN/DNA	F	2.5	7.4	3	11	KPAIRRLARRG	2368
1L1O	AB	DNA BINDING PROTEIN	B	1.5	7.4	5	18	NEFTTHILEVINAHMVLS	2369
1OXK	GH	SIGNALING PROTEIN	H	2.5	7.4	3	14	HVNQEVIKRMLNLE	2370
1PHN	AB	ELECTRON TRANSPORT	B	2.5	7.4	3	25	NRRMAACLRDMEIILRYVSYAIIAG	2371
1PZL	AB	TRANSCRIPTION	A	1.9	7.4	4	11	LDDQVALLRAH	2372
1SYQ	AB	CELL ADHESION	A	1.5	7.4	5	21	RTIESILEPVAQQISHLVIMH	2373
1TN6	AB	TRANSFERASE	A	1.9	7.4	4	13	NSVWNQRYFVISN	2374
1U0S	YA	SIGNALING PROTEIN	A	2.5	7.4	3	15	KSARIYLVFHKLEEL	2375
1VF5	RS	PHOTOSYNTHESIS	S	7.4	7.4	1	26	EMLYAALLSFGLIFVGWGLGVLLLKI	2376
1W63	BM	ENDOCYTOSIS	B	2.5	7.4	3	15	MVVANRVAALSEIAE	2377
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	I	1.9	7.4	4	10	IFIPRLLMVD	2378
1ZBB	cd	STRUCTURAL PROTEIN/DNA	d	1.9	7.4	4	18	ELAKHAVSEGTKAVTKYT	2379
1ZV8	GH	VIRAL PROTEIN	H	1.5	7.4	5	17	QKEIDRLNEVAKNLNES	2380
2A5D	AB	PROTEIN TRANSPORT/TRANSFERASE	B	3.7	7.4	2	9	RGQSEYFDR	2381
2E9X	AD	REPLICATION	D	2.5	7.4	3	32	DLKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	2382
2FFD	DE	BLOOD CLOTTING	D	1.2	7.4	6	20	RAQLVDMKRLEVDIDIKIRS	2383

2FYZ	EB	PROTEIN BINDING	B	1.9	7.4	4	29	ISTELSKVNASLQNTVKYIKESNHQLQSV	2384
2H9A	AB	OXIDOREDUCTASE	B	1.9	7.4	4	20	YALRAIHWETVTTVALIQAG	2385
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	B	1.5	7.4	5	29	SKAMGIMNSFVNDIFERIAGEASRLAHYN	2386
2HJ9	AC	SIGNALING PROTEIN	A	1.9	7.4	4	12	TRHRKFVEHVLD	2387
2I2X	CD	TRANSFERASE	C	3.7	7.4	2	17	RFETKALADAKAALEAL	2388
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	1.9	7.4	4	12	SFISILIFKGLF	2389
2UUN	IJ	ELECTRON TRANSPORT	I	2.5	7.4	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2390
2V8F	AC	PROTEIN BINDING	A	3.7	7.4	2	12	GWQSYVDNLMCD	2391
2VJH	AB	PHOTOSYNTHESIS	B	2.5	7.4	3	25	NRRMAACLRDGEIVLRYVTYALLAG	2392
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	A	2.5	7.4	3	10	LISWLSFSVL	2393
3C14	AB	LYASE/LYASE INHIBITOR	B	1.9	7.4	4	19	LECLRLLNEIIADFDDLLS	2394
3CUE	UW	PROTEIN TRANSPORT	W	3.7	7.4	2	28	FNKVNDHLYSMGYNIGCRLIEDFLARTA	2395
3DWL	DF	STRUCTURAL PROTEIN	F	2.5	7.4	3	14	LNGRARLVAETYLS	2396
3EN1	AB	OXIDOREDUCTASE	A	1.9	7.4	4	15	DDIKEEFRRQTLRTF	2397
3FBI	CD	TRANSCRIPTION	D	3.7	7.4	2	9	NFKNYLKYL	2398
3FGC	AB	OXIDOREDUCTASE	A	1.9	7.4	4	18	QTEVMKRLVNLGKASEGC	2399
5CSC	AB	OXO-ACID-LYASE	A	7.4	7.4	1	7	AAMNGLA	2400
1AM4	AE	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)	E	7.3	7.3	1	5	AILAA	2401
1B8D	AB	PHOTOSYNTHESIS	B	2.4	7.3	3	25	NRRMAACLRDGEIILRYVSYALLAG	2402
1BGY	OR	ELECTRON TRANSPORT	O	7.3	7.3	1	34	HPYITIGQLASVLYFLLILVLMPTAGTIENKLLK	2403
1FNT	JK	HYDROLASE/HYDROLASE ACTIVATOR	J	3.7	7.3	2	22	ATDVTTLNEMFRYKTNLYKLKE	2404
1GH0	CD	PHOTOSYNTHESIS	C	2.4	7.3	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2405
1GH0	EF	PHOTOSYNTHESIS	F	2.4	7.3	3	12	AFTKVVSQADTR	2406
1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.8	7.3	4	12	DEEVDEMIREAD	2407
1J8H	AB	IMMUNE SYSTEM	A	1.8	7.3	4	22	AQGALANIAVDKANLEIMTKRS	2408
1K8I	AB	IMMUNE SYSTEM	A	1.5	7.3	5	22	ASAIAFDKSFCEMLMREVSPKL	2409
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	3.7	7.3	2	6	SDGFIS	2410
1OCC	AC	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.8	7.3	4	22	PRMNNMSFWLLPPSFLLLLASS	2411
1POI	AD	TRANSFERASE	D	2.4	7.3	3	15	NVRFVGFEINEYLHK	2412
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.8	7.3	4	12	AEHENQYFRDVV	2413
1R6O	BD	HYDROLASE	D	1.8	7.3	4	18	AEVAETKVAMVNKYAREN	2414
1RCO	EM	LYASE	E	2.4	7.3	3	14	AKNYGRAVYECLRG	2415
1U9I	ED	CIRCADIAN CLOCK PROTEIN	D	2.4	7.3	3	11	PQDIIKNARSF	2416
1XK4	FH	METAL BINDING PROTEIN	H	1.8	7.3	4	17	FEEFIMLMARLTWASHE	2417
1XME	AC	OXIDOREDUCTASE	C	1.5	7.3	5	28	KGALAVILVLTLTILVFWLGVYAVFFAR	2418

1YE9	DH	OXIDOREDUCTASE	D	1.8	7.3	4	12	PETLHNVMWAMS	2419
1Z7Q	LM	HYDROLASE/HYDROLASE ACTIVATOR	L	2.4	7.3	3	23	AADCQFWETWLGSQCRLHELREK	2420
2ACL	EF	TRANSCRIPTION	E	1.8	7.3	4	8	TFLMEMLE	2421
2ACL	GH	TRANSCRIPTION	H	1.8	7.3	4	26	LMFPRMLMKLVSLRTLSSVHSEQVFA	2422
2AHM	DH	VIRAL PROTEIN, REPLICATION	H	2.4	7.3	3	68	EVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMADQAMTQMYKQARS EDKRAKVTSAMQTMLFTMLRKLD	2423
2BCJ	BG	TRANSFERASE/HYDROLASE	G	1.8	7.3	4	20	NTASIAQARKLVEQLKMEAN	2424
2C5I	TP	PROTEIN TRANSPORT	T	1.8	7.3	4	23	PFQQVVKDTKEQLNRINNYITRH	2425
2DFS	AD	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	A	1.8	7.3	4	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRD ATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	2426
2F8N	BH	STRUCTURAL PROTEIN/DNA	H	1.8	7.3	4	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	2427
2FF6	GA	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	G	1.8	7.3	4	18	QDESGAAAIFTVQLDDYL	2428
2FHH	FG	HYDROLASE	F	1.8	7.3	4	22	FNEFDNLRRGGIQFADTRGYAY	2429
2FNJ	BC	PROTEIN TRANSPORT/SIGNALING PROTEIN	C	1.8	7.3	4	17	SHVLSKVCMYFTYKVRY	2430
2G30	AP	ENDOCYTOSIS/EXOCYTOSIS	A	2.4	7.3	3	11	RQVFLATWKDI	2431
2GJ7	BE	IMMUNE SYSTEM/VIRUS/VIRAL PROTEIN	B	3.7	7.3	2	6	HQDWLN	2432
2GL7	AB	TRANSCRIPTION	B	1.8	7.3	4	11	RDLADVKSSLV	2433
2I2R	BF	TRANSPORT PROTEIN	F	3.7	7.3	2	14	FEDFVTALSILLRG	2434
2I2R	DG	TRANSPORT PROTEIN	G	2.4	7.3	3	15	KRELQVLYRGFKNEC	2435
2J0Q	FG	HYDROLASE	F	1.8	7.3	4	25	PEGLRVFYYLVQDLKCLVFSLIGLH	2436
2JIY	MH	PHOTOSYNTHESIS	M	1.8	7.3	4	26	MEGIHRWAIWMAVLVTLTGGIGILLS	2437
2JTT	AD	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	D	1.8	7.3	4	10	LMNVLKKIYE	2438
2Q8A	AH	IMMUNE SYSTEM	A	2.4	7.3	3	8	LDEMRHFY	2439
2RF4	CD	TRANSFERASE	D	1.5	7.3	5	18	LSSSISQLKRIQRDFKGL	2440
2UW1	AB	OXIDOREDUCTASE	B	2.4	7.3	3	28	AWAMWTRAWTAEENRHGDLLNKYLYLSG	2441
2VGL	AS	PROTEIN TRANSPORT	S	1.8	7.3	4	12	FYKVYTVVDEMF	2442
2ZET	AC	SIGNALING PROTEIN	C	1.8	7.3	4	42	DEEAEHVWAVVQRDFDLRRREEERLQGLKGKIQKESSKRELL	2443
3A1G	CD	TRANSFERASE	D	2.4	7.3	3	8	RIKELRNL	2444
3BZ1	AI	ELECTRON TRANSPORT	A	1.8	7.3	4	23	WFGVIMIPTLLAATICFVIAFIA	2445
3CRP	DC	PROTEIN BINDING	C	1.5	7.3	5	30	KVKQLEDAVEELLSANYHLENAVARLKKLV	2446
3D3C	CL	TRANSCRIPTION	C	2.4	7.3	3	21	AARRRARECAVQALYSWQLSQ	2447
3DAW	AB	STRUCTURAL PROTEIN/STRUCTURAL PROTEIN RE	B	2.4	7.3	3	10	IRERMLYSSC	2448
3DHH	AB	OXIDOREDUCTASE	A	1.5	7.3	5	21	PGNRNMATFGMMDELRHGQLQ	2449
3E0J	GH	TRANSFERASE	H	2.4	7.3	3	14	GPLFNTDYDILKSN	2450
3EXG	QR	OXIDOREDUCTASE	R	3.7	7.3	2	5	TYYMS	2451

3GE8	AB	OXIDOREDUCTASE	A	2.4	7.3	3	11	RQFDWAWRAYH	2452
3H0L	DF	LIGASE	D	1.8	7.3	4	19	YLKAQKVRRLITNDFLKAF	2453
1B6C	GH	COMPLEX (ISOMERASE/PROTEIN KINASE)	H	1.8	7.2	4	10	LLVQRTIART	2454
1B8D	KL	PHOTOSYNTHESIS	K	1.8	7.2	4	12	VITTTISAADAA	2455
1B9X	AB	SIGNALING PROTEIN	B	2.4	7.2	3	14	VSKCCEEFRDYVEE	2456
1BIQ	AB	OXIDOREDUCTASE	A	2.4	7.2	3	19	ISSYYDELIEMTSYWHLLG	2457
1EYS	LM	ELECTRON TRANSPORT	M	2.4	7.2	3	26	PFHMLSIAFLYGSALLFAMHGATILS	2458
1FYZ	AC	OXIDOREDUCTASE	C	1.8	7.2	4	26	PTWRDEFINRYWGAFLFNEYGLFNAH	2459
1G2C	GJ	VIRAL PROTEIN	G	2.4	7.2	3	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	2460
1G2C	WT	VIRAL PROTEIN	W	1.8	7.2	4	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	2461
1H5R	CB	TRANSFERASE	C	2.4	7.2	3	19	HQSLIEASNFIATIEERQG	2462
1IR2	DL	LYASE	D	3.6	7.2	2	21	NAPGAAANRVALEACTQARNE	2463
1LP1	AB	IMMUNE SYSTEM	B	2.4	7.2	3	13	NKEQQNAFYEILH	2464
1MHY	BG	OXIDOREDUCTASE	G	1.8	7.2	4	21	DYQYIERKIEEKLSVLKTEKL	2465
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	3.6	7.2	2	25	PKWNETMKVVSNFLEVGEYNAIAAT	2466
1PRC	MH	PHOTOSYNTHETIC REACTION CENTER	H	1.4	7.2	5	26	IAQLVWYAQWLVIWTVVLLYLRREDR	2467
1Q5Q	BI	HYDROLASE	I	1.8	7.2	4	23	AGIAIELVRLFAVELEHYEKIEG	2468
1Q5R	BI	HYDROLASE	B	2.4	7.2	3	22	YNEFENLRRAGIVHADMRGYSY	2469
1Q90	BG	PHOTOSYNTHESIS	B	1.4	7.2	5	28	GWLIRSIHRWSASMMVLMMVLHVFRVYL	2470
1RYP	CD	MULTICATALYTIC PROTEINASE	D	2.4	7.2	3	13	FQVEYALEAVKRG	2471
1W2B	FL	RIBOSOME	F	2.4	7.2	3	10	TNETTKSIER	2472
1XDK	AB	HORMONE/GROWTH FACTOR RECEPTOR	A	1.8	7.2	4	21	PAEVEALREKVYASLEAYCKH	2473
1XTG	AB	TOXIN	B	1.8	7.2	4	20	ENLEQVSGIIGNLRHMALDM	2474
1YEW	FG	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	3.6	7.2	2	25	GATVCVLGLLLGEWINRYFNFWGWT	2475
1Z7Q	TU	HYDROLASE/HYDROLASE ACTIVATOR	U	3.6	7.2	2	11	FQVEYAVKAVE	2476
1ZV8	KJ	VIRAL PROTEIN	K	1.4	7.2	5	49	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS	2477
2AK4	FH	IMMUNE SYSTEM	F	7.2	7.2	1	13	TAAQITQRKWEAA	2478
2BSK	AB	PROTEIN TRANSPORT	B	1.4	7.2	5	20	KGESVCLDRCVSKYLDIHER	2479
2D10	CG	CELL ADHESION	G	3.6	7.2	2	11	WSKKNELFSNL	2480
2D1P	DF	TRANSLATION	F	2.4	7.2	3	11	YTDFVRLTVKH	2481
2DWZ	AB	ONCOPROTEIN	B	2.4	7.2	3	14	RRQKRLIFSTITSK	2482
2E 74	AG	PHOTOSYNTHESIS	A	1.8	7.2	4	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	2483
2FHH	IJ	HYDROLASE	I	1.8	7.2	4	22	FNEFDNLRRGGIQFADTRGYAY	2484

2FJ7	AB	STRUCTURAL PROTEIN/DNA	A	1.8	7.2	4	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	2485
2G38	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	2.4	7.2	3	29	DSMLAAARAWRSLDVEMTAVQRSFNRTLL	2486
2GAG	AB	OXIDOREDUCTASE	A	3.6	7.2	2	6	FAALAG	2487
2GBW	EF	OXIDOREDUCTASE	F	2.4	7.2	3	14	FGELKQRVERLYSG	2488
2H8B	BA	HORMONE/GROWTH FACTOR	B	7.2	7.2	1	12	HHFVRALVRVCG	2489
2HV8	AD	PROTEIN TRANSPORT	D	2.4	7.2	3	31	RDELMEAIQKQEEINFRLQDYIDRIIVAIME	2490
2JBL	CM	ELECTRON TRANSPORT	C	2.4	7.2	3	19	PQRAIAWWGIRMVRDLNMN	2491
2JJ0	LM	PHOTOSYNTHESIS	L	3.6	7.2	2	5	ERKYR	2492
2PI2	DH	REPLICATION, DNA BINDING PROTEIN	D	1.8	7.2	4	22	MNEFTTHILEVINAHMVLSKAN	2493
2PMZ	AB	TRANSLATION, TRANSFERASE	A	2.4	7.2	3	34	PTELFFHAAGGREGLVDTAVRTSQSGYMQRRLIN	2494
2QKM	CD	HYDROLASE	C	1.4	7.2	5	19	EDENILRNAVNLQVLKFHY	2495
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	1.8	7.2	4	16	YAWRYVYPGMAGMGLF	2496
2RHS	AD	LIGASE	D	1.8	7.2	4	15	FFIAKGVVDRVAEKL	2497
2UUN	GH	ELECTRON TRANSPORT	G	2.4	7.2	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2498
2VE7	AC	CELL CYCLE	A	2.4	7.2	3	20	NAERLKRLQKSADLYKDRLG	2499
2VJT	AB	PHOTOSYNTHESIS	A	2.4	7.2	3	25	EKMTALCLRDLDYYLRLVTYGIVAG	2500
2ZSH	AB	HORMONE RECEPTOR	A	1.4	7.2	5	18	LNTWVLISNFKVAYNILR	2501
3BVH	DF	BLOOD CLOTTING	D	1.4	7.2	5	30	QHIQLLQKNVRAQLVDMKRLEVDIDIKIRS	2502
3CJH	AD	PROTEIN TRANSPORT	D	1.8	7.2	4	25	SQEEQCLSNCVNRFLDTNIRIVNGL	2503
3CK4	HG	PROTEIN BINDING	G	1.4	7.2	5	30	KVKQLEDVVEELLSVNYHLENVVARLKKLV	2504
3CWB	DJ	OXIDOREDUCTASE	J	2.4	7.2	3	31	TSTFALTVVLGAVLFERAFDQGADAIFEHLN	2505
3CXH	CG	OXIDOREDUCTASE	G	3.6	7.2	2	19	PVLSKLCVPVANQFINLAG	2506
3D48	PR	HORMONE/HORMONE RECEPTOR	P	2.4	7.2	3	34	EESRLSAYYNLLHCLRRDSHKIDNYLKLLKCRII	2507
3DIN	FG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	G	1.4	7.2	5	32	FGVVLVILAVTSVYFFVLDFIFSGVVSAIFKA	2508
3DS3	BD	VIRAL PROTEIN	D	1.8	7.2	4	9	FEDLLDYYG	2509
3DWL	IK	STRUCTURAL PROTEIN	K	1.8	7.2	4	14	LNGRARLVAETYLS	2510
3EBA	AB	IMMUNE SYSTEM/HYDROLASE	B	3.6	7.2	2	11	ADAVACAKRVV	2511
3FXD	CD	UNKNOWN FUNCTION	D	1.4	7.2	5	22	KDNTDAVEVLTELNTKVERAAL	2512
3HKI	DE	HYDROLASE	D	1.8	7.2	4	10	EKELLDSYID	2513
1AHJ	AB	LYASE	A	2.4	7.1	3	15	VSDRAWALFRALDGK	2514
1BGY	CD	ELECTRON TRANSPORT	C	3.6	7.1	2	27	FHPYYTIKDILGALLLILALMLLVLFA	2515
1BXR	CD	AMIDOTRANSFERASE	D	1.8	7.1	4	12	TRKLTRLLREKG	2516
1G20	AB	OXIDOREDUCTASE	B	2.4	7.1	3	16	QDYKDMLAKKRDGFEE	2517
1G2C	UV	VIRAL PROTEIN	V	1.8	7.1	4	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	2518
1GH0	WX	PHOTOSYNTHESIS	X	2.4	7.1	3	25	SRRMAACLRDMEIILRYVTYAVFAG	2519
1H1L	CD	OXIDOREDUCTASE	D	3.6	7.1	2	16	NNNMNLGLQNASALYK	2520
1H5R	CB	TRANSFERASE	B	2.4	7.1	3	19	HQSLIEASNFIATIEERQG	2521
1IZL	AD	PHOTOSYNTHESIS	D	2.4	7.1	3	11	GGALLCAIHGA	2522

1IZN	CD	PROTEIN BINDING	D	1.8	7.1	4	11	GKTKDIVNGLR	2523
1KF6	CD	OXIDOREDUCTASE	D	1.8	7.1	4	17	AIIAPVMILLVGILLPL	2524
1KTD	AB	IMMUNE SYSTEM	B	2.4	7.1	3	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	2525
1LIA	KL	LIGHT HARVESTING PROTEIN	L	2.4	7.1	3	25	NRRMAACLRDGEIILRYVSYALLAG	2526
1M8Q	GI	CONTRACTILE PROTEIN	G	3.6	7.1	2	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	2527
1MMO	DG	OXIDOREDUCTASE (MONOOXYGENASE)	D	2.4	7.1	3	9	WGERMWLAE	2528
1N9G	FE	HYDROLASE	E	2.4	7.1	3	7	TSLYIFK	2529
1OCC	AC	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.8	7.1	4	31	ASVDLTIFSLHLAGVSSILGAINFITTIINM	2530
1Q5R	EL	HYDROLASE	E	2.4	7.1	3	22	YNEFENLRRAGIVHADMRGYSY	2531
1Q90	AL	PHOTOSYNTHESIS	A	3.6	7.1	2	35	PARIQGLLVFFSFVLLTQVLLVLKKKQFEKVQLAE	2532
1R27	AB	OXIDOREDUCTASE	B	2.4	7.1	3	6	YQNLHT	2533
1RCO	RT	LYASE	T	1.8	7.1	4	14	TDQLARQVDYLLNN	2534
1RYP	OU	MULTICATALYTIC PROTEINASE	O	3.6	7.1	2	11	YQVEYAFKATN	2535
1RYP	WX	MULTICATALYTIC PROTEINASE	X	1.8	7.1	4	18	PEDLFETISQALLNAADR	2536
1S9K	DE	TRANSCRIPTION/DNA	D	1.4	7.1	5	51	RIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKE	2537
1SB3	DE	OXIDOREDUCTASE	E	3.6	7.1	2	7	EWWRSGN	2538
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	B	7.1	7.1	1	7	VEEFMSL	2539
1U35	BD	STRUCTURAL PROTEIN/DNA	B	2.4	7.1	3	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	2540
1U35	BD	STRUCTURAL PROTEIN/DNA	D	2.4	7.1	3	29	SKAMGIMNSFVNDIFERIASEASRLAHYN	2541
1W63	JR	ENDOCYTOSIS	J	2.4	7.1	3	11	PYVRKTAAVCV	2542
1X11	BD	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE)	B	2.4	7.1	3	23	AQLIAQSIGQAFSVAYQEFLRAN	2543
2A4J	AB	STRUCTURAL PROTEIN	A	7.1	7.1	1	15	KDTKEEILKAFKLFD	2544
2AK4	AC	IMMUNE SYSTEM	A	7.1	7.1	1	13	TAAQITQRKWEAA	2545
2BMO	AB	OXIDOREDUCTASE	B	1.8	7.1	4	13	YQQLKVRVEHQMD	2546
2BV8	AB	PHOTOSYNTHESIS	B	2.4	7.1	3	25	NRRMAACLRDMEIVLRYVSYAEIAG	2547
2F8N	AB	STRUCTURAL PROTEIN/DNA	A	1.8	7.1	4	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	2548
2F8N	DK	STRUCTURAL PROTEIN/DNA	D	1.8	7.1	4	18	ELAKHAVSEGTKAVTKYT	2549
2FJ7	AB	STRUCTURAL PROTEIN/DNA	B	1.8	7.1	4	11	KPAIRRLARRG	2550
2H9A	AB	OXIDOREDUCTASE	B	1.8	7.1	4	15	PKSLAEVKEHLKRIL	2551
2HVY	CD	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	C	2.4	7.1	3	13	GEYRRRWKREVLG	2552
2HZS	FK	TRANSCRIPTION	K	1.8	7.1	4	11	VDDVLKFTFTG	2553
2I3T	AB	CELL CYCLE	B	1.8	7.1	4	8	LEEVLAIS	2554
2J7A	NO	OXIDOREDUCTASE	N	3.6	7.1	2	10	RNEMRALVCG	2555
2P22	AC	TRANSPORT PROTEIN	C	1.8	7.1	4	29	ADDLDQFIKNYLDIRTQYHLRREKLATWD	2556
2PBI	AB	SIGNALING PROTEIN	A	2.4	7.1	3	14	NLEAQNLGNFIVKY	2557

2Q97	AT	STRUCTURAL PROTEIN/CELL INVASION	T	1.8	7.1	4	15	PEQAKAALLDEILRA	2558
2QIY	AC	SIGNALING PROTEIN/HYDROLASE	C	2.4	7.1	3	16	EAEFAAASVQRYELNM	2559
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	G	1.4	7.1	5	32	QKARLFITHLLLLLFIAAIMFPLLMVVAISLR	2560
2UUN	AB	ELECTRON TRANSPORT	A	2.4	7.1	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2561
2VML	IJ	PHOTOSYNTHESIS	J	2.4	7.1	3	25	NRRMAACLRDMEIILRYVSYALLAG	2562
2VZI	AB	CELL ADHESION	A	1.8	7.1	4	12	TRELDELMASLS	2563
2W73	EO	METAL BINDING PROTEIN	E	1.8	7.1	4	15	EEQIAEFKEAFSLFD	2564
2Z2S	AB	TRANSCRIPTION	A	2.4	7.1	3	19	EAAFAELFQHFAPKVKGFL	2565
2Z2T	CE	VIRAL PROTEIN/INHIBITOR	E	1.8	7.1	4	31	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK	2566
3C0T	AB	TRANSCRIPTION	B	1.4	7.1	5	14	ANQMLTDILSFMKS	2567
3CXH	DF	OXIDOREDUCTASE	F	7.1	7.1	1	5	RLFDK	2568
3DA7	AD	PROTEIN BINDING	D	3.6	7.1	2	9	LDALWDCLT	2569
3DCG	DE	LIGASE/VIRAL PROTEIN	E	1.8	7.1	4	11	LQYLALAALIK	2570
3DD7	AB	RIBOSOME INHIBITOR	B	3.6	7.1	2	9	EFASLFDTL	2571
3DWL	DF	STRUCTURAL PROTEIN	D	1.8	7.1	4	15	TDRIFGKVFLQEFVD	2572
1B9X	AC	SIGNALING PROTEIN	C	1.8	7.0	4	13	PKGVINDWRKFKL	2573
1DCE	AB	TRANSFERASE	B	2.3	7.0	3	10	SDLLGWWLCE	2574
1DE4	DF	METAL TRANSPORT INHIBITOR/RECEPTOR	D	1.8	7.0	4	28	SQMWLQLSQSLKGWDHMFTVDFWTIMEN	2575
1EM8	AB	GENE REGULATION	B	3.5	7.0	2	14	PTARAALWQQICTY	2576
1GH0	IJ	PHOTOSYNTHESIS	I	2.3	7.0	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2577
1I1R	AB	CYTOKINE	B	2.3	7.0	3	27	KDLLIQRLNWMLWVIDECFRDLCYRTG	2578
1I84	VW	CONTRACTILE PROTEIN	V	1.8	7.0	4	21	TDVIIAFQAQCRGYLARKAFA	2579
1ID3	EF	STRUCTURAL PROTEIN/DNA	E	2.3	7.0	3	13	TVALREIRRFQKS	2580
1IR2	BI	LYASE	B	2.3	7.0	3	20	WRDRFLFVAEAIYKAQAETG	2581
1IR2	DL	LYASE	L	3.5	7.0	2	14	DEQIAAQVDYIVAN	2582
1IR2	W6	LYASE	W	3.5	7.0	2	20	WRDRFLFVAEAIYKAQAETG	2583
1IWA	KL	LYASE	L	3.5	7.0	2	14	DEQIKKQIDYMISK	2584
1JOU	EF	BLOOD CLOTTING	E	1.8	7.0	4	6	ERELLE	2585
1KYO	NS	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	1.4	7.0	5	23	VLSKFFFFIFVFNFVLLGQIGAC	2586
1L4A	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.8	7.0	4	30	RLQQTQAQVEEVVDIMRVNVDKVLERDSKI	2587
1L9B	LM	PHOTOSYNTHESIS	M	2.3	7.0	3	27	PFHGLSIAFLYGSALLFAMHGATILAV	2588
1L9J	RS	PHOTOSYNTHESIS	R	7.0	7.0	1	5	PWWAN	2589
1MTY	EH	MONOOXYGENASE	E	2.3	7.0	3	10	QWGERMWLAE	2590
1NDO	AB	NON-HEME IRON DIOXYGENASE	B	2.3	7.0	3	12	FQQLKVRVEHQL	2591
1OCC	AM	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	2.3	7.0	3	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	2592

1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.8	7.0	4	31	ASVDLTIFSLHLAGVSSILGAINFITTIINM	2593
1OR0	AB	HYDROLASE	A	2.3	7.0	3	13	GDNILRLYGEARG	2594
1OR7	BF	TRANSCRIPTION	F	1.8	7.0	4	10	ISSRVMAAIE	2595
1P27	AB	RNA BINDING PROTEIN	A	2.3	7.0	3	26	PEGLRVFYYLVQDLKCLVFSLIGLHF	2596
1Q5R	DK	HYDROLASE	D	2.3	7.0	3	22	YNEFENLRRAGIVHADMRGYSY	2597
1QZ7	AB	CELL ADHESION	A	2.3	7.0	3	16	VKFLAITTDCLQILAY	2598
1TBG	DH	COMPLEX (GTP-BINDING/TRANSDUCER)	H	1.4	7.0	5	17	EKDKLKMEVDQLKKEVT	2599
1TME	13	VIRUS	1	2.3	7.0	3	5	VAFFY	2600
1TQY	EF	TRANSFERASE	F	2.3	7.0	3	15	FDFTHREFRKLWSEG	2601
1TUE	MQ	REPLICATION	M	2.3	7.0	3	14	FITFLGALKSFLKG	2602
1V54	AC	OXIDOREDUCTASE	C	1.4	7.0	5	23	PWPLTGALSALLMTSGLTMWFHF	2603
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	A	1.8	7.0	4	13	LFNKLGVFQAAIL	2604
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	3.5	7.0	2	7	YLWERYR	2605
1YEW	JK	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	1.4	7.0	5	34	HAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT	2606
1YUC	AC	TRANSCRIPTION REGULATION	C	1.8	7.0	4	9	AILYALLSS	2607
1ZV8	KL	VIRAL PROTEIN	K	1.4	7.0	5	49	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS	2608
2B87	AB	PROTEIN BINDING	A	2.3	7.0	3	15	KFNKELGWATWEIFN	2609
2BEZ	CF	VIRAL PROTEIN	C	1.4	7.0	5	74	YENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE	2610
2DD4	BC	HYDROLASE	B	1.8	7.0	4	16	YYGRWLLTAARILVDK	2611
2DFS	AC	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	A	1.8	7.0	4	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRDATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	2612
2E9X	AC	REPLICATION	C	2.3	7.0	3	7	LDDILMS	2613
2EHO	GH	REPLICATION	H	1.8	7.0	4	19	NADISQSLLQTFIGRFRRI	2614
2FHH	DE	HYDROLASE	D	1.8	7.0	4	22	FNEFDNLRRGGIQFADTRGYAY	2615
2FRV	EF	OXIDOREDUCTASE	F	2.3	7.0	3	10	PRDAQHFTQR	2616
2FRV	IJ	OXIDOREDUCTASE	J	2.3	7.0	3	10	PRDAQHFTQR	2617
2H61	HG	METAL BINDING PROTEIN, SIGNALING PROTEIN	H	2.3	7.0	3	19	FQEFMAFVAMVTTACHEFF	2618
2IO5	BC	CHAPERONE/STRUCTURAL PROTEIN	B	1.4	7.0	5	16	KLPFQRLVREIAQDFK	2619
2JBL	LM	ELECTRON TRANSPORT	M	2.3	7.0	3	27	PWHGFSIGFAYGCGLLFAAHGATILAV	2620
2JIY	LM	PHOTOSYNTHESIS	L	2.3	7.0	3	25	TLGIHRLGLLLSLSAVFFSALCMII	2621
2NU9	DE	LIGASE	D	1.8	7.0	4	14	TLDMLTVKVKLDEA	2622
2NU9	HI	LIGASE	H	1.8	7.0	4	14	TLDMLTVKVKLDEA	2623
2OF5	CJ	APOPTOSIS	J	3.5	7.0	2	12	QDVAEEVRAVLE	2624

2PMZ	TU	TRANSLATION, TRANSFERASE	U	3.5	7.0	2	8	KKLLTDVI	2625
2POP	CD	SIGNALING PROTEIN/APOPTOSIS	C	2.3	7.0	3	11	EDELFRLSQLG	2626
2Q9Q	FG	REPLICATION	G	2.3	7.0	3	19	AEEMEWFNNYKRSLATYMR	2627
2Q9Q	GH	REPLICATION	H	1.8	7.0	4	9	LDDILMSHE	2628
2QJK	PQ	ELECTRON TRANSPORT	Q	1.8	7.0	4	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	2629
2QRV	HG	TRANSFERASE/TRANSFERASE REGULATOR	G	1.8	7.0	4	15	PSWYLFQFHRLLQYA	2630
2UUN	CD	ELECTRON TRANSPORT	C	2.3	7.0	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2631
2VRW	AB	SIGNALING PROTEIN	A	2.3	7.0	3	9	DRLRPLSYP	2632
2ZCY	TU	HYDROLASE	U	3.5	7.0	2	11	YQVEYAFKATN	2633
2ZT9	AG	PHOTOSYNTHESIS	G	1.4	7.0	5	28	PLLSGIVLGLIVVTLAGLFYAAYKQYKR	2634
3A0B	ad	ELECTRON TRANSPORT	d	7.0	7.0	1	17	PVTGLWMSAIGVVGLAL	2635
3BEG	AB	TRANSFERASE/SPLICING	A	3.5	7.0	2	13	RDEDHIALIIELL	2636
3BPL	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.8	7.0	4	16	ITLQEIIKTLNSLTEQ	2637
3BVH	EF	BLOOD CLOTTING	F	1.8	7.0	4	23	QEIYNSNNQKIVNLKEKVAQLEA	2638
3C72	AB	TRANSFERASE	B	2.3	7.0	3	10	SDLLGWWLCE	2639
3C7B	AB	OXIDOREDUCTASE	A	1.8	7.0	4	14	TKALRGLCDVWEKW	2640
3CK4	EF	PROTEIN BINDING	F	1.4	7.0	5	30	KVKQLEDVVEELLSVNYHLENVVARLKKLV	2641
3CSY	IJ	IMMUNE SYSTEM/VIRAL PROTEIN	J	3.5	7.0	2	13	ILNRKAIDFLLQR	2642
3CUQ	AB	PROTEIN TRANSPORT	A	1.8	7.0	4	23	VGDFYYELGVQIIEVCLALKHRN	2643
3DAB	AB	CELL CYCLE	B	3.5	7.0	2	8	FSDLWKLL	2644
3DHW	BD	MEMBRANE PROTEIN/HYDROLASE	B	3.5	7.0	2	10	GLIEASRAMG	2645
3DTP	BD	CONTRACTILE PROTEIN	B	1.8	7.0	4	13	FQAQCRGYLARKA	2646
3EJB	EF	OXIDOREDUCTASE/LIPID TRANSPORT	E	1.4	7.0	5	14	LDTVELVMALEEEF	2647
3FWC	FH	CELL CYCLE, TRANSCRIPTION	H	1.8	7.0	4	16	WVDKVKDLTKSEMNIN	2648
3G33	CB	CELL CYCLE	C	1.8	7.0	4	17	ISTVREVALLRRLEAFE	2649
3GBM	DI	VIRAL PROTEIN / IMMUNE SYSTEM	D	2.3	7.0	3	22	KESTQKAIDGVTNKVNSIIDKM	2650
3GE8	AB	OXIDOREDUCTASE	A	2.3	7.0	3	31	PGWISTLKSHYGAIAVGEYAAVTGEGRMARF	2651
1B8D	KL	PHOTOSYNTHESIS	L	2.3	6.9	3	25	NRRMAACLRDGEIILRYVSYALLAG	2652
1BCP	CE	TOXIN	C	1.7	6.9	4	13	YDALRRLLYMIYM	2653
1BGY	OS	ELECTRON TRANSPORT	S	1.7	6.9	4	29	CILRVAPPFVAFYLVYTWGTQEFEKSKRK	2654
1BTH	JK	COMPLEX (SERINE PROTEASE/INHIBITOR)	J	1.7	6.9	4	9	ERELLESYI	2655
1CJF	AC	STRUCTURAL REGULATION PROTEIN	A	3.5	6.9	2	9	WNAYIDNLM	2656
1DGH	CD	OXIDOREDUCTASE	C	2.3	6.9	3	9	QMQHWKEQR	2657
1DIO	AG	LYASE	A	3.5	6.9	2	14	PWSKGFLASSYASR	2658
1EUV	AB	HYDROLASE	A	3.5	6.9	2	14	DTIIEFFMKYIEKS	2659
1FSX	AB	OXYGEN STORAGE/TRANSPORT	B	3.5	6.9	2	20	PENFKLLGNVLVVVLARNFG	2660
1GH0	AB	PHOTOSYNTHESIS	A	2.3	6.9	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2661
1H1L	AB	OXIDOREDUCTASE	A	1.7	6.9	4	15	DKKLSKLIEEMELLF	2662

1H3O	CD	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	C	1.7	6.9	4	24	PDVVSYVSHATQQRLQNLVEKISE	2663
1H4L	BE	KINASE/KINASE ACTIVATOR	E	2.3	6.9	3	15	KEAFWDRCLSVINLM	2664
1I7Q	AB	LYASE	A	2.3	6.9	3	21	HKELAEHLMLVDLARNDLARI	2665
1IRE	AB	LYASE	B	2.3	6.9	3	14	LEELERRTQYYREN	2666
1J1D	AC	CONTRACTILE PROTEIN	C	1.4	6.9	5	20	ASRKLQLKTLLLQIAKQELE	2667
1K3B	BC	HYDROLASE	B	3.5	6.9	2	12	EALMKLELVHHG	2668
1KFY	NO	OXIDOREDUCTASE	O	2.3	6.9	3	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	2669
1LDK	AD	LIGASE	A	2.3	6.9	3	14	SRYMELYTHVYNYC	2670
1LTX	AB	TRANSFERASE/PROTEIN BINDING	A	3.5	6.9	2	24	AAYLDDLRSKFLLENSVLKMEYAD	2671
1LVC	BE	LYASE	E	6.9	6.9	1	8	YEEFVQMM	2672
1LWU	DE	BLOOD CLOTTING	D	1.4	6.9	5	21	QVSQILRVEVDIDVALRACKG	2673
1MTY	DB	MONOOXYGENASE	B	1.7	6.9	4	26	PTWRDEFINRYWGAFLFNEYGLFNAH	2674
1NDO	EF	NON-HEME IRON DIOXYGENASE	F	2.3	6.9	3	12	FQQLKVRVEHQL	2675
1RYP	OU	MULTICATALYTIC PROTEINASE	O	1.7	6.9	4	22	IPDARNAALRAKAEAAEFRYKY	2676
1SA0	AB	CELL CYCLE	A	3.5	6.9	2	8	VHWYVGEG	2677
1SCT	CD	OXYGEN TRANSPORT	D	3.5	6.9	2	19	SKLRGHSITLMYALQNFVD	2678
1SFC	GH	TRANSPORT PROTEIN	G	1.4	6.9	5	45	ESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG	2679
1TUE	KL	REPLICATION	L	3.5	6.9	2	22	KETLSERLSALQDKIIDHYEND	2680
1V29	AB	LYASE	A	1.4	6.9	5	15	SDAIERVIKHYEHEL	2681
1VCB	HI	TRANSCRIPTION	I	1.7	6.9	4	13	LKERCLQVVRSLV	2682
1W2W	MN	ISOMERASE	M	1.7	6.9	4	17	TALGVIRSLWKDSLAKT	2683
1WYU	CD	OXIDOREDUCTASE	D	2.3	6.9	3	13	ELTLVRHYTGLSR	2684
1XL3	BD	CELL INVASION	D	1.7	6.9	4	13	LSEFMGDIVALVD	2685
1Z6O	DR	METAL BINDING PROTEIN	R	2.3	6.9	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2686
1Z6O	HX	METAL BINDING PROTEIN	X	2.3	6.9	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2687
1Z6O	KU	METAL BINDING PROTEIN	U	2.3	6.9	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2688
1Z6O	LV	METAL BINDING PROTEIN	V	2.3	6.9	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2689
1ZY8	JO	OXIDOREDUCTASE	O	2.3	6.9	3	8	PAARNILE	2690
2AGH	BC	TRANSCRIPTION	C	2.3	6.9	3	12	SDIMDFVLKNTP	2691
2AUS	AB	ISOMERASE/STRUCTURAL PROTEIN	A	2.3	6.9	3	14	LHDLVDYYHFWKED	2692
2BR2	UV	HYDROLASE	U	2.3	6.9	3	26	LQDIDQAENTARSTAVKLLEELKKHL	2693
2DOQ	BD	CELL CYCLE	B	3.5	6.9	2	11	IKNLRRVAKEL	2694
2E9X	FH	REPLICATION	F	1.4	6.9	5	23	LMEINTSGTFLTQALNHMYKLRT	2695
2EQB	AB	ENDOCYTOSIS/EXOCYTOSIS	B	2.3	6.9	3	54	NELRTKAEEEADKLNKEVEDLTASLFDEANNMVADARKEKYAIEILNKRLTEQL	2696
2FRV	EF	OXIDOREDUCTASE	E	3.5	6.9	2	5	FWDLY	2697
2FRV	IJ	OXIDOREDUCTASE	I	3.5	6.9	2	5	FWDLY	2698
2FRV	SL	OXIDOREDUCTASE	S	3.5	6.9	2	5	FWDLY	2699

2GHO	CD	TRANSFERASE	D	3.5	6.9	2	5	VLEYF	2700
2GPV	CI	TRANSCRIPTION	I	1.7	6.9	4	11	LEAIIRKALMG	2701
2JFA	AB	TRANSCRIPTION	A	1.4	6.9	5	33	LQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMK	2702
2NU9	DE	LIGASE	E	2.3	6.9	3	14	AGLAMGTMDIVKLH	2703
2PMZ	QR	TRANSLATION, TRANSFERASE	Q	3.5	6.9	2	34	PTELFFHAAGGREGLVDTAVRTSQSGYMQRRLIN	2704
2QL2	AB	TRANSCRIPTION/DNA	A	1.7	6.9	4	28	RMANNARERVRVRDINEAFRELGRMCQL	2705
2QR1	AB	TRANSFERASE	A	2.3	6.9	3	14	FLDLCAMLVCKLFS	2706
2VE7	BD	CELL CYCLE	D	3.5	6.9	2	12	RKFISDYLWSLV	2707
2VML	GH	PHOTOSYNTHESIS	G	1.7	6.9	4	12	VITEVIASADSQ	2708
2VML	KL	PHOTOSYNTHESIS	L	2.3	6.9	3	25	NRRMAACLRDMEIILRYVSYALLAG	2709
2WAX	AB	HYDROLASE	A	2.3	6.9	3	15	ERQKVHCLNTLFSRL	2710
2ZT9	AB	PHOTOSYNTHESIS	A	2.3	6.9	3	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	2711
3BEJ	BF	TRANSCRIPTION REGULATOR	B	6.9	6.9	1	25	HEDQIALLKGSAVEAMFLRSAEIFN	2712
3BZ1	AD	ELECTRON TRANSPORT	A	1.4	6.9	5	16	WADIINRANLGMEVMH	2713
3C7B	DE	OXIDOREDUCTASE	D	1.7	6.9	4	19	FVKEIKKTAELMEKAAAEG	2714
3C91	EL	HYDROLASE	L	2.3	6.9	3	22	VGDAQVLVRYMKAELELYRLQR	2715
3CXH	NR	OXIDOREDUCTASE	R	3.5	6.9	2	19	PVLSKLCVPVANQFINLAG	2716
3DAB	EF	CELL CYCLE	F	3.5	6.9	2	8	FSDLWKLL	2717
3DD7	CD	RIBOSOME INHIBITOR	C	1.7	6.9	4	16	PEELIALHDANISRYG	2718
3EDX	AB	HYDROLASE	A	1.7	6.9	4	8	EKELLDSY	2719
3H32	DE	BLOOD CLOTTING	D	1.7	6.9	4	14	LKDYEDQQKQLEQV	2720
3HKJ	DE	HYDROLASE	D	2.3	6.9	3	10	ERELLESYID	2721
1B33	HI	PHOTOSYNTHESIS	H	2.3	6.8	3	25	QEMTATCLRDLDYYLRLITYGIVAG	2722
1BGY	OP	ELECTRON TRANSPORT	O	1.7	6.8	4	24	FHPYYTIKDILGALLLILALMLLV	2723
1E7P	HL	OXIDOREDUCTASE	L	2.3	6.8	3	8	SILESYSG	2724
1EYS	MH	ELECTRON TRANSPORT	H	3.4	6.8	2	17	LYEEDKVCAYYAGGKLY	2725
1FFU	BC	HYDROLASE	C	2.3	6.8	3	22	ADYKTAMAGQMVKRALNAAWAR	2726
1G5J	AB	APOPTOSIS	A	2.3	6.8	3	14	TAYQSFEQVVNELF	2727
1GH6	AB	ANTITUMOR PROTEIN	B	2.3	6.8	3	13	IIVFYNSVFMQRL	2728
1IHF	AB	TRANSCRIPTION/DNA	A	2.3	6.8	3	12	KAEMSEYLFDKL	2729
1IWA	KL	LYASE	K	3.4	6.8	2	21	IQAGATANRVALEAMILARNE	2730
1JNR	CD	OXIDOREDUCTASE	C	3.4	6.8	2	14	YKPIIAEAAKMAVG	2731
1KXP	AD	CONTRACTILE PROTEIN/PROTEIN BINDING	D	1.7	6.8	4	33	PTVCFLKERLQLKHLSLLTTLSNRVCSQYAAYG	2732
1NH2	BD	TRANSCRIPTION/DNA	D	2.3	6.8	3	16	TIGNSLVDALDTLISD	2733
1OCC	CG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	1.4	6.8	5	25	VPLLNTSVLLASGVSITWAHHSLME	2734
1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.7	6.8	4	22	PRMNNMSFWLLPPSFLLLLASS	2735
1OXK	GH	SIGNALING PROTEIN	G	1.7	6.8	4	26	FSKGLIIQFIDQAQTTFAQMQRQLDG	2736

1Q5Q	GN	HYDROLASE	N	2.3	6.8	3	23	AGIAIELVRLFAVELEHYEKIEG	2737
1R27	CD	OXIDOREDUCTASE	D	2.3	6.8	3	6	YQNLHT	2738
1S5L	ad	PHOTOSYNTHESIS	d	3.4	6.8	2	21	FYTKNLLLNEGIRAWMAPQDQ	2739
1SCT	GH	OXYGEN TRANSPORT	H	3.4	6.8	2	20	SKLRGHSITLMYALQNFVDA	2740
1T0Q	AB	OXIDOREDUCTASE	B	1.7	6.8	4	17	ARYLFHALQMGSVYIHQ	2741
1TBG	CG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	1.7	6.8	4	17	EKDKLKMEVDQLKKEVT	2742
1TBG	DH	COMPLEX (GTP-BINDING/TRANSDUCER)	D	1.7	6.8	4	22	LDQLRQEAEQLKNQIRDARKAC	2743
1WDK	AC	LYASE,OXIDOREDUCTASE/TRANSFERASE	A	3.4	6.8	2	17	AIEQMMAFETAKGFVAG	2744
1Z6O	AO	METAL BINDING PROTEIN	O	2.3	6.8	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2745
1Z6O	GW	METAL BINDING PROTEIN	W	2.3	6.8	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2746
1Z6O	JT	METAL BINDING PROTEIN	T	2.3	6.8	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	2747
1Z7Q	DE	HYDROLASE/HYDROLASE ACTIVATOR	E	3.4	6.8	2	13	FQVEYSLEAIKLG	2748
1Z7Q	FG	HYDROLASE/HYDROLASE ACTIVATOR	G	3.4	6.8	2	11	FQVEYAVKAVE	2749
1Z8U	AB	ELECTRON TRANSPORT	A	1.7	6.8	4	19	EEDMVTVVEDWMNFYINYY	2750
1ZV8	EF	VIRAL PROTEIN	F	1.4	6.8	5	17	QKEIDRLNEVAKNLNES	2751
2AFH	AB	OXIDOREDUCTASE	A	1.7	6.8	4	15	DKKLAKLIDEVETLF	2752
2AHM	AE	VIRAL PROTEIN, REPLICATION	A	1.7	6.8	4	20	TTEAFEKMVSLLSVLLSMQG	2753
2BBV	AD	VIRUS/RNA	D	1.7	6.8	4	12	MWERVKSIIKSS	2754
2BGN	BE	HYDROLASE	E	2.3	6.8	3	19	PDEVVSLVNQGLQEGERDF	2755
2DD4	HI	HYDROLASE	I	2.3	6.8	3	14	AEDHRVWKDYVHTL	2756
2FFD	AC	BLOOD CLOTTING	C	1.4	6.8	5	36	ILTHDSSIRYLQEIYNSNNQKIVNLKEKVAQLEAQC	2757
2FUG	49	OXIDOREDUCTASE	9	6.8	6.8	1	6	LCEEAC	2758
2FUG	AC	OXIDOREDUCTASE	C	3.4	6.8	2	17	DVVREAQAGMVEFTLLN	2759
2GOX	CD	CELL ADHESION/TOXIN	D	2.3	6.8	3	14	VSAHRKAQKAVNLV	2760
2HQW	AB	METAL BINDING PROTEIN	A	3.4	6.8	2	9	YEEFVQMMT	2761
2I0Q	AB	STRUCTURAL PROTEIN/DNA	B	1.4	6.8	5	23	DEFKTTIQHFRHTALQAAINKTV	2762
2IPK	BC	IMMUNE SYSTEM	B	3.4	6.8	2	13	AVDTYCRHNYGVG	2763
2JFA	AP	TRANSCRIPTION	P	2.3	6.8	3	13	AFQLRQLILRGLQ	2764
2JJ0	MH	PHOTOSYNTHESIS	H	3.4	6.8	2	19	LLEEDKICGYVAGGLMYAA	2765
2PBD	PV	STRUCTURAL PROTEIN	P	3.4	6.8	2	9	WNAYIDNLM	2766
2QFA	AC	CELL CYCLE/CELL CYCLE/CELL CYCLE	A	1.7	6.8	4	43	LGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA	2767
2R1H	AB	OXYGEN BINDING	B	2.3	6.8	3	16	VDEIGPQALARLLIVS	2768
2UUN	QR	ELECTRON TRANSPORT	Q	2.3	6.8	3	12	PLTDAVSTADSQ	2769
2V4J	DE	OXIDOREDUCTASE	D	1.7	6.8	4	14	ADYLRQLCDIWDLR	2770
2V6X	AB	PROTEIN TRANSPORT	A	2.3	6.8	3	31	PKSKDLIRAKFTEYLNRAEQLKKHLESEEAN	2771
2V7Q	GH	HYDROLASE	G	2.3	6.8	3	75	ADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDK LTLTFNRTRQAVITKELIEIISGAAAL	2772

2VML	EF	PHOTOSYNTHESIS	E	1.7	6.8	4	12	VITEVIASADSQ	2773
2VML	IJ	PHOTOSYNTHESIS	I	2.3	6.8	3	12	VITEVIASADSQ	2774
2VOH	AB	APOPTOSIS	A	2.3	6.8	3	23	WGRIVTIFAFGGVLLKKLKQEQI	2775
2WAX	AB	HYDROLASE	B	2.3	6.8	3	12	KAAVFEEIDTYE	2776
2Z3R	OP	CYTOKINE/CYTOKINE RECEPTOR	O	3.4	6.8	2	20	KVTAMKCFLLELQVISLESG	2777
2ZCY	FG	HYDROLASE	G	3.4	6.8	2	11	YQVEYAFKATN	2778
2ZT9	BC	PHOTOSYNTHESIS	C	1.7	6.8	4	35	ANRVGWLIAFVALVMLAQVMLVLKKKQVEKVQAAE	2779
3BMC	AC	OXIDOREDUCTASE	C	1.7	6.8	4	21	SLYNMGKHALVGLTQSAALEL	2780
3BRT	CD	TRANSFERASE/TRANSCRIPTION	D	1.7	6.8	4	60	LQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQE ARKLVERLGLE	2781
3CXH	OQ	OXIDOREDUCTASE	Q	2.3	6.8	3	17	VEEFFHLQHYLDTATAP	2782
3DBJ	EF	PHOTOSYNTHESIS	F	3.4	6.8	2	13	AITAVINASDVQG	2783
3EX7	HI	HYDROLASE/RNA BINDING PROTEIN/RNA	H	2.3	6.8	3	11	FKEQIYDVYRY	2784
3F9K	gi	VIRAL PROTEIN, RECOMBINATION	g	1.7	6.8	4	12	IEPAQEEHEKYH	2785
3FLO	GH	TRANSFERASE	H	1.7	6.8	4	20	PLQLTSQIEHSIRAHISLYY	2786
3GE8	DF	OXIDOREDUCTASE	F	2.3	6.8	3	12	PMNLWYKQYRNA	2787
3GTM	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	2.3	6.8	3	11	DEFIAHRLGLI	2788
3H0L	SU	LIGASE	S	1.7	6.8	4	19	YLKAQKVRRLITNDFLKAF	2789
3H6P	BC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	C	1.7	6.8	4	24	YQGWQTQWNQALEDLVRAYQSMSG	2790
1AHJ	CD	LYASE	D	3.4	6.7	2	16	YYERYVIGVATLMVEK	2791
1AOK	AB	HYDROLASE	A	3.4	6.7	2	13	LFQFGDMILQKTG	2792
1BIQ	AB	OXIDOREDUCTASE	B	2.2	6.7	3	32	EHEKHIFISNLKYQTLLDSIQGRSPNVALLPL	2793
1BX2	EF	IMMUNE SYSTEM	E	1.7	6.7	4	22	KDILEQARAAVDTYCRHNYGVV	2794
1DIO	LM	LYASE	L	3.4	6.7	2	17	TDVAQDMLNIQKAKLTG	2795
1E1H	AB	HYDROLASE	B	3.4	6.7	2	15	KLKFDKLYKMLTEIY	2796
1F99	KL	PHOTOSYNTHESIS	L	2.2	6.7	3	25	SRRMAACLRDMEIVLRYVSYAMIAG	2797
1FNT	Tb	HYDROLASE/HYDROLASE ACTIVATOR	b	3.4	6.7	2	18	PSYIFEYLATVMYQRRSK	2798
1FOE	GH	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	G	6.7	6.7	1	8	KVASHINE	2799
1G2C	IJ	VIRAL PROTEIN	J	1.7	6.7	4	31	SDEFDASISQVNEKINQSLAFIRKSDELLHN	2800
1GH0	AB	PHOTOSYNTHESIS	A	1.7	6.7	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	2801
1GH0	KL	PHOTOSYNTHESIS	K	1.7	6.7	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	2802
1GH0	WX	PHOTOSYNTHESIS	W	1.7	6.7	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	2803
1GH0	WX	PHOTOSYNTHESIS	X	1.7	6.7	4	13	AFTKVVSQADTRG	2804
1GXS	CD	LYASE	D	3.4	6.7	2	6	NTIFDQ	2805
1HE1	AC	SIGNALING PROTEIN	A	1.7	6.7	4	25	SSAVVFKQMVLQQALPMTLKGLDKA	2806
1IB1	DH	SIGNALING PROTEIN/TRANSFERASE	D	1.7	6.7	4	32	NEERNLLSVAYKNVVGARRSSWRVVSSIEQKT	2807

1ID3	AB	STRUCTURAL PROTEIN/DNA	A	2.2	6.7	3	16	KLPFQRLVREIAQDFK	2808
1IR2	DK	LYASE	D	1.7	6.7	4	14	AKNYGRAVYECLRG	2809
1IRE	AB	LYASE	B	1.3	6.7	5	14	PELIEFVNQAVYGG	2810
1JPW	CF	CELL ADHESION	C	3.4	6.7	2	16	VKFLAITTDCLQILAY	2811
1JSU	AB	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.7	6.7	4	15	HEDIHTYLREMEVKC	2812
1JY2	NP	BLOOD CLOTTING	P	1.7	6.7	4	27	TCGIADFLNNYQTSVDKDLRTLEGILY	2813
1KYO	CH	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	2.2	6.7	3	36	VPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	2814
1LP1	AB	IMMUNE SYSTEM	A	1.7	6.7	4	14	DPQKKAFIFSLWDD	2815
1M8Q	AC	CONTRACTILE PROTEIN	A	1.1	6.7	6	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	2816
1MMO	DG	OXIDOREDUCTASE (MONOOXYGENASE)	G	2.2	6.7	3	9	LEELRKQRG	2817
1N4Q	CD	TRANSFERASE	C	3.4	6.7	2	13	KEYWRYIGRSLQS	2818
1N86	BC	BLOOD CLOTTING	B	1.3	6.7	5	32	PTNLRVLRSILENLRSKIQKLESDVSAQMEYC	2819
1NWD	AB	BINDING PROTEIN/HYDROLASE	B	2.2	6.7	3	20	DSEVQLEMITAWKKFVEEKK	2820
1NX0	AC	HYDROLASE	C	2.2	6.7	3	9	AIDALSSDF	2821
1O18	DE	CONTRACTILE PROTEIN	E	3.4	6.7	2	12	EDVIMGAFKVLD	2822
1O96	AB	ELECTRON TRANSFER	A	1.7	6.7	4	16	ISEQAAKIIQIINEFK	2823
1OCC	PT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	1.3	6.7	5	25	VPLLNTSVLLASGVSITWAHHSLME	2824
1OHZ	AB	CELL ADHESION	B	1.7	6.7	4	12	STDVLLLSRYLL	2825
1R4M	EF	CELL CYCLE	F	1.7	6.7	4	21	ASTNAVIAAVCATEVFKIATS	2826
1RHI	34	VIRUS	4	2.2	6.7	3	6	PSKFTE	2827
1RP3	CD	TRANSCRIPTION	C	2.2	6.7	3	13	EREKLVIQLIFYE	2828
1RU7	CB	VIRAL PROTEIN	B	2.2	6.7	3	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	2829
1RYP	BI	MULTICATALYTIC PROTEINASE	I	2.2	6.7	3	22	AADTEAVTQLIGSNIELHSLYT	2830
1RYP	LM	MULTICATALYTIC PROTEINASE	M	6.7	6.7	1	15	INSAARNIQHLLYGK	2831
1SB3	AC	OXIDOREDUCTASE	A	2.2	6.7	3	22	PLAVEGQTQGGVWMGMGQALSE	2832
1SFC	JL	TRANSPORT PROTEIN	J	2.2	6.7	3	65	EIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQ	2833
1SQB	CD	OXIDOREDUCTASE	C	1.7	6.7	4	20	TIKDILGALLLILALMLLVL	2834
1SQX	EJ	OXIDOREDUCTASE	J	2.2	6.7	3	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	2835
1V54	QX	OXIDOREDUCTASE	Q	1.3	6.7	5	14	EEWVAKQTKRMLDM	2836
1VG9	EF	PROTEIN BINDING/PROTEIN TRANSPORT	E	1.7	6.7	4	15	QGELPQCFCRMCAVF	2837
1W2B	FL	RIBOSOME	L	2.2	6.7	3	9	AYSYIREAW	2838
1XB2	AB	TRANSLATION	A	2.2	6.7	3	14	ELVELEIRELLTEF	2839
1YTZ	IC	CONTRACTILE PROTEIN	C	1.3	6.7	5	33	FEEFLVMMVRQMKEDAKGKSEEELANCFRIFDK	2840

1Z7Q	RS	HYDROLASE/HYDROLASE ACTIVATOR	S	3.4	6.7	2	13	FQVEYSLEAIKLG	2841
1ZOY	AB	OXIDOREDUCTASE	B	3.4	6.7	2	8	IEEREKLD	2842
2A19	AB	PROTEIN SYNTHESIS/TRANSFERASE	B	3.4	6.7	2	12	AFETSKFFTDLR	2843
2A6Q	CF	TOXIN INHIBITOR/TOXIN	F	2.2	6.7	3	12	EESWDDYLYWQE	2844
2ACL	GH	TRANSCRIPTION	G	3.4	6.7	2	13	RLPALRSIGLKCL	2845
2AFH	CD	OXIDOREDUCTASE	C	2.2	6.7	3	7	VGCGQYS	2846
2AXT	LT	ELECTRON TRANSPORT	L	2.2	6.7	3	21	RTSLYLGLLLILVLALLFSSY	2847
2BA1	FI	RNA BINDING PROTEIN	F	1.7	6.7	4	35	RDEVKQAIELAKKGALQIYEMQREAILRRYIEVGE	2848
2BR2	UV	HYDROLASE	V	1.7	6.7	4	29	PDEFRQAFDLAVKGINIIYNLEREALKSK	2849
2BV8	AB	PHOTOSYNTHESIS	A	1.7	6.7	4	12	PITEAIASADSQ	2850
2C1M	AB	PROTEIN TRANSPORT/MEMBRANE PROTEIN	A	2.2	6.7	3	15	TNIQKEATWTMSNIT	2851
2D2M	AD	OXYGEN STORAGE/TRANSPORT	D	1.7	6.7	4	19	PEFLAQVSRVVSGADIAIN	2852
2E 74	BC	PHOTOSYNTHESIS	C	1.7	6.7	4	37	PNRVKWMIAFICLVMLAQLMLILKKKQVEKVQAAEMN	2853
2EFC	CD	TRANSPORT PROTEIN	C	3.4	6.7	2	18	EAAYFFTNILSAESFISN	2854
2ERJ	FH	IMMUNE SYSTEM/CYTOKINE	H	1.7	6.7	4	17	PRDLISNINVIVLELKG	2855
2FUG	MN	OXIDOREDUCTASE	M	3.4	6.7	2	6	FEKTME	2856
2FYZ	AD	PROTEIN BINDING	D	1.7	6.7	4	28	ISTELSKVNASLQNTVKYIKESNHQLQS	2857
2FYZ	EF	PROTEIN BINDING	F	2.2	6.7	3	32	GGIDISTELSKVNASLQNTVKYIKESNHQLQS	2858
2HV8	BE	PROTEIN TRANSPORT	E	2.2	6.7	3	33	RDELMEAIQKQEEINFRLQDYIDRIIVAIMETN	2859
2HYB	JL	TRANSFERASE	L	2.2	6.7	3	11	YAGFVDLTTEC	2860
2I2R	BF	TRANSPORT PROTEIN	B	3.4	6.7	2	8	WLPFARAA	2861
2KA6	AB	TRANSCRIPTION REGULATOR	A	2.2	6.7	3	22	PQESRRLSIQRCIQSLVHACQC	2862
2NU9	FG	LIGASE	F	1.7	6.7	4	14	TLDMLTVKVKLDEA	2863
2PMZ	QG	TRANSLATION, TRANSFERASE	G	6.7	6.7	1	8	VVENIIIG	2864
2Q9Q	AB	REPLICATION	A	1.7	6.7	4	11	AAEVEFLAEKE	2865
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	2.2	6.7	3	31	PTTARTMLIIVNTWLGYPYMMILCMGLLKAI	2866
2UUN	IJ	ELECTRON TRANSPORT	I	1.7	6.7	4	27	STEIQVAFGRFRQAAAGLSAATALTSA	2867
2VSO	AE	HYDROLASE/TRANSLATION	A	3.4	6.7	2	9	ENLLRGVFG	2868
2ZHX	GH	HYDROLASE/HYDROLASE INHIBITOR	H	1.7	6.7	4	9	PEEVEEVIG	2869
2ZIV	AB	HYDROLASE	B	2.2	6.7	3	7	TFSFCLE	2870
3B5N	CD	MEMBRANE PROTEIN	C	1.3	6.7	5	68	SIKFTKQSSVASTRNTLKMAQDAERAGMNTLGMLGHQSEQLNNVEGN LDLMKVQNKVADEKVAELKKL	2871
3B9J	JK	OXIDOREDUCTASE	J	2.2	6.7	3	24	IEFRRTLTLSFFFKFYLTVLKKLG	2872
3BVH	EF	BLOOD CLOTTING	E	1.7	6.7	4	25	RSILENLRSKIQKLESDVSAQMEYC	2873
3BZ1	AC	ELECTRON TRANSPORT	A	6.7	6.7	1	7	WELSYRL	2874
3C1B	GH	STRUCTURAL PROTEIN/DNA	H	2.2	6.7	3	19	ELAKHAVSEGTKAVTKYTS	2875
3CXH	OQ	OXIDOREDUCTASE	Q	6.7	6.7	1	5	RLFDK	2876
3DA7	BC	PROTEIN BINDING	C	3.4	6.7	2	9	LDALWDCLT	2877
3DL8	AG	PROTEIN TRANSPORT	A	2.2	6.7	3	17	VALNHHINQALKAHVAM	2878

3DVE	AB	MEMBRANE PROTEIN	A	2.2	6.7	3	11	EAELQDMINEV	2879
3EAB	BH	CELL CYCLE	H	1.3	6.7	5	22	SVGTSVASAEQDELSQRLARLR	2880
3GHG	AB	BLOOD CLOTTING	A	1.3	6.7	5	63	SSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVD MKRLEVDIDIKIRSC	2881
3GTM	AK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.2	6.7	3	11	LDQVLNMLYWV	2882
3H0L	SU	LIGASE	S	1.7	6.7	4	15	PEVKRRIMLGTFALS	2883
3H0L	VX	LIGASE	V	1.7	6.7	4	15	PEVKRRIMLGTFALS	2884
4RUB	CV	LYASE(CARBON-CARBON)	C	1.7	6.7	4	20	WRDRFLFCAEALYKAQAETG	2885
1BXR	EF	AMIDOTRANSFERASE	F	1.7	6.6	4	11	TRKLTRLLREK	2886
1DFK	AZ	CONTRACTILE PROTEIN	A	2.2	6.6	3	32	VLGNLEEMRDERLSKIISMFQAHIRGYLIRKA	2887
1DGH	CD	OXIDOREDUCTASE	D	2.2	6.6	3	8	QMQHWKEQ	2888
1E7P	BF	OXIDOREDUCTASE	F	2.2	6.6	3	8	SILESYSG	2889
1F99	AB	PHOTOSYNTHESIS	A	2.2	6.6	3	24	AIGKAKCARDIGYYLRMVTYCLVV	2890
1FCC	BD	COMPLEX (ANTIBODY/ANTIGEN)	D	6.6	6.6	1	12	AEKVFKQYANDN	2891
1FFU	DE	HYDROLASE	E	3.3	6.6	2	11	RYIAADAVEAV	2892
1FLC	CD	HYDROLASE	D	1.7	6.6	4	24	KGFEKIGNDIQILKSSINIAIEKL	2893
1G2C	EF	VIRAL PROTEIN	F	1.7	6.6	4	31	SDEFDASISQVNEKINQSLAFIRKSDELLHN	2894
1GG2	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	1.7	6.6	4	16	IAQARKLVEQLKMEAN	2895
1GH0	UV	PHOTOSYNTHESIS	U	2.2	6.6	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2896
1H1L	AB	OXIDOREDUCTASE	B	2.2	6.6	3	16	QGCVAYFRTYFNRHFK	2897
1H2R	SL	OXIDOREDUCTASE	L	1.7	6.6	4	29	PETNLIATAHYLEALRLQVKAARAMAVFG	2898
1IR2	FN	LYASE	N	1.7	6.6	4	14	DEQIAAQVDYIVAN	2899
1IR2	FO	LYASE	F	1.7	6.6	4	14	AKNYGRAVYECLRG	2900
1IZL	AD	PHOTOSYNTHESIS	A	2.2	6.6	3	18	QLGVAGVFGGALFCAMHG	2901
1J7D	AB	UNKNOWN FUNCTION	A	2.2	6.6	3	15	RNFRLLEELEEGQKG	2902
1J8H	BC	IMMUNE SYSTEM	B	3.3	6.6	2	9	KDLLEQKRA	2903
1JEY	AB	DNA BINDING PROTEIN/DNA	A	1.7	6.6	4	14	PEQVGKMKAIVEKL	2904
1JNR	AB	OXIDOREDUCTASE	A	3.3	6.6	2	27	LHELMRAWELVHRVWTAEAHVRHMLFR	2905
1JOU	AB	BLOOD CLOTTING	A	1.7	6.6	4	7	ERELLES	2906
1LWU	AB	BLOOD CLOTTING	B	1.7	6.6	4	23	SVLEHLRAKMQRMEEAIKTQKEL	2907
1LZW	AB	CHAPERONE	A	1.7	6.6	4	18	AEVAETKVAMVNKYAREN	2908
1MHY	BD	OXIDOREDUCTASE	B	1.7	6.6	4	26	HHPYVKDKSEEARYTQRFLAAYSSEG	2909
1MJG	BN	OXIDOREDUCTASE	N	1.7	6.6	4	30	VALFREVYHGAITATSYAEILLNQAIRTYG	2910
1MJG	CO	OXIDOREDUCTASE	C	1.7	6.6	4	29	PQVAARKILDALEYRTWKLGVHKEVAERY	2911
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	2.2	6.6	3	16	AKEYARMEAVKDERQF	2912
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	1.7	6.6	4	26	PTWRTSSCNRYWGAFLFNEYGLFNAH	2913

1N34	CN	RIBOSOME	C	6.6	6.6	1	6	RIRGLL	2914
1NVP	BD	TRANSCRIPTION/DNA	D	2.2	6.6	3	16	TLGNSLQESLDELIQS	2915
1R6O	AC	HYDROLASE	C	1.3	6.6	5	18	AEVAETKVAMVNKYAREN	2916
1RYP	FG	MULTICATALYTIC PROTEINASE	G	3.3	6.6	2	12	FQVEYAVKAVEN	2917
1SB3	AB	OXIDOREDUCTASE	B	3.3	6.6	2	7	EWWRSGN	2918
1TUE	MQ	REPLICATION	Q	2.2	6.6	3	22	KETLSERLSALQDKIIDHYEND	2919
1V54	NQ	OXIDOREDUCTASE	N	2.2	6.6	3	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	2920
1VG9	GH	PROTEIN BINDING/PROTEIN TRANSPORT	G	2.2	6.6	3	15	QGELPQCFCRMCAVF	2921
1VRQ	AB	OXIDOREDUCTASE	A	3.3	6.6	2	6	FAALAG	2922
1VRQ	AC	OXIDOREDUCTASE	C	3.3	6.6	2	16	TEHTVHWLIDAMSEFS	2923
1VYW	AB	TRANSFERASE	B	2.2	6.6	3	15	HEDIHTYLREMEVKC	2924
1WMH	AB	TRANSFERASE/CELL CYCLE	A	1.7	6.6	4	14	QLELEEAFRLYELN	2925
1XK4	BD	METAL BINDING PROTEIN	D	1.7	6.6	4	18	QLERNIETIINTFHQYSV	2926
1XK4	FH	METAL BINDING PROTEIN	H	1.7	6.6	4	18	QLERNIETIINTFHQYSV	2927
1XK4	IK	METAL BINDING PROTEIN	I	1.7	6.6	4	20	FQEFLILVIKMGVAAHKKSH	2928
1XK4	IK	METAL BINDING PROTEIN	K	1.7	6.6	4	18	QLERNIETIINTFHQYSV	2929
1XLS	AE	TRANSCRIPTION	A	3.3	6.6	2	29	RFAKLLLRLPALRSIGLKCLEHLFFFKLI	2930
1YHU	UW	OXYGEN STORAGE/TRANSPORT	U	1.7	6.6	4	20	PEFKAHIARVLGGLDRVISM	2931
1ZV8	AF	VIRAL PROTEIN	F	1.7	6.6	4	17	QKEIDRLNEVAKNLNES	2932
1ZV8	CB	VIRAL PROTEIN	B	2.2	6.6	3	16	QKEIDRLNEVAKNLNE	2933
2A1T	DS	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.7	6.6	4	21	EQQKEFQATARKFAREEIIPV	2934
2AXT	LT	ELECTRON TRANSPORT	T	1.7	6.6	4	21	ETITYVFIFACIIALFFFAIF	2935
2AXT	lt	ELECTRON TRANSPORT	t	1.7	6.6	4	21	ETITYVFIFACIIALFFFAIF	2936
2BNQ	AE	IMMUNE SYSTEM/RECEPTOR	A	2.2	6.6	3	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	2937
2FU5	AD	SIGNALING PROTEIN	D	2.2	6.6	3	7	TFISTIG	2938
2G30	AP	ENDOCYTOSIS/EXOCYTOSIS	P	3.3	6.6	2	11	DEAFSRLAQSR	2939
2H61	HG	METAL BINDING PROTEIN, SIGNALING PROTEIN	G	2.2	6.6	3	19	FQEFMAFVAMVTTACHEFF	2940
2H7V	AC	SIGNALING PROTEIN	A	1.7	6.6	4	9	EDYDRLRPL	2941
2HQW	AB	METAL BINDING PROTEIN	A	2.2	6.6	3	12	EEEIREAFRVFD	2942
2HVY	AB	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	2.2	6.6	3	13	IRSLIHHIGLALG	2943
2I2R	BE	TRANSPORT PROTEIN	E	2.2	6.6	3	15	KRELQVLYRGFKNEC	2944
2IVF	BC	OXIDOREDUCTASE	C	6.6	6.6	1	5	PFLAL	2945
2JIZ	LN	HYDROLASE	N	1.7	6.6	4	69	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAA	2946
2NQB	BD	STRUCTURAL PROTEIN/DNA	B	3.3	6.6	2	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	2947
2NZD	BD	STRUCTURAL PROTEIN/DNA	B	3.3	6.6	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	2948

2OZA	AB	SIGNALING PROTEIN/TRANSFERASE	B	2.2	6.6	3	21	DDHVQFLIYQILRGLKYIHSA	2949
2P58	AC	TRANSPORT PROTEIN/CHAPERONE	C	1.7	6.6	4	14	LNVLLAEIALIGTG	2950
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	H	2.2	6.6	3	16	SLRQVLANAERSYNQL	2951
2PMZ	QR	TRANSLATION, TRANSFERASE	Q	6.6	6.6	1	7	EIIAKTL	2952
2Q97	AT	STRUCTURAL PROTEIN/CELL INVASION	T	1.3	6.6	5	17	TEQQKAYEQVQRDLSQL	2953
2QL2	CD	TRANSCRIPTION/DNA	C	1.7	6.6	4	30	RMANNARERVRVRDINEAFRELGRMCQLHL	2954
2RGN	EF	SIGNALING PROTEIN COMPLEX	F	2.2	6.6	3	7	DRLRPLS	2955
2RHS	CB	LIGASE	B	2.2	6.6	3	15	FFIAKGVVDRVAEKL	2956
2UUN	EF	ELECTRON TRANSPORT	E	2.2	6.6	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2957
2UUN	MN	ELECTRON TRANSPORT	M	2.2	6.6	3	12	PLTDAVSTADSQ	2958
2V6X	AB	PROTEIN TRANSPORT	B	1.7	6.6	4	12	DDLQARLNTLKK	2959
2Z2T	CF	VIRAL PROTEIN/INHIBITOR	C	2.2	6.6	3	35	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	2960
3A1G	CD	TRANSFERASE	C	1.7	6.6	4	11	QRCCNLFEKFF	2961
3BO0	AC	RIBOSOME	C	2.2	6.6	3	20	PEHVIGVTVAFVIIEAILTY	2962
3CF4	AG	OXIDOREDUCTASE	G	3.3	6.6	2	14	KFYINQVLSAAKNF	2963
3DTU	AB	OXIDOREDUCTASE	B	1.7	6.6	4	24	TIVPIVILVAIGAFSLPVLFNQQE	2964
3DWL	DF	STRUCTURAL PROTEIN	F	1.7	6.6	4	24	KHKLVDFIIEFMEEVDAEISEMKL	2965
3E7S	AB	OXIDOREDUCTASE	A	2.2	6.6	3	20	WKDKAAVEINLAVLHSFQLA	2966
3ECH	AC	TRANSCRIPTION, TRANSCRIPTION REGULATION	A	1.7	6.6	4	24	DEGLAIHLHAELIMSRVHDELFAP	2967
3F6Q	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	B	1.7	6.6	4	9	EHDFQMLFA	2968
3FH6	FG	TRANSPORT PROTEIN	F	6.6	6.6	1	22	AAAIATLIFLLVGALAIVNLKA	2969
3FSH	BC	LIGASE	C	1.7	6.6	4	17	LVQRKDELLQQARKRFL	2970
3GJX	ED	PROTEIN TRANSPORT	E	2.2	6.6	3	11	SMEELSQALAS	2971
3H32	AB	BLOOD CLOTTING	B	1.3	6.6	5	40	DETVNSNIPTNLRVLRSILENLRSKIQKLESDVSAQMEYC	2972
1AGR	DH	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	D	1.6	6.5	4	10	RSERKKWIHC	2973
1AQD	DE	COMPLEX (MHC PROTEIN/ANTIGEN)	D	2.2	6.5	3	22	AQGALANIAVDKANLEIMTKRS	2974
1AVO	KL	PROTEASOME ACTIVATOR	L	1.6	6.5	4	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	2975
1BXR	AB	AMIDOTRANSFERASE	B	2.2	6.5	3	11	TRKLTRLLREK	2976
1CA0	BC	COMPLEX (SERINE PROTEASE/INHIBITOR)	C	1.6	6.5	4	9	VNWVQQTLA	2977
1CG5	AB	OXYGEN TRANSPORT	A	3.3	6.5	2	16	AEAWGADALARLFELH	2978
1DCE	AB	TRANSFERASE	A	2.2	6.5	3	16	YSSWHYRSCLLPQLHP	2979
1DD4	AC	RIBOSOME	C	1.6	6.5	4	11	TIDEIIEAIEK	2980
1DGH	AB	OXIDOREDUCTASE	A	2.2	6.5	3	9	QMQHWKEQR	2981
1ED3	AC	IMMUNE SYSTEM	A	2.2	6.5	3	29	PEYWEQQTRIAKEWEQIYRVDLRTLRGYY	2982
1EF1	AC	MEMBRANE PROTEIN	C	2.2	6.5	3	10	TKQRIDEFES	2983

1EYS	LM	ELECTRON TRANSPORT	L	2.2	6.5	3	29	PAHMLAISFFFTNCLALSMHGSLILSVTN	2984
1F66	AB	STRUCTURAL PROTEIN/DNA	A	2.2	6.5	3	16	KLPFQRLVREIAQDFK	2985
1F66	EF	STRUCTURAL PROTEIN/DNA	E	1.6	6.5	4	14	KLPFQRLVREIAQD	2986
1GH0	GH	PHOTOSYNTHESIS	G	2.2	6.5	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	2987
1HDM	AB	IMMUNE SYSTEM	B	1.6	6.5	4	18	GLQNCATHTQPFWGSLTN	2988
1ID3	EF	STRUCTURAL PROTEIN/DNA	F	2.2	6.5	3	11	KPAIRRLARRG	2989
1II8	AB	REPLICATION	A	6.5	6.5	1	12	DEAREKVVREVL	2990
1IR2	CJ	LYASE	C	3.3	6.5	2	20	WRDRFLFVAEAIYKAQAETG	2991
1IR2	Z5	LYASE	Z	2.2	6.5	3	20	WRDRFLFVAEAIYKAQAETG	2992
1IRU	EL	HYDROLASE	L	1.3	6.5	5	22	AADCSFWERLLARQCRIYELRN	2993
1IZN	AB	PROTEIN BINDING	A	3.3	6.5	2	5	WNKIL	2994
1LNU	GH	SUGAR BINDING PROTEIN	G	1.6	6.5	4	22	PQGGLQNIAVVKHNLGVLTKRS	2995
1M1J	BC	BLOOD CLOTTING	C	1.6	6.5	4	56	IEQLTQKSKKIIEEIIRYENTILAHENTIQQLTDMHIMNSNKITQLKQKIAQ LESH	2996
1M56	GH	OXIDOREDUCTASE	G	1.3	6.5	5	30	LTQQSYFMMATMVIAVPTGIKIFSWIATMW	2997
1MDU	AB	STRUCTURAL PROTEIN	A	2.2	6.5	3	18	QDESGAAAIFTVQLDDYL	2998
1N5W	AC	OXIDOREDUCTASE	C	3.3	6.5	2	7	PQIRYMG	2999
1NBW	AB	HYDROLASE	B	2.2	6.5	3	14	AGAINELCWGLEEQ	3000
1O96	EF	ELECTRON TRANSFER	E	1.6	6.5	4	15	ISEQAAKIIQIINEF	3001
1OAO	AD	OXIDOREDUCTASE	A	1.6	6.5	4	29	PQVAARKILDALEYRTWKLGVHKEVAERY	3002
1OAO	AD	OXIDOREDUCTASE	D	1.6	6.5	4	30	VALFREVYHGAITATSYAEILLNQAIRTYG	3003
1PGR	EF	CYTOKINE	E	2.2	6.5	3	29	QSFLLKCLEQVRKIQGDGAALQEKLCATY	3004
1RE0	AB	PROTEIN TRANSPORT	B	1.6	6.5	4	19	ADSVFVLSYSIIMLNTDSH	3005
1SB0	AB	TRANSCRIPTION	B	2.2	6.5	3	21	EKRIKELELLLMSTENELKGQ	3006
1SQX	DJ	OXIDOREDUCTASE	J	2.2	6.5	3	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	3007
1T3M	AB	HYDROLASE	A	1.6	6.5	4	24	LQQELRYIEALSAIVETGQKMLEA	3008
1T3M	CD	HYDROLASE	C	1.6	6.5	4	24	LQQELRYIEALSAIVETGQKMLEA	3009
1TA3	AB	HYDROLASE INHIBITOR/HYDROLASE	A	1.6	6.5	4	13	PKNVYYGVAPVAQ	3010
1TBG	AE	COMPLEX (GTP-BINDING/TRANSDUCER)	E	2.2	6.5	3	16	KDKLKMEVDQLKKEVT	3011
1TBG	BF	COMPLEX (GTP-BINDING/TRANSDUCER)	B	1.6	6.5	4	23	LDQLRQEAEQLKNQIRDARKACA	3012
1TII	AC	ENTEROTOXIN	C	1.6	6.5	4	32	CASLTNKLSQHDLADFKKYIKRKFTLMTLLSI	3013
1TY4	BD	APOPTOSIS	D	2.2	6.5	3	11	IGYEIGSKLAA	3014
1ULI	CD	OXIDOREDUCTASE	C	2.2	6.5	3	17	VFEQDDGENWVEIQQVL	3015
1V54	AL	OXIDOREDUCTASE	A	2.2	6.5	3	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	3016
1V54	QX	OXIDOREDUCTASE	X	1.6	6.5	4	22	GNAVLASGATFCVAVWVYMATQ	3017
1VF5	NO	PHOTOSYNTHESIS	N	3.3	6.5	2	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	3018
1XIU	AE	TRANSCRIPTION/TRANSFERASE	A	1.6	6.5	4	24	LEDQVILLRAGWNELLIAGFSHRS	3019
1XK4	EG	METAL BINDING PROTEIN	G	1.6	6.5	4	18	QLERNIETIINTFHQYSV	3020

1XL3	AC	CELL INVASION	C	1.6	6.5	4	13	LSEFMGDIVALVD	3021
1YE9	AE	OXIDOREDUCTASE	E	2.2	6.5	3	9	YSHPRLFWL	3022
1Z6O	BN	METAL BINDING PROTEIN	B	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3023
1Z6O	CO	METAL BINDING PROTEIN	C	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3024
1Z6O	DP	METAL BINDING PROTEIN	D	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3025
1Z6O	FR	METAL BINDING PROTEIN	F	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3026
1Z6O	GS	METAL BINDING PROTEIN	G	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3027
1Z6O	HT	METAL BINDING PROTEIN	H	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3028
1Z6O	IU	METAL BINDING PROTEIN	I	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3029
1Z6O	KW	METAL BINDING PROTEIN	K	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3030
1Z6O	LX	METAL BINDING PROTEIN	L	2.2	6.5	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3031
1Z7Q	IJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.6	6.5	4	18	PEDLFETISQALLNAADR	3032
2AXT	lt	ELECTRON TRANSPORT	l	2.2	6.5	3	21	RTSLYLGLLLILVLALLFSSY	3033
2DYM	CD	PROTEIN TURNOVER/PROTEIN TURNOVER	D	1.6	6.5	4	18	MDDLLIRRLTDRNDKEAH	3034
2FK0	KL	VIRAL PROTEIN	L	1.3	6.5	5	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	3035
2FUG	CD	OXIDOREDUCTASE	D	2.2	6.5	3	10	VIYHFKHYTE	3036
2GBW	CD	OXIDOREDUCTASE	D	2.2	6.5	3	11	FGELKQRVERL	3037
2I2R	AH	TRANSPORT PROTEIN	H	3.3	6.5	2	15	KRELQVLYRGFKNEC	3038
2ICW	EF	IMMUNE SYSTEM	E	1.6	6.5	4	13	AVDTYCRHNYGVG	3039
2ISS	AD	LYASE, TRANSFERASE	A	2.2	6.5	3	14	PRKMAKAMVLAVTY	3040
2IUC	AB	HYDROLASE	B	2.2	6.5	3	10	LSQISSTFYF	3041
2JJ0	LM	PHOTOSYNTHESIS	L	3.3	6.5	2	26	TLGIHRLGLLLSLSAVFFSALCMIIT	3042
2JKR	LI	ENDOCYTOSIS	I	2.2	6.5	3	12	FYKVYTVVDEMF	3043
2P58	AC	TRANSPORT PROTEIN/CHAPERONE	A	2.2	6.5	3	26	AKQYQVWQRESKALESAIAIIHYVAG	3044
2Q0O	AC	TRANSCRIPTION	C	1.6	6.5	4	33	GPVLQTLQDEYVARQKRSEAQQEELSDILDALG	3045
2QKM	GH	HYDROLASE	G	1.3	6.5	5	19	EDENILRNAVNLQVLKFHY	3046
2QRV	HG	TRANSFERASE/TRANSFERASE REGULATOR	H	1.6	6.5	4	16	TGRLFFEFYRLLHDAR	3047
2RF4	CD	TRANSFERASE	D	3.3	6.5	2	16	TDEVLQFLESFIDEKE	3048
2UUN	UV	ELECTRON TRANSPORT	U	2.2	6.5	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	3049
2UW1	AB	OXIDOREDUCTASE	A	3.3	6.5	2	28	AWAMWTRAWTAEENRHGDLLNKYLYLSG	3050
2V4J	AC	OXIDOREDUCTASE	C	3.3	6.5	2	9	VRILSKNTG	3051
2V7Q	GI	HYDROLASE	I	2.2	6.5	3	14	YIRYSQICAKAVRD	3052
2VE7	BD	CELL CYCLE	B	3.3	6.5	2	9	ADLYKDRLG	3053
2VJH	AB	PHOTOSYNTHESIS	A	1.6	6.5	4	12	VVTTVLAAADAA	3054
2ZAE	CD	HYDROLASE	D	1.6	6.5	4	21	KEKKKIAIERIDTLFTLAERV	3055
2ZLE	ID	HYDROLASE	I	6.5	6.5	1	5	ELAKA	3056
3BOW	BC	HYDROLASE/HYDROLASE INHIBITOR	C	2.2	6.5	3	9	PIDALSEDL	3057

3BZ1	LM	ELECTRON TRANSPORT	L	1.6	6.5	4	24	RTSLYLGLLLILVLALLFSSYFFN	3058
3CFI	GH	PROTEIN TRANSPORT/IMMUNE SYSTEM	G	2.2	6.5	3	22	YLEQKMFAAMVADNQMAMVMLN	3059
3DGE	BD	TRANSFERASE/SIGNALING PROTEIN	D	2.2	6.5	3	13	AVLRKIVSFNLKK	3060
3EZQ	MN	APOPTOSIS	N	1.3	6.5	5	16	NLVADLVQEVQQARDL	3061
3FAL	AB	SIGNALING PROTEIN	B	1.6	6.5	4	26	PLMFPRMLMKLVSLRTLSSVHSEQVF	3062
3FH6	HI	TRANSPORT PROTEIN	H	6.5	6.5	1	22	AAAIATLIFLLVGALAIVNLKA	3063
3GE8	AB	OXIDOREDUCTASE	B	1.6	6.5	4	19	LRYLFHCLQMSSAYVQQMA	3064
3GE8	AB	OXIDOREDUCTASE	B	2.2	6.5	3	12	PMNLWYKQYRNA	3065
3H0L	GI	LIGASE	G	2.2	6.5	3	15	PEVKRRIMLGTFALS	3066
1AIP	AC	COMPLEX OF TWO ELONGATION FACTORS	C	3.2	6.4	2	6	DFVARN	3067
1CC1	SL	OXIDOREDUCTASE	L	1.3	6.4	5	32	GAKADATNTYGLNQYLKALEIRRICHEMVAMF	3068
1CM1	AB	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	A	2.1	6.4	3	15	EEQIAEFKEAFSLFD	3069
1E 08	AD	HYDROGENASE	A	2.1	6.4	3	20	EFTADVTIWEEGSEFVERLT	3070
1E1H	CD	HYDROLASE	D	3.2	6.4	2	12	LQYMKNVFKEKY	3071
1E7P	EC	OXIDOREDUCTASE	C	2.1	6.4	3	8	SILESYSG	3072
1E7P	EF	OXIDOREDUCTASE	E	2.1	6.4	3	8	DEDYYELI	3073
1FM6	UV	TRANSCRIPTION	V	2.1	6.4	3	9	KILHRLLQE	3074
1G0U	HI	HYDROLASE	I	3.2	6.4	2	18	PEDLFETISQALLNAADR	3075
1I3R	AB	IMMUNE SYSTEM	B	3.2	6.4	2	5	NFLVP	3076
1ID3	EF	STRUCTURAL PROTEIN/DNA	E	2.1	6.4	3	29	SSAIGALQESVEAYLVSLFEDTNLAAIHA	3077
1IK9	AC	GENE REGULATION/LIGASE	A	1.6	6.4	4	93	PAEVIRELIAYALDTIAENQAKNEHLQKENERLLRDWNDVQGRFEKAV SAKEALETDLYKRFILVLNEKKTKIRSLHNKLLNAAQEREKDIKQ	3078
1KF6	CD	OXIDOREDUCTASE	C	2.1	6.4	3	28	VIVIINLITLAAALLHTKTWFELAPKAA	3079
1KF6	OP	OXIDOREDUCTASE	P	1.3	6.4	5	27	EPVFWGLFGAGGMWSAIIAPVMILLVG	3080
1KFU	LS	HYDROLASE	L	1.6	6.4	4	22	FDNFVRCLVRLETLFKIFKQLD	3081
1KIL	CD	MEMBRANE PROTEIN	C	1.3	6.4	5	70	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLD RVEEGMNHINQDMKEAEKNLKD	3082
1MHY	BD	OXIDOREDUCTASE	D	1.6	6.4	4	26	AKEYARMEAAKDERQFGTLLDGLTRL	3083
1MTY	EC	MONOOXYGENASE	C	1.6	6.4	4	33	PTWRDEFINRYWGAFLFNEYGLFNAHSQGAREA	3084
1NTK	CD	OXIDOREDUCTASE	D	2.1	6.4	3	13	YAMKRHKWSVLKS	3085
1NVP	BD	TRANSCRIPTION/DNA	B	1.6	6.4	4	16	VPKLYRSVIEDVINDV	3086
1OE9	AB	ATPASE/MYOSIN	A	2.1	6.4	3	39	QVAYLEKIRADKLRAACIRIQKTIRGWLMRKKYMRMRRG	3087
1PD7	AB	TRANSCRIPTION	B	1.6	6.4	4	20	IQMLLEAADYLERREREAEH	3088
1PHN	AB	ELECTRON TRANSPORT	A	1.6	6.4	4	12	PITEAIAAADNQ	3089
1PHN	AB	ELECTRON TRANSPORT	A	3.2	6.4	2	25	AVGKAKCARDIGYYLRMVTYCLVVG	3090
1RYP	AG	MULTICATALYTIC PROTEINASE	A	3.2	6.4	2	11	YQVEYAFKATN	3091

1RYP	TU	MULTICATALYTIC PROTEINASE	U	3.2	6.4	2	12	FQVEYAVKAVEN	3092
1S5L	AD	PHOTOSYNTHESIS	A	3.2	6.4	2	12	IVAAHGYFGRLI	3093
1U7F	CB	SIGNALING PROTEIN	C	6.4	6.4	1	9	AAVELTRRH	3094
1U9I	ED	CIRCADIAN CLOCK PROTEIN	E	1.6	6.4	4	19	SSVVRRELFRLVARLKQIG	3095
1ULI	EF	OXIDOREDUCTASE	F	2.1	6.4	3	11	AQMMRGRLRKI	3096
1VF5	AB	PHOTOSYNTHESIS	A	3.2	6.4	2	25	ELTWISGVILAVITVSFGVTGYSLP	3097
1WQL	AB	OXIDOREDUCTASE	A	2.1	6.4	3	15	EDIKEEYRRKNIFTF	3098
1XK4	AC	METAL BINDING PROTEIN	C	1.6	6.4	4	20	QLERNIETIINTFHQYSVKL	3099
1XKM	AB	ANTIBIOTIC	B	2.1	6.4	3	23	LVSGLIEARKYLEQLHRKLKNCK	3100
1XMN	CD	BLOOD CLOTTING	C	2.1	6.4	3	8	ERELLESY	3101
1YE9	AE	OXIDOREDUCTASE	A	2.1	6.4	3	12	PETLHNVMWAMS	3102
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.6	6.4	4	14	LVPGAIILDTVLML	3103
1Z7Q	ST	HYDROLASE/HYDROLASE ACTIVATOR	T	3.2	6.4	2	13	FQVEYALEAIKQG	3104
1Z7Q	WX	HYDROLASE/HYDROLASE ACTIVATOR	X	1.6	6.4	4	18	PEDLFETISQALLNAADR	3105
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	D	1.6	6.4	4	19	ELAKHAVSEGTKAVTKYTS	3106
2AA1	AB	OXYGEN STORAGE/TRANSPORT	B	2.1	6.4	3	14	VVGPATLARCLVVY	3107
2AFH	AB	OXIDOREDUCTASE	A	2.1	6.4	3	7	VGCGQYS	3108
2BE6	CF	MEMBRANE PROTEIN	C	2.1	6.4	3	15	EEQIAEFKEAFSLFD	3109
2BG9	AB	ION CHANNEL/RECEPTOR	A	6.4	6.4	1	28	LYFVVNVIIPCLLFSFLTVLVFYLPTDS	3110
2C5I	TP	PROTEIN TRANSPORT	P	2.1	6.4	3	14	LNKDRRLLLREFYN	3111
2FHH	OP	HYDROLASE	P	1.6	6.4	4	23	AAVAVEFARLYAVELEHYEKLEG	3112
2FYN	PQ	OXIDOREDUCTASE	P	6.4	6.4	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	3113
2FYZ	EB	PROTEIN BINDING	E	1.6	6.4	4	53	LGSAVSLVQAQTNARAIAAMKNSIQATNRAVFEVKEGTQRLAIAVQAIQDHIN	3114
2GAG	AD	OXIDOREDUCTASE	D	2.1	6.4	3	9	DKQWSRYLF	3115
2GOX	AB	CELL ADHESION/TOXIN	B	1.6	6.4	4	14	VSAHRKAQKAVNLV	3116
2GPP	BD	TRANSCRIPTION	D	1.6	6.4	4	8	LLLHLLKS	3117
2HLD	SV	HYDROLASE	S	2.1	6.4	3	14	RSTVAQLVQTLEQH	3118
2I2R	DH	TRANSPORT PROTEIN	D	2.1	6.4	3	8	WLPFARAA	3119
2J0Q	BF	HYDROLASE	F	6.4	6.4	1	25	PEGLRVFYYLVQDLKCLVFSLIGLH	3120
2JF9	AP	TRANSCRIPTION	A	1.6	6.4	4	24	LHDQVHLLECAWLEILMIGLVWRS	3121
2JGD	AB	OXIDOREDUCTASE	B	3.2	6.4	2	10	QVVIDQFISS	3122
2JKI	AS	CHAPERONE	A	1.6	6.4	4	8	KSDLVNNL	3123
2K8B	AB	PROTEIN BINDING	B	2.1	6.4	3	17	PMFLDQVAKFIIDNTKG	3124
2KC8	AB	TOXIN/TOXIN REPRESSOR	B	1.6	6.4	4	15	EDAELVEIVKERLRN	3125
2O8A	BJ	HYDROLASE/INHIBITOR	J	2.1	6.4	3	18	PEEREKKRQFEMKRKLHY	3126
2O8F	AB	DNA BINDING PROTEIN/DNA	A	2.1	6.4	3	20	TYDGFGLAWAISEYIATKIG	3127
2PBI	AB	SIGNALING PROTEIN	B	1.6	6.4	4	24	ETLASLKSEAESLKGKLEEERAKL	3128
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	V	1.6	6.4	4	32	KLQNLAQRVFASKARLNYALNDKAQKYNTLIE	3129

2PQA	AB	REPLICATION	A	1.6	6.4	4	20	NEFTTHILEVINAHMVLSKA	3130
2RF4	AB	TRANSFERASE	B	3.2	6.4	2	17	TDEVLQFLESFIDEKEN	3131
2UUN	ST	ELECTRON TRANSPORT	S	2.1	6.4	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	3132
2VBO	AB	HYDROLASE	B	2.1	6.4	3	14	KEFLLYLAGFVDGD	3133
2VYR	DH	IMMUNE SYSTEM	D	1.6	6.4	4	15	VKEVMHYLGQYIMVK	3134
2VZG	AB	CELL ADHESION	A	1.6	6.4	4	12	ELDRLLLELNAV	3135
2WAQ	DL	TRANSCRIPTION	D	1.6	6.4	4	14	LEFVNAIRRAAMLY	3136
3A1G	AB	TRANSFERASE	B	2.1	6.4	3	8	RIKELRNL	3137
3B5N	JK	MEMBRANE PROTEIN	K	1.3	6.4	5	64	FTKQSSVASTRNTLKMAQDAERAGMNTLGMLGHQSEQLNNVEGNLDL MKVQNKVADEKVAELKK	3138
3C1B	CD	STRUCTURAL PROTEIN/DNA	D	3.2	6.4	2	19	ELAKHAVSEGTKAVTKYTS	3139
3CHW	PV	STRUCTURAL PROTEIN	P	3.2	6.4	2	9	WNAYIDNLM	3140
3CXH	CH	OXIDOREDUCTASE	C	2.1	6.4	3	35	PYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	3141
3D24	AB	TRANSCRIPTION	B	2.1	6.4	3	8	SELLKYLT	3142
3DI2	CD	CYTOKINE/CYTOKINE RECEPTOR	C	2.1	6.4	3	18	DFDLHLLKVSEGTTILLK	3143
3DL8	HD	PROTEIN TRANSPORT	H	6.4	6.4	1	17	LTLLLIIALIIAIIVGI	3144
3EXG	IJ	OXIDOREDUCTASE	J	3.2	6.4	2	15	IDQVINSAAKTYYMS	3145
3EZJ	CD	PROTEIN TRANSPORT	C	1.6	6.4	4	16	VRELAPILRQMIDSAG	3146
3FGC	AB	OXIDOREDUCTASE	B	3.2	6.4	2	11	PLTVAGFLLGM	3147
3FSG	BD	HYDROLASE	B	3.2	6.4	2	16	REAVGFHFDLFLDELN	3148
3GE8	AB	OXIDOREDUCTASE	A	1.6	6.4	4	22	YPEYVSIQREKDAGAYSVKAAL	3149
3GZ1	BP	CHAPERONE	B	2.1	6.4	3	17	DDMMDDIYSYAYDFYNK	3150
3H0L	AB	LIGASE	A	1.6	6.4	4	13	IFEMYARTRDEGF	3151
3H6P	AC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	C	2.1	6.4	3	19	YAGTLQSLGADIASEQAVL	3152
3HAY	CD	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	C	2.1	6.4	3	13	GEYRRRWKREVLG	3153
1AFV	AH	VIRAL PROTEIN/IMMUNE SYSTEM	A	3.2	6.3	2	21	QAAMQMLKETINEEAAEWDRL	3154
1B27	BE	HYDROLASE/HYDROLASE INHIBITOR	E	3.2	6.3	2	9	LDALWDALT	3155
1CP9	AB	HYDROLASE	A	2.1	6.3	3	12	EQLGVEFFNQIN	3156
1EFU	AB	COMPLEX (TWO ELONGATION FACTORS)	B	3.2	6.3	2	5	DFVAK	3157
1EQZ	EF	STRUCTURAL PROTEIN/DNA	F	1.6	6.3	4	12	SIYVYKVLKQVH	3158
1FCD	BD	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	D	3.2	6.3	2	13	TPYLQYAMSDFRE	3159
1FYZ	CE	OXIDOREDUCTASE	E	2.1	6.3	3	6	EVDFRH	3160
1G20	CD	OXIDOREDUCTASE	D	2.1	6.3	3	14	QDYKDMLAKKRDGF	3161
1G2C	MP	VIRAL PROTEIN	P	2.1	6.3	3	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	3162
1H2A	SL	OXIDOREDUCTASE	L	2.1	6.3	3	10	PRDAQHFTQR	3163
1HL6	CD	SIGNAL PROTEIN	C	1.6	6.3	4	13	EDGDQGIVRLKEK	3164

1KN1	AB	ELECTRON TRANSPORT	B	2.1	6.3	3	25	TRRYAACIRDLDYYLRYATYAMLAG	3165
1LTX	AR	TRANSFERASE/PROTEIN BINDING	R	3.2	6.3	2	7	RADVFNS	3166
1MO1	CD	TRANSPORT PROTEIN	C	2.1	6.3	3	13	EQEALEKLAAYVQ	3167
1NU9	DF	HYDROLASE/PROTEIN BINDING	F	3.2	6.3	2	40	KDAKDKLMTRILGEDQYLLERKKVQYEEYKKLYKKYKEEN	3168
1NVM	GH	LYASE/OXIDOREDUCTASE	G	2.1	6.3	3	15	EDMIVDVALDLLAAH	3169
1OCC	AD	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	1.6	6.3	4	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	3170
1PRC	MH	PHOTOSYNTHETIC REACTION CENTER	M	2.1	6.3	3	27	PWHGFSIGFAYGCGLLFAAHGATILAV	3171
1R4M	AB	CELL CYCLE	A	2.1	6.3	3	21	HTIAAFLGGAAAQEVIKIITK	3172
1RD8	CD	VIRAL PROTEIN	D	1.3	6.3	5	24	NERTLDFHDSNVRNLYEKVKSQLK	3173
1RYP	OP	MULTICATALYTIC PROTEINASE	P	2.1	6.3	3	18	GPDYRVLVDKSRKVAHTS	3174
1S5L	bd	PHOTOSYNTHESIS	d	2.1	6.3	3	20	LFVPVTGLWMSAIGVVGLAL	3175
1T2K	CD	TRANSCRIPTION/DNA	D	1.3	6.3	5	60	RRKFLERNRAAASRSRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQLLLA	3176
1TI2	AB	OXIDOREDUCTASE	B	2.1	6.3	3	12	NCFMGCMDEHEL	3177
1TUE	FG	REPLICATION	F	1.6	6.3	4	11	WRPIVQFLRYQ	3178
1V54	AD	OXIDOREDUCTASE	A	1.6	6.3	4	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	3179
1V5I	AB	HYDROLASE/PROTEIN BINDING	A	2.1	6.3	3	14	YSWIINGIEWAIAN	3180
1VF5	RS	PHOTOSYNTHESIS	R	3.2	6.3	2	25	ILGAVFYIVFIALFFGIAVGIIFAI	3181
1XB2	AB	TRANSLATION	B	3.2	6.3	2	6	DFVSRN	3182
1Y96	AB	RNA BINDING PROTEIN	B	2.1	6.3	3	24	LESQEQRARAALRERYLRSLLAMV	3183
1YE9	JN	OXIDOREDUCTASE	N	2.1	6.3	3	10	YSHPRLFWLS	3184
1Z6O	HO	METAL BINDING PROTEIN	O	3.2	6.3	2	13	EALGEFIFDKKLL	3185
1Z6O	LQ	METAL BINDING PROTEIN	Q	3.2	6.3	2	13	EALGEFIFDKKLL	3186
2APO	AB	ISOMERASE/RNA BINDING PROTEIN	A	2.1	6.3	3	14	LQDLLDAYVFWKED	3187
2C9W	AC	TRANSCRIPTION REGULATION	C	2.1	6.3	3	11	ALELLMAANFL	3188
2DXB	WX	HYDROLASE	X	3.2	6.3	2	6	RDCLIG	3189
2F9I	CD	TRANSFERASE	C	3.2	6.3	2	14	RDEIANDRFEKFRN	3190
2FK0	IJ	VIRAL PROTEIN	J	1.3	6.3	5	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	3191
2GL7	DE	TRANSCRIPTION	E	2.1	6.3	3	9	ADVKSSLVN	3192
2I2X	MN	TRANSFERASE	M	3.2	6.3	2	17	RFETKALADAKAALEAL	3193
2INP	AC	OXIDOREDUCTASE	C	1.6	6.3	4	29	TTVSQMHIYTGMDRLGIGQYLSRIALMID	3194
2JBL	LM	ELECTRON TRANSPORT	M	2.1	6.3	3	7	PLQFFRQ	3195
2JEA	AB	HYDROLASE	B	3.2	6.3	2	18	RREIELSKVIREALESAV	3196
2ODE	AB	SIGNALING PROTEIN	A	2.1	6.3	3	10	RSERKKWIHC	3197
2P5T	EF	TRANSCRIPTION REGULATOR	F	2.1	6.3	3	12	KTTIHRIKQKEF	3198
2QKL	AB	HYDROLASE	A	1.6	6.3	4	18	DENILRNAVNLQVLKFHY	3199
2RGN	DE	SIGNALING PROTEIN COMPLEX	E	2.1	6.3	3	21	IQQIYEWHRDYFLQELQRCLK	3200
2W73	EO	METAL BINDING PROTEIN	O	1.6	6.3	4	16	IRNKIRAIGKMARVFS	3201

2WD7	AC	OXIDOREDUCTASE	A	1.3	6.3	5	24	SLYNMGKHALVGLTQSAALELAPY	3202
3B5N	KL	MEMBRANE PROTEIN	K	1.3	6.3	5	64	FTKQSSVASTRNTLKMAQDAERAGMNTLGMLGHQSEQLNNVEGNLDL MKVQNKVADEKVAELKK	3203
3B9J	BC	OXIDOREDUCTASE	B	2.1	6.3	3	24	IEFRRTLTLSFFFKFYLTVLKKLG	3204
3BOW	AC	HYDROLASE/HYDROLASE INHIBITOR	C	1.6	6.3	4	12	DDALDELSDSLG	3205
3CSY	OP	IMMUNE SYSTEM/VIRAL PROTEIN	P	2.1	6.3	3	15	FSILNRKAIDFLLQR	3206
3CWB	CD	OXIDOREDUCTASE	C	1.6	6.3	4	21	YYSFKDILGLTLMLTPFLTLA	3207
3DBJ	CD	PHOTOSYNTHESIS	D	3.2	6.3	2	25	TRRYAACIRDLDYYLRYATYAMLAG	3208
3DGE	AC	TRANSFERASE/SIGNALING PROTEIN	C	1.6	6.3	4	14	AVLRKIVSFNLKKE	3209
3DMT	BC	OXIDOREDUCTASE	B	2.1	6.3	3	10	AEYFAYQMRY	3210
3EXG	CD	OXIDOREDUCTASE	D	2.1	6.3	3	14	EMGFAGIAVGAAMA	3211
3EXG	GH	OXIDOREDUCTASE	H	3.2	6.3	2	5	TYYMS	3212
3EXH	EF	OXIDOREDUCTASE	F	3.2	6.3	2	5	TYYMS	3213
3EZQ	CD	APOPTOSIS	D	1.3	6.3	5	16	NLVADLVQEVQQARDL	3214
3G5O	DC	TOXIN/ANTITOXIN	D	2.1	6.3	3	8	EDEIRAEF	3215
1AVO	AB	PROTEASOME ACTIVATOR	B	1.6	6.2	4	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	3216
1B33	CD	PHOTOSYNTHESIS	D	2.1	6.2	3	25	TRRYAACIRDLDYYLRYATYAMLAG	3217
1DCE	CD	TRANSFERASE	C	2.1	6.2	3	11	QSAWFYHRWLL	3218
1DD4	AC	RIBOSOME	A	2.1	6.2	3	9	IDEIIEAIE	3219
1E1C	CD	ISOMERASE	C	1.6	6.2	4	22	FFMEVAKLRAARMLWAKLVHQF	3220
1E6V	BC	OXIDOREDUCTASE	C	2.1	6.2	3	20	EELLQVVQRIHELRTLAGYR	3221
1E6Y	AC	OXIDOREDUCTASE	A	3.1	6.2	2	7	PTALEDH	3222
1E7P	KI	OXIDOREDUCTASE	I	2.1	6.2	3	8	SILESYSG	3223
1EM8	CD	GENE REGULATION	D	3.1	6.2	2	14	PTARAALWQQICTY	3224
1FFU	BC	HYDROLASE	B	2.1	6.2	3	11	SYRVWKSLKEH	3225
1GXS	CD	LYASE	D	3.1	6.2	2	10	AVFNSINYLN	3226
1H3O	CD	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	D	2.1	6.2	3	22	LQIADDFIESVVTAACQLARHR	3227
1IR2	V4	LYASE	4	2.1	6.2	3	14	DEQIAAQVDYIVAN	3228
1KI6	AB	PHOSPHOTRANSFERASE	A	2.1	6.2	3	16	NVFAWALDVLAKRLRS	3229
1KQF	AB	OXIDOREDUCTASE	B	3.1	6.2	2	10	ACQVACSEWN	3230
1KYO	OQ	OXIDOREDUCTASE/ELECTRON TRANSPORT	Q	6.2	6.2	1	6	RLFDKL	3231
1MF8	AB	HYDROLASE, LIGASE	B	3.1	6.2	2	15	ADEIKRLGKRFKKLD	3232
1MZN	CD	TRANSCRIPTION	D	2.1	6.2	3	9	KILHRLLQD	3233
1N4Q	EF	TRANSFERASE	E	2.1	6.2	3	10	ESAWNYLKGI	3234
1NHG	AC	OXIDOREDUCTASE	C	2.1	6.2	3	13	FIDYAIEYSEKYA	3235
1NIK	BC	TRANSCRIPTION	C	2.1	6.2	3	11	DEFIAHRLGLI	3236
1OOK	AB	HYDROLASE	A	2.1	6.2	3	7	ERELLES	3237
1Q90	AR	PHOTOSYNTHESIS	A	1.6	6.2	4	35	PARIQGLLVFFSFVLLTQVLLVLKKKQFEKVQLAE	3238

1R5V	AB	SIGNALING PROTEIN	A	2.1	6.2	3	23	AQGALANIAVDKANLDVMKERSN	3239
1R5V	FD	SIGNALING PROTEIN	D	1.2	6.2	5	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	3240
1R8U	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	A	2.1	6.2	3	12	EEVLMSLVIEMG	3241
1RU7	AF	VIRAL PROTEIN	F	3.1	6.2	2	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	3242
1S6C	AB	TRANSPORT PROTEIN	A	2.1	6.2	3	12	EETFKQIYAQFF	3243
1SUY	AD	CIRCADIAN CLOCK PROTEIN	A	2.1	6.2	3	24	DILLDYRLTLIDVIAHLCEMYRRS	3244
1T3Q	DE	OXIDOREDUCTASE	D	2.1	6.2	3	8	ETIIDAIT	3245
1TI2	KL	OXIDOREDUCTASE	L	1.6	6.2	4	13	NCFMGCMDEHELN	3246
1U35	AB	STRUCTURAL PROTEIN/DNA	B	3.1	6.2	2	11	KPAIRRLARRG	3247
1U35	BD	STRUCTURAL PROTEIN/DNA	B	3.1	6.2	2	11	AMDVVYALKRQ	3248
1WDC	AB	MUSCLE PROTEIN	A	2.1	6.2	3	13	QWWKLYSKVKPLL	3249
1WYU	GH	OXIDOREDUCTASE	H	1.2	6.2	5	15	FLALVRAWAYIRTLG	3250
1XME	AB	OXIDOREDUCTASE	B	1.6	6.2	4	35	HKAHKAILAYEKGWLAFSLAMLFVFIALIAYTLAT	3251
1YE9	KO	OXIDOREDUCTASE	O	2.1	6.2	3	13	PYIRERVVDQLAH	3252
1YHU	QS	OXYGEN STORAGE/TRANSPORT	Q	3.1	6.2	2	20	PEFKAHIARVLGGLDRVISM	3253
1YKE	AB	GENE REGULATION	A	1.6	6.2	4	39	RPHQSRESLIMLLEEQLEYKRGEIREIEQVCKQVHDKLT	3254
1Z6O	BP	METAL BINDING PROTEIN	P	3.1	6.2	2	13	EALGEFIFDKKLL	3255
1Z6O	JT	METAL BINDING PROTEIN	J	2.1	6.2	3	16	LSLALYVFDEYLQKTV	3256
1Z7Q	EF	HYDROLASE/HYDROLASE ACTIVATOR	F	3.1	6.2	2	13	FQVEYALEAIKQG	3257
1ZV8	GL	VIRAL PROTEIN	L	2.1	6.2	3	16	QKEIDRLNEVAKNLNE	3258
2A4J	AB	STRUCTURAL PROTEIN	B	3.1	6.2	2	8	WKLLAKGL	3259
2ADV	AC	HYDROLASE	C	3.1	6.2	2	7	REQVEAA	3260
2AXT	ad	ELECTRON TRANSPORT	a	3.1	6.2	2	16	WADIINRANLGMEVMH	3261
2B59	AB	HYDROLASE/STRUCTURAL PROTEIN	B	1.6	6.2	4	10	MQDIMIVHKH	3262
2B8K	AB	TRANSFERASE	B	3.1	6.2	2	11	EMERDCMIAHG	3263
2CJS	AC	EXOCYTOSIS	A	2.1	6.2	3	20	EEEARYWAKKLEQLNAKLNS	3264
2D1P	GI	TRANSLATION	G	2.1	6.2	3	16	QQASSAFQFAQALIAD	3265
2DXB	MW	HYDROLASE	W	2.1	6.2	3	17	LTELHNKIVEMRERVAS	3266
2E9X	AD	REPLICATION	A	1.2	6.2	5	37	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY	3267
2EHO	JL	REPLICATION	L	2.1	6.2	3	8	LWLAKGLF	3268
2F8N	AB	STRUCTURAL PROTEIN/DNA	B	2.1	6.2	3	11	KPAIRRLARRG	3269
2F9I	AB	TRANSFERASE	A	3.1	6.2	2	14	RDEIANDRFEKFRN	3270
2FFD	AC	BLOOD CLOTTING	A	2.1	6.2	3	33	EKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRS	3271
2FHH	MN	HYDROLASE	M	1.6	6.2	4	22	FNEFDNLRRGGIQFADTRGYAY	3272
2FU5	BC	SIGNALING PROTEIN	C	2.1	6.2	3	6	FISTIG	3273
2H9A	AB	OXIDOREDUCTASE	A	2.1	6.2	3	14	PYQAVMEASVYIAK	3274
2HLD	AE	HYDROLASE	E	1.2	6.2	5	15	TREGNDLYREMKETG	3275
2HTM	CG	BIOSYNTHETIC PROTEIN	C	2.1	6.2	3	16	AEEAVRLARLGRLLTG	3276

2HYB	PQ	TRANSFERASE	Q	2.1	6.2	3	16	IYAWEALEVVLIGAAF	3277
2I2X	AB	TRANSFERASE	A	2.1	6.2	3	17	RFETKALADAKAALEAL	3278
2IVF	AB	OXIDOREDUCTASE	B	3.1	6.2	2	6	HKEVFY	3279
2J0S	AT	HYDROLASE	A	3.1	6.2	2	13	KGFKEQIYDVYRY	3280
2JJ0	LM	PHOTOSYNTHESIS	L	3.1	6.2	2	25	HIPFAFAFAILAYLTLVLFRPVMMG	3281
2JKR	LB	ENDOCYTOSIS	B	6.2	6.2	1	13	DNADELLESFLEG	3282
2OCY	BC	ENDOCYTOSIS/EXOCYTOSIS	B	6.2	6.2	1	10	TASLFDEANN	3283
2PHG	AB	TRANSCRIPTION	A	2.1	6.2	3	13	KKEIGRCFKLILK	3284
2PKQ	QP	OXIDOREDUCTASE	Q	3.1	6.2	2	10	VKSATHLLKY	3285
2Q9Q	AB	REPLICATION	B	2.1	6.2	3	32	DLKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	3286
2QRV	EF	TRANSFERASE/TRANSFERASE REGULATOR	F	3.1	6.2	2	16	PSWYLFQFHRLLQYAR	3287
2RAX	EF	CELL CYCLE	F	2.1	6.2	3	5	WLDYF	3288
2VBL	AB	HYDROLASE	B	2.1	6.2	3	14	KEFLLYLAGFVDAD	3289
2VDW	CD	TRANSFERASE	C	2.1	6.2	3	14	FATIIERSKKFING	3290
2VE7	BD	CELL CYCLE	D	3.1	6.2	2	20	TTVTIPSAVYVAQLYHQVSK	3291
2Z3R	IJ	CYTOKINE/CYTOKINE RECEPTOR	I	3.1	6.2	2	20	KVTAMKCFLLELQVISLESG	3292
2ZCY	TU	HYDROLASE	U	1.6	6.2	4	22	IPDARNAALRAKAEAAEFRYKY	3293
3C1B	GH	STRUCTURAL PROTEIN/DNA	G	3.1	6.2	2	7	EELNKLL	3294
3CUE	CE	PROTEIN TRANSPORT	E	3.1	6.2	2	28	FNKVNDHLYSMGYNIGCRLIEDFLARTA	3295
3CUE	OQ	PROTEIN TRANSPORT	Q	6.2	6.2	1	28	FNKVNDHLYSMGYNIGCRLIEDFLARTA	3296
3DHH	AB	OXIDOREDUCTASE	B	2.1	6.2	3	12	PMNLWYKQYRNA	3297
3EI2	AB	DNA BINDING PROTEIN/DNA	B	1.6	6.2	4	10	ILHYIYKSSL	3298
3EXG	OP	OXIDOREDUCTASE	O	2.1	6.2	3	16	AQVPLGAGIALACKYN	3299
3FMP	AB	ONCOPROTEIN/HYDROLASE	B	2.1	6.2	3	11	HQDQSIRIQRM	3300
3FXD	AB	UNKNOWN FUNCTION	A	1.6	6.2	4	23	NFLRVIGKKLIAIRDRFLKRIGA	3301
3GLI	DO	TRANSFERASE/DNA	D	3.1	6.2	2	17	PTDIQLYYQTLLIGRKE	3302
3HD7	CD	EXOCYTOSIS	C	1.2	6.2	5	61	ADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNL	3303
3HOY	AK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	3.1	6.2	2	10	DQVLNMLYWV	3304
1B33	EF	PHOTOSYNTHESIS	F	2.0	6.1	3	27	TAALEKLKSYFSTGELRVRAATTIAAN	3305
1B33	JK	PHOTOSYNTHESIS	J	3.1	6.1	2	25	QEMTATCLRDLDYYLRLITYGIVAG	3306
1BCP	IK	TOXIN	I	1.5	6.1	4	14	YDALRRLLYMIYMS	3307
1E7P	BC	OXIDOREDUCTASE	B	2.0	6.1	3	8	DEDYYELI	3308
1E7P	KL	OXIDOREDUCTASE	K	2.0	6.1	3	8	DEDYYELI	3309
1FM6	AD	TRANSCRIPTION	A	2.0	6.1	3	23	PAEVEALREKVYASLEAYCKHKY	3310
1G0U	PW	HYDROLASE	W	1.5	6.1	4	22	ATDVTTLNEMFRYKTNLYKLKE	3311
1G0U	VL	HYDROLASE	L	1.5	6.1	4	18	VEEVIKLVRDSFTSATER	3312
1GH0	UV	PHOTOSYNTHESIS	U	1.5	6.1	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	3313

1H6K	AX	NUCLEAR PROTEIN	A	3.1	6.1	2	14	PQMIAVLVDKMIRT	3314
1I3R	CD	IMMUNE SYSTEM	D	3.1	6.1	2	5	NFLVP	3315
1IR2	W6	LYASE	W	2.0	6.1	3	14	AKNYGRAVYECLRG	3316
1IR2	Z5	LYASE	Z	1.5	6.1	4	14	AKNYGRAVYECLRG	3317
1IRE	AB	LYASE	A	1.5	6.1	4	10	PQYRSRVVRE	3318
1JD2	EL	HYDROLASE	E	3.1	6.1	2	22	APDARVLSNYLRQQCNYSSLVF	3319
1KYO	NR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	6.1	6.1	1	19	PVLSKLCVPVANQFINLAG	3320
1L9J	ST	PHOTOSYNTHESIS	S	1.5	6.1	4	26	MEGIHRWAIWMAVLVTLTGGIGILLS	3321
1LIA	AB	LIGHT HARVESTING PROTEIN	B	2.0	6.1	3	25	NRRMAACLRDGEIILRYVSYALLAG	3322
1M93	AB	VIRAL PROTEIN	A	2.0	6.1	3	9	STAEQLSKY	3323
1MWN	AX	STRUCTURAL PROTEIN	A	6.1	6.1	1	12	QEVVDKVMETLD	3324
1MXE	BF	METAL BINDING PROTEIN	B	1.5	6.1	4	15	EEQIAEFKEAFSLFD	3325
1N95	AB	TRANSFERASE	A	2.0	6.1	3	14	KEYWRYIGRSLQSK	3326
1NEK	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.5	6.1	4	33	ITAIASILHRVSGVITFVAVGILLWLLGTSLSS	3327
1NTK	CG	OXIDOREDUCTASE	C	2.0	6.1	3	22	PLSQCLFWALVADLLTLTWIGG	3328
1NTK	DJ	OXIDOREDUCTASE	J	2.0	6.1	3	30	TSTFALTIVVGALFFERAFDQGADAIYEHI	3329
1NU7	BD	HYDROLASE/PROTEIN BINDING	D	2.0	6.1	3	40	KDAKDKLMTRILGEDQYLLERKKVQYEEYKKLYKKYKEEN	3330
1OCC	AL	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	2.0	6.1	3	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	3331
1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.5	6.1	4	31	LFVWSVMITAVLLLLSLPVLAAGITMLLTDR	3332
1OCC	NY	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.0	6.1	3	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	3333
1QHH	BD	HYDROLASE	B	1.5	6.1	4	17	EADEAQFVAGRIREAVE	3334
1RD8	AB	VIRAL PROTEIN	B	1.5	6.1	4	29	RRIENLNKKVDDGFLDIWTYNAELLVLLE	3335
1RU7	CB	VIRAL PROTEIN	C	3.1	6.1	2	10	YEELREQLSS	3336
1SCJ	AB	HYDROLASE	A	6.1	6.1	1	19	TCMATPHVAGAAALILSKH	3337
1SFC	JK	TRANSPORT PROTEIN	K	1.5	6.1	4	48	LVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG	3338
1SUY	BC	CIRCADIAN CLOCK PROTEIN	B	2.0	6.1	3	24	DILLDYRLTLIDVIAHLCEMYRRS	3339
1TBG	AE	COMPLEX (GTP-BINDING/TRANSDUCER)	A	1.5	6.1	4	24	ELDQLRQEAEQLKNQIRDARKACA	3340
1V54	AC	OXIDOREDUCTASE	A	2.0	6.1	3	31	ASVDLTIFSLHLAGVSSILGAINFITTIINM	3341
1V54	NP	OXIDOREDUCTASE	N	2.0	6.1	3	31	ASVDLTIFSLHLAGVSSILGAINFITTIINM	3342
1X11	AC	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE)	A	2.0	6.1	3	23	AQLIAQSIGQAFSVAYQEFLRAN	3343
1X86	GH	SIGNALING PROTEIN/MEMBRANE PROTEIN	H	3.1	6.1	2	5	DRLRP	3344

1XK4	JL	METAL BINDING PROTEIN	L	1.5	6.1	4	20	QLERNIETIINTFHQYSVKL	3345
1YOV	AB	SIGNALING PROTEIN	A	2.0	6.1	3	11	DDYVHEFCRYG	3346
1Z7Q	YL	HYDROLASE/HYDROLASE ACTIVATOR	Y	2.0	6.1	3	14	YSGFYTFSLLDHHY	3347
1ZAV	AV	STRUCTURAL PROTEIN	A	1.5	6.1	4	41	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK	3348
1ZBB	ab	STRUCTURAL PROTEIN/DNA	a	1.5	6.1	4	16	KLPFQRLVREIAQDFK	3349
1ZVV	AW	TRANSCRIPTION/DNA	A	6.1	6.1	1	14	MYDIGAVAMRLLTK	3350
2AFH	AB	OXIDOREDUCTASE	B	2.0	6.1	3	14	QDYKDMLAKKRDGF	3351
2AFH	CD	OXIDOREDUCTASE	C	2.0	6.1	3	10	IKEKFIFQKM	3352
2AHM	CG	VIRAL PROTEIN, REPLICATION	G	2.0	6.1	3	12	DALNNIINNARD	3353
2AXT	EF	ELECTRON TRANSPORT	E	2.0	6.1	3	17	ITIPALFIAGWLFVSTG	3354
2BR2	EF	HYDROLASE	E	2.0	6.1	3	26	LQDIDQAENTARSTAVKLLEELKKHL	3355
2BSK	AD	PROTEIN TRANSPORT	A	3.1	6.1	2	20	FKEFLGTYNKLTETCFLDCV	3356
2C1M	AB	PROTEIN TRANSPORT/MEMBRANE PROTEIN	A	2.0	6.1	3	17	FKTQKEAAWAITNYTSG	3357
2DOI	XC	HYDROLASE	C	2.0	6.1	3	20	DAELQRLKNERHEEAELERL	3358
2DXB	NO	HYDROLASE	O	1.5	6.1	4	10	PNYRRRLVRW	3359
2F9I	AB	TRANSFERASE	B	2.0	6.1	3	17	SVIGEKICRIIDYCTEN	3360
2FFD	EF	BLOOD CLOTTING	F	2.0	6.1	3	18	NNQKIVNLKEKVAQLEAQ	3361
2FHH	QR	HYDROLASE	R	1.5	6.1	4	23	AAVAVEFARLYAVELEHYEKLEG	3362
2FNJ	AC	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	3.1	6.1	2	10	LMDLCRRTIR	3363
2FUG	JL	OXIDOREDUCTASE	J	6.1	6.1	1	16	EKDVENLEALLPLIEG	3364
2GUZ	KL	CHAPERONE, PROTEIN TRANSPORT	K	2.0	6.1	3	18	PFLATKINEAKDFLEKRG	3365
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	B	2.0	6.1	3	20	ELAKHAVSEGTKAVTKYTSS	3366
2HJ9	AC	SIGNALING PROTEIN	C	3.1	6.1	2	5	NAHFY	3367
2HY5	AC	TRANSFERASE	C	2.0	6.1	3	11	YAGFVDLTTEC	3368
2INP	BD	OXIDOREDUCTASE	B	3.1	6.1	2	25	MDAYWKYQAEKEKKLYAIFDAFAQN	3369
2IZV	BC	TRANSCRIPTION	C	2.0	6.1	3	17	SHVLSKVCMYFTYKVRY	3370
2JBL	LM	ELECTRON TRANSPORT	M	1.5	6.1	4	26	IESVHRWGWFFSLMVMVSASVGILLT	3371
2JKR	AS	ENDOCYTOSIS	S	2.0	6.1	3	12	FYKVYTVVDEMF	3372
2NOJ	AB	IMMUNE SYSTEM	B	2.0	6.1	3	14	VATHRKAQRAVNLI	3373
2NU9	FG	LIGASE	G	2.0	6.1	3	14	AGLAMGTMDIVKLH	3374
2NZ0	CD	MEMBRANE PROTEIN	C	2.0	6.1	3	14	FEDFVTALSILLRG	3375
2O01	14	PHOTOSYNTHESIS	4	6.1	6.1	1	14	ILSHYVEIRRWQDI	3376
2O98	AP	PROTEIN BINDING	A	2.0	6.1	3	21	YKDSTLIMQLLRDNLTLWTSD	3377
2ODY	DF	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	F	1.5	6.1	4	8	EEECELVC	3378
2PMZ	AC	TRANSLATION, TRANSFERASE	C	2.0	6.1	3	8	QSVGEPGT	3379
2PT7	AG	HYDROLASE/PROTEIN BINDING	G	1.5	6.1	4	18	YRYKALSYLLFNWIHPTY	3380

2Q9Q	AD	REPLICATION	A	3.1	6.1	2	16	GTFLTQALNHMYKLRT	3381
2QOG	AC	HYDROLASE	C	2.0	6.1	3	13	LLQFNKMIKFETR	3382
2V4J	DB	OXIDOREDUCTASE	B	3.1	6.1	2	9	WERFFSLTG	3383
2W73	FO	METAL BINDING PROTEIN	O	1.5	6.1	4	16	IRNKIRAIGKMARVFS	3384
2WIN	HN	IMMUNE SYSTEM	N	2.0	6.1	3	24	FKKMSEAKYQLQKIYNEIDEALKS	3385
2Z2S	AB	TRANSCRIPTION	A	3.1	6.1	2	11	VATWIFTIARN	3386
2ZAL	CD	HYDROLASE	C	1.5	6.1	4	24	LQQELRYIEALSAIVETGQKMLEA	3387
2ZCY	ST	HYDROLASE	S	2.0	6.1	3	15	VERAGHLLCDKAQKN	3388
2ZL1	AB	PROTEIN BINDING	B	2.0	6.1	3	20	ARVTAAIASNIWAAYDRNGN	3389
2ZT9	AG	PHOTOSYNTHESIS	A	2.0	6.1	3	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	3390
3BPQ	CD	TOXIN	C	2.0	6.1	3	22	RKEYEKIEEILDIGLAKAMEET	3391
3BZ1	BD	ELECTRON TRANSPORT	B	1.5	6.1	4	26	PRGWFTFAHAVFALLFFFGHIWHGAR	3392
3C01	BF	MEMBRANE PROTEIN, PROTEIN TRANSPORT	B	2.0	6.1	3	9	EQVKSDIEN	3393
3C5J	BC	MEMBRANE PROTEIN	B	1.5	6.1	4	16	QVDNYCRHNYGVVESF	3394
3CFA	LA	FLUORESCENT PROTEIN	L	3.1	6.1	2	6	FDILST	3395
3DF0	BC	HYDROLASE	C	3.1	6.1	2	8	DALSSDFT	3396
3DW8	DE	HYDROLASE	D	2.0	6.1	3	16	DSVRLLAVEACVNIAQ	3397
3EH3	BC	OXIDOREDUCTASE	B	1.5	6.1	4	30	AILAYEKGWLAFSLAMLFVFIALIAYTLAT	3398
3EXG	12	OXIDOREDUCTASE	2	3.1	6.1	2	15	IDQVINSAAKTYYMS	3399
3EXH	DC	OXIDOREDUCTASE	D	3.1	6.1	2	15	IDQVINSAAKTYYMS	3400
3F9K	gi	VIRAL PROTEIN, RECOMBINATION	i	2.0	6.1	3	10	TEMITTLKKI	3401
3GLI	AE	TRANSFERASE/DNA	E	1.5	6.1	4	17	RELLITDLLLRIEHYLQ	3402
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	2.0	6.1	3	12	YAAKLLFQELMA	3403
3H0L	KL	LIGASE	K	3.1	6.1	2	14	KRAVEYAIRASLAL	3404
3HD7	GH	EXOCYTOSIS	G	2.0	6.1	3	52	TRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAE KNLKD	3405
3HOU	AP	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	P	1.5	6.1	4	15	DDELERILKELSNLE	3406
3HOU	OW	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	O	2.0	6.1	3	22	VVRGIDTLQKKVASILLALTQM	3407
1CP9	AB	HYDROLASE	B	3.0	6.0	2	13	ELTSLMAWVKQGQ	3408
1DOA	AB	CELL CYCLE	A	2.0	6.0	3	5	DRLRP	3409
1E1C	AB	ISOMERASE	B	2.0	6.0	3	22	QFLTIARLRALREAWARIGEVF	3410
1E6V	AC	OXIDOREDUCTASE	A	1.5	6.0	4	19	AQAGLNGWYLSQILHKEGQ	3411
1E6V	DF	OXIDOREDUCTASE	D	1.5	6.0	4	19	AQAGLNGWYLSQILHKEGQ	3412
1ED3	DF	IMMUNE SYSTEM	D	2.0	6.0	3	29	PEYWEQQTRIAKEWEQIYRVDLRTLRGYY	3413
1F2U	AB	REPLICATION	A	3.0	6.0	2	13	KSSLLDAILVGLY	3414
1FM6	AD	TRANSCRIPTION	A	3.0	6.0	2	17	RLPALRSIGLKCLEHLF	3415

1I7Y	AB	PHOTOSYNTHESIS	B	3.0	6.0	2	25	NRRMAACLRDMEIILRYVTYAILAG	3416
1IBX	AB	HYDROLASE/HYDROLASE INHIBITOR	B	6.0	6.0	1	6	DYFLCL	3417
1ID3	AB	STRUCTURAL PROTEIN/DNA	A	2.0	6.0	3	13	TVALREIRRFQKS	3418
1IRU	SZ	HYDROLASE	Z	1.2	6.0	5	22	AADCSFWERLLARQCRIYELRN	3419
1IW7	NP	TRANSFERASE	P	2.0	6.0	3	19	FLDLIQEGNQGLIRAVEKF	3420
1IZN	AB	PROTEIN BINDING	A	3.0	6.0	2	7	TTFKALR	3421
1JJ2	FL	RIBOSOME	L	3.0	6.0	2	9	AYSYIREAW	3422
1KFY	BC	OXIDOREDUCTASE	C	3.0	6.0	2	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	3423
1KFY	OP	OXIDOREDUCTASE	O	2.0	6.0	3	26	VIVIINLITLAAALLHTKTWFELAPK	3424
1KQS	FL	RIBOSOME	L	3.0	6.0	2	9	AYSYIREAW	3425
1KX4	CD	STRUCTURAL PROTEIN/DNA	D	1.5	6.0	4	20	ELAKHAVSEGTKAVTKYTSA	3426
1MHY	BD	OXIDOREDUCTASE	D	1.5	6.0	4	10	PLWKGMKRVF	3427
1MIO	AB	MOLYBDENUM-IRON PROTEIN	B	2.0	6.0	3	16	GSNIKTAVKNIFSLYN	3428
1N5W	DF	OXIDOREDUCTASE	F	3.0	6.0	2	7	PQIRYMG	3429
1N86	EF	BLOOD CLOTTING	E	3.0	6.0	2	8	ILENLRSK	3430
1NRL	BD	TRANSCRIPTION	D	2.0	6.0	3	9	KILHRLLQE	3431
1NVM	CD	LYASE/OXIDOREDUCTASE	C	3.0	6.0	2	14	EDMIVDVALDLLAA	3432
1OL5	AB	TRANSFERASE/CELL CYCLE	B	3.0	6.0	2	9	SWFEEKANL	3433
1OQO	AC	IMMUNE SYSTEM	C	3.0	6.0	2	12	MQCQRRFYEALH	3434
1PH1	AB	DNA BINDING PROTEIN/DNA	B	1.5	6.0	4	20	DEFKTTIQHFRHTALQAAIN	3435
1QHH	BD	HYDROLASE	B	2.0	6.0	3	12	KRILQAANEVIE	3436
1QLE	AC	OXIDOREDUCTASE/IMMUNE SYSTEM	C	2.0	6.0	3	28	PVVRIGLQYGFILFIMSEVMFFVAWFWA	3437
1RYP	QX	MULTICATALYTIC PROTEINASE	X	1.5	6.0	4	23	ATDVTTLNEMFRYKTNLYKLKEE	3438
1TI2	GH	OXIDOREDUCTASE	H	2.0	6.0	3	12	NCFMGCMDEHEL	3439
1TN6	AB	TRANSFERASE	A	2.0	6.0	3	15	KEYWRYIGRSLQSKH	3440
1TQY	GH	TRANSFERASE	G	2.0	6.0	3	12	ATSLEREYLLLS	3441
1TY4	AC	APOPTOSIS	C	2.0	6.0	3	6	DDFDAQ	3442
1U7B	AB	REPLICATION	B	3.0	6.0	2	5	LDDFF	3443
1XFV	CQ	LYASE/METAL BINDING PROTEIN	C	3.0	6.0	2	15	SLEKQKGVTNLLIKY	3444
1XMN	EF	BLOOD CLOTTING	E	1.5	6.0	4	8	ERELLESY	3445
1XXH	FJ	TRANSFERASE	F	1.5	6.0	4	19	QTQLRQAVQLLTRTELTLK	3446
1YE9	BF	OXIDOREDUCTASE	B	3.0	6.0	2	9	DTFWDYVSL	3447
1YE9	KO	OXIDOREDUCTASE	O	2.0	6.0	3	13	FHRRELWEAIEAG	3448
1Z6O	AM	METAL BINDING PROTEIN	A	2.0	6.0	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3449
1Z6O	EQ	METAL BINDING PROTEIN	E	2.0	6.0	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3450
1Z6O	GR	METAL BINDING PROTEIN	R	3.0	6.0	2	13	EALGEFIFDKKLL	3451
1Z6O	JV	METAL BINDING PROTEIN	J	2.0	6.0	3	26	VATELQAYAKLHLERSYDYLLSAAYF	3452
1ZBB	gh	STRUCTURAL PROTEIN/DNA	h	2.0	6.0	3	19	ELAKHAVSEGTKAVTKYTS	3453
1ZBB	GH	STRUCTURAL PROTEIN/DNA	H	2.0	6.0	3	19	ELAKHAVSEGTKAVTKYTS	3454

1ZRT	PR	OXIDOREDUCTASE/METAL TRANSPORT	P	6.0	6.0	1	26	MRYIHANGASLFFLAVYIHIFRGLYY	3455
1ZUN	AB	TRANSFERASE	A	2.0	6.0	3	20	HLKQLEAESIHIIREVAAEF	3456
2AK4	QS	IMMUNE SYSTEM	Q	6.0	6.0	1	13	TAAQITQRKWEAA	3457
2BEQ	CF	VIRAL PROTEIN	C	1.2	6.0	5	35	QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	3458
2BR2	UV	HYDROLASE	U	2.0	6.0	3	17	NAIELARVVDRSLRDSK	3459
2BRU	BC	OXIDOREDUCTASE	B	3.0	6.0	2	13	AGLAAIGAANSLG	3460
2BV8	ON	PHOTOSYNTHESIS	N	1.5	6.0	4	25	NRRMAACLRDMEIVLRYVSYAEIAG	3461
2CKF	EF	OXIDOREDUCTASE	E	3.0	6.0	2	15	PATKSAIQREATRTF	3462
2DFS	AB	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	A	1.2	6.0	5	38	QVAYLEKIRADKLRAACIRIQKTIRGWLMRKKYMRMRR	3463
2EHO	IJ	REPLICATION	I	3.0	6.0	2	13	NTESYLKNVALKH	3464
2FFD	EF	BLOOD CLOTTING	E	1.5	6.0	4	28	RVLRSILENLRSKIQKLESDVSAQMEYC	3465
2FUG	DE	OXIDOREDUCTASE	E	1.5	6.0	4	11	EREVYDLFGIV	3466
2FUG	SU	OXIDOREDUCTASE	U	3.0	6.0	2	17	DVVREAQAGMVEFTLLN	3467
2FYZ	CF	PROTEIN BINDING	C	1.5	6.0	4	49	AVSLVQAQTNARAIAAMKNSIQATNRAVFEVKEGTQRLAIAVQAIQDHI	3468
2GAG	AB	OXIDOREDUCTASE	A	3.0	6.0	2	9	VEHIKRYTS	3469
2HLD	LM	HYDROLASE	L	3.0	6.0	2	12	VFYLHSRLLERA	3470
2HOD	KL	BLOOD CLOTTING	K	1.5	6.0	4	15	KIQKLESDVSAQMEY	3471
2I2X	GH	TRANSFERASE	G	3.0	6.0	2	17	RFETKALADAKAALEAL	3472
2IBZ	DH	OXIDOREDUCTASE	H	6.0	6.0	1	6	RLFDKL	3473
2INN	BD	OXIDOREDUCTASE	B	2.0	6.0	3	23	AYWKYQAEKEKKLYAIFDAFAQN	3474
2ISS	AD	LYASE, TRANSFERASE	A	3.0	6.0	2	12	WIIKKGFAEMFK	3475
2IX2	BC	REPLICATION	B	3.0	6.0	2	13	TITFADIIDELSD	3476
2J0S	AC	HYDROLASE	A	3.0	6.0	2	13	DDIRILRDIEQYY	3477
2JIY	LM	PHOTOSYNTHESIS	L	3.0	6.0	2	24	HIPFAFAFAILAYLTLVLFRPVMM	3478
2JRI	AC	HYDROLASE/SIGNALING PROTEIN	A	2.0	6.0	3	22	PVELSSIAHQLDEEERMRMAEG	3479
2O01	BC	PHOTOSYNTHESIS	B	6.0	6.0	1	6	QGIAQD	3480
2ODE	CD	SIGNALING PROTEIN	C	2.0	6.0	3	10	RSERKKWIHC	3481
2PQR	BD	APOPTOSIS	B	1.5	6.0	4	15	RRECLYYLTIGCYKL	3482
2V52	BM	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	M	2.0	6.0	3	9	DYLKRKIRS	3483
2W73	FM	METAL BINDING PROTEIN	M	2.0	6.0	3	15	IRNKIRAIGKMARVF	3484
2WAX	CD	HYDROLASE	D	2.0	6.0	3	11	KAAVFEEIDTY	3485
2WD7	AC	OXIDOREDUCTASE	C	1.5	6.0	4	24	SLYNMGKHALVGLTQSAALELAPY	3486
2ZCY	EF	HYDROLASE	F	3.0	6.0	2	13	FQVEYAVKAVENG	3487
2ZCY	PW	HYDROLASE	W	1.5	6.0	4	23	ATDVTTLNEMFRYKTNLYKLKEE	3488
3CJH	AB	PROTEIN TRANSPORT	A	2.0	6.0	3	26	DACIDQCLAKYMRSWNVISKAYISRI	3489
3CJH	IJ	PROTEIN TRANSPORT	I	2.0	6.0	3	24	DACIDQCLAKYMRSWNVISKAYIS	3490

3CJH	KL	PROTEIN TRANSPORT	L	2.0	6.0	3	20	KQKVQMSIHQFTNICFKKCV	3491
3D24	CD	TRANSCRIPTION	D	2.0	6.0	3	8	SELLKYLT	3492
3D5A	CN	RIBOSOME	C	3.0	6.0	2	18	YRHLLLEDQRIRGLLEKE	3493
3EX7	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	3.0	6.0	2	11	FKEQIYDVYRY	3494
3EXG	34	OXIDOREDUCTASE	4	2.0	6.0	3	15	IDQVINSAAKTYYMS	3495
3F1I	HS	PROTEIN BINDING	H	1.5	6.0	4	26	HEQFLKALQNAVTTFVNRMKSNHMRG	3496
3FS4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	2.0	6.0	3	16	AEEYGAETLERMFITY	3497
3GHG	BC	BLOOD CLOTTING	B	1.5	6.0	4	29	SNIPTNLRVLRSILENLRSKIQKLESDVS	3498
3HAY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	2.0	6.0	3	15	LHDLVDYYYFWKEDG	3499
3HD7	AB	EXOCYTOSIS	A	1.5	6.0	4	41	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA	3500
3HOU	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	E	3.0	6.0	2	11	SDEKRELLKRY	3501
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	2.0	6.0	3	7	VSENVIL	3502
1AOI	EF	DNA BINDING PROTEIN/DNA	E	2.0	5.9	3	14	KLPFQRLVREIAQD	3503
1AVO	CD	PROTEASOME ACTIVATOR	D	1.5	5.9	4	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	3504
1B0N	AB	TRANSCRIPTION REGULATOR	B	2.0	5.9	3	11	PEEIRKYLLLN	3505
1B33	EF	PHOTOSYNTHESIS	E	1.5	5.9	4	13	PGELDRIKSFVSS	3506
1BCC	DH	OXIDOREDUCTASE	D	5.9	5.9	1	17	MSQVAKDVCTFLRWAAE	3507
1E7P	EF	OXIDOREDUCTASE	E	3.0	5.9	2	5	ACHDV	3508
1ECI	AB	TOXIN	B	1.5	5.9	4	17	TIVKLTICPTLKSMAKK	3509
1EYX	AB	PHOTOSYNTHESIS	B	2.0	5.9	3	25	NRRMAACLRDGEIILRYISYALLAG	3510
1FMH	AB	TRANSCRIPTION	B	1.5	5.9	4	29	VQALKKRVQALKARNYAAKQKVQALRHKC	3511
1FQJ	AB	SIGNALING PROTEIN	A	2.0	5.9	3	10	RSERKKWIHC	3512
1G0U	KL	HYDROLASE	L	5.9	5.9	1	15	INSAARNIQHLLYGK	3513
1G20	CD	OXIDOREDUCTASE	C	2.0	5.9	3	15	DKKLAKLIDEVETLF	3514
1G2C	QR	VIRAL PROTEIN	Q	2.0	5.9	3	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	3515
1GH0	ST	PHOTOSYNTHESIS	S	1.5	5.9	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	3516
1H1L	AB	OXIDOREDUCTASE	A	2.0	5.9	3	7	VGCGQYS	3517
1H3O	AB	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	B	2.0	5.9	3	22	LQIADDFIESVVTAACQLARHR	3518
1I7Y	AB	PHOTOSYNTHESIS	A	1.5	5.9	4	27	NTELQAVDGRFKRAVASMEAARALTNN	3519
1IR2	Y8	LYASE	Y	1.5	5.9	4	14	AKNYGRAVYECLRG	3520
1IW7	CD	TRANSFERASE	D	3.0	5.9	2	8	KRMALELF	3521
1IWP	LM	LYASE	M	2.0	5.9	3	12	DERILAIYNALR	3522
1L9B	MH	PHOTOSYNTHESIS	H	2.0	5.9	3	24	LASLAIYSFWIFLAGLIYYLQTEN	3523

1NGM	EF	TRANSCRIPTION/DNA	E	2.0	5.9	3	19	EDDSKLASRKYARIIQKIG	3524
1OQS	AB	HYDROLASE	A	3.0	5.9	2	13	LFQFGEMILQKTG	3525
1OR7	AC	TRANSCRIPTION	C	2.0	5.9	3	11	ISSRVMAAIEE	3526
1Q7L	CD	HYDROLASE	D	3.0	5.9	2	13	PWWAAFSRVCKDM	3527
1RUY	LK	VIRAL PROTEIN	K	2.0	5.9	3	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	3528
1RYP	Z1	MULTICATALYTIC PROTEINASE	1	5.9	5.9	1	15	INSAARNIQHLLYGK	3529
1S5L	bd	PHOTOSYNTHESIS	b	1.5	5.9	4	12	FFGHIWHGARTL	3530
1S5L	DL	PHOTOSYNTHESIS	L	1.5	5.9	4	24	RTSLYLGLLLILVLALLFSSYFFN	3531
1TQY	EF	TRANSFERASE	E	2.0	5.9	3	12	ATSLEREYLLLS	3532
1U8T	BF	SIGNALING PROTEIN	F	2.0	5.9	3	7	QAEIDAL	3533
1UZD	OM	LYASE	O	3.0	5.9	2	20	WRDRFLFVAEAIYKAQAETG	3534
1V54	AB	OXIDOREDUCTASE	A	2.0	5.9	3	8	SSLDIVLH	3535
1V54	NY	OXIDOREDUCTASE	N	3.0	5.9	2	6	INRWLF	3536
1WYU	CD	OXIDOREDUCTASE	C	1.5	5.9	4	24	PEGLREVALKSVEMAHKLHALLLE	3537
1Y14	CD	TRANSFERASE	C	3.0	5.9	2	23	LSEARLVIKEALVERRRAFKRSQ	3538
1YE9	AE	OXIDOREDUCTASE	E	2.0	5.9	3	13	FHRRELWEAIEAG	3539
1YNJ	CD	TRANSFERASE	D	3.0	5.9	2	11	KPFLLKKMEEK	3540
1Z6O	CU	METAL BINDING PROTEIN	U	3.0	5.9	2	13	EALGEFIFDKKLL	3541
1Z6O	DW	METAL BINDING PROTEIN	W	3.0	5.9	2	13	EALGEFIFDKKLL	3542
1Z6O	EM	METAL BINDING PROTEIN	M	3.0	5.9	2	13	EALGEFIFDKKLL	3543
1Z7S	13	VIRUS	3	2.0	5.9	3	7	MMELAEI	3544
1ZAV	AV	STRUCTURAL PROTEIN	V	1.5	5.9	4	15	VSELAELVKKLEDKF	3545
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	2.0	5.9	3	33	ITAIASILHRVSGVITFVAVGILLWLLGTSLSS	3546
2AXT	ad	ELECTRON TRANSPORT	d	2.0	5.9	3	21	FYTKNLLLNEGIRAWMAPQDQ	3547
2BC4	CD	IMMUNE SYSTEM	D	2.0	5.9	3	19	GLQNCATHTQPFWGSLTNR	3548
2BEQ	BE	VIRAL PROTEIN	E	1.5	5.9	4	13	QKEIDRLNEVAKN	3549
2CKF	CD	OXIDOREDUCTASE	C	3.0	5.9	2	15	PATKSAIQREATRTF	3550
2CLY	DF	HYDROLASE	D	1.5	5.9	4	64	QKRHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMRQKEQEHMINWVEKRVV	3551
2CZV	AC	HYDROLASE	C	2.0	5.9	3	10	VEYLRFALML	3552
2DD4	AK	HYDROLASE	K	3.0	5.9	2	17	LTELHNKIVEMRERVAS	3553
2DD4	KL	HYDROLASE	K	2.0	5.9	3	17	LTELHNKIVEMRERVAS	3554
2DXB	EF	HYDROLASE	E	2.0	5.9	3	18	LTELHNKIVEMRERVASG	3555
2DXB	TU	HYDROLASE	T	2.0	5.9	3	18	LTELHNKIVEMRERVASG	3556
2EHB	AD	SIGNALLING PROTEIN/TRANSFERASE	A	2.0	5.9	3	15	REELKEMVVALLHES	3557
2EKV	AB	CONTRACTILE PROTEIN	A	3.0	5.9	2	11	RNVRKWLVLRN	3558
2F9I	CD	TRANSFERASE	D	2.0	5.9	3	17	SVIGEKICRIIDYCTEN	3559
2FYZ	AB	PROTEIN BINDING	B	1.5	5.9	4	29	ISTELSKVNASLQNTVKYIKESNHQLQSV	3560

2GEZ	AB	HYDROLASE	A	1.5	5.9	4	15	PLDVVELVVRELENI	3561
2GUZ	GH	CHAPERONE, PROTEIN TRANSPORT	G	2.0	5.9	3	18	PFLATKINEAKDFLEKRG	3562
2GUZ	IJ	CHAPERONE, PROTEIN TRANSPORT	I	2.0	5.9	3	18	PFLATKINEAKDFLEKRG	3563
2HYB	DF	TRANSFERASE	F	2.0	5.9	3	11	YAGFVDLTTEC	3564
2I2R	AE	TRANSPORT PROTEIN	A	5.9	5.9	1	8	WLPFARAA	3565
2I2R	KN	TRANSPORT PROTEIN	N	2.0	5.9	3	15	KRELQVLYRGFKNEC	3566
2I2X	OP	TRANSFERASE	O	2.0	5.9	3	17	RFETKALADAKAALEAL	3567
2JKR	LE	ENDOCYTOSIS	E	2.0	5.9	3	16	PDLRDRGYIYWRLLST	3568
2OM0	QR	HORMONE	R	2.0	5.9	3	19	VNQHLCGSHLVEALYLVCG	3569
2OV2	GO	PROTEIN BINDING/TRANSFERASE	G	3.0	5.9	2	9	DRLRPLSYP	3570
2P7V	AB	TRANSCRIPTION	A	1.5	5.9	4	27	KALDDFCQSLVDYLSAGHFSIYERILH	3571
2PQR	AC	APOPTOSIS	A	1.5	5.9	4	18	VNDERLGVKILTDIYKEA	3572
2PT7	DH	HYDROLASE/PROTEIN BINDING	H	1.5	5.9	4	19	YRYKALSYLLFNWIHPTYG	3573
2Q9Q	EH	REPLICATION	E	2.0	5.9	3	29	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	3574
2QM6	AB	TRANSFERASE	A	3.0	5.9	2	7	RERFLKY	3575
2RAX	AB	CELL CYCLE	B	2.0	5.9	3	5	WLDYF	3576
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	A	2.0	5.9	3	34	ITAEFLVKSKHRDLTALCKEYDELAETQGKLEEK	3577
2V4I	EF	TRANSFERASE	F	2.0	5.9	3	14	PAEQDRLFRRVMDR	3578
2VBL	AB	HYDROLASE	A	2.0	5.9	3	14	KEFLLYLAGFVDGD	3579
2VJH	AB	PHOTOSYNTHESIS	A	2.0	5.9	3	27	GSDLESVQGNIQRSAARLEAAEKLAAG	3580
2WAX	CD	HYDROLASE	C	3.0	5.9	2	14	ERQKVHCLNTLFSR	3581
2Z2L	BC	BIOSYNTHETIC PROTEIN	C	3.0	5.9	2	11	PGDLAEELRRN	3582
2Z3R	MN	CYTOKINE/CYTOKINE RECEPTOR	M	3.0	5.9	2	20	KVTAMKCFLLELQVISLESG	3583
2ZAL	AB	HYDROLASE	A	1.5	5.9	4	24	LQQELRYIEALSAIVETGQKMLEA	3584
2ZCY	KL	HYDROLASE	L	5.9	5.9	1	15	INSAARNIQHLLYGK	3585
3BLW	MN	OXIDOREDUCTASE	N	2.0	5.9	3	11	IDNSVLKVVTN	3586
3BOW	BC	HYDROLASE/HYDROLASE INHIBITOR	B	2.0	5.9	3	14	EERQFRKLFVQLAG	3587
3BZ1	DL	ELECTRON TRANSPORT	L	2.0	5.9	3	24	RTSLYLGLLLILVLALLFSSYFFN	3588
3BZ1	LT	ELECTRON TRANSPORT	T	2.0	5.9	3	21	ETITYVFIFACIIALFFFAIF	3589
3C1B	EF	STRUCTURAL PROTEIN/DNA	E	2.0	5.9	3	13	TVALREIRRYQKS	3590
3CFA	MB	FLUORESCENT PROTEIN	M	3.0	5.9	2	6	FDILST	3591
3CI0	IJ	PROTEIN TRANSPORT	I	2.0	5.9	3	22	HVLEEKTVAGWVAENQTALLYL	3592
3CJH	KL	PROTEIN TRANSPORT	K	2.0	5.9	3	26	DACIDQCLAKYMRSWNVISKAYISRI	3593
3DBJ	EF	PHOTOSYNTHESIS	F	3.0	5.9	2	25	TRRYAACIRDLDYYLRYATYAMLAG	3594
3DUF	GH	OXIDOREDUCTASE/TRANSFERASE	H	1.5	5.9	4	14	ESGIGGLAIGLALQ	3595
3EJB	AB	OXIDOREDUCTASE/LIPID TRANSPORT	A	1.5	5.9	4	14	LDTVELVMALEEEF	3596
3EXG	UV	OXIDOREDUCTASE	U	3.0	5.9	2	16	AQVPLGAGIALACKYN	3597
3F1F	X2	RIBOSOME	2	2.0	5.9	3	25	SPVELEKLVREKKRELMELRFQASI	3598
3FAL	AD	SIGNALING PROTEIN	A	1.5	5.9	4	8	FLMEMLEA	3599
3FGC	AB	OXIDOREDUCTASE	A	3.0	5.9	2	7	DKDFRVF	3600

3FKS	SW	HYDROLASE	S	3.0	5.9	2	7	SRLLERA	3601
3FWC	JK	CELL CYCLE, TRANSCRIPTION	K	2.0	5.9	3	14	WVDKVKDLTKSEMN	3602
3GTU	CD	TRANSFERASE	C	1.5	5.9	4	27	EKEQIREDILENQFMDSRMQLAKLCYD	3603
3HOU	AK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	3.0	5.9	2	11	LDQVLNMLYWV	3604
4RUB	AT	LYASE(CARBON-CARBON)	A	2.0	5.9	3	20	WRDRFLFCAEALYKAQAETG	3605
1BGY	OS	ELECTRON TRANSPORT	O	2.9	5.8	2	22	PLSQCLFWALVADLLTLTWIGG	3606
1BX2	AC	IMMUNE SYSTEM	A	1.2	5.8	5	23	AQGALANIAVDKANLEIMTKRSN	3607
1DIO	LM	LYASE	M	1.9	5.8	3	17	KICAAFVREAATLYVER	3608
1E1H	AB	HYDROLASE	A	1.9	5.8	3	13	DLGRMLLTSIVRG	3609
1E1H	CD	HYDROLASE	D	1.9	5.8	3	8	FEELRTFG	3610
1E3A	AB	ANTIBIOTIC RESISTANCE	A	1.9	5.8	3	10	VKFDKDIRRN	3611
1EF1	AC	MEMBRANE PROTEIN	C	1.5	5.8	4	16	ERVQKHLKALTSELAN	3612
1F99	AB	PHOTOSYNTHESIS	B	2.9	5.8	2	12	AFAKVVAQADAR	3613
1FE8	CJ	IMMUNE SYSTEM	C	1.9	5.8	3	10	KAHLLSLVDV	3614
1FFU	EF	HYDROLASE	E	1.9	5.8	3	11	SYRVWKSLKEH	3615
1FYZ	BF	OXIDOREDUCTASE	B	1.9	5.8	3	33	PASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYG	3616
1GZS	BA	TOXIN/CELL CYCLE	A	1.5	5.8	4	9	DRLRPLSYP	3617
1H1L	AB	OXIDOREDUCTASE	A	1.9	5.8	3	11	IKEKYIFQKMG	3618
1H1L	CD	OXIDOREDUCTASE	D	2.9	5.8	2	13	DEYQELFRNKRQL	3619
1HIA	AB	COMPLEX (PROTEASE/INHIBITOR)	B	2.9	5.8	2	11	LDWIDDTITEN	3620
1HIA	XY	COMPLEX (PROTEASE/INHIBITOR)	Y	1.9	5.8	3	11	LDWIDDTITEN	3621
1HLU	AP	COMPLEX (ACETYLATION/ACTIN-BINDING)	P	1.5	5.8	4	18	GGMINKKCYEMASHLRRS	3622
1I7Q	AB	LYASE	B	1.9	5.8	3	11	TYNLVDQLRAS	3623
1JD2	RS	HYDROLASE	R	1.9	5.8	3	22	AADCQFWETWLGSQCRLHELRE	3624
1KX4	GH	STRUCTURAL PROTEIN/DNA	H	1.9	5.8	3	18	LAKHAVSEGTKAVTKYTS	3625
1L9J	ST	PHOTOSYNTHESIS	T	1.9	5.8	3	21	LAIYSFWIFLAGLIYYLQTEN	3626
1LWU	AB	BLOOD CLOTTING	A	1.5	5.8	4	21	QVSQILRVEVDIDVALRACKG	3627
1M1J	AC	BLOOD CLOTTING	C	1.9	5.8	3	31	CGIADFFNKYRLTTDGELLEIEGLLQQATNS	3628
1M1J	BC	BLOOD CLOTTING	C	1.9	5.8	3	31	CGIADFFNKYRLTTDGELLEIEGLLQQATNS	3629
1OCC	NG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.9	5.8	2	31	LFVWSVMITAVLLLLSLPVLAAGITMLLTDR	3630
1OCC	YZ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Y	1.5	5.8	4	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	3631
1PSB	AC	METAL BINDING PROTEIN	C	1.9	5.8	3	16	KETEFLRLKRTRLGLE	3632
1RH5	AC	PROTEIN TRANSPORT	C	1.9	5.8	3	20	PEHVIGVTVAFVIIEAILTY	3633
1RVF	13	VIRUS/IMMUNE SYSTEM	1	5.8	5.8	1	8	VQLRKKLE	3634
1S5L	lt	PHOTOSYNTHESIS	l	1.9	5.8	3	24	RTSLYLGLLLILVLALLFSSYFFN	3635
1S9V	AB	IMMUNE SYSTEM	A	1.5	5.8	4	22	PQFALTNIAVLKHNLNSLIKRS	3636

1SQB	EJ	OXIDOREDUCTASE	E	1.5	5.8	4	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	3637
1T0F	AC	DNA BINDING PROTEIN	C	1.9	5.8	3	7	LRYIYSQ	3638
1T3Q	AB	OXIDOREDUCTASE	A	1.9	5.8	3	8	ETIIDAIT	3639
1TUE	DE	REPLICATION	D	1.5	5.8	4	11	WRPIVQFLRYQ	3640
1TUE	MQ	REPLICATION	M	1.9	5.8	3	11	WRPIVQFLRYQ	3641
1UZD	EJ	LYASE	E	2.9	5.8	2	20	WRDRFLFVAEAIYKAQAETG	3642
1UZD	RP	LYASE	R	2.9	5.8	2	20	WRDRFLFVAEAIYKAQAETG	3643
1V54	EI	OXIDOREDUCTASE	E	2.9	5.8	2	11	KEIYPYVIQEL	3644
1VF5	NO	PHOTOSYNTHESIS	N	5.8	5.8	1	10	QVGYWAVKIV	3645
1VG0	AB	PROTEIN BINDING/PROTEIN TRANSPORT	A	1.9	5.8	3	15	QGELPQCFCRMCAVF	3646
1XCG	AB	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	B	2.9	5.8	2	7	LRPLSYP	3647
1XCQ	AB	IMMUNE SYSTEM	A	2.9	5.8	2	5	SEQLT	3648
1XQ5	CB	OXYGEN STORAGE/TRANSPORT	B	1.9	5.8	3	7	PWTQRYF	3649
1YE9	KO	OXIDOREDUCTASE	O	1.9	5.8	3	10	YSHPRLFWLS	3650
1YHU	EG	OXYGEN STORAGE/TRANSPORT	G	1.5	5.8	4	20	PEFQGHVVRVMGGLDILINA	3651
1Z6O	AX	METAL BINDING PROTEIN	X	2.9	5.8	2	13	EALGEFIFDKKLL	3652
1Z6O	IS	METAL BINDING PROTEIN	S	1.9	5.8	3	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	3653
1Z6O	IT	METAL BINDING PROTEIN	T	2.9	5.8	2	13	EALGEFIFDKKLL	3654
1Z7Q	Fg	HYDROLASE/HYDROLASE ACTIVATOR	F	2.9	5.8	2	13	FQVEYALEAIKQG	3655
1ZV8	AB	VIRAL PROTEIN	B	1.5	5.8	4	16	QKEIDRLNEVAKNLNE	3656
2DXB	NO	HYDROLASE	N	1.9	5.8	3	18	LTELHNKIVEMRERVASG	3657
2DXB	VT	HYDROLASE	T	1.9	5.8	3	17	SSIREEVHRHLGTVALM	3658
2F4O	AB	HYDROLASE	A	1.9	5.8	3	19	ESRRKELLQRIIVELVEFI	3659
2FBW	NO	OXIDOREDUCTASE	N	2.9	5.8	2	21	QDAIHYMTEQAPAAVIELENY	3660
2FHH	12	HYDROLASE	1	1.9	5.8	3	22	FNEFDNLRRGGIQFADTRGYAY	3661
2FYZ	CD	PROTEIN BINDING	D	1.9	5.8	3	28	ISTELSKVNASLQNTVKYIKESNHQLQS	3662
2GTL	NO	OXYGEN STORAGE/TRANSPORT	N	1.9	5.8	3	24	AFLIIRLDRIIEKLRTKLDEAEKI	3663
2GV5	BC	CELL CYCLE	C	1.5	5.8	4	16	LKKFRERLLEIVKSEE	3664
2H4C	GH	HYDROLASE	G	2.9	5.8	2	11	FFQFAEMIVKM	3665
2HGJ	ES	RIBOSOME	S	1.9	5.8	3	11	LIKLVESRYVR	3666
2HYB	EC	TRANSFERASE	E	5.8	5.8	1	5	GVYQL	3667
2HYB	GI	TRANSFERASE	I	1.9	5.8	3	11	YAGFVDLTTEC	3668
2HYB	PQ	TRANSFERASE	P	1.5	5.8	4	11	LGQLVEAAIQA	3669
2J59	EQ	HYDROLASE	Q	1.5	5.8	4	22	EEDTGVTNRDLISRRIKEYNNL	3670
2JF9	BQ	TRANSCRIPTION	B	1.5	5.8	4	24	LHDQVHLLECAWLEILMIGLVWRS	3671
2JFA	BQ	TRANSCRIPTION	Q	1.9	5.8	3	14	AFQLRQLILRGLQD	3672
2JTT	BC	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	C	1.9	5.8	3	10	LMNVLKKIYE	3673

2NPI	AC	TRANSCRIPTION	C	5.8	5.8	1	7	DSQWAAF	3674
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.5	5.8	4	8	PVYNTVAK	3675
2OV2	BJ	PROTEIN BINDING/TRANSFERASE	B	2.9	5.8	2	9	DRLRPLSYP	3676
2PA8	DL	TRANSFERASE	D	2.9	5.8	2	14	LEFVNAIRRASMLY	3677
2QOW	CN	RIBOSOME	C	1.5	5.8	4	21	KEFADNLDSDFKVRQYLTKEL	3678
2R1H	CD	OXYGEN BINDING	D	2.9	5.8	2	16	VDEIGPQALARLLIVS	3679
2RAX	EF	CELL CYCLE	F	1.5	5.8	4	38	FLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	3680
2V4J	AB	OXIDOREDUCTASE	B	1.9	5.8	3	15	ITHIREMCDIADKYC	3681
2V6X	AB	PROTEIN TRANSPORT	A	1.5	5.8	4	18	FLTKGIELVQKAIDLDTA	3682
2VE7	AC	CELL CYCLE	A	1.9	5.8	3	16	DEMNAELQSKLKDLFN	3683
2VOF	AB	APOPTOSIS	A	2.9	5.8	2	22	WGRIVTIFAFGGVLLKKLKQES	3684
2VOH	AB	APOPTOSIS	A	2.9	5.8	2	6	KSYLDD	3685
2VSO	BF	HYDROLASE/TRANSLATION	B	2.9	5.8	2	9	ENLLRGVFG	3686
2W2X	BC	SIGNALING PROTEIN/HYDROLASE	C	2.9	5.8	2	16	VEELFEWFQSIREITW	3687
2W72	AB	OXYGEN TRANSPORT	B	2.9	5.8	2	16	VDEVGGEAYGRLLVVY	3688
2ZCY	YZ	HYDROLASE	Z	5.8	5.8	1	15	INSAARNIQHLLYGK	3689
2ZT9	AB	PHOTOSYNTHESIS	A	2.9	5.8	2	17	QVGYWAVKIVSGVPEAI	3690
3BJI	BC	SIGNALING PROTEIN	C	1.9	5.8	3	5	DRLRP	3691
3C7B	DE	OXIDOREDUCTASE	D	1.5	5.8	4	15	TKALRGLCDVWEKWG	3692
3CF6	ER	SIGNALING PROTEIN/GTP-BINDING PROTEIN	R	1.5	5.8	4	11	TAMRDLYMKNG	3693
3CJH	GH	PROTEIN TRANSPORT	G	1.9	5.8	3	25	DACIDQCLAKYMRSWNVISKAYISR	3694
3CJH	IL	PROTEIN TRANSPORT	I	1.9	5.8	3	15	ELVNKISENCFEKCL	3695
3CM8	AB	RNA BINDING PROTEIN/TRANSFERASE	B	1.9	5.8	3	5	PTLLF	3696
3CQG	AB	PROTEIN TRANSPORT	B	1.9	5.8	3	17	FAKKKTLLGLSKLAALA	3697
3D32	AC	TRANSPORT PROTEIN	A	1.9	5.8	3	12	VGQFYFLIRKRI	3698
3DAC	AB	CELL CYCLE	B	2.9	5.8	2	8	FSDLWKLL	3699
3DW8	AC	HYDROLASE	A	1.5	5.8	4	17	YLHRMTTLFCINVLSEV	3700
3EUB	34	OXIDOREDUCTASE	3	1.9	5.8	3	24	IEFRRTLTLSFFFKFYLTVLKKLG	3701
3EXG	AB	OXIDOREDUCTASE	B	2.9	5.8	2	5	TYYMS	3702
3EXG	OP	OXIDOREDUCTASE	P	2.9	5.8	2	15	IDQVINSAAKTYYMS	3703
3EXH	AB	OXIDOREDUCTASE	B	2.9	5.8	2	15	IDQVINSAAKTYYMS	3704
3H32	BC	BLOOD CLOTTING	C	1.5	5.8	4	34	THDSSIRYLQEIYNSNNQKIVNLKEKVAQLEAQC	3705
3HKZ	AB	TRANSFERASE	A	5.8	5.8	1	6	FAYVMA	3706
3HOU	NO	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	O	1.9	5.8	3	11	DEFIAHRLGLI	3707
3I1H	AB	APOPTOSIS	A	1.9	5.8	3	22	WGRIVTIFAFEGILIKKLLRQQ	3708
1BXN	GK	LYASE	G	1.9	5.7	3	14	GRNYGRVVYEGLKG	3709
1BXR	GH	AMIDOTRANSFERASE	G	2.9	5.7	2	21	RWFLVQIEELVRLEEKVAEVG	3710

1DIO	LM	LYASE	L	2.9	5.7	2	14	PWSKGFLASSYASR	3711
1DIO	LM	LYASE	M	1.9	5.7	3	11	DDRILEIYNAL	3712
1E1H	AB	HYDROLASE	A	2.9	5.7	2	21	DNEKDNYLKGVTKLFERIYST	3713
1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.9	5.7	2	16	PFDVAMIFVGTMANRF	3714
1E6Y	BC	OXIDOREDUCTASE	B	1.9	5.7	3	24	VPKWNACAAVGTLAATLVNCGAGR	3715
1F66	CD	STRUCTURAL PROTEIN/DNA	D	2.9	5.7	2	21	ELAKHAVSEGTKAVTKYTSAK	3716
1FOE	AD	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	D	1.9	5.7	3	19	PASFENVRAKWYPEVRHHC	3717
1FQJ	AC	SIGNALING PROTEIN	A	1.9	5.7	3	10	RSERKKWIHC	3718
1G20	AB	OXIDOREDUCTASE	A	1.9	5.7	3	7	VGCGQYS	3719
1G2C	OR	VIRAL PROTEIN	O	1.9	5.7	3	49	HLEGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	3720
1GH0	AB	PHOTOSYNTHESIS	B	1.9	5.7	3	12	AFTKVVSQADTR	3721
1HDS	AD	OXYGEN TRANSPORT	D	2.9	5.7	2	7	PWTQRFF	3722
1IBR	CD	CELL CYCLE, TRANSLATION	C	1.4	5.7	4	10	VPNWHRDLVR	3723
1JB0	AB	PHOTOSYNTHESIS	A	1.4	5.7	4	18	RGYWQELIESIVWAHNKL	3724
1JMU	DH	VIRAL PROTEIN	H	2.9	5.7	2	12	GHQIVDLINNAF	3725
1JPW	CF	CELL ADHESION	C	1.9	5.7	3	18	DSVLFYAITTLHNLLLHQ	3726
1JYO	DE	CHAPERONE	E	2.9	5.7	2	15	QKILQTFLHALTEKY	3727
1K6L	LM	PHOTOSYNTHESIS	L	2.9	5.7	2	17	HIPFAFAFAILAYLTLV	3728
1KF6	BC	OXIDOREDUCTASE	C	1.9	5.7	3	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	3729
1KYO	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.9	5.7	3	32	PEHDERKRLGLKTVIILSSLYLLSIWVKKFKW	3730
1L9B	LM	PHOTOSYNTHESIS	L	1.9	5.7	3	29	GLWQIITICATGAFVSWALREVEICRKLG	3731
1N4Q	GH	TRANSFERASE	G	1.9	5.7	3	10	ESAWNYLKGI	3732
1NDO	CD	NON-HEME IRON DIOXYGENASE	D	1.9	5.7	3	12	FQQLKVRVEHQL	3733
1OAO	BC	OXIDOREDUCTASE	C	1.9	5.7	3	9	EAVEQLLEE	3734
1OCC	DK	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	K	1.4	5.7	4	27	FHDKYGNAVLASGATFCVAVWVYMATQ	3735
1OCC	QX	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	X	1.4	5.7	4	27	FHDKYGNAVLASGATFCVAVWVYMATQ	3736
1R27	AB	OXIDOREDUCTASE	B	1.9	5.7	3	11	TCSVTCKNVWT	3737
1R3I	HC	MEMBRANE PROTEIN	C	2.9	5.7	2	29	LHWRAAGAATVLLVIVLLAGSYLAVLAER	3738
1RM6	DE	OXIDOREDUCTASE	D	2.9	5.7	2	14	PDRITELLDAKEAA	3739
1RYP	J1	MULTICATALYTIC PROTEINASE	J	1.4	5.7	4	12	SDQLFGMCESLY	3740
1RYP	V2	MULTICATALYTIC PROTEINASE	2	1.9	5.7	3	20	ISDMQHIERLLKDLVTENAY	3741
1S5L	LM	PHOTOSYNTHESIS	L	1.9	5.7	3	24	RTSLYLGLLLILVLALLFSSYFFN	3742
1T6O	AB	VIRAL PROTEIN	B	1.9	5.7	3	17	DSRRSADALLRLQAMAG	3743
1TQY	AB	TRANSFERASE	A	1.9	5.7	3	12	ATSLEREYLLLS	3744
1V54	DE	OXIDOREDUCTASE	D	2.9	5.7	2	12	IDEKVELYRLKF	3745

1V54	YZ	OXIDOREDUCTASE	Z	1.4	5.7	4	25	PKEQAIGLSVTFLSFLLPAGWVLYH	3746
1VRQ	AB	OXIDOREDUCTASE	B	2.9	5.7	2	16	LGDVRESIRRVEANKF	3747
1WDK	BD	LYASE,OXIDOREDUCTASE/TRANSFERASE	B	2.9	5.7	2	17	AIEQMMAFETAKGFVAG	3748
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	A	1.9	5.7	3	12	NTLNLLTSARSD	3749
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	E	1.9	5.7	3	10	IFIPRLLMVD	3750
1YHU	NP	OXYGEN STORAGE/TRANSPORT	N	1.9	5.7	3	16	EPVLNTQLAHLAKQHE	3751
1YKE	AB	GENE REGULATION	A	1.9	5.7	3	24	YQYKIQELRKLLKSLLLNYLELIG	3752
1YOV	CD	SIGNALING PROTEIN	C	1.4	5.7	4	21	HTIAAFLGGAAAQEVIKIITK	3753
1Z6O	BM	METAL BINDING PROTEIN	B	1.9	5.7	3	16	LSLALYVFDEYLQKTV	3754
1Z6O	FV	METAL BINDING PROTEIN	V	2.9	5.7	2	13	EALGEFIFDKKLL	3755
1Z6O	LV	METAL BINDING PROTEIN	L	1.9	5.7	3	16	LSLALYVFDEYLQKTV	3756
1ZAV	AU	STRUCTURAL PROTEIN	U	1.9	5.7	3	16	VSELAELVKKLEDKFG	3757
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.9	5.7	3	10	YEEFVQMMTA	3758
2A1D	AB	HYDROLASE	A	2.9	5.7	2	9	EKELFESYI	3759
2BE6	CF	MEMBRANE PROTEIN	C	1.4	5.7	4	12	EEEIREAFRVFD	3760
2BEQ	CE	VIRAL PROTEIN	C	1.4	5.7	4	35	QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	3761
2BSK	AD	PROTEIN TRANSPORT	D	1.9	5.7	3	20	KGESVCLDRCVSKYLDIHER	3762
2CCI	BF	CELL CYCLE	B	1.9	5.7	3	8	VAEFVYIT	3763
2D2M	AC	OXYGEN STORAGE/TRANSPORT	A	1.9	5.7	3	18	RLEQILVKTQWAQSYGEA	3764
2DD4	AE	HYDROLASE	E	1.9	5.7	3	15	IREEVHRHLGTVALM	3765
2DD4	DH	HYDROLASE	H	2.9	5.7	2	18	LTELHNKIVEMRERVASG	3766
2DD4	EF	HYDROLASE	E	1.9	5.7	3	16	YYGRWLLTAARILVDK	3767
2DXB	HI	HYDROLASE	H	1.9	5.7	3	16	YYGRWLLTAARILVDK	3768
2E9X	BD	REPLICATION	B	1.9	5.7	3	9	AAEVEFLAE	3769
2FCW	AB	LIPID TRANSPORT/ENDOCYTOSIS/CHAPERONE	A	1.9	5.7	3	41	DKELEAFREELKHFEAKIEKHNHYQKQLEIAHEKLRHAESV	3770
2FHH	QR	HYDROLASE	Q	1.9	5.7	3	22	FNEFDNLRRGGIQFADTRGYAY	3771
2FK0	GH	VIRAL PROTEIN	H	1.4	5.7	4	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQL	3772
2FOI	BD	OXIDOREDUCTASE	D	2.9	5.7	2	12	FIDYAIEYSEKY	3773
2GPP	BD	TRANSCRIPTION	B	1.9	5.7	3	11	LADQMSLLQSA	3774
2GUZ	EF	CHAPERONE, PROTEIN TRANSPORT	E	1.9	5.7	3	18	PFLATKINEAKDFLEKRG	3775
2H1O	DH	GENE REGULATION/DNA COMPLEX	H	1.9	5.7	3	12	LGSMLASIGQEI	3776
2HYB	AC	TRANSFERASE	C	1.9	5.7	3	11	YAGFVDLTTEC	3777
2I2R	IM	TRANSPORT PROTEIN	I	5.7	5.7	1	8	WLPFARAA	3778
2I3T	EF	CELL CYCLE	F	2.9	5.7	2	9	LEEVLAISR	3779

2IAN	BC	IMMUNE SYSTEM	B	2.9	5.7	2	25	KDLLEQRRAAVDTYCRHNYGVGESF	3780
2IE3	AC	SIGNALING PROTEIN,HYDROLASE	A	2.9	5.7	2	14	ANVRFNVAKSLQKI	3781
2JDQ	AE	PROTEIN TRANSPORT	A	2.9	5.7	2	18	FRTRKEAAWAITNATSGG	3782
2JKR	EU	ENDOCYTOSIS	U	1.9	5.7	3	19	AAMVFEFLYKMCDVMAAYF	3783
2KA6	AB	TRANSCRIPTION REGULATOR	A	1.9	5.7	3	13	PFCLNIKHKLRQQ	3784
2KIN	AB	MOTOR PROTEIN	B	1.9	5.7	3	6	KMTRIL	3785
2NU9	DI	LIGASE	I	2.9	5.7	2	11	PYQGRELAFKL	3786
2NVU	AB	PROTEIN TURNOVER, LIGASE	A	1.9	5.7	3	7	DRQLRLW	3787
2O3B	AB	HYDROLASE/HYDROLASE INHIBITOR	A	2.9	5.7	2	6	PDNNRN	3788
2OV2	FN	PROTEIN BINDING/TRANSFERASE	N	5.7	5.7	1	7	RQWQSLI	3789
2P2C	KL	HYDROLASE	L	2.9	5.7	2	13	WYIEALAQVFSER	3790
2PF4	BF	HYDROLASE REGULATOR/VIRAL PROTEIN	B	2.9	5.7	2	10	PMVRRAAASK	3791
2PG1	DK	STRUCTURAL PROTEIN	D	1.9	5.7	3	16	EKDIAAYIKKEFDKKY	3792
2PQR	BD	APOPTOSIS	D	2.9	5.7	2	9	SATTFRILA	3793
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	1.4	5.7	4	14	KAVYRVLLILPYAV	3794
2V4J	AE	OXIDOREDUCTASE	E	2.9	5.7	2	9	WERFFSLTG	3795
2V5P	BC	RECEPTOR/GLYCOPROTEIN	C	1.9	5.7	3	12	GELVDTLQFVCG	3796
2VML	KL	PHOTOSYNTHESIS	K	1.4	5.7	4	27	NTELQAANGRFQRATASMEAARALTSN	3797
2W72	DC	OXYGEN TRANSPORT	D	2.9	5.7	2	16	VDEVGGEAYGRLLVVY	3798
2WAQ	AB	TRANSCRIPTION	B	5.7	5.7	1	5	LPSRM	3799
2WIN	FM	IMMUNE SYSTEM	M	1.9	5.7	3	24	FKKMSEAKYQLQKIYNEIDEALKS	3800
2ZCY	AB	HYDROLASE	B	2.9	5.7	2	12	YQVEYALESISH	3801
2ZCY	ST	HYDROLASE	T	2.9	5.7	2	13	FQVEYAVKAVENG	3802
2ZNV	AB	HYDROLASE/SIGNALING PROTEIN	A	1.9	5.7	3	14	SVDLHTHCSYQLML	3803
2ZSH	AB	HORMONE RECEPTOR	A	1.9	5.7	3	8	RHLAEYLD	3804
2ZT9	BC	PHOTOSYNTHESIS	B	1.9	5.7	3	26	PNDLLYVFPIVIMGSFACIVALAVLD	3805
3BLW	OP	OXIDOREDUCTASE	P	1.9	5.7	3	11	IDNSVLKVVTN	3806
3BTP	AB	DNA BINDING PROTEIN, CHAPERONE	A	2.9	5.7	2	8	PWTQALKE	3807
3CFA	RG	FLUORESCENT PROTEIN	R	2.9	5.7	2	6	FDILST	3808
3DHH	AB	OXIDOREDUCTASE	B	1.9	5.7	3	19	LRYLFHCLQMSSAYVQQMA	3809
3DTU	CD	OXIDOREDUCTASE	C	1.9	5.7	3	8	ASVDRYYH	3810
3EAB	AG	CELL CYCLE	A	1.9	5.7	3	28	SMEAERVRVFHKQAFEYISIALRIDEDE	3811
3EO1	HL	IMMUNE SYSTEM/CYTOKINE	L	2.9	5.7	2	12	THSTVLGLYNTL	3812
3EZJ	AB	PROTEIN TRANSPORT	A	1.4	5.7	4	15	ERQYYQLFLNLLEAQ	3813
3F1I	HS	PROTEIN BINDING	S	1.9	5.7	3	13	EDKMDQLLQMLQS	3814
3HOU	OW	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	W	2.9	5.7	2	29	PKDALKNACNSIINKLGALKTNFETEWNL	3815
4RUB	CU	LYASE(CARBON-CARBON)	C	1.4	5.7	4	22	NAPGAVANRVALEACVKARNEG	3816

1AXC	EF	COMPLEX (DNA-BINDING PROTEIN/DNA)	F	2.8	5.6	2	5	MTDFY	3817
1BB1	BC	DE NOVO PROTEIN DESIGN	C	1.4	5.6	4	32	IAAIKYKQAAIKNEIAAIKQEIAAIEQMIAAI	3818
1CG5	AB	OXYGEN TRANSPORT	B	2.8	5.6	2	16	HKQITAKALERVFVVY	3819
1CP9	AB	HYDROLASE	A	1.4	5.6	4	24	SQEQDILRGYADGMNAWIKQINTK	3820
1DD4	BD	RIBOSOME	B	1.9	5.6	3	9	IDEIIEAIE	3821
1DIO	AG	LYASE	G	1.9	5.6	3	11	DDRILEIYNAL	3822
1E1C	AB	ISOMERASE	B	2.8	5.6	2	18	PYVNILRGSIATFSASVG	3823
1E6Y	DF	OXIDOREDUCTASE	D	2.8	5.6	2	7	PTALEDH	3824
1EJH	BF	TRANSLATION	B	1.9	5.6	3	10	VEDFWALYNH	3825
1F99	KL	PHOTOSYNTHESIS	L	1.9	5.6	3	14	GNKRLDVVNKITNN	3826
1G0U	TU	HYDROLASE	U	2.8	5.6	2	14	YQVEYAFKATNQTN	3827
1GH0	CD	PHOTOSYNTHESIS	C	1.4	5.6	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	3828
1GH0	IJ	PHOTOSYNTHESIS	I	1.4	5.6	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	3829
1GO3	EF	TRANSFERASE	F	2.8	5.6	2	13	YEQGCALDYLQKF	3830
1H0H	AB	DEHYDROGENASE	A	2.8	5.6	2	7	PWLLEAE	3831
1H0H	KL	DEHYDROGENASE	K	2.8	5.6	2	7	PWLLEAE	3832
1H2R	SL	OXIDOREDUCTASE	S	2.8	5.6	2	5	FWDAM	3833
1H4L	AD	KINASE/KINASE ACTIVATOR	D	2.8	5.6	2	15	KEAFWDRCLSVINLM	3834
1I7M	DC	LYASE	C	1.9	5.6	3	12	LVPLLKLARDYS	3835
1I7Q	CD	LYASE	D	1.4	5.6	4	11	TYNLVDQLRAS	3836
1ICE	AB	CYTOKINE	B	1.4	5.6	4	13	VFIGRLIEHMQEY	3837
1IRU	AH	HYDROLASE	H	1.9	5.6	3	23	AADTQAVADAVTYQLGFHSIELN	3838
1IRU	LM	HYDROLASE	L	2.8	5.6	2	22	AADCSFWERLLARQCRIYELRN	3839
1IRU	OV	HYDROLASE	V	1.9	5.6	3	23	AADTQAVADAVTYQLGFHSIELN	3840
1IRU	Z1	HYDROLASE	Z	2.8	5.6	2	22	AADCSFWERLLARQCRIYELRN	3841
1IZL	AD	PHOTOSYNTHESIS	D	2.8	5.6	2	7	FMLFVPV	3842
1JIW	PI	HYDROLASE/HYROLASE INHIBITOR	P	1.9	5.6	3	15	YGRQTLTHEIGHTLG	3843
1JRO	GH	OXIDOREDUCTASE	H	2.8	5.6	2	13	PEAVLAAVRRAEG	3844
1JYO	AE	CHAPERONE	E	2.8	5.6	2	8	FINLIKSK	3845
1K6L	MH	PHOTOSYNTHESIS	H	1.4	5.6	4	24	LASLAIYSFWIFLAGLIYYLQTEN	3846
1KFY	OP	OXIDOREDUCTASE	O	1.4	5.6	4	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	3847
1LWU	GH	BLOOD CLOTTING	H	1.4	5.6	4	12	MEEAIKTQKELC	3848
1M56	AC	OXIDOREDUCTASE	C	1.9	5.6	3	21	IWPFMASVGAFVMLFGAVLWM	3849
1MIO	CB	MOLYBDENUM-IRON PROTEIN	B	1.9	5.6	3	17	ASIEEERGQLIDLMIDA	3850
1MKW	LH	COMPLEX (BLOOD COAGULATION/PROENZYME)	L	1.9	5.6	3	9	EKELFESYI	3851
1MU2	AB	TRANSFERASE	B	2.8	5.6	2	11	REIWEQWWDNY	3852
1N4Q	KL	TRANSFERASE	L	1.9	5.6	3	13	EKELNRIKRWCIM	3853
1NGM	IJ	TRANSCRIPTION/DNA	I	1.9	5.6	3	17	DSKLASRKYARIIQKIG	3854

1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	B	1.4	5.6	4	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	3855
1OXK	IJ	SIGNALING PROTEIN	J	1.4	5.6	4	14	HVNQEVIKRMLNLE	3856
1RCO	KT	LYASE	K	1.9	5.6	3	20	WRDRFLFCAEALYKAQAETG	3857
1RYP	IJ	MULTICATALYTIC PROTEINASE	J	1.9	5.6	3	17	PEDLFETISQALLNAAD	3858
1SMP	AI	COMPLEX (METALLOPROTEASE/INHIBITOR)	A	1.9	5.6	3	16	DYGRQTFTHEIGHALG	3859
1SQX	KJ	OXIDOREDUCTASE	K	1.9	5.6	3	19	VPTASLWGAVGAVGLVWAT	3860
1U35	CD	STRUCTURAL PROTEIN/DNA	D	5.6	5.6	1	12	SREVQTAVRLLL	3861
1VG9	CD	PROTEIN BINDING/PROTEIN TRANSPORT	C	2.8	5.6	2	13	ELPQCFCRMCAVF	3862
1XFV	AO	LYASE/METAL BINDING PROTEIN	A	1.9	5.6	3	15	SLEKQKGVTNLLIKY	3863
1XQS	AC	CHAPERONE	C	1.9	5.6	3	20	GEDFDNRLVNHFVEEFKRKH	3864
1YE9	JN	OXIDOREDUCTASE	N	1.9	5.6	3	13	FHRRELWEAIEAG	3865
1YQ3	AB	OXIDOREDUCTASE	A	2.8	5.6	2	12	APAAVIELENYG	3866
1YQ3	BD	OXIDOREDUCTASE	D	5.6	5.6	1	27	PAVDYSLAAALTLHGHWGLGQVITDYV	3867
1ZV8	GL	VIRAL PROTEIN	G	1.4	5.6	4	49	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS	3868
2ADV	BC	HYDROLASE	C	1.9	5.6	3	12	LRAQQSVRLMSE	3869
2B9S	AB	ISOMERASE/DNA	A	1.9	5.6	3	19	AKVFRTYNASITLDRWFKE	3870
2BEQ	BD	VIRAL PROTEIN	B	1.4	5.6	4	35	QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	3871
2BV8	OP	PHOTOSYNTHESIS	P	1.9	5.6	3	25	NRRMAACLRDMEIVLRYVSYAEIAG	3872
2CCL	CD	CELL ADHESION	D	2.8	5.6	2	12	STDLTMLKRSVL	3873
2CKF	AB	OXIDOREDUCTASE	A	2.8	5.6	2	15	PATKSAIQREATRTF	3874
2D2M	BC	OXYGEN STORAGE/TRANSPORT	C	5.6	5.6	1	23	ADFRAHCVRVVNGLDVAINMLND	3875
2DD4	KL	HYDROLASE	K	1.9	5.6	3	16	YYGRWLLTAARILVDK	3876
2DXB	NO	HYDROLASE	N	1.9	5.6	3	16	YYGRWLLTAARILVDK	3877
2FBW	AB	OXIDOREDUCTASE	A	2.8	5.6	2	21	QDAIHYMTEQAPAAVIELENY	3878
2FBW	CD	OXIDOREDUCTASE	D	1.9	5.6	3	28	DTPIKVANTGLYVLSAITFTGLCYFNYY	3879
2FHH	AH	HYDROLASE	A	1.9	5.6	3	22	FNEFDNLRRGGIQFADTRGYAY	3880
2FHH	MN	HYDROLASE	N	1.4	5.6	4	23	AAVAVEFARLYAVELEHYEKLEG	3881
2G38	CD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	1.9	5.6	3	31	DSMLAAARAWRSLDVEMTAVQRSFNRTLLSL	3882
2GAG	AC	OXIDOREDUCTASE	C	2.8	5.6	2	15	TEHTVHWLVDAMSEF	3883
2GV5	EF	CELL CYCLE	F	1.9	5.6	3	50	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK	3884
2H0D	AB	METAL BINDING PROTEIN/LIGASE	A	1.9	5.6	3	16	LFKNEMKRRRDFYAAH	3885
2H1O	AE	GENE REGULATION/DNA COMPLEX	E	1.9	5.6	3	12	LGSMLASIGQEI	3886
2H4M	AC	PROTEIN TRANSPORT	A	1.9	5.6	3	19	ISVCNNATWAIGEISIQMG	3887
2HL5	BD	STRUCTURAL PROTEIN	B	1.9	5.6	3	35	MQQVNVLKLTVEDLEKERDFYFGKLRNIELICQEN	3888

2HYB	MO	TRANSFERASE	O	1.9	5.6	3	11	YAGFVDLTTEC	3889
2IHB	AB	SIGNALING PROTEIN	B	1.4	5.6	4	21	QKLQDQIFNLMKYDSYSRFLK	3890
2INN	AC	OXIDOREDUCTASE	A	2.8	5.6	2	22	AYWKYQAEKEKKLYAIFDAFAQ	3891
2INN	BE	OXIDOREDUCTASE	B	2.8	5.6	2	7	PVHQIYQ	3892
2IOF	AK	HYDROLASE	A	1.9	5.6	3	11	WMCYKNAMELG	3893
2J5G	CD	HYDROLASE	C	1.9	5.6	3	27	QRLKRLVNEGIGYGLALEGITATDLRN	3894
2NNU	AB	TRANSCRIPTION	A	1.9	5.6	3	24	LRDHIDYWKHMRLECAIYYKAREM	3895
2OM0	ij	HORMONE	j	1.9	5.6	3	19	VNQHLCGSHLVEALYLVCG	3896
2OV2	HP	PROTEIN BINDING/TRANSFERASE	P	5.6	5.6	1	5	RQWQS	3897
2PV2	AE	ISOMERASE	E	2.8	5.6	2	8	TLKFWDIF	3898
2QKM	CD	HYDROLASE	D	1.9	5.6	3	13	FSQVLDDLSARFI	3899
2RF4	AB	TRANSFERASE	B	1.4	5.6	4	18	LSSSISQLKRIQRDFKGL	3900
2UZ1	DC	LYASE	C	1.9	5.6	3	10	DTIFQACLDH	3901
2UZ1	DC	LYASE	D	2.8	5.6	2	8	YHGVAAAF	3902
2VH3	AB	UNKNOWN FUNCTION	A	1.9	5.6	3	11	LGSLCTLFQKL	3903
2VWE	AE	IMMUNE SYSTEM	A	2.8	5.6	2	9	WIDVYTRAT	3904
2WAX	CD	HYDROLASE	D	2.8	5.6	2	6	FEGNLA	3905
2Z2S	EF	TRANSCRIPTION	E	1.9	5.6	3	16	GTIKSRIRLALDRLRQ	3906
2ZCY	SZ	HYDROLASE	S	2.8	5.6	2	22	APDARVLSNYLRQQCNYSSLVF	3907
2ZIV	AB	HYDROLASE	B	1.9	5.6	3	15	RVDAEEALVDLQLHT	3908
2ZT9	EH	PHOTOSYNTHESIS	H	1.9	5.6	3	25	AILTLGWVSLLVVFTWSIAMVVWGR	3909
3C59	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	B	1.9	5.6	3	6	IEWLKN	3910
3C5Z	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	C	1.9	5.6	3	21	PQGGLQNIAVVKHNLGVLTKR	3911
3C5Z	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	G	1.9	5.6	3	21	PQGGLQNIAVVKHNLGVLTKR	3912
3C72	AB	TRANSFERASE	A	2.8	5.6	2	21	AAYLDDLRSKFLLENSVLKME	3913
3CSY	IJ	IMMUNE SYSTEM/VIRAL PROTEIN	J	1.4	5.6	4	23	LICGLRQLANETTQALQLFLRAT	3914
3CXH	OP	OXIDOREDUCTASE	O	1.9	5.6	3	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	3915
3D2E	CD	CHAPERONE	C	1.4	5.6	4	29	AQDKLVAETEDRKNTLEEYIYTLRGKLEE	3916
3D4X	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	2.8	5.6	2	16	VDEVGGEALGRLLVVY	3917
3DCO	NA	MOTOR PROTEIN	N	2.8	5.6	2	18	LSETLSTLRFGTSAKAAA	3918
3DHR	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	2.8	5.6	2	16	VADCGAEALARLLIVY	3919
3DXR	AB	PROTEIN TRANSPORT	B	1.4	5.6	4	28	KNESSCLDRCVAKYFETNVQVGENMQKM	3920
3E3Q	PR	IMMUNE SYSTEM	P	1.9	5.6	3	24	AAEYYRAYLEGECVEWLHRYLKNG	3921
3EXG	YZ	OXIDOREDUCTASE	Y	1.9	5.6	3	16	AQVPLGAGIALACKYN	3922
3EXH	BC	OXIDOREDUCTASE	B	2.8	5.6	2	6	KILEDN	3923

3EZJ	AB	PROTEIN TRANSPORT	A	1.4	5.6	4	16	VRELAPILRQMIDSAG	3924
3FGC	CD	OXIDOREDUCTASE	C	1.9	5.6	3	15	PVRQAEDVNLLDQMS	3925
3HRD	GH	OXIDOREDUCTASE	G	1.9	5.6	3	7	PQIRNLG	3926
1AHJ	CD	LYASE	C	1.8	5.5	3	10	FEYRARVVRE	3927
1BCP	KL	TOXIN	L	1.8	5.5	3	16	TWFDTMLGFAISAYAL	3928
1CP9	AB	HYDROLASE	A	2.8	5.5	2	15	EIDNLALLTALKDKY	3929
1DE4	AC	METAL TRANSPORT INHIBITOR/RECEPTOR	C	1.8	5.5	3	23	QWLYSARGDFFRATSRLTTDFGN	3930
1DFL	BW	CONTRACTILE PROTEIN	B	1.4	5.5	4	9	IRKWLVLRN	3931
1E1H	CD	HYDROLASE	C	1.8	5.5	3	13	DLGRMLLTSIVRG	3932
1E6Y	DF	OXIDOREDUCTASE	D	1.4	5.5	4	19	ANAGLSGWYLSMYLHKEAW	3933
1FDH	AG	OXYGEN TRANSPORT	G	2.8	5.5	2	18	ENFKLLGNVLVTVLAIHF	3934
1FM6	DE	TRANSCRIPTION	E	1.4	5.5	4	10	KILHRLLQEG	3935
1FS2	AB	LIGASE	B	2.8	5.5	2	15	QGTLFELILAANYLD	3936
1FYZ	CE	OXIDOREDUCTASE	E	2.8	5.5	2	15	KWEAEKIHIGFRQAY	3937
1G0U	SZ	HYDROLASE	Z	1.8	5.5	3	21	AADGDALVKRFKNSVKWYHFD	3938
1G2C	MN	VIRAL PROTEIN	N	1.8	5.5	3	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	3939
1GH0	GH	PHOTOSYNTHESIS	G	1.4	5.5	4	12	PLTEAVSVADSQ	3940
1GO3	MN	TRANSFERASE	N	1.8	5.5	3	14	VSEAAEIMYNRAQI	3941
1GO3	MN	TRANSFERASE	N	2.8	5.5	2	13	YEQGCALDYLQKF	3942
1IR2	AL	LYASE	A	2.8	5.5	2	20	WRDRFLFVAEAIYKAQAETG	3943
1JMU	BG	VIRAL PROTEIN	G	2.8	5.5	2	12	GHQIVDLINNAF	3944
1JY2	RS	BLOOD CLOTTING	S	1.8	5.5	3	27	TCGIADFLNNYQTSVDKDLRTLEGILY	3945
1K6L	LM	PHOTOSYNTHESIS	M	1.8	5.5	3	27	PFHGLSIAFLYGSALLFAMHGATILAV	3946
1KTD	AB	IMMUNE SYSTEM	B	5.5	5.5	1	10	RPDAENWNSQ	3947
1KYO	DE	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.8	5.5	3	32	PEHDERKRLGLKTVIILSSLYLLSIWVKKFKW	3948
1KYO	OT	OXIDOREDUCTASE/ELECTRON TRANSPORT	O	1.8	5.5	3	34	DERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	3949
1L9B	LM	PHOTOSYNTHESIS	L	1.8	5.5	3	13	PDHEDTFFRDLVG	3950
1L9J	LM	PHOTOSYNTHESIS	M	1.8	5.5	3	27	PFHGLSIAFLYGSALLFAMHGATILAV	3951
1M1J	EF	BLOOD CLOTTING	F	1.8	5.5	3	37	NTILAHENTIQQLTDMHIMNSNKITQLKQKIAQLESH	3952
1M56	AB	OXIDOREDUCTASE	B	2.8	5.5	2	21	SPLEIAWTIVPIVILVAIGAF	3953
1MJG	AM	OXIDOREDUCTASE	A	1.4	5.5	4	16	DLIYSILTQIASDVYG	3954
1MJG	BN	OXIDOREDUCTASE	B	1.4	5.5	4	16	DLIYSILTQIASDVYG	3955
1N86	EF	BLOOD CLOTTING	E	1.8	5.5	3	15	IQKLESDVSAQMEYC	3956
1NEK	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	2.8	5.5	2	11	GPEAILELEHM	3957
1OCC	PW	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	1.8	5.5	3	30	MTLLMIGLTTNMLTMYQWWRDVIRESTFQG	3958

1OQS	EF	HYDROLASE	F	2.8	5.5	2	13	LFQFARMINGKLG	3959
1RYP	DE	MULTICATALYTIC PROTEINASE	E	2.8	5.5	2	11	FQVEYSLEAIK	3960
1S5L	AD	PHOTOSYNTHESIS	D	1.8	5.5	3	21	FYTKNLLLNEGIRAWMAPQDQ	3961
1SYQ	AB	CELL ADHESION	A	1.4	5.5	4	23	TAPVAAVQAAVSNLVRVGKETVQ	3962
1U35	BD	STRUCTURAL PROTEIN/DNA	D	1.8	5.5	3	12	SREVQTAVRLLL	3963
1UVQ	BC	IMMUNOLOGY	B	1.8	5.5	3	9	RPDAEYWNS	3964
1V54	DK	OXIDOREDUCTASE	D	1.4	5.5	4	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	3965
1WCM	AE	TRANSCRIPTION	A	5.5	5.5	1	10	LFCCLLRSRL	3966
1XDK	EF	HORMONE/GROWTH FACTOR RECEPTOR	F	1.8	5.5	3	7	MFPKILM	3967
1XQS	AC	CHAPERONE	C	5.5	5.5	1	18	KRAVRRLRTACERAKRTL	3968
1YE9	CG	OXIDOREDUCTASE	G	2.8	5.5	2	10	YSHPRLFWLS	3969
1YE9	DE	OXIDOREDUCTASE	E	2.8	5.5	2	17	LLQGRLFSYTDTQISRL	3970
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.8	5.5	3	9	IADIQGYNY	3971
1YKE	CD	GENE REGULATION	C	1.4	5.5	4	22	YQYKIQELRKLLKSLLLNYLEL	3972
1YNJ	CD	TRANSFERASE	D	2.8	5.5	2	7	VLEYFIS	3973
1YQ3	CD	OXIDOREDUCTASE	D	1.8	5.5	3	29	DTPIKVANTGLYVLSAITFTGLCYFNYYD	3974
1Z6O	KN	METAL BINDING PROTEIN	N	2.8	5.5	2	13	EALGEFIFDKKLL	3975
1ZV8	AB	VIRAL PROTEIN	A	1.4	5.5	4	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	3976
1ZV8	CB	VIRAL PROTEIN	C	1.4	5.5	4	45	KQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQ	3977
2AVU	BE	TRANSCRIPTION ACTIVATOR	E	2.8	5.5	2	20	WEQNVHASMFCNAWQFLLKT	3978
2BKR	AB	PROTEIN BINDING/HYDROLASE	A	2.8	5.5	2	8	PAEIAMFL	3979
2DD4	GE	HYDROLASE	E	2.8	5.5	2	17	LTELHNKIVEMRERVAS	3980
2DD4	HI	HYDROLASE	H	1.8	5.5	3	16	YYGRWLLTAARILVDK	3981
2DSR	BI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	B	1.8	5.5	3	7	PLHTLMH	3982
2ES4	AD	HYDROLASE	A	1.8	5.5	3	15	PVAVIRTHVNRLKLQ	3983
2ES4	BE	HYDROLASE	B	1.8	5.5	3	15	PVAVIRTHVNRLKLQ	3984
2GWW	AB	CELL ADHESION, STRUCTURAL PROTEIN	B	1.8	5.5	3	15	NIYKAAKDVTTSLSK	3985
2H1L	CO	VIRAL PROTEIN	C	1.8	5.5	3	15	QSRIVEWKERLDKEF	3986
2H7V	BD	SIGNALING PROTEIN	B	1.4	5.5	4	10	YDRLRPLSYP	3987
2HLD	JN	HYDROLASE	J	1.8	5.5	3	11	VFYLHSRLLER	3988
2HYB	HI	TRANSFERASE	I	2.8	5.5	2	9	SLESCLKFA	3989
2HYB	JK	TRANSFERASE	K	1.8	5.5	3	15	YAWEALEVVLIGAAF	3990

2HYI	GI	HYDROLASE/RNA BINDING PROTEIN/RNA	I	1.8	5.5	3	13	DDIRILRDIEQYY	3991
2I26	OM	IMMUNE SYSTEM	M	2.8	5.5	2	5	SRWWC	3992
2I2R	KO	TRANSPORT PROTEIN	K	5.5	5.5	1	8	WLPFARAA	3993
2I3T	CD	CELL CYCLE	D	2.8	5.5	2	9	LEEVLAISR	3994
2INP	AC	OXIDOREDUCTASE	A	1.4	5.5	4	31	AGARVACQMQAIDELRHSQTQQHAMSHYNKH	3995
2IVF	AB	OXIDOREDUCTASE	A	2.8	5.5	2	7	DIYRKEW	3996
2J5G	FD	HYDROLASE	D	1.8	5.5	3	27	QRLKRLVNEGIGYGLALEGITATDLRN	3997
2JBL	CL	ELECTRON TRANSPORT	L	1.8	5.5	3	15	ILSHLDWVNNFGYQY	3998
2JBY	AB	APOPTOSIS	B	1.8	5.5	3	13	TMGQVGRQLAIIG	3999
2NYL	DE	HYDROLASE	E	1.8	5.5	3	18	RAYIRKQINNIFYRFIYE	4000
2OF5	EK	APOPTOSIS	E	2.8	5.5	2	11	DRQINQLAQRL	4001
2OV2	BJ	PROTEIN BINDING/TRANSFERASE	J	5.5	5.5	1	7	RQWQSLI	4002
2P2C	LU	HYDROLASE	L	5.5	5.5	1	15	VADMLVKVNALIKDR	4003
2P58	BC	TRANSPORT PROTEIN/CHAPERONE	C	1.8	5.5	3	12	EPWLALCEYRLG	4004
2QJK	PQ	ELECTRON TRANSPORT	P	1.8	5.5	3	24	YFIIKDVFALAVVLLVFFAIVGFM	4005
2QJP	GH	ELECTRON TRANSPORT	H	1.8	5.5	3	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	4006
2R6G	BF	HYDROLASE/TRANSPORT PROTEIN	F	1.8	5.5	3	10	DDLYEASAMD	4007
2RF4	EF	TRANSFERASE	F	1.4	5.5	4	18	LSSSISQLKRIQRDFKGL	4008
2RGN	AB	SIGNALING PROTEIN COMPLEX	B	1.8	5.5	3	26	PAISQAWIKHVAQILESQRDFLNALQ	4009
2UUN	OP	ELECTRON TRANSPORT	P	2.8	5.5	2	12	AFTKVAAQADTR	4010
2UZ1	AB	LYASE	A	1.8	5.5	3	10	DTIFQACLDH	4011
2UZ1	AB	LYASE	B	1.8	5.5	3	10	DTIFQACLDH	4012
2V1S	EL	OXIDOREDUCTASE	L	2.8	5.5	2	9	LSRLLSYAG	4013
2V4J	AB	OXIDOREDUCTASE	A	5.5	5.5	1	6	HCINTM	4014
2VML	KL	PHOTOSYNTHESIS	K	1.8	5.5	3	12	VITEVIASADSQ	4015
2VSO	AE	HYDROLASE/TRANSLATION	E	5.5	5.5	1	18	SRIKFKLIDIKELRHDKN	4016
2ZCY	BI	HYDROLASE	I	1.4	5.5	4	23	ATDVTTLNEMFRYKTNLYKLKEE	4017
3B5N	AD	MEMBRANE PROTEIN	D	1.4	5.5	4	61	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRLAG	4018
3C1B	AB	STRUCTURAL PROTEIN/DNA	A	1.8	5.5	3	13	TVALREIRRYQKS	4019
3CHX	AB	MEMBRANE PROTEIN	A	5.5	5.5	1	8	TIIGYAVT	4020
3CQC	AB	PROTEIN TRANSPORT	B	1.8	5.5	3	18	FAKKKTLLGLSKLAALAS	4021
3CQX	AD	CHAPERONE	A	1.8	5.5	3	18	KRAVRRLRTACERAKRTL	4022
3D32	BD	TRANSPORT PROTEIN	B	1.8	5.5	3	12	VGQFYFLIRKRI	4023
3DBJ	AB	PHOTOSYNTHESIS	B	2.8	5.5	2	25	TRRYAACIRDLDYYLRYATYAMLAG	4024
3DZU	AD	TRANSCRIPTION/DNA	A	2.8	5.5	2	11	QYCRYQKCLAM	4025
3E0J	GH	TRANSFERASE	H	1.8	5.5	3	20	VNQAKQMLYDYVERKRKENS	4026
3E7S	AB	OXIDOREDUCTASE	B	2.8	5.5	2	19	HHAATVSFMKHLDNEQKAR	4027

3ECH	AC	TRANSCRIPTION, TRANSCRIPTION REGULATION	A	2.8	5.5	2	25	PDLMPALMAVFQHVRTRIQSELDCQ	4028
3EH3	AB	OXIDOREDUCTASE	A	1.8	5.5	3	36	PTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLR	4029
3ETR	MN	OXIDOREDUCTASE	M	1.8	5.5	3	24	IEFRRTLTLSFFFKFYLTVLKKLG	4030
3EUH	BE	CELL CYCLE	B	1.8	5.5	3	40	HFVDRLVFDLQSKLDRIISWGQQSIDLWIGYDRHVHKFIR	4031
3EXG	EF	OXIDOREDUCTASE	F	2.8	5.5	2	5	TYYMS	4032
3EXG	YZ	OXIDOREDUCTASE	Z	2.8	5.5	2	15	IDQVINSAAKTYYMS	4033
3EXH	EF	OXIDOREDUCTASE	E	2.8	5.5	2	17	AQVPLGAGIALACKYNG	4034
3F6Z	CD	HYDROLASE	C	2.8	5.5	2	5	SRWWC	4035
3FKU	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.4	5.5	4	35	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLD	4036
3FMO	AB	ONCOPROTEIN/HYDROLASE	B	1.8	5.5	3	11	HQDQSIRIQRM	4037
3FWC	FH	CELL CYCLE, TRANSCRIPTION	H	1.4	5.5	4	16	FTQILSTVEPKALEMV	4038
3H0L	SU	LIGASE	S	1.4	5.5	4	13	IFEMYARTRDEGF	4039
3HKZ	OV	TRANSFERASE	V	1.8	5.5	3	21	PKDALLKAIENIRGMTSHYID	4040
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA/RNA HYBRID	B	1.8	5.5	3	11	EMERDCMIAHG	4041
1AIP	AC	COMPLEX OF TWO ELONGATION FACTORS	C	1.8	5.4	3	11	MMDVKRALEDA	4042
1B33	JK	PHOTOSYNTHESIS	K	2.7	5.4	2	25	TRRYAACIRDLDYYLRYATYAMLAG	4043
1B35	AC	VIRUS	A	1.4	5.4	4	5	IRQLI	4044
1DEE	FH	IMMUNE SYSTEM	H	1.4	5.4	4	14	EAQRNGFIQSLKDD	4045
1DOW	AB	CELL ADHESION	A	1.8	5.4	3	26	AHVLAASVEQATENFLEKGDKIAKES	4046
1E3D	CD	HYDROGENASE	C	5.4	5.4	1	9	IDTLILDTI	4047
1E6Y	AC	OXIDOREDUCTASE	A	1.4	5.4	4	19	ANAGLSGWYLSMYLHKEAW	4048
1EFU	AB	COMPLEX (TWO ELONGATION FACTORS)	B	2.7	5.4	2	9	FAAEVAAMS	4049
1EYS	MH	ELECTRON TRANSPORT	M	2.7	5.4	2	14	MESIHRWAWWCAVL	4050
1F3M	AC	TRANSFERASE	C	1.8	5.4	3	12	PLRALYLIATNG	4051
1F5Q	AB	TRANSFERASE	A	1.8	5.4	3	13	STAIREISLLKEL	4052
1FM6	XY	TRANSCRIPTION	Y	1.8	5.4	3	9	KILHRLLQE	4053
1FYZ	BF	OXIDOREDUCTASE	F	1.8	5.4	3	9	LEELRKQRG	4054
1G0U	BI	HYDROLASE	I	1.4	5.4	4	23	ATDVTTLNEMFRYKTNLYKLKEE	4055
1G2C	AB	VIRAL PROTEIN	B	1.4	5.4	4	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	4056
1G2C	MN	VIRAL PROTEIN	M	1.4	5.4	4	46	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPI	4057
1G2C	MP	VIRAL PROTEIN	M	1.8	5.4	3	46	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPI	4058
1G3N	EG	CELL CYCLE, SIGNALING PROTEIN	G	1.8	5.4	3	15	RQELIDQEKELLEKL	4059
1GH0	CD	PHOTOSYNTHESIS	D	1.8	5.4	3	13	AFTKVVSQADTRG	4060
1GH0	OP	PHOTOSYNTHESIS	O	1.4	5.4	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	4061

1HLE	AB	HYDROLASE INHIBITOR (SERINE PROTEINASE)	A	1.8	5.4	3	22	EQLSTANTHFAVDLFRALNESD	4062
1J1E	EF	CONTRACTILE PROTEIN	F	1.8	5.4	3	39	ASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRAQ	4063
1JD2	PL	HYDROLASE	P	5.4	5.4	1	18	PEDLFETISQALLNAADR	4064
1JEK	AB	VIRAL PROTEIN	A	1.8	5.4	3	39	SLANATAAQQEVLEASYAMVQHIAKGIRILEARVARVEA	4065
1JOU	CD	BLOOD CLOTTING	C	1.4	5.4	4	8	ERELLESY	4066
1K3B	AB	HYDROLASE	B	1.8	5.4	3	13	PYLIAGKYAQDFG	4067
1K6L	LM	PHOTOSYNTHESIS	L	1.8	5.4	3	12	PDHEDTFFRDLV	4068
1KYO	CG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	5.4	5.4	1	19	PVLSKLCVPVANQFINLAG	4069
1LIA	KL	LIGHT HARVESTING PROTEIN	K	2.7	5.4	2	12	VITTTISAADAA	4070
1LTX	AB	TRANSFERASE/PROTEIN BINDING	B	1.8	5.4	3	12	SDLLGWWLCERQ	4071
1M56	AC	OXIDOREDUCTASE	A	1.8	5.4	3	23	PRMNNLSYWLYVAGTSLAVASLF	4072
1N5W	AB	OXIDOREDUCTASE	B	2.7	5.4	2	11	RYVAADAIELV	4073
1NHG	AC	OXIDOREDUCTASE	C	2.7	5.4	2	13	STDIGSVASFLLS	4074
1NHG	BD	OXIDOREDUCTASE	D	2.7	5.4	2	13	STDIGSVASFLLS	4075
1NIK	AB	TRANSCRIPTION	B	2.7	5.4	2	13	YAAKLLFQELMAM	4076
1O9U	AB	KINASE	B	1.8	5.4	3	17	EPQKFAEELIHRLEAVQ	4077
1OCC	BI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	I	1.8	5.4	3	40	LLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFY	4078
1OCC	OV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	V	1.8	5.4	3	40	LLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFY	4079
1OW3	AB	GENE REGULATION/SIGNALING PROTEIN	B	1.8	5.4	3	9	DRLRPLSYP	4080
1P4E	AC	DNA BINDING PROTEIN/RECOMBINATION/DNA	C	1.8	5.4	3	14	ITDIVSSLQLQFES	4081
1Q5Q	FM	HYDROLASE	F	1.8	5.4	3	22	YNEFENLRRAGIVHADMRGYSY	4082
1Q90	BD	PHOTOSYNTHESIS	B	2.7	5.4	2	17	QVGYWAVKIVTGVPDAI	4083
1RYP	FG	MULTICATALYTIC PROTEINASE	G	1.8	5.4	3	22	IPDGRHLVNRGREEAASFKKLY	4084
1RYP	OP	MULTICATALYTIC PROTEINASE	P	2.7	5.4	2	12	GQIDYALTAVKQ	4085
1RYP	QR	MULTICATALYTIC PROTEINASE	R	2.7	5.4	2	23	NADSRILIEKARVEAQSHRLTLE	4086
1S5L	lm	PHOTOSYNTHESIS	l	1.8	5.4	3	24	RTSLYLGLLLILVLALLFSSYFFN	4087
1SQX	EJ	OXIDOREDUCTASE	E	1.8	5.4	3	35	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMS	4088
1T0Q	AB	OXIDOREDUCTASE	A	2.7	5.4	2	7	LYFPYAN	4089
1T0Q	AB	OXIDOREDUCTASE	A	1.8	5.4	3	22	YPEYVSIQREKDSGAYSIKAAL	4090
1TIL	AB	TRANSCRIPTION	A	2.7	5.4	2	12	ESFARVTVAAFV	4091
1TUE	FG	REPLICATION	G	2.7	5.4	2	22	KETLSERLSALQDKIIDHYEND	4092
1UZD	AT	LYASE	A	2.7	5.4	2	20	WRDRFLFVAEAIYKAQAETG	4093
1V54	PW	OXIDOREDUCTASE	W	1.8	5.4	3	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	4094
1VRQ	AD	OXIDOREDUCTASE	A	2.7	5.4	2	5	KRSFS	4095

1XFU	FT	LYASE/METAL BINDING PROTEIN	T	1.4	5.4	4	13	SEEEIREAFRVFD	4096
1XV9	CG	DNA BINDING PROTEIN	G	2.7	5.4	2	7	KILHRLL	4097
1Y64	AB	STRUCTURAL PROTEIN	B	5.4	5.4	1	5	KRKED	4098
1YE9	CG	OXIDOREDUCTASE	G	2.7	5.4	2	17	PFEQRHIVDGFSFELSK	4099
1YE9	IM	OXIDOREDUCTASE	I	2.7	5.4	2	9	DTFWDYVSL	4100
1YHU	NP	OXYGEN STORAGE/TRANSPORT	N	1.8	5.4	3	20	PAFRAHATRVLGGLDMCIAL	4101
1YMM	BC	IMMUNE SYSTEM	B	1.8	5.4	3	9	YCRHNYGVV	4102
1Z6O	FQ	METAL BINDING PROTEIN	F	1.8	5.4	3	16	LSLALYVFDEYLQKTV	4103
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	D	1.4	5.4	4	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	4104
2BA0	FI	RNA BINDING PROTEIN	I	1.4	5.4	4	17	ENSIELARVVDRGIRES	4105
2BC4	CD	IMMUNE SYSTEM	D	1.4	5.4	4	14	NSLANVLSQHLNQK	4106
2BCJ	BG	TRANSFERASE/HYDROLASE	B	1.8	5.4	3	10	ELDQLRQEAE	4107
2BE6	CF	MEMBRANE PROTEIN	C	1.8	5.4	3	12	DEEVDEMIREAD	4108
2BV8	OP	PHOTOSYNTHESIS	O	1.8	5.4	3	12	PITEAIASADSQ	4109
2BYK	DC	DNA-BINDING PROTEIN	D	2.7	5.4	2	29	KEARAAIARAASVFAIFVTSSSTALAHKQ	4110
2DD4	BC	HYDROLASE	C	1.8	5.4	3	5	EWYRS	4111
2DXB	BC	HYDROLASE	B	1.8	5.4	3	17	LTELHNKIVEMRERVAS	4112
2DXB	QR	HYDROLASE	Q	1.8	5.4	3	16	YYGRWLLTAARILVDK	4113
2EFC	AB	TRANSPORT PROTEIN	B	2.7	5.4	2	6	LAPMYY	4114
2EHO	AB	REPLICATION	A	1.8	5.4	3	14	RIRYVLSSYLRCRL	4115
2EHO	IK	REPLICATION	I	1.8	5.4	3	14	RIRYVLSSYLRCRL	4116
2FHH	BC	HYDROLASE	C	1.4	5.4	4	23	AAVAVEFARLYAVELEHYEKLEG	4117
2FK0	MN	VIRAL PROTEIN	N	1.8	5.4	3	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	4118
2FRV	AB	OXIDOREDUCTASE	A	2.7	5.4	2	5	FWDLY	4119
2FRV	CD	OXIDOREDUCTASE	C	2.7	5.4	2	5	FWDLY	4120
2FRV	GH	OXIDOREDUCTASE	G	2.7	5.4	2	5	FWDLY	4121
2FYZ	CF	PROTEIN BINDING	F	1.8	5.4	3	32	GGIDISTELSKVNASLQNTVKYIKESNHQLQS	4122
2GD4	AB	HYDROLASE	B	5.4	5.4	1	10	DWAESTLMTQ	4123
2GPV	BH	TRANSCRIPTION	H	1.8	5.4	3	11	LEAIIRKALMG	4124
2GYK	EF	ANTIBIOTIC/ANTIBIOTIC INHIBITOR	E	1.8	5.4	3	16	EEELVKLVTHFEEMTE	4125
2H1O	BF	GENE REGULATION/DNA COMPLEX	F	1.8	5.4	3	12	LGSMLASIGQEI	4126
2H1O	CG	GENE REGULATION/DNA COMPLEX	G	1.8	5.4	3	12	LGSMLASIGQEI	4127
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	D	2.7	5.4	2	11	KPAIRRLARRG	4128
2IAN	QR	IMMUNE SYSTEM	Q	1.8	5.4	3	16	AVDTYCRHNYGVGESF	4129
2IBF	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.8	5.4	3	47	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVA	4130
2INN	AC	OXIDOREDUCTASE	A	2.7	5.4	2	12	VPKSFFDDARSA	4131
2IV8	AP	ENDOCYTOSIS/REGULATOR	P	2.7	5.4	2	12	DDIVFEDFARQR	4132

2J28	JQ	RIBOSOME	Q	5.4	5.4	1	6	ADIAVF	4133
2JBA	AB	TRANSCRIPTION	A	1.8	5.4	3	14	APIREMVCFVLEQN	4134
2JIY	MH	PHOTOSYNTHESIS	M	1.8	5.4	3	27	PFHGLSIAFLYGSALLFAMHGATILAV	4135
2JKR	LI	ENDOCYTOSIS	L	2.7	5.4	2	16	TNLRYLALESMCTLAS	4136
2OM0	34	HORMONE	4	1.8	5.4	3	18	NQHLCGSHLVEALYLVCG	4137
2OT3	AB	PROTEIN TRANSPORT	A	2.7	5.4	2	18	EDGYYFTNLCCAVAFIEK	4138
2OV2	EM	PROTEIN BINDING/TRANSFERASE	M	5.4	5.4	1	5	RQWQS	4139
2QIY	BD	SIGNALING PROTEIN/HYDROLASE	D	2.7	5.4	2	15	AEFAAASVQRYELNM	4140
2R1H	CD	OXYGEN BINDING	C	2.7	5.4	2	19	PEIHLSVDKFLQQLALALA	4141
2RFK	AB	ISOMERASE/RNA	A	2.7	5.4	2	14	LHDLVDYYYFWKED	4142
2UZ6	BL	RECEPTOR	L	2.7	5.4	2	6	PPCILN	4143
2V4J	DB	OXIDOREDUCTASE	B	2.7	5.4	2	5	DPAYY	4144
2V4J	DB	OXIDOREDUCTASE	D	1.8	5.4	3	8	ITEYRKRH	4145
2V7Q	GH	HYDROLASE	G	5.4	5.4	1	51	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYE	4146
2W2X	AD	SIGNALING PROTEIN/HYDROLASE	D	5.4	5.4	1	16	VEELFEWFQSIREITW	4147
2WAQ	AB	TRANSCRIPTION	B	1.8	5.4	3	8	AMLLKDRL	4148
2WAQ	AC	TRANSCRIPTION	C	1.4	5.4	4	11	VKHLLDAAARG	4149
2WBJ	EF	IMMUNE SYSTEM	E	1.8	5.4	3	22	AQGALANIAVDKANLEIMTKRS	4150
2ZCY	EF	HYDROLASE	F	1.8	5.4	3	22	IPDGRHLVNRGREEAASFKKLY	4151
2ZIV	AB	HYDROLASE	A	1.8	5.4	3	11	RFREQKFRLKR	4152
3A1G	AB	TRANSFERASE	A	1.8	5.4	3	11	QRCCNLFEKFF	4153
3BUA	AE	DNA BINDING PROTEIN	A	1.4	5.4	4	19	EHTVSRLLRVMQCLSRIEE	4154
3BZ1	DF	ELECTRON TRANSPORT	F	1.8	5.4	3	24	VRWVAVHTLAVPTIFFLGAIAAMQ	4155
3CXH	OT	OXIDOREDUCTASE	O	1.8	5.4	3	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	4156
3D5A	GK	RIBOSOME	K	2.7	5.4	2	18	PYAAQLAALDAAKKAMAY	4157
3D5A	JN	RIBOSOME	N	2.7	5.4	2	11	RICLRELAHKG	4158
3D7V	AB	APOPTOSIS	A	1.4	5.4	4	11	KSLSRVMIHVF	4159
3DRA	AB	TRANSFERASE	A	1.8	5.4	3	13	YTIWIYRFNILKN	4160
3EXH	DC	OXIDOREDUCTASE	C	2.7	5.4	2	17	AQVPLGAGIALACKYNG	4161
3EXH	EG	OXIDOREDUCTASE	G	1.8	5.4	3	13	GQIFEAYNMAALW	4162
3EXH	HG	OXIDOREDUCTASE	H	5.4	5.4	1	14	EMGFAGIAVGAAMA	4163
3FGC	CD	OXIDOREDUCTASE	D	1.8	5.4	3	15	PVRVAEEACLLDQMS	4164
3FWC	FH	CELL CYCLE, TRANSCRIPTION	H	1.4	5.4	4	16	NYELISNELKARLLQE	4165
3G9V	AB	CYTOKINE/CYTOKINE RECEPTOR	A	2.7	5.4	2	5	PWWET	4166
3GM1	BC	TRANSFERASE	C	1.8	5.4	3	10	ELDELMASLS	4167
3H0L	GI	LIGASE	G	1.8	5.4	3	19	YLKAQKVRRLITNDFLKAF	4168
3I1H	AB	APOPTOSIS	B	1.8	5.4	3	14	VGRQLAIIGDDINR	4169
3KIN	CD	MOTOR PROTEIN	D	1.8	5.4	3	17	EAETKSTLMFGQRAKTI	4170
5CSC	AB	OXO-ACID-LYASE	B	2.7	5.4	2	22	KDVLAALIPKEQARIKTFRQQH	4171

1AIP	FH	COMPLEX OF TWO ELONGATION FACTORS	H	1.8	5.3	3	11	MMDVKRALEDA	4172
1AOI	AB	DNA BINDING PROTEIN/DNA	A	1.8	5.3	3	13	TVALREIRRYQKS	4173
1CPC	KL	LIGHT HARVESTING PROTEIN	K	1.8	5.3	3	12	PLTEAVAAADSQ	4174
1E6E	AB	OXIDOREDUCTASE	B	1.8	5.3	3	9	DEENDMLDL	4175
1FOE	GH	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	H	1.8	5.3	3	5	DRLRP	4176
1G0U	WL	HYDROLASE	L	1.8	5.3	3	13	ASLIMPFLDNQVN	4177
1G20	AB	OXIDOREDUCTASE	A	1.8	5.3	3	15	DKKLAKLIDEVETLF	4178
1G20	AB	OXIDOREDUCTASE	B	1.8	5.3	3	16	QGCVAYFRSYFNRHFR	4179
1G4U	SR	SIGNALING PROTEIN	S	5.3	5.3	1	8	EVERWVDK	4180
1GH0	AB	PHOTOSYNTHESIS	B	2.7	5.3	2	25	SRRMAACLRDMEIILRYVTYAVFAG	4181
1GOT	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	1.3	5.3	4	17	EKDKLKMEVDQLKKEVT	4182
1IAK	AB	HISTOCOMPATIBILITY ANTIGEN I-AK	A	1.8	5.3	3	22	PQGGLQNIATGKHNLEILTKRS	4183
1IBC	AB	COMPLEX (HYDROLASE/PEPTIDE)	B	1.3	5.3	4	13	VFIGRLIEHMQEY	4184
1JNR	AB	OXIDOREDUCTASE	A	1.3	5.3	4	10	VSQALLWACQ	4185
1K3Z	AD	TRANSCRIPTION	A	2.7	5.3	2	10	YETFKSIMKK	4186
1K74	AD	TRANSCRIPTION	D	1.3	5.3	4	29	LFAKLLQKMTDLRQIVTEHVQLLQVIKKT	4187
1KF6	OP	OXIDOREDUCTASE	O	1.8	5.3	3	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	4188
1KI1	AB	SIGNALING PROTEIN	A	2.7	5.3	2	7	LRPLSYP	4189
1KX4	FH	STRUCTURAL PROTEIN/DNA	F	2.7	5.3	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	4190
1L1O	BC	DNA BINDING PROTEIN	C	1.8	5.3	3	18	YREYGRRLVMSIRRSALM	4191
1LQB	BC	GENE REGULATION	B	5.3	5.3	1	17	SHVLSKVCMYFTYKVRY	4192
1LVC	CF	LYASE	F	1.8	5.3	3	11	EEVDEMIREAD	4193
1LVC	CF	LYASE	F	1.8	5.3	3	10	YEEFVQMMTA	4194
1N2D	BC	CELL CYCLE	B	1.8	5.3	3	11	TEDFVKAFQVF	4195
1N4Q	EF	TRANSFERASE	E	2.7	5.3	2	13	KEYWRYIGRSLQS	4196
1N4Q	GH	TRANSFERASE	G	2.7	5.3	2	13	KEYWRYIGRSLQS	4197
1N95	AB	TRANSFERASE	A	2.7	5.3	2	14	YTVWHFRRVLLRSL	4198
1NTK	CD	OXIDOREDUCTASE	C	1.8	5.3	3	17	DILGALLLILALMLLVL	4199
1NWD	AB	BINDING PROTEIN/HYDROLASE	A	5.3	5.3	1	9	YEEFVQMMT	4200
1NZY	CB	LYASE	B	1.3	5.3	4	25	VAGVRDHFRIAALWWHQMIHKIIRV	4201
1O96	AB	ELECTRON TRANSFER	B	2.7	5.3	2	7	RPIADAG	4202
1OCC	CJ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	1.8	5.3	3	23	PWPLTGALSALLMTSGLTMWFHF	4203
1PRC	MH	PHOTOSYNTHETIC REACTION CENTER	M	1.3	5.3	4	26	IESVHRWGWFFSLMVMVSASVGILLT	4204
1Q5R	BI	HYDROLASE	I	1.8	5.3	3	23	AGIAIELVRLFAVELEHYEKIEG	4205
1Q90	BD	PHOTOSYNTHESIS	B	2.7	5.3	2	28	GWLIRSIHRWSASMMVLMMVLHVFRVYL	4206
1R27	CD	OXIDOREDUCTASE	D	1.8	5.3	3	11	TCSVTCKNVWT	4207

1R27	CD	OXIDOREDUCTASE	D	1.8	5.3	3	24	KPVLRALKRMLAMRHYKRAETVDG	4208
1RP3	GH	TRANSCRIPTION	G	1.3	5.3	4	18	EEVIKRELTEKVKEAVSK	4209
1RSO	CB	NEUROPEPTIDE/MEMBRANE PROTEIN	C	5.3	5.3	1	12	NLFQALIDIQEF	4210
1S5L	LT	PHOTOSYNTHESIS	L	1.8	5.3	3	24	RTSLYLGLLLILVLALLFSSYFFN	4211
1S5R	AB	TRANSCRIPTION	A	1.3	5.3	4	12	AVYVLSSMARQR	4212
1SCJ	AB	HYDROLASE	A	1.8	5.3	3	14	YSWIINGIEWAISN	4213
1SCT	AB	OXYGEN TRANSPORT	A	5.3	5.3	1	20	SKLRGHAITLTYALNNFVDS	4214
1SHZ	AF	SIGNALING PROTEIN	F	1.8	5.3	3	19	SQQVAVGRQLEDFRSKRLM	4215
1SQ0	AB	BLOOD CLOTTING	A	1.3	5.3	4	13	TSEVLKYTLFQIF	4216
1SQX	DJ	OXIDOREDUCTASE	D	1.3	5.3	4	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	4217
1U35	FH	STRUCTURAL PROTEIN/DNA	F	2.7	5.3	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	4218
1ULI	AB	OXIDOREDUCTASE	A	2.7	5.3	2	15	EEMKEEYRQQTLRTF	4219
1ULI	EF	OXIDOREDUCTASE	E	2.7	5.3	2	15	EEMKEEYRQQTLRTF	4220
1VCB	GH	TRANSCRIPTION	H	1.3	5.3	4	18	SHVLSKVCMYFTYKVRYT	4221
1XMN	GH	BLOOD CLOTTING	G	1.8	5.3	3	8	ERELLESY	4222
1XQ5	CD	OXYGEN STORAGE/TRANSPORT	D	1.8	5.3	3	16	YEAVGGATLARCLIVY	4223
1YA7	FP	HYDROLASE/HYDROLASE ACTIVATOR	F	2.7	5.3	2	12	FQVEYAREAVKK	4224
1YNJ	CD	TRANSFERASE	C	2.7	5.3	2	10	EMEVWALEAY	4225
1YOV	AB	SIGNALING PROTEIN	B	2.7	5.3	2	6	NHVKKF	4226
1Z00	AB	HYDROLASE	B	2.7	5.3	2	12	AANAKQLYDFIH	4227
1Z6O	JS	METAL BINDING PROTEIN	S	2.7	5.3	2	13	EALGEFIFDKKLL	4228
1Z6O	KU	METAL BINDING PROTEIN	K	1.8	5.3	3	16	LSLALYVFDEYLQKTV	4229
1Z7Q	LM	HYDROLASE/HYDROLASE ACTIVATOR	M	5.3	5.3	1	15	INSAARNIQHLLYGK	4230
1ZBB	bd	STRUCTURAL PROTEIN/DNA	b	2.7	5.3	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	4231
2A3I	AB	TRANSFERASE	B	1.8	5.3	3	7	LLQQLLT	4232
2AXT	BD	ELECTRON TRANSPORT	B	5.3	5.3	1	23	TVLSSSIAAVFFAAFVVAGTMWY	4233
2CCI	CD	CELL CYCLE	D	2.7	5.3	2	16	YHEDIHTYLREMEVKC	4234
2DXB	PN	HYDROLASE	N	2.7	5.3	2	16	SIREEVHRHLGTVALM	4235
2DXB	SQ	HYDROLASE	Q	2.7	5.3	2	17	LTELHNKIVEMRERVAS	4236
2DXB	TU	HYDROLASE	T	1.8	5.3	3	16	YYGRWLLTAARILVDK	4237
2DXB	VN	HYDROLASE	N	2.7	5.3	2	18	LTELHNKIVEMRERVASG	4238
2F5Z	EM	OXIDOREDUCTASE/PROTEIN BINDING	M	2.7	5.3	2	10	PAARNILEKH	4239
2FBW	PQ	OXIDOREDUCTASE	Q	1.8	5.3	3	28	DTPIKVANTGLYVLSAITFTGLCYFNYY	4240
2FHH	KL	HYDROLASE	L	1.3	5.3	4	23	AAVAVEFARLYAVELEHYEKLEG	4241
2FNJ	AC	PROTEIN TRANSPORT/SIGNALING PROTEIN	C	2.7	5.3	2	17	SHVLSKVCMYFTYKVRY	4242
2FUG	DG	OXIDOREDUCTASE	D	2.7	5.3	2	10	VIYHFKHYTE	4243
2GBW	AB	OXIDOREDUCTASE	A	2.7	5.3	2	15	PATKSMIQREAIRTF	4244
2GEZ	CD	HYDROLASE	C	1.8	5.3	3	14	PLDVVELVVRELEN	4245
2GTL	NO	OXYGEN STORAGE/TRANSPORT	O	1.8	5.3	3	19	RTNKITTSISHVESLLDDR	4246

2GUZ	CD	CHAPERONE, PROTEIN TRANSPORT	C	1.8	5.3	3	18	PFLATKINEAKDFLEKRG	4247
2H9A	AB	OXIDOREDUCTASE	A	1.8	5.3	3	15	PADILPLITLRLNIY	4248
2HRK	AB	LIGASE/RNA BINDING PROTEIN	B	2.7	5.3	2	14	RHILRWIDYMQNLL	4249
2HYE	AB	PROTEIN BINDING	B	1.8	5.3	3	11	TVEYFTSQQVT	4250
2J59	CO	HYDROLASE	O	1.8	5.3	3	20	EEDTGVTNRDLISRRIKEYN	4251
2JGD	AB	OXIDOREDUCTASE	A	2.7	5.3	2	5	AWYCS	4252
2JIY	LM	PHOTOSYNTHESIS	M	1.8	5.3	3	15	IFSHLDWTNNFSLVH	4253
2JKR	LB	ENDOCYTOSIS	B	5.3	5.3	1	15	QELVQQVLSLATQDS	4254
2NTS	PA	TOXIN/IMMUNE SYSTEM	A	1.8	5.3	3	11	IGIDNLRNFYT	4255
2NZ0	AB	MEMBRANE PROTEIN	A	1.8	5.3	3	14	FEDFVTALSILLRG	4256
2OM0	CD	HORMONE	D	1.8	5.3	3	19	VNQHLCGSHLVEALYLVCG	4257
2OV2	CK	PROTEIN BINDING/TRANSFERASE	K	5.3	5.3	1	6	RQWQSL	4258
2QJP	AB	ELECTRON TRANSPORT	A	2.7	5.3	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	4259
2RGN	EF	SIGNALING PROTEIN COMPLEX	E	2.7	5.3	2	32	QKKKALERSMYVLSELVETEKMYVDDLGQIVE	4260
2V1Y	AB	TRANSFERASE	B	2.7	5.3	2	25	RTAIEAFNETIKIFEEQCQTQERYS	4261
2VTB	AB	LYASE/DNA	B	1.8	5.3	3	18	SEEVDVERLVNQGLKRVG	4262
2VUS	BJ	TRANSCRIPTION	B	2.7	5.3	2	12	VGPALLQIFKDG	4263
2VYR	CG	IMMUNE SYSTEM	C	1.8	5.3	3	15	VKEVMHYLGQYIMVK	4264
2ZAL	CD	HYDROLASE	C	1.8	5.3	3	15	ALDVVTEAVRLLEEC	4265
2ZIV	AB	HYDROLASE	B	1.8	5.3	3	10	LALVWRRQIQ	4266
3A0B	AD	ELECTRON TRANSPORT	D	2.7	5.3	2	6	YNAIAF	4267
3BL2	BD	VIRAL PROTEIN/APOPTOSIS	B	1.8	5.3	3	22	LVDVSKIITLTQEFRRHYDSVY	4268
3BLH	AB	TRANSCRIPTION	B	2.7	5.3	2	16	GNSVAPAALFLAAKVE	4269
3BPS	PA	HYDROLASE/LIPID TRANSPORT	A	1.8	5.3	3	18	VSGTLIGLEFIRKSQLVQ	4270
3C91	PW	HYDROLASE	P	1.8	5.3	3	23	VADARVLVDFARISAQQEKVTYG	4271
3CL3	AD	VIRAL PROTEIN/SIGNALING PROTEIN	D	1.8	5.3	3	53	HSVQVDQLRMQGQSVEAALRMERQAASEEKRKLAQLQVAYHQLFQEYDNHIKS	4272
3CSY	OP	IMMUNE SYSTEM/VIRAL PROTEIN	P	1.8	5.3	3	20	GLRQLANETTQALQLFLRAT	4273
3DBO	AB	TOXIN/ANTITOXIN	A	1.3	5.3	4	11	PGLRNDLAVLA	4274
3DHH	AB	OXIDOREDUCTASE	B	2.7	5.3	2	15	PGWQGLRELMEKQLT	4275
3DHR	GH	OXYGEN STORAGE, OXYGEN TRANSPORT	H	1.8	5.3	3	16	VADCGAEALARLLIVY	4276
3EUB	TU	OXIDOREDUCTASE	T	2.7	5.3	2	24	IEFRRTLTLSFFFKFYLTVLKKLG	4277
3EXG	ST	OXIDOREDUCTASE	S	1.8	5.3	3	17	AQVPLGAGIALACKYNG	4278
3GJX	BA	PROTEIN TRANSPORT	A	2.7	5.3	2	14	WKFLKTVVNKLFEF	4279
3H32	BC	BLOOD CLOTTING	B	1.3	5.3	4	40	DETVNSNIPTNLRVLRSILENLRSKIQKLESDVSAQMEYC	4280
3H4S	AE	MOTOR PROTEIN/CALCIUM BINDING PROTEIN	A	1.8	5.3	3	21	EMVRLKKLVAYWKEQAGKKGE	4281
3HOU	MR	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	R	2.7	5.3	2	17	KYERARILGTRALQISM	4282

3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.7	5.3	2	10	VEILFEAGAS	4283
1ALL	AB	LIGHT HARVESTING PROTEIN	B	2.6	5.2	2	12	AITSVINSSDVQ	4284
1B6C	EF	COMPLEX (ISOMERASE/PROTEIN KINASE)	F	1.7	5.2	3	10	LLVQRTIART	4285
1BR1	AB	MUSCLE PROTEIN	A	1.7	5.2	3	21	TDVIIAFQAQCRGYLARKAFA	4286
1BX2	BC	IMMUNE SYSTEM	B	1.3	5.2	4	24	DILEQARAAVDTYCRHNYGVVESF	4287
1D8D	AB	TRANSFERASE	A	5.2	5.2	1	14	YHAWQHRQWVIQEF	4288
1DGH	AB	OXIDOREDUCTASE	B	2.6	5.2	2	8	QMQHWKEQ	4289
1DIO	AB	LYASE	B	1.3	5.2	4	14	QAKSAILHIKETKY	4290
1DKF	AB	HORMONE/GROWTH FACTOR RECEPTOR	A	2.6	5.2	2	23	PAEVEALREKVYASLEAYCKHKY	4291
1E 08	AD	HYDROGENASE	A	5.2	5.2	1	6	PAVRYA	4292
1EJH	AE	TRANSLATION	E	1.7	5.2	3	7	REFLLDF	4293
1F66	FH	STRUCTURAL PROTEIN/DNA	F	2.6	5.2	2	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	4294
1FFU	DE	HYDROLASE	E	1.7	5.2	3	22	PMIIEGQIHGGLTEGYAVAMGQ	4295
1FS2	CD	LIGASE	D	2.6	5.2	2	15	QGTLFELILAANYLD	4296
1G2C	ST	VIRAL PROTEIN	T	1.7	5.2	3	32	SDEFDASISQVNEKINQSLAFIRKSDELLHNV	4297
1G2C	WX	VIRAL PROTEIN	W	1.7	5.2	3	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	4298
1GH0	QR	PHOTOSYNTHESIS	R	1.3	5.2	4	12	AFTKVVSQADTR	4299
1I5K	BC	BLOOD CLOTTING	C	1.7	5.2	3	22	ADAELQRLKNERHEEAELERLK	4300
1ID3	EF	STRUCTURAL PROTEIN/DNA	F	1.7	5.2	3	11	IYEEVRAVLKS	4301
1IK9	BC	GENE REGULATION/LIGASE	B	2.6	5.2	2	30	LETDLYKRFILVLNEKKTKIRSLHNKLLNA	4302
1IR2	EM	LYASE	M	2.6	5.2	2	14	DEQIAAQVDYIVAN	4303
1IR2	T1	LYASE	T	2.6	5.2	2	20	WRDRFLFVAEAIYKAQAETG	4304
1MUJ	AC	IMMUNE SYSTEM	A	1.3	5.2	4	22	PQGGLQNIAVVKHNLGVLTKRS	4305
1N52	AB	RNA BINDING PROTEIN	B	1.7	5.2	3	11	EEQIYELFSKS	4306
1N86	AB	BLOOD CLOTTING	A	1.3	5.2	4	18	DMKRLEVDIDIKIRSCRG	4307
1NGM	EF	TRANSCRIPTION/DNA	F	2.6	5.2	2	15	EEASKLKERIWIGLN	4308
1P8V	BC	MEMBRANE PROTEIN/HYDROLASE	B	1.7	5.2	3	8	ERELLESY	4309
1Q7L	AB	HYDROLASE	B	2.6	5.2	2	13	PWWAAFSRVCKDM	4310
1Q90	BG	PHOTOSYNTHESIS	G	1.7	5.2	3	27	PLLCGIVLGLVPVTIAGLFVTAYLQYL	4311
1R27	AB	OXIDOREDUCTASE	B	1.7	5.2	3	25	TKPVLRALKRMLAMRHYKRAETVDG	4312
1R4M	CD	CELL CYCLE	C	1.7	5.2	3	21	HTIAAFLGGAAAQEVIKIITK	4313
1R5W	CD	SIGNALING PROTEIN	C	2.6	5.2	2	23	AQGALANIAVDKANLDVMKERSN	4314
1RYP	CD	MULTICATALYTIC PROTEINASE	D	2.6	5.2	2	22	NADSRILIEKARVEAQSHRLTL	4315
1RYP	ST	MULTICATALYTIC PROTEINASE	T	2.6	5.2	2	12	FQVEYALEAIKQ	4316
1S5L	BD	PHOTOSYNTHESIS	B	1.7	5.2	3	12	FFGHIWHGARTL	4317
1SFC	EF	TRANSPORT PROTEIN	F	1.7	5.2	3	42	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID	4318

1SFC	GH	TRANSPORT PROTEIN	H	1.7	5.2	3	47	IGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKML	4319
1SQX	DH	OXIDOREDUCTASE	H	2.6	5.2	2	23	TEELLDFLHARDHCVAHKLFNSL	4320
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.7	5.2	3	16	QRLVQNCLWTLRNLSD	4321
1U3H	GH	IMMUNE SYSTEM	G	1.7	5.2	3	6	VLTKRS	4322
1UKL	BE	PROTEIN TRANSPORT/DNA BINDING PROTEIN	E	1.7	5.2	3	23	VLRKAIDYIKYLQQVNHKLRQEN	4323
1V54	CG	OXIDOREDUCTASE	G	1.7	5.2	3	24	ARTWRFLTFGLALPSVALCTLNSW	4324
1V54	NO	OXIDOREDUCTASE	O	1.3	5.2	4	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	4325
1VCB	JK	TRANSCRIPTION	K	1.7	5.2	3	18	SHVLSKVCMYFTYKVRYT	4326
1VF5	AD	PHOTOSYNTHESIS	D	5.2	5.2	1	22	LAFGTVTGVALGALYPLVKYFI	4327
1VYJ	IJ	DNA-BINDING PROTEIN	J	2.6	5.2	2	5	ITDYF	4328
1W7P	AD	PROTEIN TRANSPORT	A	1.7	5.2	3	24	TVNDFYYEVCLKVIEICRQTKDMN	4329
1WPX	AB	HYDROLASE	B	2.6	5.2	2	12	FAQASIDSYKKH	4330
1YE9	CF	OXIDOREDUCTASE	F	1.7	5.2	3	13	FHRRELWEAIEAG	4331
1YE9	IM	OXIDOREDUCTASE	M	1.7	5.2	3	7	FFAENEQ	4332
1YE9	KM	OXIDOREDUCTASE	K	1.7	5.2	3	12	FILREKITHFDH	4333
1Z6O	DR	METAL BINDING PROTEIN	D	1.7	5.2	3	16	LSLALYVFDEYLQKTV	4334
1ZOY	CD	OXIDOREDUCTASE	D	1.7	5.2	3	28	DALQKAAKAGLLALSAFTFAGLCYFNYH	4335
2AA1	CD	OXYGEN STORAGE/TRANSPORT	D	2.6	5.2	2	14	VVGPATLARCLVVY	4336
2ADF	AH	BLOOD CLOTTING/IMMUNE SYSTEM	A	2.6	5.2	2	13	IGDALGFAVRYLT	4337
2AFH	CD	OXIDOREDUCTASE	C	1.3	5.2	4	15	DKKLAKLIDEVETLF	4338
2AHM	BF	VIRAL PROTEIN, REPLICATION	B	1.7	5.2	3	20	TTEAFEKMVSLLSVLLSMQG	4339
2AK4	DE	IMMUNE SYSTEM	E	1.7	5.2	3	7	EAEISHT	4340
2AL2	AB	LYASE	A	1.7	5.2	3	23	FAEALRIGSEVYHNLKSLTKKRY	4341
2B9S	AB	ISOMERASE/DNA	B	1.3	5.2	4	9	LGTSKINYI	4342
2BA0	EH	RNA BINDING PROTEIN	H	1.7	5.2	3	17	ENSIELARVVDRGIRES	4343
2BL0	AB	MUSCLE PROTEIN	B	1.7	5.2	3	11	YESFVDMLVTG	4344
2BR2	OP	HYDROLASE	O	1.7	5.2	3	26	LQDIDQAENTARSTAVKLLEELKKHL	4345
2CZY	AB	GENE REGULATION	A	1.7	5.2	3	17	PATYNGFLEIMKEFKSQ	4346
2DD4	DB	HYDROLASE	B	2.6	5.2	2	16	SIREEVHRHLGTVALM	4347
2DF4	AC	LIGASE	A	2.6	5.2	2	15	KEVKRRIFLGTFALS	4348
2DPP	AB	LYASE	A	1.7	5.2	3	10	PAYRARVVKE	4349
2DXB	DH	HYDROLASE	H	2.6	5.2	2	18	LTELHNKIVEMRERVASG	4350
2DXB	PT	HYDROLASE	T	2.6	5.2	2	18	LTELHNKIVEMRERVASG	4351
2FHH	WX	HYDROLASE	W	1.7	5.2	3	22	FNEFDNLRRGGIQFADTRGYAY	4352
2FSE	DF	IMMUNE SYSTEM, STRUCTURAL PROTEIN	D	2.6	5.2	2	10	RPDAEYWNSQ	4353

2GC4	AF	OXIDOREDUCTASE, ELECTRON TRANSPORT	A	1.3	5.2	4	20	QAQETQGQAAARAAAADLAA	4354
2GUZ	AB	CHAPERONE, PROTEIN TRANSPORT	A	1.7	5.2	3	18	PFLATKINEAKDFLEKRG	4355
2GV5	BC	CELL CYCLE	C	1.3	5.2	4	50	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK	4356
2HGJ	V4	RIBOSOME	V	5.2	5.2	1	10	KVRLVVDLIR	4357
2HLD	UV	HYDROLASE	U	2.6	5.2	2	12	VFYLHSRLLERA	4358
2HP0	AB	ISOMERASE	A	1.7	5.2	3	14	HSVQVALKYVAATG	4359
2HWN	CF	TRANSFERASE	C	1.3	5.2	4	16	LTELLQGYTVEVLRQQ	4360
2IBZ	CF	OXIDOREDUCTASE	F	1.7	5.2	3	20	EDESYARAYRIIRAHQTELT	4361
2IUC	AB	HYDROLASE	A	1.7	5.2	3	10	LSQISSTFYF	4362
2IZX	AC	KINASE	C	1.7	5.2	3	17	IEYLAKQIVDNAIQQAK	4363
2J0Q	AT	HYDROLASE	A	1.7	5.2	3	14	KGFKEQIYDVYRYL	4364
2J5G	AD	HYDROLASE	D	2.6	5.2	2	20	PREWDKTYWEGKKVLQNLLD	4365
2JIY	LM	PHOTOSYNTHESIS	L	1.7	5.2	3	5	ERKYR	4366
2O98	BQ	PROTEIN BINDING	B	1.7	5.2	3	23	EESYKDSTLIMQLLRDNLTLWTS	4367
2OM0	GH	HORMONE	H	1.7	5.2	3	18	NQHLCGSHLVEALYLVCG	4368
2OM0	KL	HORMONE	L	1.7	5.2	3	18	NQHLCGSHLVEALYLVCG	4369
2OM0	XY	HORMONE	Y	1.7	5.2	3	18	NQHLCGSHLVEALYLVCG	4370
2OV2	DL	PROTEIN BINDING/TRANSFERASE	L	5.2	5.2	1	7	RQWQSLI	4371
2P22	AC	TRANSPORT PROTEIN	A	1.7	5.2	3	34	MQESIARFHEIIAIDKNHLRAVEQAIEQTMHSLN	4372
2QL5	AB	HYDROLASE	A	1.7	5.2	3	16	TDKDAEALFKCFRSLG	4373
2RAO	AB	OXYGEN BINDING	B	2.6	5.2	2	16	VEEVGGEALGRLLVVY	4374
2RAX	XY	CELL CYCLE	X	1.7	5.2	3	19	LGEFLKLDRERAKNKIAKE	4375
2RHK	BD	VIRAL PROTEIN/NUCLEAR PROTEIN	D	2.6	5.2	2	6	YFYSKF	4376
2SEB	BE	COMPLEX (MHC CLASS II/SUPERANTIGEN)	B	1.7	5.2	3	23	KDLLEQKRAAVDTYCRHNYGVGE	4377
2UUN	EF	ELECTRON TRANSPORT	E	1.7	5.2	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	4378
2VE7	AC	CELL CYCLE	C	1.7	5.2	3	12	RKFISDYLWSLV	4379
2VGL	MS	PROTEIN TRANSPORT	S	1.3	5.2	4	17	DDEKQKLIEEVHAVVTV	4380
2W84	AB	PROTEIN TRANSPORT	A	2.6	5.2	2	12	LATRRAFLKKKG	4381
2WAQ	EF	TRANSCRIPTION	F	1.7	5.2	3	13	NLLQRTYDYLNSV	4382
2ZAL	AB	HYDROLASE	A	1.7	5.2	3	15	ALDVVTEAVRLLEEC	4383
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	A	1.7	5.2	3	16	DTVIEDIIDKTFEEAD	4384
2ZME	AB	PROTEIN TRANSPORT	A	2.6	5.2	2	19	VGDFYYELGVQIIEVCLAL	4385
2ZNV	DE	HYDROLASE/SIGNALING PROTEIN	D	2.6	5.2	2	10	EELFNVQDQH	4386
2ZT9	AD	PHOTOSYNTHESIS	D	1.7	5.2	3	31	MGRRQFMNLLTFGTVTGVALGALYPVVNYFI	4387
3CUE	HJ	PROTEIN TRANSPORT	H	1.7	5.2	3	19	LSAMAFLFQEMISQLHRTC	4388
3CUE	NP	PROTEIN TRANSPORT	N	1.7	5.2	3	19	LSAMAFLFQEMISQLHRTC	4389
3DUF	CD	OXIDOREDUCTASE/TRANSFERASE	C	1.7	5.2	3	16	AQYIQAAGVALGLKMR	4390

3DUF	CD	OXIDOREDUCTASE/TRANSFERASE	D	1.7	5.2	3	14	ESGIGGLAIGLALQ	4391
3DUF	EF	OXIDOREDUCTASE/TRANSFERASE	F	1.7	5.2	3	9	QMARIRYRT	4392
3EH3	AB	OXIDOREDUCTASE	B	1.7	5.2	3	30	AILAYEKGWLAFSLAMLFVFIALIAYTLAT	4393
3EXG	MN	OXIDOREDUCTASE	N	2.6	5.2	2	15	IDQVINSAAKTYYMS	4394
3EXH	EG	OXIDOREDUCTASE	E	1.7	5.2	3	13	GQIFEAYNMAALW	4395
3EXH	FG	OXIDOREDUCTASE	F	2.6	5.2	2	6	KILEDN	4396
3FKS	LM	HYDROLASE	M	2.6	5.2	2	15	TREGNDLYREMKETG	4397
3FKU	CF	VIRAL PROTEIN/IMMUNE SYSTEM	C	1.7	5.2	3	10	YEELKHLLSR	4398
3GHG	HI	BLOOD CLOTTING	I	1.7	5.2	3	29	DLQSLEDILHQVENKTSEVKQLIKAIQLT	4399
3H0L	PR	LIGASE	P	2.6	5.2	2	15	PEVKRRIMLGTFALS	4400
3H11	AB	APOPTOSIS	A	1.3	5.2	4	17	LLDLHIELNGYMYDWNS	4401
3HD7	CD	EXOCYTOSIS	D	1.3	5.2	4	47	HMARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKA	4402
3HRD	CD	OXIDOREDUCTASE	C	1.7	5.2	3	7	PQIRNLG	4403
1AOI	CD	DNA BINDING PROTEIN/DNA	D	1.7	5.1	3	12	AIYVYKVLKQVH	4404
1AVF	QJ	ASPARTIC PROTEASE	Q	2.6	5.1	2	8	IRETMKEK	4405
1B35	AB	VIRUS	B	1.7	5.1	3	8	PNRVTLIN	4406
1BCC	DF	OXIDOREDUCTASE	F	1.7	5.1	3	20	ENLYDDRMFRIKRALDLNMR	4407
1CKK	AB	CALMODULIN-PEPTIDE COMPLEX	B	2.6	5.1	2	11	WTTVILVKSML	4408
1D8D	AB	TRANSFERASE	A	2.6	5.1	2	14	KEYWRYIGRSLQSK	4409
1D9K	HQ	IMMUNE SYSTEM	H	5.1	5.1	1	5	EYWNK	4410
1DD4	BD	RIBOSOME	B	1.3	5.1	4	16	VSELAELVKKLEDKFG	4411
1DIO	AG	LYASE	G	1.3	5.1	4	17	KICAAFVREAATLYVER	4412
1E1H	AB	HYDROLASE	B	2.6	5.1	2	12	LQYMKNVFKEKY	4413
1E8O	CD	ALU RIBONUCLEOPROTEIN PARTICLE	C	1.7	5.1	3	17	VKKIEKFHSQLMRLMVA	4414
1EJH	AE	TRANSLATION	A	2.6	5.1	2	10	VEDFWALYNH	4415
1EUV	AB	HYDROLASE	A	2.6	5.1	2	10	SFFYTNLSER	4416
1EYS	LM	ELECTRON TRANSPORT	L	1.7	5.1	3	29	GLWQIITICAAGAFISWALREVEICRKLG	4417
1F51	AE	TRANSFERASE	A	1.3	5.1	4	31	TALTNELIHLLGHSRHDWMNKLQLIKGNLSL	4418
1FLC	CD	HYDROLASE	D	1.7	5.1	3	43	LEIENARSEALLGELGIIRALLVGNISIGLQESLWELASEITN	4419
1FNT	OP	HYDROLASE/HYDROLASE ACTIVATOR	O	1.7	5.1	3	19	CDVLAKRMANLSQIYTQRA	4420
1FQV	IJ	LIGASE	I	1.7	5.1	3	8	KRWYRLAS	4421
1G0U	GH	HYDROLASE	G	1.7	5.1	3	18	CDVLAKRMANLSQIYTQR	4422
1G2C	GH	VIRAL PROTEIN	H	1.7	5.1	3	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	4423
1G3N	AC	CELL CYCLE, SIGNALING PROTEIN	A	1.7	5.1	3	17	LSTIREVAVLRHLETFE	4424
1GCV	CD	OXYGEN STORAGE/TRANSPORT	C	2.6	5.1	2	16	PEAYGAECLARLFVTH	4425
1GH0	GH	PHOTOSYNTHESIS	G	1.3	5.1	4	27	STEIQVAFGRFRQAKAGLEAAKALTSK	4426
1GH0	KL	PHOTOSYNTHESIS	L	1.7	5.1	3	12	AFTKVVSQADTR	4427
1GZL	AC	GLYCOPROTEIN	A	2.6	5.1	2	43	MKQIEDKIEEIESKQKKIENEIARIKKLLQLTVWGIKQLQARI	4428
1GZL	BD	GLYCOPROTEIN	B	1.7	5.1	3	44	MKQIEDKIEEIESKQKKIENEIARIKKLLQLTVWGIKQLQARIL	4429

1GZS	BA	TOXIN/CELL CYCLE	B	1.7	5.1	3	30	PAYASQTREAILSAVYSKNKDQCCNLLISK	4430
1HBM	AC	METHANOGENESIS	A	2.6	5.1	2	7	PALLEDQ	4431
1HH4	AD	SIGNALING PROTEIN/INHIBITOR	A	2.6	5.1	2	13	VRAKWYPEVRHHC	4432
1HWM	AB	HYDROLASE	A	1.7	5.1	3	13	RYIEQEVRRSLQQ	4433
1ID3	EF	STRUCTURAL PROTEIN/DNA	E	1.7	5.1	3	14	KLPFQRLVREIAQD	4434
1IRU	DE	HYDROLASE	E	2.6	5.1	2	12	FQVEYDIEAIKL	4435
1KF6	NO	OXIDOREDUCTASE	O	2.6	5.1	2	32	PFYRFYMLREGTAVPAVWFSIELIFGLFALKN	4436
1KFU	LS	HYDROLASE	L	2.6	5.1	2	9	LISWLCFSV	4437
1KZ7	CD	SIGNALING PROTEIN	D	1.7	5.1	3	7	DRLRPLS	4438
1L9J	RS	PHOTOSYNTHESIS	R	1.7	5.1	3	29	PAHMIAISFFFTNALALALHGALVLSAAN	4439
1LOT	AB	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	A	1.7	5.1	3	33	PTVCFLKERLQLKHLSLLTTLSNRVCSQYAAYG	4440
1LVC	CF	LYASE	F	1.3	5.1	4	11	EEIREAFRVFD	4441
1MTY	EH	MONOOXYGENASE	H	1.7	5.1	3	20	VNYFLDGERQLGTRLMELRN	4442
1N1J	AB	DNA BINDING PROTEIN	B	2.6	5.1	2	9	LARIKKIMK	4443
1NRL	AC	TRANSCRIPTION	C	1.3	5.1	4	8	KILHRLLQ	4444
1NVM	AB	LYASE/OXIDOREDUCTASE	A	2.6	5.1	2	16	EDMIVDVALDLLAAHK	4445
1NY7	12	VIRUS	2	1.7	5.1	3	9	MPNSWISMW	4446
1O96	AB	ELECTRON TRANSFER	A	2.6	5.1	2	11	STGISVASYLN	4447
1Q90	AD	PHOTOSYNTHESIS	A	1.7	5.1	3	35	PARIQGLLVFFSFVLLTQVLLVLKKKQFEKVQLAE	4448
1QLE	AB	OXIDOREDUCTASE/IMMUNE SYSTEM	A	1.3	5.1	4	28	LTQQAYFMLATMTIAVPTGIKVFSWIAT	4449
1QPW	AB	OXYGEN TRANSPORT	B	2.6	5.1	2	19	PDVQAAFQKVVAGVANALA	4450
1R4M	CD	CELL CYCLE	D	1.7	5.1	3	21	ASTNAVIAAVCATEVFKIATS	4451
1RCO	KM	LYASE	K	1.7	5.1	3	21	NAPGAVANRVALEACVQARNE	4452
1RD8	CD	VIRAL PROTEIN	D	1.7	5.1	3	23	QKSTQNAIDGITNKVNSVIEKMN	4453
1SQB	DJ	OXIDOREDUCTASE	D	1.7	5.1	3	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	4454
1SQB	JK	OXIDOREDUCTASE	K	1.7	5.1	3	20	VPTAQLWGAVGAVGLVWATD	4455
1SXJ	DE	REPLICATION	E	1.3	5.1	4	19	TTNKSSIIEYSSVFDERLS	4456
1SYQ	AB	CELL ADHESION	A	1.3	5.1	4	49	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVAEV	4457
1T0F	AC	DNA BINDING PROTEIN	A	1.7	5.1	3	17	ERTLEKLELERRYWQQK	4458
1T3M	AB	HYDROLASE	A	1.7	5.1	3	15	ALDVVTEAVRLLEEC	4459
1TBG	BF	COMPLEX (GTP-BINDING/TRANSDUCER)	F	1.3	5.1	4	17	EKDKLKMEVDQLKKEVT	4460
1UZD	EF	LYASE	F	2.6	5.1	2	14	DEQIAAQVDYIVAN	4461
1UZD	KI	LYASE	K	1.7	5.1	3	15	AKNYGRAVYECLRGG	4462
1UZH	RP	LYASE	R	2.6	5.1	2	14	AKNYGRAVYECLRG	4463
1V54	AL	OXIDOREDUCTASE	A	2.6	5.1	2	6	INRWLF	4464
1VF6	BD	PROTEIN BINDING/PROTEIN TRANSPORT	B	1.7	5.1	3	24	PLFNQILTLQQSIKQLKGQLNHIL	4465

1VF6	BD	PROTEIN BINDING/PROTEIN TRANSPORT	D	1.7	5.1	3	16	SQSQEDISLLLQLVQN	4466
1VRQ	AD	OXIDOREDUCTASE	D	2.6	5.1	2	9	DKEWSRYLF	4467
1WDC	AC	MUSCLE PROTEIN	C	2.6	5.1	2	11	FADYMEAFKTF	4468
1XK4	EG	METAL BINDING PROTEIN	E	1.7	5.1	3	20	FQEFLILVIKMGVAAHKKSH	4469
1YCP	LH	COMPLEX (SERINE PROTEASE/PEPTIDE)	L	2.6	5.1	2	9	EKELFESYI	4470
1YE9	LP	OXIDOREDUCTASE	L	5.1	5.1	1	9	DTFWDYVSL	4471
1Z2C	AB	SIGNALING PROTEIN	A	2.6	5.1	2	5	DRLRP	4472
1Z6O	HX	METAL BINDING PROTEIN	H	1.7	5.1	3	16	LSLALYVFDEYLQKTV	4473
1Z7S	13	VIRUS	1	2.6	5.1	2	5	LESFF	4474
1ZBB	cd	STRUCTURAL PROTEIN/DNA	d	1.7	5.1	3	12	AIYVYKVLKQVH	4475
1ZBB	CD	STRUCTURAL PROTEIN/DNA	D	1.7	5.1	3	12	AIYVYKVLKQVH	4476
2A5T	AB	METAL TRANSPORT,MEMBRANE PROTEIN	A	1.3	5.1	4	15	WKQNVSLSILKSHEN	4477
2A78	AB	PROTEIN BINDING/TRANSFERASE	A	2.6	5.1	2	11	AAIRDNYFRSG	4478
2AA1	AD	OXYGEN STORAGE/TRANSPORT	A	2.6	5.1	2	7	PQTKIYF	4479
2AFH	AB	OXIDOREDUCTASE	A	2.6	5.1	2	10	IKEKFIFQKM	4480
2AGH	AB	TRANSCRIPTION	B	1.3	5.1	4	16	QDLRSHLVHKLVQAIF	4481
2AUS	AB	ISOMERASE/STRUCTURAL PROTEIN	B	1.7	5.1	3	12	GEYRRRLKRELL	4482
2C9W	AC	TRANSCRIPTION REGULATION	C	2.6	5.1	2	17	SHVLSKVCMYFTYKVRY	4483
2CNW	CF	SIGNAL RECOGNITION	F	1.7	5.1	3	12	GGTQLSEWGKRL	4484
2DD4	GK	HYDROLASE	K	2.6	5.1	2	16	SIREEVHRHLGTVALM	4485
2EHO	BD	REPLICATION	B	2.6	5.1	2	7	LIRELHR	4486
2FHH	UV	HYDROLASE	U	1.7	5.1	3	22	FNEFDNLRRGGIQFADTRGYAY	4487
2GTL	AG	OXYGEN STORAGE/TRANSPORT	A	5.1	5.1	1	12	YEDRREIRHIWD	4488
2GTL	EH	OXYGEN STORAGE/TRANSPORT	H	1.3	5.1	4	19	PEFGAHSQRVLSGLDITIS	4489
2INN	AC	OXIDOREDUCTASE	A	1.7	5.1	3	14	AIDELRHSQTQQHA	4490
2J0S	AC	HYDROLASE	C	1.7	5.1	3	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	4491
2JF9	AP	TRANSCRIPTION	P	1.7	5.1	3	8	REWFKDML	4492
2KA6	AB	TRANSCRIPTION REGULATOR	A	1.7	5.1	3	17	PVCKQLIALCCYHAKHC	4493
2NYL	EF	HYDROLASE	F	2.6	5.1	2	9	FYDECLRKY	4494
2NZ8	AB	SIGNALING PROTEIN, CELL CYCLE	B	2.6	5.1	2	34	RRKEFIMAELIQTEKAYVRDLRECMDTYLWEMTS	4495
2NZD	CD	STRUCTURAL PROTEIN/DNA	D	1.7	5.1	3	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	4496
2OM0	UV	HORMONE	V	1.7	5.1	3	18	NQHLCGSHLVEALYLVCG	4497
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.7	5.1	3	5	LRGFL	4498
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.3	5.1	4	8	PVYNTVAK	4499
2Q6W	DF	IMMUNE SYSTEM	D	1.3	5.1	4	22	AQGALANIAVDKANLEIMTKRS	4500

2QKM	AB	HYDROLASE	B	2.6	5.1	2	22	VERLCFQIEQAHWFYEDFIRAQ	4501
2QLV	AB	TRANSFERASE/PROTEIN BINDING	A	2.6	5.1	2	14	LDVMGEIYIALKNL	4502
2QR1	BG	TRANSFERASE	G	2.6	5.1	2	11	VKTSLSLLTLN	4503
2RGN	DE	SIGNALING PROTEIN COMPLEX	E	1.7	5.1	3	7	DFLNALQ	4504
2UUN	GH	ELECTRON TRANSPORT	G	1.7	5.1	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	4505
2UUN	MN	ELECTRON TRANSPORT	M	1.7	5.1	3	25	QRGKDKCARDIGYYLRMVTYCLIAG	4506
2UUN	UV	ELECTRON TRANSPORT	U	1.7	5.1	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	4507
2VE7	AC	CELL CYCLE	C	2.6	5.1	2	21	MEGFLPFSNLVTHLDSFLPIC	4508
2VN5	AB	CELL ADHESION	B	1.7	5.1	3	13	ALDFAGLKKYIMA	4509
2VOF	CD	APOPTOSIS	C	2.6	5.1	2	22	WGRIVTIFAFGGVLLKKLKQEQ	4510
2VZD	BD	CELL ADHESION	D	2.6	5.1	2	10	DDLDALLADL	4511
2WBJ	EH	IMMUNE SYSTEM	E	1.7	5.1	3	22	AQGALANIAVDKANLEIMTKRS	4512
3BCQ	AB	TRANSPORT PROTEIN/OXYGEN BINDING	B	1.7	5.1	3	16	VDEIGPQALSRLLIVY	4513
3BOW	AC	HYDROLASE/HYDROLASE INHIBITOR	C	1.7	5.1	3	8	PEYRHLLD	4514
3BVH	BC	BLOOD CLOTTING	C	1.7	5.1	3	26	YLQEIYNSNNQKIVNLKEKVAQLEAQ	4515
3CFV	AF	HISTONE/CHAPERONE	F	1.7	5.1	3	10	KPAIRRLARR	4516
3CWB	CD	OXIDOREDUCTASE	D	1.7	5.1	3	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	4517
3CXH	CG	OXIDOREDUCTASE	G	1.3	5.1	4	14	FTSIARIGDYILKS	4518
3CXH	OT	OXIDOREDUCTASE	T	2.6	5.1	2	8	WKDVKARI	4519
3DTP	AC	CONTRACTILE PROTEIN	C	1.7	5.1	3	11	FEDYVEGLRVF	4520
3E8C	EK	TRANSFERASE	K	2.6	5.1	2	8	TYADFIAS	4521
3EXG	ST	OXIDOREDUCTASE	T	1.7	5.1	3	14	EMGFAGIAVGAAMA	4522
3EYM	CF	VIRAL PROTEIN	F	2.6	5.1	2	52	RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLR	4523
3EYQ	CD	IMMUNE SYSTEM	C	5.1	5.1	1	5	EQLKS	4524
3F6Q	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	2.6	5.1	2	8	PLHYACFW	4525
3F75	AP	HYDROLASE	P	2.6	5.1	2	8	RDEFRRKY	4526
3FBI	CD	TRANSCRIPTION	D	2.6	5.1	2	12	RFEVELEFIQSL	4527
3FWC	BC	CELL CYCLE, TRANSCRIPTION	C	1.7	5.1	3	17	DSTRETVLKQIREFLEE	4528
3FWC	NO	CELL CYCLE, TRANSCRIPTION	O	1.7	5.1	3	20	DSTRETVLKQIREFLEEIVD	4529
3GHG	KL	BLOOD CLOTTING	L	1.3	5.1	4	23	LHQVENKTSEVKQLIKAIQLTYN	4530
3H0L	VX	LIGASE	V	1.3	5.1	4	19	YLKAQKVRRLITNDFLKAF	4531
3H2U	AB	CELL ADHESION	A	2.6	5.1	2	21	DIIAAAKRMALLMAEMSRLVR	4532
3H6P	AC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.7	5.1	3	58	FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQAN	4533
1A9N	CD	RNA BINDING PROTEIN/RNA	D	1.7	5.0	3	12	KEELKRSLYALF	4534
1AYY	AB	HYDROLASE	A	1.7	5.0	3	15	ALDAVEKGVRLVEDD	4535
1B33	EF	PHOTOSYNTHESIS	E	1.7	5.0	3	12	IVTKSIVNADAE	4536

1BGY	CF	ELECTRON TRANSPORT	F	2.5	5.0	2	6	GFNKLG	4537
1DIO	LM	LYASE	L	5.0	5.0	1	12	GLEVVKALAQGG	4538
1E7P	EF	OXIDOREDUCTASE	E	2.5	5.0	2	14	LQSKIAYLRRKMVS	4539
1FCD	BD	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	D	5.0	5.0	1	8	TIMGRIAK	4540
1FFT	FG	OXIDOREDUCTASE	F	2.5	5.0	2	14	AIPTGVKIFNWLFT	4541
1FFU	EF	HYDROLASE	F	2.5	5.0	2	22	ADYKTAMAGQMVKRALNAAWAR	4542
1FLC	EF	HYDROLASE	F	1.7	5.0	3	43	LEIENARSEALLGELGIIRALLVGNISIGLQESLWELASEITN	4543
1FQV	KL	LIGASE	L	5.0	5.0	1	14	QGTLFELILAANYL	4544
1FQV	MN	LIGASE	M	1.7	5.0	3	7	KRWYRLA	4545
1G0U	EF	HYDROLASE	E	2.5	5.0	2	15	VERAGHLLCDKAQKN	4546
1G20	CD	OXIDOREDUCTASE	C	2.5	5.0	2	8	EKFIFQKM	4547
1H1L	CD	OXIDOREDUCTASE	C	2.5	5.0	2	10	IKEKYIFQKM	4548
1H2A	SL	OXIDOREDUCTASE	L	2.5	5.0	2	6	LEIILK	4549
1I9R	KM	CYTOKINE/IMMUNE SYSTEM	M	2.5	5.0	2	5	DEQLK	4550
1IZN	CD	PROTEIN BINDING	C	2.5	5.0	2	14	DEEKVRIAAKFITH	4551
1JNR	AB	OXIDOREDUCTASE	A	2.5	5.0	2	17	KKKLKHIYEEAFEDFLD	4552
1JYO	AF	CHAPERONE	A	2.5	5.0	2	22	TYHIISQLESFVNQQEALKNIL	4553
1KDX	AB	TRANSCRIPTION REGULATION COMPLEX	A	1.7	5.0	3	21	RDEYYHLLAEKIYKIQKELEE	4554
1KVD	CD	TOXIN	D	1.3	5.0	4	17	KNDLQNMSADLAKNGFK	4555
1L4A	AB	ENDOCYTOSIS/EXOCYTOSIS	B	1.7	5.0	3	42	TQQAKQTLADIEARHADIMKLETSIRELHDMFMDMAMLVESQ	4556
1N4Q	CD	TRANSFERASE	C	1.7	5.0	3	10	ESAWNYLKGI	4557
1NDO	CD	NON-HEME IRON DIOXYGENASE	C	1.7	5.0	3	19	FWESDDNDNMETASQNGKK	4558
1NIK	BI	TRANSCRIPTION	B	2.5	5.0	2	9	WQMLEMLKP	4559
1OCC	AC	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.7	5.0	3	31	LFVWSVMITAVLLLLSLPVLAAGITMLLTDR	4560
1OUU	AD	OXYGEN TRANSPORT	D	1.7	5.0	3	7	PWTQRYF	4561
1PGR	GH	CYTOKINE	G	1.7	5.0	3	29	QSFLLKCLEQVRKIQGDGAALQEKLCATY	4562
1PK1	AB	TRANSCRIPTION REPRESSION	B	1.7	5.0	3	14	LGPALKICNLVNKV	4563
1POV	13	VIRUS	3	2.5	5.0	2	6	MMELAE	4564
1Q5R	GN	HYDROLASE	G	2.5	5.0	2	22	YNEFENLRRAGIVHADMRGYSY	4565
1Q90	DG	PHOTOSYNTHESIS	G	1.7	5.0	3	27	PLLCGIVLGLVPVTIAGLFVTAYLQYL	4566
1R4M	GH	CELL CYCLE	G	1.7	5.0	3	21	HTIAAFLGGAAAQEVIKIITK	4567
1RCO	OI	LYASE	O	1.7	5.0	3	14	AKNYGRAVYECLRG	4568
1RKE	AB	CELL ADHESION, STRUCTURAL PROTEIN	B	1.7	5.0	3	20	ERIPTISTQLKILSTVKATM	4569
1RYP	AB	MULTICATALYTIC PROTEINASE	B	2.5	5.0	2	12	GQIDYALTAVKQ	4570
1RYP	PQ	MULTICATALYTIC PROTEINASE	Q	2.5	5.0	2	11	YQVEYALESIS	4571
1SP4	AB	HYDROLASE	B	2.5	5.0	2	12	PSGAWNFWTKKG	4572

1SUV	AC	METAL TRANSPORT	A	5.0	5.0	1	17	RFVMKKLNDRVMRVEYH	4573
1SXJ	BC	REPLICATION	C	1.3	5.0	4	19	EETRVHLLTKLADIEYSIS	4574
1T0Q	AB	OXIDOREDUCTASE	A	1.7	5.0	3	21	PGNRNMATFGMMDENRHGQIQ	4575
1TUE	HJ	REPLICATION	H	2.5	5.0	2	14	FITFLGALKSFLKG	4576
1UEL	AB	GENE REGULATION/PROTEIN BINDING	B	1.3	5.0	4	16	EEEQIAYAMQMSLQGA	4577
1UPT	BA	HYDROLASE/PROTEIN-BINDING	B	2.5	5.0	2	13	TEFEYLRKVLFEY	4578
1UPT	FE	HYDROLASE/PROTEIN-BINDING	F	2.5	5.0	2	13	TEFEYLRKVLFEY	4579
1UZH	KI	LYASE	K	1.3	5.0	4	14	AKNYGRAVYECLRG	4580
1V02	FE	HYDROLASE	F	1.7	5.0	3	8	FSMRVSAR	4581
1V54	DK	OXIDOREDUCTASE	D	1.3	5.0	4	14	EEWVAKQTKRMLDM	4582
1VF5	AB	PHOTOSYNTHESIS	A	2.5	5.0	2	10	QVGYWAVKIV	4583
1VRA	AB	TRANSFERASE	B	1.7	5.0	3	14	HGHLQGALSAITNE	4584
1VRQ	AB	OXIDOREDUCTASE	B	1.7	5.0	3	15	FHVIEEQMAAAVELF	4585
1WYU	GH	OXIDOREDUCTASE	G	1.7	5.0	3	14	PEYRAVLRAYLEAV	4586
1XB2	AB	TRANSLATION	B	2.5	5.0	2	15	ASSKELLMKLRRKTG	4587
1XKM	CD	ANTIBIOTIC	D	1.7	5.0	3	19	LIEARKYLEQLHRKLKNCK	4588
1YE9	DH	OXIDOREDUCTASE	H	2.5	5.0	2	11	YYSHPRLFWLS	4589
1YHU	EG	OXYGEN STORAGE/TRANSPORT	E	2.5	5.0	2	20	PEFKAHIARVLGGLDRVISM	4590
1YKE	AB	GENE REGULATION	B	1.3	5.0	4	42	AEEQLRKIDMLQKKLVEVEDEKIEAIKKKEKLLRHVDSLIED	4591
1YKE	CD	GENE REGULATION	C	1.7	5.0	3	22	PDMYERKVENIRTILVNIHHLL	4592
1YNJ	AC	TRANSFERASE	A	1.3	5.0	4	16	FGVTLGNPLRRILLSS	4593
1Z7Q	EL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.7	5.0	3	23	AADCQFWETWLGSQCRLHELREK	4594
1Z7Q	Za	HYDROLASE/HYDROLASE ACTIVATOR	a	5.0	5.0	1	15	INSAARNIQHLLYGK	4595
1ZBB	ab	STRUCTURAL PROTEIN/DNA	a	1.7	5.0	3	13	TVALREIRRYQKS	4596
1ZBB	AB	STRUCTURAL PROTEIN/DNA	A	1.7	5.0	3	13	TVALREIRRYQKS	4597
1ZBB	BD	STRUCTURAL PROTEIN/DNA	B	2.5	5.0	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	4598
1ZBB	GH	STRUCTURAL PROTEIN/DNA	H	1.7	5.0	3	12	AIYVYKVLKQVH	4599
1ZV8	IH	VIRAL PROTEIN	I	1.3	5.0	4	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	4600
2AXT	AI	ELECTRON TRANSPORT	A	2.5	5.0	2	10	LWERFCNWVT	4601
2BEQ	CF	VIRAL PROTEIN	F	1.7	5.0	3	13	QKEIDRLNEVAKN	4602
2BTQ	AB	STRUCTURAL PROTEIN	B	2.5	5.0	2	6	THWYEN	4603
2CKF	EF	OXIDOREDUCTASE	E	5.0	5.0	1	6	TLESDD	4604
2DD4	JH	HYDROLASE	H	2.5	5.0	2	17	SSIREEVHRHLGTVALM	4605
2DXB	KL	HYDROLASE	K	2.5	5.0	2	18	LTELHNKIVEMRERVASG	4606
2DXB	MQ	HYDROLASE	Q	2.5	5.0	2	15	IREEVHRHLGTVALM	4607
2E9X	AD	REPLICATION	A	1.7	5.0	3	25	EDGLRQVLEEMKALYEQNQSDVNEA	4608
2E9X	EH	REPLICATION	E	1.7	5.0	3	27	EDGLRQVLEEMKALYEQNQSDVNEAKS	4609
2F8N	EF	STRUCTURAL PROTEIN/DNA	E	1.7	5.0	3	13	TVALREIRRYQKS	4610
2FHH	AH	HYDROLASE	H	1.7	5.0	3	23	AAVAVEFARLYAVELEHYEKLEG	4611

2FJ7	EF	STRUCTURAL PROTEIN/DNA	F	1.7	5.0	3	11	KPAIRRLARRG	4612
2FJH	VH	HORMONE/GROWTH FACTOR/IMMUNE SYSTEM	V	1.7	5.0	3	8	FMDVYQRS	4613
2FRV	CD	OXIDOREDUCTASE	D	1.7	5.0	3	10	PRDAQHFTQR	4614
2G9H	BC	IMMUNE SYSTEM	B	2.5	5.0	2	10	RPDAEYWNSQ	4615
2G9H	BC	IMMUNE SYSTEM	B	1.7	5.0	3	22	KDLLEQRRAAVDTYCRHNYGVG	4616
2H8P	CD	MEMBRANE PROTEIN	D	1.7	5.0	3	36	LWGRLVAVVVMVAGITSFGLVTAALATWFVGREQER	4617
2HGR	GH	RIBOSOME	H	2.5	5.0	2	11	AVPRAILELAG	4618
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	C	2.5	5.0	2	6	IAQDFK	4619
2I2R	CG	TRANSPORT PROTEIN	C	2.5	5.0	2	8	WLPFARAA	4620
2IAE	AC	HYDROLASE	A	1.7	5.0	3	12	YLHRMTTLFCIN	4621
2IAM	BP	IMMUNE SYSTEM	B	2.5	5.0	2	12	ELGRPDAEYWNS	4622
2J8X	AB	HYDROLASE/INHIBITOR	B	1.7	5.0	3	9	PEEVEEVIG	4623
2J8X	CD	HYDROLASE/INHIBITOR	C	2.5	5.0	2	5	PLAQN	4624
2J9U	AB	PROTEIN TRANSPORT	A	1.7	5.0	3	19	KDQLHPLLAELLISINRVT	4625
2JBL	LM	ELECTRON TRANSPORT	L	2.5	5.0	2	24	HVPLAFCVPIFMFCVLQVFRPLLL	4626
2JBL	LM	ELECTRON TRANSPORT	M	5.0	5.0	1	15	IWPHIDWLTAFSIRY	4627
2JDQ	AE	PROTEIN TRANSPORT	A	2.5	5.0	2	16	EDVQEQAVWALGNIAG	4628
2JIZ	CF	HYDROLASE	C	2.5	5.0	2	15	LSKQAVAYRQMSLLL	4629
2JTT	AC	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	C	2.5	5.0	2	14	DDMKRTINKAWVES	4630
2K9J	AB	MEMBRANE PROTEIN	B	1.3	5.0	4	33	ILVVLLSVMGAILLIGLAALLIWKLLITIHDRK	4631
2NNW	AB	TRANSFERASE	A	1.7	5.0	3	17	WFEEYYKVGVALTRMRI	4632
2NQB	BD	STRUCTURAL PROTEIN/DNA	D	5.0	5.0	1	29	SKAMSIMNSFVNDIFERIAAEASRLAHYN	4633
2NV2	EF	LYASE/TRANSFERASE	E	1.7	5.0	3	11	ERVKRGMAEMQ	4634
2NVU	AB	PROTEIN TURNOVER, LIGASE	A	1.7	5.0	3	21	HTIAAFLGGAAAQEVIKIITK	4635
2NZ0	AB	MEMBRANE PROTEIN	A	1.7	5.0	3	12	EDTFKQIYAQFF	4636
2P1L	AB	APOPTOSIS	A	2.5	5.0	2	22	QMAAVKQALREAGDEFELRYRR	4637
2P2C	BP	HYDROLASE	P	5.0	5.0	1	9	PLHLAAKTG	4638
2PBI	AB	SIGNALING PROTEIN	A	5.0	5.0	1	5	PWITD	4639
2PBI	CD	SIGNALING PROTEIN	C	5.0	5.0	1	5	PWITD	4640
2Q9Q	FG	REPLICATION	G	1.3	5.0	4	37	IPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	4641
2QM6	CD	TRANSFERASE	C	2.5	5.0	2	7	SSSKKYF	4642
2R6G	AG	HYDROLASE/TRANSPORT PROTEIN	G	2.5	5.0	2	10	SSLEEAAALD	4643
2RI4	IJ	OXYGEN STORAGE, OXYGEN TRANSPORT	I	5.0	5.0	1	19	PAVHASLDKFLANVSTVLT	4644
2RNR	AB	TRANSCRIPTION	B	5.0	5.0	1	19	AVKERDAVKDLLQQLLPKF	4645
2UUN	ST	ELECTRON TRANSPORT	S	1.7	5.0	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	4646
2UUN	WX	ELECTRON TRANSPORT	W	1.7	5.0	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	4647

2UZ1	AB	LYASE	B	2.5	5.0	2	8	YHGVAAAF	4648
2UZ1	DC	LYASE	C	2.5	5.0	2	8	YHGVAAAF	4649
2V4J	AB	OXIDOREDUCTASE	A	1.7	5.0	3	16	TPQLEEIFFELTHNLN	4650
2VAS	AB	MOTOR PROTEIN	B	2.5	5.0	2	15	EEQIAEFKEAFSLFD	4651
2VGL	AS	PROTEIN TRANSPORT	A	2.5	5.0	2	14	YTEKQIGYLFISVL	4652
2VTB	AB	LYASE/DNA	A	1.7	5.0	3	17	SEEVDVERLVNQGLKRV	4653
2W19	BD	TRANSFERASE/ISOMERASE	D	1.7	5.0	3	11	HSREMKVIERY	4654
2WH2	X2	RIBOSOME	2	2.5	5.0	2	19	PVELEKLVREKKRELMELR	4655
2ZCY	EF	HYDROLASE	E	2.5	5.0	2	15	VERAGHLLCDKAQKN	4656
2ZCY	OP	HYDROLASE	P	2.5	5.0	2	12	YQVEYALESISH	4657
2ZCY	RY	HYDROLASE	Y	2.5	5.0	2	22	AADCQFWETWLGSQCRLHELRE	4658
2ZFB	AB	METAL BINDING PROTEIN	B	2.5	5.0	2	19	PENFRLLGDILIIVLAGHF	4659
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	A	5.0	5.0	1	11	LFADRVFDLFD	4660
2ZT9	FH	PHOTOSYNTHESIS	H	1.7	5.0	3	25	AILTLGWVSLLVVFTWSIAMVVWGR	4661
2ZXX	BC	CELL CYCLE/REPLICATION	B	1.7	5.0	3	38	SQYWKEVAEQRRKALYEALKENEKLHKEIEQKDSEIAR	4662
3A0B	ck	ELECTRON TRANSPORT	c	1.7	5.0	3	12	GLIVFWAGAMTL	4663
3B8E	AB	HYDROLASE/TRANSPORT PROTEIN	B	1.7	5.0	3	21	YVIFYGCLAGIFIGTIQVMLL	4664
3BGO	PS	HYDROLASE	S	2.5	5.0	2	14	ASWIINGIEWAIAN	4665
3BZ1	FJ	ELECTRON TRANSPORT	J	1.7	5.0	3	24	LWIVATVAGMGVIVIVGLFFYGAY	4666
3C1B	BD	STRUCTURAL PROTEIN/DNA	D	1.7	5.0	3	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	4667
3C9A	BD	HORMONE/SIGNALING PROTEIN	D	2.5	5.0	2	8	ETFDAWYC	4668
3CUQ	AB	PROTEIN TRANSPORT	B	1.7	5.0	3	21	ISEAFEDLSKLMIKAKEMVEL	4669
3CWB	DH	OXIDOREDUCTASE	H	5.0	5.0	1	23	TEELFDFLHARDHCVAHKLFNKL	4670
3CXH	DI	OXIDOREDUCTASE	I	5.0	5.0	1	8	WKDVKARI	4671
3D24	CD	TRANSCRIPTION	C	2.5	5.0	2	11	LSDQMSVLQSV	4672
3D5D	FP	RIBOSOME	F	2.5	5.0	2	12	PHLLWEVVRWQL	4673
3DTP	AE	CONTRACTILE PROTEIN	A	1.7	5.0	3	26	KAFAKRQQQLTAMKVIQRNCAAYLKL	4674
3DUF	GH	OXIDOREDUCTASE/TRANSFERASE	G	2.5	5.0	2	13	GDFYEGINFAGAF	4675
3DXC	AB	PROTEIN BINDING	B	1.7	5.0	3	13	PEERHLSKMQQNG	4676
3E0J	GH	TRANSFERASE	G	1.7	5.0	3	16	GESLLGTQLLVDVVTG	4677
3E0J	GH	TRANSFERASE	H	2.5	5.0	2	8	YKWLSYTL	4678
3EXG	UV	OXIDOREDUCTASE	V	2.5	5.0	2	15	IDQVINSAAKTYYMS	4679
3G5O	AB	TOXIN/ANTITOXIN	B	1.7	5.0	3	12	PRILAAVVEFAF	4680
3GE8	DF	OXIDOREDUCTASE	F	2.5	5.0	2	15	PGWQGLRELMEKQLT	4681
3GHG	EF	BLOOD CLOTTING	F	1.3	5.0	4	24	QEIYNSNNQKIVNLKEKVAQLEAQ	4682
3GM1	BD	TRANSFERASE	D	1.7	5.0	3	10	RELDELMASL	4683
3MON	EF	SWEET-TASTING PROTEIN	F	2.5	5.0	2	18	PFTQNLGKFAVDEENKIG	4684
1B33	AB	PHOTOSYNTHESIS	B	1.6	4.9	3	12	AITAVINSSDVQ	4685
1B4U	CD	DIOXYGENASE	D	1.2	4.9	4	8	HIQYLRES	4686
1BB1	AC	DE NOVO PROTEIN DESIGN	C	1.6	4.9	3	32	IAAIKYKQAAIKNEIAAIKQEIAAIEQMIAAI	4687

1BGY	CG	ELECTRON TRANSPORT	C	2.5	4.9	2	22	PLSQCLFWALVADLLTLTWIGG	4688
1D8D	AB	TRANSFERASE	A	2.5	4.9	2	14	YTVWHFRRVLLRSL	4689
1DML	EF	DNA BINDING PROTEIN/TRANSFERASE	F	1.6	4.9	3	15	AEETRRMLHRAFDTL	4690
1DS6	AB	SIGNALING PROTEIN	A	2.5	4.9	2	5	DRLRP	4691
1E 08	AD	HYDROGENASE	A	2.5	4.9	2	17	PIGMNGALAKTYGAERM	4692
1EQZ	AB	STRUCTURAL PROTEIN/DNA	B	1.6	4.9	3	19	ELAKHAVSEGTKAVTKYTS	4693
1EQZ	FH	STRUCTURAL PROTEIN/DNA	F	2.5	4.9	2	29	SKAMGIMNSFVNDIFERIAGEASRLAHYN	4694
1ES7	AD	CYTOKINE	D	2.5	4.9	2	7	SDFQCKD	4695
1F99	KL	PHOTOSYNTHESIS	K	1.2	4.9	4	27	NTELQVVNGRYNRATSSLEAAKALTAN	4696
1FPP	BA	PRENYLTRANSFERASE	A	2.5	4.9	2	15	KEYWRYIGRSLQSKH	4697
1FQV	EF	LIGASE	E	2.5	4.9	2	7	KRWYRLA	4698
1FS0	EG	HYDROLASE	G	1.6	4.9	3	37	PKALLDTLLRRYVESQVYQGVVENLASEQAARMVAMK	4699
1FSX	CD	OXYGEN STORAGE/TRANSPORT	D	2.5	4.9	2	16	VDEVGGEALGRLLVVY	4700
1GH0	OP	PHOTOSYNTHESIS	P	1.6	4.9	3	12	AFTKVVSQADTR	4701
1GK0	AB	HYDROLASE	A	1.6	4.9	3	13	GDNILRLYGEARG	4702
1H6K	AX	NUCLEAR PROTEIN	A	4.9	4.9	1	11	FSHSFSALAKF	4703
1HX1	AB	CHAPERONE/CHAPERONE INHIBITOR	B	2.5	4.9	2	27	KDSRLKRKGLVKKVQAFLAECDTVEQN	4704
1IRU	EL	HYDROLASE	E	2.5	4.9	2	22	IADAKTLIDKARVETQNHWFTY	4705
1IRU	RS	HYDROLASE	S	2.5	4.9	2	12	FQVEYDIEAIKL	4706
1IRU	TU	HYDROLASE	U	2.5	4.9	2	12	FQVEYAMKAVEN	4707
1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	2.5	4.9	2	11	AAELRHVMTNL	4708
1IZN	AB	PROTEIN BINDING	A	2.5	4.9	2	13	DEEKVRIAAKFIT	4709
1JD2	KL	HYDROLASE	L	4.9	4.9	1	15	INSAARNIQHLLYGK	4710
1JFI	AB	TRANSCRIPTION/DNA	A	2.5	4.9	2	9	PARIKKIMQ	4711
1JNR	AB	OXIDOREDUCTASE	A	2.5	4.9	2	14	YKPIIAEAAKMAVG	4712
1JNR	CD	OXIDOREDUCTASE	C	2.5	4.9	2	17	KKKLKHIYEEAFEDFLD	4713
1JR3	DE	TRANSFERASE	E	1.6	4.9	3	17	RELLITDLLLRIEHYLQ	4714
1KUP	AB	CELL ADHESION	A	2.5	4.9	2	5	WKVGF	4715
1KX4	AB	STRUCTURAL PROTEIN/DNA	A	1.6	4.9	3	13	TVALREIRRYQKS	4716
1KYO	PT	OXIDOREDUCTASE/ELECTRON TRANSPORT	P	1.6	4.9	3	31	KGRSYAYFMVGAMGLLSSAGAKSTVETFISS	4717
1LVC	AD	LYASE	D	1.6	4.9	3	11	EEIREAFRVFD	4718
1M1Y	KL	OXIDOREDUCTASE	L	1.6	4.9	3	14	QDYKDMLAKKRDGF	4719
1MHY	BD	OXIDOREDUCTASE	B	2.5	4.9	2	12	SGARATVQEIWQ	4720
1N4Q	AB	TRANSFERASE	A	2.5	4.9	2	13	KEYWRYIGRSLQS	4721
1OCC	BD	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	4.9	4.9	1	14	EEWVAKQTKRMLDM	4722
1OCC	DE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	2.5	4.9	2	12	IDEKVELYRLKF	4723

1OCC	NQ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	1.6	4.9	3	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	4724
1OCC	OQ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	4.9	4.9	1	14	EEWVAKQTKRMLDM	4725
1OQO	BD	IMMUNE SYSTEM	D	2.5	4.9	2	12	MQCQRRFYEALH	4726
1OSV	AC	DNA BINDING PROTEIN	C	1.6	4.9	3	8	ALLRYLLD	4727
1P7T	AB	LYASE	B	4.9	4.9	1	40	AAAFWRNFDEIVHDLAPENRQLLAERDRIQAALDEWHRSN	4728
1PRC	CM	PHOTOSYNTHETIC REACTION CENTER	C	2.5	4.9	2	18	LSDAYATFALMMSISDSL	4729
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	2.5	4.9	2	7	PLQFFRQ	4730
1Q86	HN	RIBOSOME	N	2.5	4.9	2	9	AYSYIREAW	4731
1R5V	CD	SIGNALING PROTEIN	C	1.6	4.9	3	23	AQGALANIAVDKANLDVMKERSN	4732
1R8Q	AE	PROTEIN TRANSPORT/EXCHANGE FACTOR	A	2.5	4.9	2	8	RPLWRHYF	4733
1RD8	CD	VIRAL PROTEIN	D	1.6	4.9	3	29	RRIENLNKKVDDGFLDIWTYNAELLVLLE	4734
1RE0	AB	PROTEIN TRANSPORT	A	1.6	4.9	3	6	WRHYFQ	4735
1RKE	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.6	4.9	3	28	RTIESILEPVAQQISHLVIMHEEGEVDG	4736
1RUZ	LK	VIRAL PROTEIN	L	2.5	4.9	2	10	YEELREQLSS	4737
1RYP	BC	MULTICATALYTIC PROTEINASE	C	2.5	4.9	2	11	YQVEYALESIS	4738
1T3M	CD	HYDROLASE	C	1.6	4.9	3	15	ALDVVTEAVRLLEEC	4739
1TFC	AC	TRANSCRIPTION	C	1.6	4.9	3	10	KILHRLLQEG	4740
1USP	AB	OXIDOREDUCTASE	B	2.5	4.9	2	24	PEQLFAAGYAACFQGALGVVSRRN	4741
1UZD	RP	LYASE	R	1.6	4.9	3	15	AKNYGRAVYECLRGG	4742
1V54	AB	OXIDOREDUCTASE	B	1.6	4.9	3	23	TILPAIILILIALPSLRILYMMD	4743
1V54	AC	OXIDOREDUCTASE	C	2.5	4.9	2	29	TLLMIGLTTNMLTMYQWWRDVIRESTFQG	4744
1YE9	BF	OXIDOREDUCTASE	F	2.5	4.9	2	10	YSHPRLFWLS	4745
1YEW	JK	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	4.9	4.9	1	25	GATVCVLGLLLGEWINRYFNFWGWT	4746
1YHU	AC	OXYGEN STORAGE/TRANSPORT	A	1.6	4.9	3	20	PEFKAHIARVLGGLDRVISM	4747
1Z6O	CN	METAL BINDING PROTEIN	N	2.5	4.9	2	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	4748
1Z7Q	EM	HYDROLASE/HYDROLASE ACTIVATOR	E	2.5	4.9	2	23	TADARSMIEHARTAAVTHNLYYD	4749
1Z7Q	OU	HYDROLASE/HYDROLASE ACTIVATOR	O	2.5	4.9	2	10	YQVEYAFKAT	4750
1ZA3	BS	IMMUNE SYSTEM/SIGNALING PROTEIN	B	1.6	4.9	3	7	YYSYYYS	4751
1ZAV	AY	STRUCTURAL PROTEIN	A	1.6	4.9	3	41	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK	4752
1ZBB	gh	STRUCTURAL PROTEIN/DNA	h	1.6	4.9	3	12	AIYVYKVLKQVH	4753
1ZNV	CD	HYDROLASE/PROTEIN BINDING	C	2.5	4.9	2	6	TDLIYY	4754
2A1T	DS	OXIDOREDUCTASE/ELECTRON TRANSPORT	S	2.5	4.9	2	10	LPNIMKAKKK	4755
2AXT	ad	ELECTRON TRANSPORT	d	2.5	4.9	2	10	MVTANRFWSQ	4756

2AXT	bd	ELECTRON TRANSPORT	b	4.9	4.9	1	23	TVLSSSIAAVFFAAFVVAGTMWY	4757
2BA0	BE	RNA BINDING PROTEIN	E	1.6	4.9	3	11	IEVGEEMDEIT	4758
2BA1	FI	RNA BINDING PROTEIN	F	2.5	4.9	2	18	RRSIEISKVSKEAFEAVI	4759
2BE6	AD	MEMBRANE PROTEIN	A	1.6	4.9	3	15	EEQIAEFKEAFSLFD	4760
2BR2	MN	HYDROLASE	N	1.2	4.9	4	18	RREIELSKVIREALESAV	4761
2C35	AB	POLYMERASE	A	2.5	4.9	2	13	EVFMKTLNYTARF	4762
2C35	CD	POLYMERASE	C	2.5	4.9	2	13	EVFMKTLNYTARF	4763
2DXB	DB	HYDROLASE	B	2.5	4.9	2	16	SIREEVHRHLGTVALM	4764
2DXB	GK	HYDROLASE	K	2.5	4.9	2	16	SIREEVHRHLGTVALM	4765
2DXB	SW	HYDROLASE	W	2.5	4.9	2	16	SIREEVHRHLGTVALM	4766
2F2L	AX	MEMBRANE PROTEIN, IMMUNE SYSTEM, TOXIN	X	2.5	4.9	2	20	REVCSARVNVVQSFHMDSWG	4767
2F93	AB	MEMBRANE PROTEIN	A	1.6	4.9	3	33	PTVDVALIVYLDLVTKVGFGFIALDAAATLRAE	4768
2F95	AB	MEMBRANE PROTEIN	A	1.6	4.9	3	33	PTVDVALIVYLDLVTKVGFGFIALDAAATLRAE	4769
2FIF	CD	PROTEIN TURNOVER/ENDOCYTOSIS	D	1.6	4.9	3	35	SKCWREEYHKARQKQIQEDWELAERLQREEEEAFA	4770
2FRV	AB	OXIDOREDUCTASE	B	1.6	4.9	3	10	PRDAQHFTQR	4771
2FRV	GH	OXIDOREDUCTASE	H	1.6	4.9	3	10	PRDAQHFTQR	4772
2G38	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	2.5	4.9	2	36	TAQIADLDQEYDDFWDEDGEVMRDYRLRVSDALSKL	4773
2G9J	DB	STRUCTURAL PROTEIN	B	1.6	4.9	3	31	DAIKKKMQMLKLDNYHLENEVARLKKLVGER	4774
2GBW	CD	OXIDOREDUCTASE	C	2.5	4.9	2	17	TLESDDGENMSSATYIN	4775
2GEZ	EF	HYDROLASE	E	1.6	4.9	3	14	PLDVVELVVRELEN	4776
2GHO	CD	TRANSFERASE	D	4.9	4.9	1	6	LNDLYR	4777
2GL7	AC	TRANSCRIPTION	C	1.6	4.9	3	22	QEQLEHRERSLQTLRDIQRMLF	4778
2GYA	CJ	RIBOSOME	C	4.9	4.9	1	9	VVAYAAGAR	4779
2GZD	BD	PROTEIN TRANSPORT	D	4.9	4.9	1	18	DTHIRELEDYIDNLLVRV	4780
2HY5	AB	TRANSFERASE	A	1.2	4.9	4	11	LGQLVEAAIQA	4781
2HYB	PR	TRANSFERASE	R	1.6	4.9	3	11	YAGFVDLTTEC	4782
2INN	BL	OXIDOREDUCTASE	B	2.5	4.9	2	8	TVTFGFSA	4783
2INP	BD	OXIDOREDUCTASE	D	1.6	4.9	3	25	YGAYVGNRAKMQESAETSFGFCEKR	4784
2J59	DP	HYDROLASE	P	1.6	4.9	3	21	EEDTGVTNRDLISRRIKEYNN	4785
2JIZ	HN	HYDROLASE	N	2.5	4.9	2	69	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAA	4786
2JM6	AB	APOPTOSIS	A	1.2	4.9	4	24	LKDECAQLRRIGDKVNLRQKLLNM	4787
2ODB	AB	PROTEIN BINDING	B	4.9	4.9	1	5	PQWQN	4788
2OM0	gh	HORMONE	h	1.6	4.9	3	18	NQHLCGSHLVEALYLVCG	4789
2OM0	IJ	HORMONE	J	1.6	4.9	3	19	VNQHLCGSHLVEALYLVCG	4790
2OS8	AC	CONTRACTILE PROTEIN	A	2.5	4.9	2	22	VLGNLEEMRDERLSKIISMFQA	4791
2OV2	DL	PROTEIN BINDING/TRANSFERASE	D	2.5	4.9	2	9	DRLRPLSYP	4792
2PHG	AB	TRANSCRIPTION	B	1.6	4.9	3	9	QMFTDALGI	4793

2PXY	CD	IMMUNE SYSTEM	C	2.5	4.9	2	6	VLTKRS	4794
2Q9Q	GH	REPLICATION	G	1.2	4.9	4	37	IPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	4795
2QJK	MN	ELECTRON TRANSPORT	M	2.5	4.9	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	4796
2QKM	EF	HYDROLASE	F	2.5	4.9	2	23	VERLCFQIEQAHWFYEDFIRAQN	4797
2UUN	AB	ELECTRON TRANSPORT	A	1.6	4.9	3	12	PLTDAVSTADSQ	4798
2VBO	AB	HYDROLASE	A	1.6	4.9	3	14	KEFLLYLAGFVDGD	4799
2VE7	BD	CELL CYCLE	B	1.6	4.9	3	15	DEMNAELQSKLKDLF	4800
2VGO	AD	TRANSFERASE	D	2.5	4.9	2	13	NLLTQAIRQQYYK	4801
2WB1	AB	TRANSCRIPTION	A	4.9	4.9	1	7	ITQMAAM	4802
2ZCY	DE	HYDROLASE	E	2.5	4.9	2	13	FQVEYALEAIKQG	4803
2ZCY	EL	HYDROLASE	E	1.6	4.9	3	22	APDARVLSNYLRQQCNYSSLVF	4804
2ZIV	AB	HYDROLASE	A	1.2	4.9	4	10	VREVFARQLM	4805
2ZT9	CH	PHOTOSYNTHESIS	H	1.6	4.9	3	25	AILTLGWVSLLVVFTWSIAMVVWGR	4806
2ZVN	CH	SIGNALING PROTEIN/TRANSCRIPTION	H	1.6	4.9	3	51	IVMETVPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKL	4807
2ZXX	DF	CELL CYCLE/REPLICATION	D	1.6	4.9	3	43	YWKEVAEQRRKALYEALKENEKLHKEIEQKDSEIARLRKENKD	4808
3BPQ	AB	TOXIN	B	1.6	4.9	3	8	RKSIYDYF	4809
3BRT	AB	TRANSFERASE/TRANSCRIPTION	B	2.5	4.9	2	60	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	4810
3BUA	CG	DNA BINDING PROTEIN	C	1.2	4.9	4	17	YGDFRQIRDIMQALLVR	4811
3C7B	AB	OXIDOREDUCTASE	A	2.5	4.9	2	19	FVKEIKKTAELMEKAAAEG	4812
3CWB	EJ	OXIDOREDUCTASE	J	1.6	4.9	3	31	TSTFALTVVLGAVLFERAFDQGADAIFEHLN	4813
3CWB	RW	OXIDOREDUCTASE	W	1.6	4.9	3	31	TSTFALTVVLGAVLFERAFDQGADAIFEHLN	4814
3D36	AC	TRANSFERASE/TRANSFERASE INHIBITOR	A	2.5	4.9	2	20	ISHEIRNPLTAARGFIQLIE	4815
3D3C	AJ	TRANSCRIPTION	J	1.2	4.9	4	18	HRLIDQATAEIVETAKRT	4816
3D4X	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	2.5	4.9	2	16	VDEVGGEALGRLLVVY	4817
3DGC	MR	CYTOKINE/SIGNALING PROTEIN	M	1.6	4.9	3	17	PYMQEVVPFLARLSNRL	4818
3DMT	BC	OXIDOREDUCTASE	C	2.5	4.9	2	10	AEYFAYQMRY	4819
3DUF	AB	OXIDOREDUCTASE/TRANSFERASE	B	1.6	4.9	3	14	ESGIGGLAIGLALQ	4820
3EXH	AC	OXIDOREDUCTASE	A	1.6	4.9	3	13	GQIFEAYNMAALW	4821
3EZJ	EF	PROTEIN TRANSPORT	E	1.6	4.9	3	15	ERQYYQLFLNLLEAQ	4822
3FWC	BC	CELL CYCLE, TRANSCRIPTION	C	2.5	4.9	2	11	FTQILSTVEPK	4823
3G3A	CD	HYDROLASE/IMMUNE SYSTEM	D	2.5	4.9	2	8	VAWRNRCK	4824
3G5O	AB	TOXIN/ANTITOXIN	B	1.6	4.9	3	9	TTARRDLHK	4825
3G5O	DC	TOXIN/ANTITOXIN	C	1.6	4.9	3	12	PRILAAVVEFAF	4826
3GHG	AC	BLOOD CLOTTING	C	1.6	4.9	3	19	TCGIADFLSTYQTKVDKDL	4827
3GHG	GH	BLOOD CLOTTING	H	1.6	4.9	3	36	DETVNSNIPTNLRVLRSILENLRSKIQKLESDVSAQ	4828
3HKZ	AG	TRANSFERASE	A	4.9	4.9	1	9	GKQVISAFL	4829

3HKZ	IM	TRANSFERASE	M	1.6	4.9	3	14	DKIFDLAIKEYSEG	4830
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.5	4.9	2	23	PQVCAKLFGNIQKVVNFWLLHNG	4831
3HOU	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	2.5	4.9	2	11	DEFIAHRLGLI	4832
3HOY	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.6	4.9	3	13	LAMANSLRRVMIA	4833
1AIP	FH	COMPLEX OF TWO ELONGATION FACTORS	F	2.4	4.8	2	17	ELLDLVEMEVRDLLNQY	4834
1AOK	AB	HYDROLASE	B	1.6	4.8	3	13	LFQFAKMINGKLG	4835
1C08	BC	IMMUNE SYSTEM/HYDROLASE	C	4.8	4.8	1	11	TASVNCAKKIV	4836
1CFF	AB	CALMODULIN	A	1.6	4.8	3	12	DEEVDEMIREAD	4837
1DOW	AB	CELL ADHESION	B	1.6	4.8	3	10	KHAVVNLINY	4838
1E1C	CD	ISOMERASE	D	1.6	4.8	3	19	DFPLRIARNTGIVLAEEVN	4839
1E1H	CD	HYDROLASE	C	2.4	4.8	2	21	DNEKDNYLKGVTKLFERIYST	4840
1EQZ	EF	STRUCTURAL PROTEIN/DNA	F	1.6	4.8	3	20	GELAKHAVSEGTKAVTKYTS	4841
1G2C	CF	VIRAL PROTEIN	C	2.4	4.8	2	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	4842
1GH0	EF	PHOTOSYNTHESIS	E	1.6	4.8	3	12	PLTEAVSVADSQ	4843
1GH0	UV	PHOTOSYNTHESIS	V	1.6	4.8	3	12	AFTKVVSQADTR	4844
1GK0	CD	HYDROLASE	C	1.6	4.8	3	13	GDNILRLYGEARG	4845
1H1L	CD	OXIDOREDUCTASE	D	2.4	4.8	2	8	AEYEALNF	4846
1HBM	DB	METHANOGENESIS	D	4.8	4.8	1	19	AQTGLSGWYLSMYLHKEQH	4847
1I94	EH	RIBOSOME	E	1.6	4.8	3	6	ADVERL	4848
1IR2	S4	LYASE	S	2.4	4.8	2	20	WRDRFLFVAEAIYKAQAETG	4849
1IRU	SZ	HYDROLASE	S	2.4	4.8	2	22	IADAKTLIDKARVETQNHWFTY	4850
1IW7	MN	TRANSFERASE	N	4.8	4.8	1	5	WLSAA	4851
1J7V	LR	CYTOKINE/RECEPTOR	L	2.4	4.8	2	15	NLPNMLRDLRDAFSR	4852
1JCH	AB	RIBOSOME INHIBITOR, HYDROLASE	B	1.6	4.8	3	8	EWVPLLQP	4853
1JCH	CD	RIBOSOME INHIBITOR, HYDROLASE	D	1.6	4.8	3	8	EWVPLLQP	4854
1K5D	JL	SIGNALING PROTEIN/SIGNALING ACTIVATOR	J	4.8	4.8	1	11	RVTYKNVPNWH	4855
1KFY	AB	OXIDOREDUCTASE	A	1.6	4.8	3	11	PFICELAKAYV	4856
1KTD	AB	IMMUNE SYSTEM	A	2.4	4.8	2	7	EEFAKFA	4857
1L4A	BD	ENDOCYTOSIS/EXOCYTOSIS	B	2.4	4.8	2	42	TQQAKQTLADIEARHADIMKLETSIRELHDMFMDMAMLVESQ	4858
1LIA	KL	LIGHT HARVESTING PROTEIN	K	4.8	4.8	1	16	HEAVVKEAGDACFSKY	4859
1M1E	AB	STRUCTURAL PROTEIN	A	2.4	4.8	2	15	EGVATYAAAVLFRMS	4860
1M1Y	KL	OXIDOREDUCTASE	K	1.6	4.8	3	15	DKKLAKLIDEVETLF	4861
1M63	EF	HYDROLASE/ISOMERASE	F	1.6	4.8	3	14	DTQLQQIVDKTIIN	4862
1MF8	AB	HYDROLASE, LIGASE	B	4.8	4.8	1	5	PELQQ	4863

1MHY	BG	OXIDOREDUCTASE	B	2.4	4.8	2	27	GAHNRTFLNAWTEHYLASSVAALKDFV	4864
1MJG	CO	OXIDOREDUCTASE	C	1.2	4.8	4	16	DLIYSILTQIASDVYG	4865
1MJG	DP	OXIDOREDUCTASE	D	1.6	4.8	3	29	PQVAARKILDALEYRTWKLGVHKEVAERY	4866
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	1.6	4.8	3	7	AQEVHRW	4867
1MZN	AB	TRANSCRIPTION	A	2.4	4.8	2	8	TFLMEMLE	4868
1N86	DE	BLOOD CLOTTING	E	4.8	4.8	1	6	LRVLRS	4869
1N95	AB	TRANSFERASE	A	2.4	4.8	2	14	YHAWQHRQWVIQEF	4870
1NH2	BD	TRANSCRIPTION/DNA	D	1.6	4.8	3	22	ASLAMRVLETFDKVVAETLKDN	4871
1NTK	EJ	OXIDOREDUCTASE	E	2.4	4.8	2	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	4872
1O96	QZ	ELECTRON TRANSFER	Z	1.6	4.8	3	12	IFDIEEELKAQL	4873
1OCC	AF	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	2.4	4.8	2	5	LEWLN	4874
1OCC	NS	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.4	4.8	2	5	LEWLN	4875
1P4E	AD	DNA BINDING PROTEIN/RECOMBINATION/DNA	A	2.4	4.8	2	15	ITDIVSSLQLQFESG	4876
1PMA	N1	PROTEASE	1	1.6	4.8	3	22	VGDAQVLVRYMKAELELYRLQR	4877
1Q7L	AB	HYDROLASE	A	1.6	4.8	3	17	KCVSIQYLEAVRRLKVE	4878
1QVF	FL	RIBOSOME	L	2.4	4.8	2	9	AYSYIREAW	4879
1R1K	DA	HORMONE/GROWTH FACTOR RECEPTOR	A	1.6	4.8	3	22	RQEVEVLREKMFLCLDEYCRRS	4880
1R27	AB	OXIDOREDUCTASE	A	2.4	4.8	2	13	TPDAHFFTEVRYK	4881
1RJC	AB	IMMUNE SYSTEM/HYDROLASE	B	1.6	4.8	3	8	VAWRNRCK	4882
1RM6	EF	OXIDOREDUCTASE	E	1.6	4.8	3	9	TDLLPNLRR	4883
1RP3	EF	TRANSCRIPTION	E	1.6	4.8	3	20	VEEEVIKRELTEKVKEAVSK	4884
1RYP	EF	MULTICATALYTIC PROTEINASE	F	2.4	4.8	2	12	FQVEYALEAIKQ	4885
1SQX	KJ	OXIDOREDUCTASE	J	1.6	4.8	3	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	4886
1SVD	AM	LYASE	M	1.6	4.8	3	14	AERIRAQIKYAIAQ	4887
1T1K	AB	HORMONE/GROWTH FACTOR	B	2.4	4.8	2	12	SDLAEALYLVCG	4888
1TI2	AB	OXIDOREDUCTASE	A	1.6	4.8	3	6	HTARLV	4889
1UM9	CB	OXIDOREDUCTASE	C	1.6	4.8	3	12	WHLLRQEALLKE	4890
1UZH	HW	LYASE	H	1.6	4.8	3	14	AKNYGRAVYECLRG	4891
1V4U	AD	OXYGEN STORAGE/TRANSPORT	D	2.4	4.8	2	6	PWTQRY	4892
1V54	QR	OXIDOREDUCTASE	Q	2.4	4.8	2	12	IDEKVELYRLKF	4893
1V54	QR	OXIDOREDUCTASE	Q	4.8	4.8	1	5	FAEMN	4894
1W2W	AB	ISOMERASE	A	2.4	4.8	2	14	DNGAKYLIDVLQKD	4895
1WDC	AB	MUSCLE PROTEIN	B	1.6	4.8	3	12	FTMFLSIFSDKL	4896
1XB2	AB	TRANSLATION	B	2.4	4.8	2	11	FINCKKALETC	4897
1XFV	ES	LYASE/METAL BINDING PROTEIN	E	1.2	4.8	4	15	SLEKQKGVTNLLIKY	4898

1XXI	AE	TRANSFERASE	A	1.6	4.8	3	19	QTQLRQAVQLLTRTELTLK	4899
1XXI	FG	TRANSFERASE	F	1.6	4.8	3	15	LLALAQALERLSLLW	4900
1YAG	AG	CONTRACTILE PROTEIN	G	1.6	4.8	3	18	QDESGAAAIFTVQLDDYL	4901
1YE9	CG	OXIDOREDUCTASE	C	4.8	4.8	1	9	DTFWDYVSL	4902
1YE9	IM	OXIDOREDUCTASE	M	1.6	4.8	3	17	PFEQRHIVDGFSFELSK	4903
1YOV	AB	SIGNALING PROTEIN	A	1.2	4.8	4	21	HTIAAFLGGAAAQEVIKIITK	4904
1YOV	CD	SIGNALING PROTEIN	C	1.6	4.8	3	7	DRQLRLW	4905
1Z6O	EP	METAL BINDING PROTEIN	P	2.4	4.8	2	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	4906
1Z6O	IS	METAL BINDING PROTEIN	I	1.6	4.8	3	16	LSLALYVFDEYLQKTV	4907
1Z7Q	AG	HYDROLASE/HYDROLASE ACTIVATOR	A	2.4	4.8	2	10	YQVEYAFKAT	4908
1ZY3	AB	APOPTOSIS	A	1.6	4.8	3	14	QQRFTQVSDELFQG	4909
2A1T	RS	OXIDOREDUCTASE/ELECTRON TRANSPORT	S	1.6	4.8	3	10	QTGQMTAGFL	4910
2AFH	CD	OXIDOREDUCTASE	D	2.4	4.8	2	16	QGCVAYFRSYFNRHFR	4911
2AHM	BF	VIRAL PROTEIN, REPLICATION	F	1.6	4.8	3	21	KRAKVTSAMQTMLFTMLRKLD	4912
2AVU	DF	TRANSCRIPTION ACTIVATOR	F	2.4	4.8	2	20	EQNVHASMFCNAWQFLLKTG	4913
2AXT	AC	ELECTRON TRANSPORT	A	1.6	4.8	3	26	SRSLHFFLAAWPVVGVWFTALGISTM	4914
2AXT	ef	ELECTRON TRANSPORT	e	2.4	4.8	2	17	ITIPALFIAGWLFVSTG	4915
2BA0	AD	RNA BINDING PROTEIN	D	1.6	4.8	3	30	RDEVKQAIELAKKGALQIYEMQREAILRRY	4916
2BA1	EH	RNA BINDING PROTEIN	H	1.6	4.8	3	18	DENSIELARVVDRGIRES	4917
2BE6	BE	MEMBRANE PROTEIN	B	1.2	4.8	4	14	FPEFLTMMARKMKD	4918
2BSK	EF	PROTEIN TRANSPORT	F	1.6	4.8	3	20	KGESVCLDRCVSKYLDIHER	4919
2C52	AB	TRANSFERASE	A	4.8	4.8	1	6	KYVANQ	4920
2DXB	BC	HYDROLASE	B	1.6	4.8	3	16	YYGRWLLTAARILVDK	4921
2DXB	GE	HYDROLASE	E	2.4	4.8	2	18	LTELHNKIVEMRERVASG	4922
2DXB	QR	HYDROLASE	R	1.6	4.8	3	10	PNYRRRLVRW	4923
2EFC	AB	TRANSPORT PROTEIN	A	1.6	4.8	3	16	ADEFLPVLIYVTIKAN	4924
2EHO	GH	REPLICATION	H	1.6	4.8	3	18	RGLFQTGQKGLNDFQCWE	4925
2F8N	FH	STRUCTURAL PROTEIN/DNA	H	2.4	4.8	2	12	SREIQTAVRLLL	4926
2FHJ	CD	TRANSFERASE	C	2.4	4.8	2	9	VGYKLSFFG	4927
2FHX	AB	HYDROLASE, METAL BINDING PROTEIN	B	2.4	4.8	2	22	DLTKQLRLEENKKDRIKAAEFY	4928
2FUG	MP	OXIDOREDUCTASE	M	2.4	4.8	2	11	AVIYHFKHYTE	4929
2FUG	VY	OXIDOREDUCTASE	V	2.4	4.8	2	10	VIYHFKHYTE	4930
2FYN	PQ	OXIDOREDUCTASE	Q	1.6	4.8	3	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	4931
2FYZ	AD	PROTEIN BINDING	A	1.6	4.8	3	50	VSLVQAQTNARAIAAMKNSIQATNRAVFEVKEGTQRLAIAVQAIQDHINT	4932
2GBW	AB	OXIDOREDUCTASE	A	2.4	4.8	2	17	TLESDDGENMSSATYIN	4933
2GBW	EF	OXIDOREDUCTASE	E	2.4	4.8	2	15	PATKSMIQREAIRTF	4934
2GD4	LH	HYDROLASE	H	4.8	4.8	1	10	DWAESTLMTQ	4935

2GUZ	GF	CHAPERONE, PROTEIN TRANSPORT	F	1.6	4.8	3	15	MDKINNRFNYLFEVN	4936
2H4M	BD	PROTEIN TRANSPORT	B	4.8	4.8	1	11	LPLKERLAAFY	4937
2H8P	CD	MEMBRANE PROTEIN	C	1.6	4.8	3	29	LHWRAAGAATVLLVIVLLAGSYLAVLAER	4938
2HYI	AC	HYDROLASE/RNA BINDING PROTEIN/RNA	C	2.4	4.8	2	13	DDIRILRDIEQYY	4939
2HYI	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	2.4	4.8	2	11	FKEQIYDVYRY	4940
2I2R	JN	TRANSPORT PROTEIN	N	2.4	4.8	2	14	FEDFVTALSILLRG	4941
2I2X	EH	TRANSFERASE	H	4.8	4.8	1	6	YNVALE	4942
2IAN	QR	IMMUNE SYSTEM	Q	2.4	4.8	2	11	ELGRPDAEYWN	4943
2J0Q	AT	HYDROLASE	A	2.4	4.8	2	11	VGEDIRKLDYG	4944
2J0Q	BI	HYDROLASE	B	1.6	4.8	3	14	KGFKEQIYDVYRYL	4945
2JF9	CR	TRANSCRIPTION	C	1.2	4.8	4	23	LHDQVHLLECAWLEILMIGLVWR	4946
2JGB	AB	TRANSLATION	A	2.4	4.8	2	10	VEQFWRFYSH	4947
2JIZ	AD	HYDROLASE	A	1.6	4.8	3	14	RSTVAQLVKRLTDA	4948
2JJ0	MH	PHOTOSYNTHESIS	H	1.6	4.8	3	24	LASLAIYSFWIFLAGLIYYLQTEN	4949
2KIN	AB	MOTOR PROTEIN	B	1.6	4.8	3	16	EAETKSTLMFGQRAKT	4950
2NU9	HE	LIGASE	E	2.4	4.8	2	11	PYQGRELAFKL	4951
2O60	AB	METAL BINDING PROTEIN	A	4.8	4.8	1	9	IREAFRVFD	4952
2P22	CD	TRANSPORT PROTEIN	D	2.4	4.8	2	13	SNKKFDQWYKEQY	4953
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	H	1.6	4.8	3	15	KTTIDQLHNSLNAAS	4954
2PQR	BD	APOPTOSIS	B	2.4	4.8	2	14	IQSRFNYAWGLIKS	4955
2QJP	DE	ELECTRON TRANSPORT	E	2.4	4.8	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	4956
2QJY	DE	OXIDOREDUCTASE	D	2.4	4.8	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	4957
2QL5	CD	HYDROLASE	C	1.6	4.8	3	16	TDKDAEALFKCFRSLG	4958
2R1H	CD	OXYGEN BINDING	C	2.4	4.8	2	16	SDEIGEQALSRMLVVY	4959
2UUN	OP	ELECTRON TRANSPORT	O	1.6	4.8	3	12	PLTDAVSTADSQ	4960
2UUN	QR	ELECTRON TRANSPORT	Q	1.6	4.8	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	4961
2VE7	AC	CELL CYCLE	A	1.6	4.8	3	19	NKLFLDYTIKCYESFMSGA	4962
2VJT	AB	PHOTOSYNTHESIS	B	1.6	4.8	3	25	TRRYAACIRDMDYFLRYATYAMLAG	4963
2W72	BC	OXYGEN TRANSPORT	B	2.4	4.8	2	6	PWTQRF	4964
2W73	AK	METAL BINDING PROTEIN	K	1.6	4.8	3	14	IRNKIRAIGKMARV	4965
2WH4	FP	RIBOSOME	F	2.4	4.8	2	15	PHLLWEVVRWQLAKR	4966
2ZCY	AG	HYDROLASE	A	2.4	4.8	2	13	GQIDYALTAVKQG	4967
2ZCY	ST	HYDROLASE	T	1.6	4.8	3	22	IPDGRHLVNRGREEAASFKKLY	4968
2ZME	AB	PROTEIN TRANSPORT	A	4.8	4.8	1	15	QDDLIRAIKKLKALG	4969
2ZSH	AB	HORMONE RECEPTOR	B	2.4	4.8	2	16	MADVAQKLEQLEVMMS	4970
2ZXE	AG	HYDROLASE/TRANSPORT PROTEIN	A	2.4	4.8	2	20	KILIFGLFEETALAAFLSYC	4971
3BL2	AC	VIRAL PROTEIN/APOPTOSIS	A	2.4	4.8	2	25	SAVLVDVSKIITLTQEFRRHYDSVY	4972

3BRV	AD	TRANSFERASE/TRANSCRIPTION	D	1.2	4.8	4	60	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	4973
3C72	AB	TRANSFERASE	A	2.4	4.8	2	13	QSAWFYHRWLLGA	4974
3C7B	AB	OXIDOREDUCTASE	A	2.4	4.8	2	12	TLELCYDLTMTY	4975
3CJH	IL	PROTEIN TRANSPORT	I	1.6	4.8	3	24	DACIDQCLAKYMRSWNVISKAYIS	4976
3CPH	GA	PROTEIN TRANSPORT	G	2.4	4.8	2	15	LGELPQGFARLSAIY	4977
3CQX	BC	CHAPERONE	B	2.4	4.8	2	18	KRAVRRLRTACERAKRTL	4978
3D36	AC	TRANSFERASE/TRANSFERASE INHIBITOR	C	2.4	4.8	2	14	DELLIESYFKAKEL	4979
3D4X	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	4.8	4.8	1	19	PAVHASLDKFFSAVSTVLT	4980
3D85	CD	IMMUNE SYSTEM/CYTOKINE	C	1.6	4.8	3	32	PWQRLLLRFKILRSLQAFVAVAARVFAHGAAT	4981
3DF0	AB	HYDROLASE	B	2.4	4.8	2	20	FDNFISCLVRLDAMFRAFRS	4982
3DRA	AB	TRANSFERASE	A	1.6	4.8	3	10	SNFWDYQISK	4983
3DUF	CD	OXIDOREDUCTASE/TRANSFERASE	C	4.8	4.8	1	13	GDFYEGINFAGAF	4984
3EAB	EK	CELL CYCLE	E	1.6	4.8	3	28	EQCERARRLQAKMMTNLVMAKDRLQLLE	4985
3ECH	BC	TRANSCRIPTION, TRANSCRIPTION REGULATION	B	1.6	4.8	3	23	LMPALMAVFQHVRTRIQSELDCQ	4986
3EXG	GH	OXIDOREDUCTASE	G	2.4	4.8	2	10	GIALACKYNG	4987
3EXG	WX	OXIDOREDUCTASE	X	2.4	4.8	2	5	TYYMS	4988
3EXH	AB	OXIDOREDUCTASE	A	2.4	4.8	2	17	AQVPLGAGIALACKYNG	4989
3FWB	BC	CELL CYCLE, TRANSCRIPTION	C	1.6	4.8	3	15	FTQILSTVEPKALEM	4990
3GJX	ED	PROTEIN TRANSPORT	D	2.4	4.8	2	14	WKFLKTVVNKLFEF	4991
3GLI	AE	TRANSFERASE/DNA	A	1.6	4.8	3	19	QTQLRQAVQLLTRTELTLK	4992
3GTM	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	F	1.6	4.8	3	10	KYERARILGT	4993
3H4P	Jj	HYDROLASE	j	1.6	4.8	3	6	LYKMRT	4994
3HD7	GH	EXOCYTOSIS	H	1.6	4.8	3	54	DENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT	4995
3HRD	AB	OXIDOREDUCTASE	A	1.6	4.8	3	12	GPAVITRATVHC	4996
3HRD	AB	OXIDOREDUCTASE	B	1.6	4.8	3	21	GEPALIPMIPAVVAAIEDALG	4997
3UBP	BC	HYDROLASE	C	1.6	4.8	3	8	RQQYAESY	4998
1AGR	AE	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	A	1.6	4.7	3	10	RSERKKWIHC	4999
1AOI	CD	DNA BINDING PROTEIN/DNA	D	2.4	4.7	2	19	ELAKHAVSEGTKAVTKYTS	5000
1B4U	AB	DIOXYGENASE	B	1.6	4.7	3	8	HIQYLRES	5001
1BUH	AB	TRANSFERASE	A	1.6	4.7	3	12	EIDQLFRIFRTL	5002
1DGW	AX	PLANT PROTEIN	X	2.4	4.7	2	7	SQLRDLD	5003
1DX5	OK	SERINE PROTEINASE	K	2.4	4.7	2	5	ECENG	5004
1ECI	AB	TOXIN	A	1.6	4.7	3	17	KKIWETVCPTVEPWAKK	5005

1EZQ	AB	HYDROLASE	A	4.7	4.7	1	9	RDWAESTLM	5006
1FQJ	AC	SIGNALING PROTEIN	C	2.4	4.7	2	5	PWEAF	5007
1FYZ	BD	OXIDOREDUCTASE	D	1.6	4.7	3	33	PTWRDEFINRYWGAFLFNEYGLFNAHSQGAREA	5008
1G0U	ST	HYDROLASE	T	2.4	4.7	2	12	FQVEYAVKAVEN	5009
1G20	CD	OXIDOREDUCTASE	D	2.4	4.7	2	16	QGCVAYFRSYFNRHFR	5010
1G73	BD	APOPTOSIS/APOPTOSIS INHIBITOR	B	1.6	4.7	3	48	EEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQT	5011
1GH0	AB	PHOTOSYNTHESIS	A	1.6	4.7	3	12	PLTEAVSVADSQ	5012
1GH0	MN	PHOTOSYNTHESIS	M	1.6	4.7	3	27	STEIQVAFGRFRQAKAGLEAAKALTSK	5013
1HDM	AB	IMMUNE SYSTEM	B	2.4	4.7	2	7	DTLMQRL	5014
1HE1	AC	SIGNALING PROTEIN	A	2.4	4.7	2	5	LQQWG	5015
1I3Q	BJ	TRANSCRIPTION	J	1.6	4.7	3	10	YCCRRMILTH	5016
1IBR	CD	CELL CYCLE, TRANSLATION	D	2.4	4.7	2	18	TRVRVAALQNLVKIMSLY	5017
1J1E	DF	CONTRACTILE PROTEIN	D	1.6	4.7	3	11	DDIEELMKDGD	5018
1J2J	AB	PROTEIN TRANSPORT	A	2.4	4.7	2	7	RPLWRHY	5019
1J8H	BC	IMMUNE SYSTEM	B	2.4	4.7	2	9	RPDAEYWNS	5020
1JEY	AB	DNA BINDING PROTEIN/DNA	A	1.6	4.7	3	15	PVLQQHFRNLEALAL	5021
1JL4	AB	IMMUNE SYSTEM	A	1.6	4.7	3	22	PQGGLQNIATGKHNLEILTKRS	5022
1JMO	HA	BLOOD CLOTTING	A	1.6	4.7	3	7	LEKIFSE	5023
1JMU	FI	VIRAL PROTEIN	I	2.4	4.7	2	12	GHQIVDLINNAF	5024
1JNR	CD	OXIDOREDUCTASE	C	2.4	4.7	2	27	LHELMRAWELVHRVWTAEAHVRHMLFR	5025
1JRO	CD	OXIDOREDUCTASE	C	2.4	4.7	2	8	LLELLRAE	5026
1JRO	GH	OXIDOREDUCTASE	G	2.4	4.7	2	9	PVQQAMIDH	5027
1JSU	BC	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.6	4.7	3	15	KKQVLRMEHLVLKVL	5028
1K74	AD	TRANSCRIPTION	A	2.4	4.7	2	23	PAEVEALREKVYASLEAYCKHKY	5029
1KEN	EF	VIRAL PROTEIN/IMMUNE SYSTEM	F	2.4	4.7	2	21	IQDLEKYVEDTKIDLWSYNAE	5030
1KQF	AB	OXIDOREDUCTASE	B	2.4	4.7	2	6	VDRVSV	5031
1KX4	CD	STRUCTURAL PROTEIN/DNA	D	2.4	4.7	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	5032
1KYO	NR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	4.7	4.7	1	5	FDDLI	5033
1L1O	EF	DNA BINDING PROTEIN	F	1.6	4.7	3	17	YREYGRRLVMSIRRSAL	5034
1L8C	AB	GENE REGULATION	A	1.6	4.7	3	16	AHCASSRQIISHWKNC	5035
1LTX	AR	TRANSFERASE/PROTEIN BINDING	A	2.4	4.7	2	18	ENVLLKELELVQNAFFTD	5036
1LWU	BC	BLOOD CLOTTING	B	1.6	4.7	3	15	VKIRIESTVAGSLRS	5037
1M1Y	IJ	OXIDOREDUCTASE	I	1.6	4.7	3	15	DKKLAKLIDEVETLF	5038
1MDY	AB	TRANSCRIPTION/DNA	A	2.4	4.7	2	18	KVEILRNAIRYIEGLQAL	5039
1MJG	BN	OXIDOREDUCTASE	N	1.6	4.7	3	9	EAVEQLLEE	5040
1MJG	CO	OXIDOREDUCTASE	O	1.6	4.7	3	30	VALFREVYHGAITATSYAEILLNQAIRTYG	5041
1MXE	AE	METAL BINDING PROTEIN	A	1.6	4.7	3	12	DEEVDEMIREAD	5042

1N5W	DE	OXIDOREDUCTASE	D	4.7	4.7	1	17	YCTPGMIMRSHRLLQEN	5043
1NDO	EF	NON-HEME IRON DIOXYGENASE	E	2.4	4.7	2	19	FWESDDNDNMETASQNGKK	5044
1NEK	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	2.4	4.7	2	9	YEVWIGFFA	5045
1NGM	MN	TRANSCRIPTION/DNA	N	2.4	4.7	2	15	EEASKLKERIWIGLN	5046
1NI4	CD	OXIDOREDUCTASE	C	2.4	4.7	2	17	AQVPLGAGIALACKYNG	5047
1NRL	AC	TRANSCRIPTION	A	2.4	4.7	2	11	IEDQISLLKGA	5048
1NVM	EF	LYASE/OXIDOREDUCTASE	E	2.4	4.7	2	14	EDMIVDVALDLLAA	5049
1NX0	AC	HYDROLASE	A	4.7	4.7	1	21	FEEFKYLWNNIKKWQAIYKQF	5050
1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.6	4.7	3	8	SSLDIVLH	5051
1ONK	AB	HYDROLASE/SUGER BINDING PROTEIN	A	4.7	4.7	1	14	NPILWRYRQYINSG	5052
1ORQ	BC	MEMBRANE PROTEIN	C	4.7	4.7	1	10	FRLVRLLRFL	5053
1OXK	AB	SIGNALING PROTEIN	A	4.7	4.7	1	10	WTILNEIISM	5054
1PGR	AB	CYTOKINE	A	1.6	4.7	3	29	QSFLLKCLEQVRKIQGDGAALQEKLCATY	5055
1PUM	AB	SUGAR BINDING PROTEIN	A	4.7	4.7	1	13	NPILWRARQYINS	5056
1Q16	AB	OXIDOREDUCTASE	B	1.6	4.7	3	6	YPRIEA	5057
1Q16	AB	OXIDOREDUCTASE	B	2.4	4.7	2	25	TKPVLRALKRMLAMRHYKRAETVDG	5058
1Q16	BC	OXIDOREDUCTASE	C	4.7	4.7	1	5	VEYLT	5059
1Q5R	AH	HYDROLASE	A	2.4	4.7	2	22	YNEFENLRRAGIVHADMRGYSY	5060
1Q90	BR	PHOTOSYNTHESIS	R	2.4	4.7	2	31	MNKRNIMNLILAGGAGLPITTLALGYGAFFV	5061
1R27	CD	OXIDOREDUCTASE	C	2.4	4.7	2	10	AHFFTEVRYK	5062
1RD8	AD	VIRAL PROTEIN	D	1.6	4.7	3	29	RRIENLNKKVDDGFLDIWTYNAELLVLLE	5063
1RP3	AB	TRANSCRIPTION	B	1.6	4.7	3	16	KIEDKVTLSKIAQELS	5064
1RU7	IH	VIRAL PROTEIN	H	2.4	4.7	2	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	5065
1RZR	AD	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	D	1.6	4.7	3	15	IFYAELARGIEDIAT	5066
1SCT	EF	OXYGEN TRANSPORT	F	2.4	4.7	2	20	SKLRGHSITLMYALQNFVDA	5067
1SQB	CD	OXIDOREDUCTASE	C	2.4	4.7	2	12	AFSSVTHICRDV	5068
1T3Q	DE	OXIDOREDUCTASE	D	2.4	4.7	2	8	RDEVREVM	5069
1TB6	LH	HYDROLASE/BLOOD CLOTTING	L	1.6	4.7	3	8	ERELLESY	5070
1TBG	BF	COMPLEX (GTP-BINDING/TRANSDUCER)	F	2.4	4.7	2	5	PLVKG	5071
1TN6	AB	TRANSFERASE	A	4.7	4.7	1	14	YHAWQHRQWVIQEF	5072
1TU3	EJ	PROTEIN TRANSPORT	J	1.6	4.7	3	31	LQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	5073
1ULI	CD	OXIDOREDUCTASE	C	2.4	4.7	2	15	EEMKEEYRQQTLRTF	5074
1V02	FE	HYDROLASE	E	1.6	4.7	3	8	FSMRVSAR	5075
1V54	NP	OXIDOREDUCTASE	P	2.4	4.7	2	29	TLLMIGLTTNMLTMYQWWRDVIRESTFQG	5076
1V54	NY	OXIDOREDUCTASE	N	2.4	4.7	2	30	HKDIGTLYLLFGAWAGMVGTALSLLIRAEL	5077

1V54	OV	OXIDOREDUCTASE	O	1.2	4.7	4	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	5078
1VSA	DJ	RIBOSOME	D	4.7	4.7	1	10	VVRWQLAKRR	5079
1VYW	CD	TRANSFERASE	D	2.4	4.7	2	13	HEDIHTYLREMEV	5080
1WCM	AB	TRANSCRIPTION	A	4.7	4.7	1	6	VEILFE	5081
1WDW	KL	LYASE	K	1.6	4.7	3	8	YNPIYRAG	5082
1WPX	AB	HYDROLASE	A	2.4	4.7	2	22	VWSCVPATIYCNNAQLAPYQRT	5083
1WRD	AB	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	1.6	4.7	3	28	PADLELLQELNRTCRAMQQRVLELIPQI	5084
1XCG	EF	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	F	1.6	4.7	3	9	DRLRPLSYP	5085
1Y14	AB	TRANSFERASE	A	2.4	4.7	2	21	LSEARLVIKEALVERRRAFKR	5086
1YA7	CT	HYDROLASE/HYDROLASE ACTIVATOR	C	1.6	4.7	3	11	FQVEYAREAVK	5087
1YA7	GN	HYDROLASE/HYDROLASE ACTIVATOR	N	2.4	4.7	2	23	VGDAQVLVRYMKAELELYRLQRR	5088
1YE9	DH	OXIDOREDUCTASE	D	4.7	4.7	1	9	DTFWDYVSL	5089
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	A	1.6	4.7	3	21	DRKVAMGFLAATILIVVMAMS	5090
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	1.6	4.7	3	14	LVPGAIILDTVLML	5091
1YFN	DH	PROTEIN BINDING	H	2.4	4.7	2	6	PHQWQK	5092
1YOV	AB	SIGNALING PROTEIN	B	1.6	4.7	3	21	ASTNAVIAAVCATEVFKIATS	5093
1YQ3	CD	OXIDOREDUCTASE	C	1.6	4.7	3	30	LPMAMSITHRGTGVALSLGVSLFSLAALLL	5094
1Z6O	AO	METAL BINDING PROTEIN	A	1.6	4.7	3	16	LSLALYVFDEYLQKTV	5095
1Z7Q	KZ	HYDROLASE/HYDROLASE ACTIVATOR	K	2.4	4.7	2	14	YSGFYTFSLLDHHY	5096
2A40	AC	STRUCTURAL PROTEIN	C	1.6	4.7	3	12	ARSDLLSAIRQG	5097
2A7U	AB	HYDROLASE	B	1.6	4.7	3	13	ENGQNLIRVMAEN	5098
2B5L	AC	PROTEIN BINDING/VIRALPROTEIN	C	2.4	4.7	2	11	TVEYFTSQQVT	5099
2BA0	AD	RNA BINDING PROTEIN	D	1.6	4.7	3	11	IEVGEEMDEIT	5100
2BMO	AB	OXIDOREDUCTASE	A	2.4	4.7	2	15	EDLKRRVADAVQRSI	5101
2BR2	QR	HYDROLASE	Q	2.4	4.7	2	26	LQDIDQAENTARSTAVKLLEELKKHL	5102
2C9W	BC	TRANSCRIPTION REGULATION	C	2.4	4.7	2	17	SHVLSKVCMYFTYKVRY	5103
2CG9	AX	CHAPERONE	A	2.4	4.7	2	23	KIMKVIRKNIVKKLIEAFNEIAE	5104
2DD4	EF	HYDROLASE	E	2.4	4.7	2	17	LTELHNKIVEMRERVAS	5105
2DF4	AB	LIGASE	A	2.4	4.7	2	13	LEELYKMSRSEGF	5106
2DSR	BI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	2.4	4.7	2	12	AELVDALQFVCG	5107
2DT7	AB	RNA BINDING PROTEIN	B	2.4	4.7	2	18	AFDLDVVKLTAQFVARNG	5108
2DXB	AE	HYDROLASE	E	2.4	4.7	2	15	IREEVHRHLGTVALM	5109
2DXB	AK	HYDROLASE	K	2.4	4.7	2	18	LTELHNKIVEMRERVASG	5110
2DXB	JH	HYDROLASE	H	2.4	4.7	2	17	SSIREEVHRHLGTVALM	5111

2DXB	WX	HYDROLASE	X	1.6	4.7	3	10	PNYRRRLVRW	5112
2E 32	CD	LIGASE	C	1.6	4.7	3	11	EPLLLRVLAEL	5113
2E9X	EH	REPLICATION	E	1.2	4.7	4	38	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	5114
2EHO	EF	REPLICATION	E	2.4	4.7	2	14	RIRYVLSSYLRCRL	5115
2EHO	FD	REPLICATION	F	2.4	4.7	2	6	NALRFH	5116
2EHO	IK	REPLICATION	K	1.6	4.7	3	10	LWLAINLKQR	5117
2FBW	PQ	OXIDOREDUCTASE	P	1.6	4.7	3	30	LPMAMSITHRGTGVALSLGVSLFSVAALLL	5118
2FHJ	CD	TRANSFERASE	D	2.4	4.7	2	10	VGYKLSFFGD	5119
2FK0	KL	VIRAL PROTEIN	L	1.6	4.7	3	23	KESTQKAIDGVTNKVNSIIDKMN	5120
2HDN	KL	TRANSLATION	L	1.6	4.7	3	18	AEWEAKILELAGFLDSYI	5121
2HOD	EF	BLOOD CLOTTING	F	1.6	4.7	3	30	SSIRYLQEIYNSNNQKIVNLKEKVAQLEAQ	5122
2HY5	AC	TRANSFERASE	A	2.4	4.7	2	16	QASDSAYQFAKAALEK	5123
2J0Q	AT	HYDROLASE	A	2.4	4.7	2	14	KRKVDWLTEKMREA	5124
2JGD	AB	OXIDOREDUCTASE	A	2.4	4.7	2	7	GDFANGA	5125
2JIZ	JK	HYDROLASE	J	1.6	4.7	3	12	VFYLHSRLLERA	5126
2JKR	BM	ENDOCYTOSIS	M	2.4	4.7	2	19	AAMVFEFLYKMCDVMAAYF	5127
2NV2	ST	LYASE/TRANSFERASE	S	1.6	4.7	3	10	ERVKRGMAEM	5128
2O8F	AB	DNA BINDING PROTEIN/DNA	B	1.6	4.7	3	16	EEVIQKGHRKAREFEK	5129
2ODE	CD	SIGNALING PROTEIN	D	1.6	4.7	3	21	DQAQGKVHSLMEKDSYPRFLR	5130
2OV2	EM	PROTEIN BINDING/TRANSFERASE	E	2.4	4.7	2	9	DRLRPLSYP	5131
2P5T	AB	TRANSCRIPTION REGULATOR	B	2.4	4.7	2	17	DSEFKHALARNLRSLTR	5132
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	V	2.4	4.7	2	6	GKISEI	5133
2Q0O	AC	TRANSCRIPTION	A	1.6	4.7	3	12	PREMLCLVWASK	5134
2Q9Q	BC	REPLICATION	C	1.6	4.7	3	27	EDGLRQVLEEMKALYEQNQSDVNEAKS	5135
2Q9Q	FG	REPLICATION	G	1.6	4.7	3	26	EDGLRQVLEEMKALYEQNQSDVNEAK	5136
2QRV	AB	TRANSFERASE/TRANSFERASE REGULATOR	A	4.7	4.7	1	11	VSDKRDISRFL	5137
2R1H	AB	OXYGEN BINDING	A	2.4	4.7	2	16	SDEIGEQALSRMLVVY	5138
2RHK	AC	VIRAL PROTEIN/NUCLEAR PROTEIN	A	4.7	4.7	1	18	IEDVKNAIGVLIGGLEWN	5139
2SIV	ED	ENVELOPE GLYCOPROTEIN	E	1.2	4.7	4	35	GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT	5140
2UUN	GH	ELECTRON TRANSPORT	G	1.6	4.7	3	12	PLTDAVSTADSQ	5141
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	B	1.2	4.7	4	34	AATTVLRQLDMELVSVKRQIQNIKQTNSALKEKL	5142
2V1S	CJ	OXIDOREDUCTASE	J	2.4	4.7	2	10	RLSRLLSYAG	5143
2V4J	DE	OXIDOREDUCTASE	D	2.4	4.7	2	16	TPQLEEIFFELTHNLN	5144
2V51	BF	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	F	1.6	4.7	3	9	NVLQLKLQQ	5145
2VDW	EF	TRANSFERASE	F	1.6	4.7	3	14	YFLQISRVNDLNRM	5146
2W72	AB	OXYGEN TRANSPORT	A	2.4	4.7	2	16	AGEYGAEAYERMFLSF	5147
2W73	BL	METAL BINDING PROTEIN	L	1.6	4.7	3	16	IRNKIRAIGKMARVFS	5148

2W73	FM	METAL BINDING PROTEIN	F	1.6	4.7	3	15	EEQIAEFKEAFSLFD	5149
2WAQ	AB	TRANSCRIPTION	A	4.7	4.7	1	6	FAYVMA	5150
2WAQ	AB	TRANSCRIPTION	B	4.7	4.7	1	11	EMERDCLIGFG	5151
2WB1	WY	TRANSCRIPTION	W	1.2	4.7	4	16	RTSQSGYMQRRLINAL	5152
2WHP	AB	HYDROLASE	B	2.4	4.7	2	17	AQTCAFWNRFLPKLLSA	5153
2ZCY	FG	HYDROLASE	G	1.6	4.7	3	22	IPDARNAALRAKAEAAEFRYKY	5154
2ZCY	OU	HYDROLASE	O	2.4	4.7	2	13	GQIDYALTAVKQG	5155
3A0B	AC	ELECTRON TRANSPORT	C	1.2	4.7	4	31	PRSWLATSHFVLAFFFLVGHLWHAGRARAAA	5156
3BLW	CD	OXIDOREDUCTASE	D	1.6	4.7	3	11	IDNSVLKVVTN	5157
3BRT	AD	TRANSFERASE/TRANSCRIPTION	D	1.6	4.7	3	60	LQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQE ARKLVERLGLE	5158
3CJH	AB	PROTEIN TRANSPORT	B	2.4	4.7	2	20	KQKVQMSIHQFTNICFKKCV	5159
3CJT	IJ	TRANSFERASE/RIBOSOMAL PROTEIN	I	1.6	4.7	3	8	LPGLFDGG	5160
3CM8	AB	RNA BINDING PROTEIN/TRANSFERASE	A	2.4	4.7	2	11	SWIQSEFNKAC	5161
3CM8	AB	RNA BINDING PROTEIN/TRANSFERASE	A	2.4	4.7	2	18	PWVLLNASWFNSFLTHAL	5162
3CW2	BL	TRANSLATION	L	2.4	4.7	2	8	EYVEMLDR	5163
3CWB	AC	OXIDOREDUCTASE	A	2.4	4.7	2	7	YNRIRSG	5164
3CXH	AB	OXIDOREDUCTASE	A	1.6	4.7	3	20	DTEVERAKSLLKLQLGQLYE	5165
3DBH	GH	CELL CYCLE	G	4.7	4.7	1	31	YIKLQNVYREKAKKDAAAVGNHVAKLLQSIG	5166
3E0J	AB	TRANSFERASE	B	2.4	4.7	2	20	VNQAKQMLYDYVERKRKENS	5167
3EAB	AG	CELL CYCLE	G	1.6	4.7	3	22	SVGTSVASAEQDELSQRLARLR	5168
3EJB	CD	OXIDOREDUCTASE/LIPID TRANSPORT	C	1.2	4.7	4	14	LDTVELVMALEEEF	5169
3EN1	AB	OXIDOREDUCTASE	A	2.4	4.7	2	16	FEQDDGENWVEIQHIL	5170
3ESW	AB	HYDROLASE	A	2.4	4.7	2	7	FDSIAKM	5171
3EXG	WX	OXIDOREDUCTASE	W	2.4	4.7	2	17	AQVPLGAGIALACKYNG	5172
3FGC	AB	OXIDOREDUCTASE	A	2.4	4.7	2	15	PVRQAEDVNLLDQMS	5173
3FH9	AB	OXYGEN TRANSPORT	B	2.4	4.7	2	14	EVGGEALGRLLVVY	5174
3FUB	AB	HORMONE	A	4.7	4.7	1	15	DTCKKYRSAYITPCT	5175
3G5O	AB	TOXIN/ANTITOXIN	A	1.2	4.7	4	14	IRESIAEADADIAS	5176
3H0L	AC	LIGASE	A	2.4	4.7	2	15	PEVKRRIMLGTFALS	5177
3HAX	CD	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	C	2.4	4.7	2	13	GEYRRRWKREVLG	5178
1AQD	GH	COMPLEX (MHC PROTEIN/ANTIGEN)	G	2.3	4.6	2	5	EEFGR	5179
1AVO	MN	PROTEASOME ACTIVATOR	N	1.5	4.6	3	32	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI	5180
1B33	HI	PHOTOSYNTHESIS	H	2.3	4.6	2	12	IVTKSIVNADAE	5181
1B33	LM	PHOTOSYNTHESIS	M	2.3	4.6	2	13	TAALEKLKSYFST	5182
1BGY	DH	ELECTRON TRANSPORT	H	2.3	4.6	2	14	RERLELCDERVSSR	5183
1BSX	AX	HORMONE/GROWTH FACTOR	X	1.5	4.6	3	6	ILHRLL	5184
1BSX	BY	HORMONE/GROWTH FACTOR	Y	1.5	4.6	3	6	ILHRLL	5185
1BXR	EF	AMIDOTRANSFERASE	E	1.5	4.6	3	19	DKEYQIMRNASMAVLREIG	5186

1DCE	CD	TRANSFERASE	C	2.3	4.6	2	23	AAYLDDLRSKFLLENSVLKMEYA	5187
1E 08	AD	HYDROGENASE	D	2.3	4.6	2	17	IKDYMLDRINGVYGADA	5188
1E1C	AB	ISOMERASE	A	1.5	4.6	3	23	FFMEVAKLRAARMLWAKLVHQFG	5189
1EAH	13	VIRUS	3	2.3	4.6	2	6	MMELAE	5190
1EJH	CG	TRANSLATION	G	1.5	4.6	3	8	REFLLDFQ	5191
1FYZ	AC	OXIDOREDUCTASE	A	1.5	4.6	3	10	PLWKGMKRVF	5192
1FYZ	AC	OXIDOREDUCTASE	A	2.3	4.6	2	21	AKEYARMEAVKDERQFGSLQD	5193
1G0U	BC	HYDROLASE	B	1.5	4.6	3	18	VEILVRRLSDIKQGYTQH	5194
1G0U	BC	HYDROLASE	C	2.3	4.6	2	13	FQVEYALEAVKRG	5195
1G2C	WX	VIRAL PROTEIN	X	1.2	4.6	4	31	SDEFDASISQVNEKINQSLAFIRKSDELLHN	5196
1G5J	AB	APOPTOSIS	B	2.3	4.6	2	15	QRYGRELRRMSDEFV	5197
1GK0	CD	HYDROLASE	C	4.6	4.6	1	11	VPERAQQWYAQ	5198
1GXS	CB	LYASE	C	4.6	4.6	1	14	DHEDMIGMFESWWH	5199
1I3Q	AB	TRANSCRIPTION	B	1.5	4.6	3	9	ASFLKERLM	5200
1IR2	U2	LYASE	U	2.3	4.6	2	20	WRDRFLFVAEAIYKAQAETG	5201
1IRU	IJ	HYDROLASE	I	4.6	4.6	1	23	AADTDMTTQLISSNLELHSLSTG	5202
1J1D	AB	CONTRACTILE PROTEIN	A	1.5	4.6	3	12	EEELSDLFRMFD	5203
1JMO	LH	BLOOD CLOTTING	L	1.5	4.6	3	8	ERELLESY	5204
1JN5	AB	TRANSPORT PROTEIN	A	1.5	4.6	3	25	FKTYVDQACRAAEEFVNVYYTTMDK	5205
1KEN	CD	VIRAL PROTEIN/IMMUNE SYSTEM	D	2.3	4.6	2	21	IQDLEKYVEDTKIDLWSYNAE	5206
1KI6	AB	PHOSPHOTRANSFERASE	B	1.5	4.6	3	17	SIPTICDLARTFAREMG	5207
1L4A	BC	ENDOCYTOSIS/EXOCYTOSIS	C	1.2	4.6	4	45	ELEEIQQQCNQVTDDSLESTRRMLNMCEESKEAGIRTLVMLDEQG	5208
1L4A	CD	ENDOCYTOSIS/EXOCYTOSIS	D	1.5	4.6	3	29	IGNLRNMAIDMGNEIGSQNRQVDRIQQKA	5209
1L8C	AB	GENE REGULATION	B	2.3	4.6	2	11	EELLRALDQVN	5210
1MIO	CB	MOLYBDENUM-IRON PROTEIN	B	4.6	4.6	1	15	VSATDEFIMALSEAT	5211
1NZY	CB	LYASE	C	2.3	4.6	2	13	PHFMPCLTRFLDG	5212
1O18	DF	CONTRACTILE PROTEIN	D	1.2	4.6	4	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	5213
1OCC	CG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	1.5	4.6	3	29	RKHMLQALFITITLGVYFTLLQASEYYEA	5214
1OCC	DI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	I	2.3	4.6	2	40	LLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFY	5215
1OCC	LM	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	L	1.5	4.6	3	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	5216
1OCC	QV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	V	2.3	4.6	2	40	LLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFY	5217
1OED	BC	ION CHANNEL/RECEPTOR	C	2.3	4.6	2	29	MSTAISVLLAQAVFLLLTSQRLPETALAV	5218
1OR0	CD	HYDROLASE	C	4.6	4.6	1	11	VPERAQQWYAQ	5219
1OSV	BD	DNA BINDING PROTEIN	D	2.3	4.6	2	8	ALLRYLLD	5220
1Q5R	CJ	HYDROLASE	C	2.3	4.6	2	22	YNEFENLRRAGIVHADMRGYSY	5221

1Q5R	FM	HYDROLASE	F	2.3	4.6	2	22	YNEFENLRRAGIVHADMRGYSY	5222
1Q90	BD	PHOTOSYNTHESIS	D	2.3	4.6	2	5	TVPFI	5223
1QLE	AB	OXIDOREDUCTASE/IMMUNE SYSTEM	B	1.5	4.6	3	23	TLVPVLILVAIGAFSLPILFRSQ	5224
1QVI	AY	CONTRACTILE PROTEIN	Y	2.3	4.6	2	11	FTMFLSIFSDK	5225
1R1R	AD	OXIDOREDUCTASE	A	1.5	4.6	3	14	MQQLLKDLLTAYKF	5226
1R4M	AB	CELL CYCLE	B	4.6	4.6	1	13	KAEVAAEFLNDRV	5227
1RFN	AB	COAGULATION FACTOR	A	4.6	4.6	1	10	KEYTNIFLKF	5228
1RK8	AB	TRANSLATION	B	1.5	4.6	3	15	QSVMEELKRIIIDSE	5229
1RP3	AB	TRANSCRIPTION	A	1.5	4.6	3	15	PYSNQIEREELILKY	5230
1RYP	T1	MULTICATALYTIC PROTEINASE	T	2.3	4.6	2	22	APDARVLSNYLRQQCNYSSLVF	5231
1SCT	AB	OXYGEN TRANSPORT	B	2.3	4.6	2	20	SKLRGHSITLMYALQNFVDA	5232
1SQB	AB	OXIDOREDUCTASE	A	1.5	4.6	3	10	NALEKEVESM	5233
1SXJ	CD	REPLICATION	C	2.3	4.6	2	16	DQIQGSAVIGAIKASF	5234
1TBG	DH	COMPLEX (GTP-BINDING/TRANSDUCER)	H	2.3	4.6	2	5	PLVKG	5235
1U3H	HI	IMMUNE SYSTEM	H	1.5	4.6	3	33	RPDAEYYNKQYLERTRAELDTVCRYNYEETEVP	5236
1UZD	OM	LYASE	O	1.5	4.6	3	14	AKNYGRAVYECLRG	5237
1UZH	BC	LYASE	C	2.3	4.6	2	14	DEQIAAQVDYIVAN	5238
1V54	AL	OXIDOREDUCTASE	A	2.3	4.6	2	30	HKDIGTLYLLFGAWAGMVGTALSLLIRAEL	5239
1VYW	AB	TRANSFERASE	B	2.3	4.6	2	18	KLQLVGTAAMLLASKFEE	5240
1VYW	CD	TRANSFERASE	D	2.3	4.6	2	17	LQLVGTAAMLLASKFEE	5241
1VZJ	HJ	HYDROLASE	H	4.6	4.6	1	9	HWKNQFDHY	5242
1WDW	GH	LYASE	G	1.5	4.6	3	8	YNPIYRAG	5243
1XDK	AB	HORMONE/GROWTH FACTOR RECEPTOR	A	2.3	4.6	2	21	RLPALRSIGLKCLEHLFFFKL	5244
1XFV	BP	LYASE/METAL BINDING PROTEIN	B	1.5	4.6	3	15	SLEKQKGVTNLLIKY	5245
1XLS	AI	TRANSCRIPTION	I	1.5	4.6	3	7	ALLRYLL	5246
1XMN	AB	BLOOD CLOTTING	A	1.5	4.6	3	8	ERELLESY	5247
1Y3A	BF	SIGNALING PROTEIN	B	2.3	4.6	2	8	RKKWIHCF	5248
1YE9	AH	OXIDOREDUCTASE	H	2.3	4.6	2	13	FHRRELWEAIEAG	5249
1Z0K	AB	PROTEIN TRANSPORT	B	1.5	4.6	3	19	PLLQQIHNITSFIRQAKAA	5250
1Z6O	CU	METAL BINDING PROTEIN	C	2.3	4.6	2	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	5251
1Z6O	GW	METAL BINDING PROTEIN	G	1.5	4.6	3	16	LSLALYVFDEYLQKTV	5252
1ZV8	ED	VIRAL PROTEIN	E	1.5	4.6	3	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	5253
2A0L	BF	MEMBRANE PROTEIN	B	1.5	4.6	3	23	FRLVRLLRFLRILLIISRGSKFL	5254
2AXT	ac	ELECTRON TRANSPORT	a	1.5	4.6	3	26	SRSLHFFLAAWPVVGVWFTALGISTM	5255
2AXT	AI	ELECTRON TRANSPORT	A	4.6	4.6	1	7	WELSYRL	5256
2B5I	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.5	4.6	3	17	PRDLISNINVIVLELKG	5257
2B5T	AB	BLOOD CLOTTING	A	1.5	4.6	3	8	ERELLESY	5258

2BEC	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	B	1.5	4.6	3	22	INEEIHTQFLDHLLTGIEDICG	5259
2BH1	AX	TRANSPORT PROTEIN	X	1.5	4.6	3	12	MEALVETKRVVK	5260
2BR2	ST	HYDROLASE	S	2.3	4.6	2	26	LQDIDQAENTARSTAVKLLEELKKHL	5261
2BSK	CF	PROTEIN TRANSPORT	F	4.6	4.6	1	8	SACHRKCV	5262
2BV8	AB	PHOTOSYNTHESIS	A	1.5	4.6	3	27	NGELQSINGRYQRATASLEAARSLTSN	5263
2DD4	BC	HYDROLASE	B	2.3	4.6	2	18	LTELHNKIVEMRERVASG	5264
2DFK	CD	CELL CYCLE	D	1.5	4.6	3	5	DRLRP	5265
2DPP	AB	LYASE	B	1.5	4.6	3	5	PVDYL	5266
2DXB	HI	HYDROLASE	I	1.5	4.6	3	10	PNYRRRLVRW	5267
2DXB	TU	HYDROLASE	U	1.5	4.6	3	10	PNYRRRLVRW	5268
2E1M	AC	OXIDOREDUCTASE	A	1.5	4.6	3	13	LKLRYLDVLIDNG	5269
2E9X	EG	REPLICATION	G	2.3	4.6	2	7	LDDILMS	5270
2EHO	EF	REPLICATION	E	1.5	4.6	3	13	NTESYLKNVALKH	5271
2FBW	CD	OXIDOREDUCTASE	C	1.5	4.6	3	30	LPMAMSITHRGTGVALSLGVSLFSVAALLL	5272
2FHH	FG	HYDROLASE	G	1.5	4.6	3	23	AAVAVEFARLYAVELEHYEKLEG	5273
2FJ7	AB	STRUCTURAL PROTEIN/DNA	B	1.5	4.6	3	16	GLIYEETRGVLKVFLE	5274
2FUG	LM	OXIDOREDUCTASE	M	2.3	4.6	2	11	AVIYHFKHYTE	5275
2FYN	JK	OXIDOREDUCTASE	K	2.3	4.6	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	5276
2GAG	AB	OXIDOREDUCTASE	B	1.5	4.6	3	15	FHVIQEQMAAAVELF	5277
2GUZ	KD	CHAPERONE, PROTEIN TRANSPORT	D	2.3	4.6	2	23	FYLQSKVYRAAERLKWELAQREK	5278
2HLD	NP	HYDROLASE	P	2.3	4.6	2	46	SARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGASS	5279
2HLD	TX	HYDROLASE	T	1.5	4.6	3	12	VFYLHSRLLERA	5280
2HWN	CF	TRANSFERASE	F	2.3	4.6	2	18	LAWKIAKMIVSDVMQQCK	5281
2HYB	GH	TRANSFERASE	G	1.5	4.6	3	11	LGQLVEAAIQA	5282
2I2R	JM	TRANSPORT PROTEIN	M	1.5	4.6	3	15	KRELQVLYRGFKNEC	5283
2I2X	KJ	TRANSFERASE	J	4.6	4.6	1	6	YNVALE	5284
2I2X	MP	TRANSFERASE	P	4.6	4.6	1	5	YNVAL	5285
2IBZ	DI	OXIDOREDUCTASE	I	2.3	4.6	2	7	WKDVKAR	5286
2INN	AC	OXIDOREDUCTASE	A	1.5	4.6	3	18	SGISPLEHAAFQGYSKVG	5287
2IPK	AB	IMMUNE SYSTEM	A	2.3	4.6	2	22	AQGALANIAVDKANLEIMTKRS	5288
2J0S	AT	HYDROLASE	A	1.5	4.6	3	14	KRKVDWLTEKMREA	5289
2JEL	HP	COMPLEX (ANTIBODY/ANTIGEN)	P	2.3	4.6	2	13	EQKAVEHLVKLMA	5290
2JIZ	HL	HYDROLASE	H	1.5	4.6	3	12	VFYLHSRLLERA	5291
2JJ0	MH	PHOTOSYNTHESIS	M	1.5	4.6	3	26	MEGIHRWAIWMAVLVTLTGGIGILLS	5292
2NZ0	AD	MEMBRANE PROTEIN	D	4.6	4.6	1	5	EKEFF	5293
2O02	AP	PROTEIN BINDING/TOXIN	A	2.3	4.6	2	19	YKDSTLIMQLLRDNLTLWT	5294
2O97	AB	DNA BINDING PROTEIN	A	2.3	4.6	2	22	KTQAKAALESTLAAITESLKEG	5295
2P2C	GH	HYDROLASE	G	2.3	4.6	2	5	PEFYQ	5296

2PQN	AB	APOPTOSIS	A	2.3	4.6	2	14	IQSRFNYAWGLIKS	5297
2QKM	GH	HYDROLASE	H	1.5	4.6	3	12	SQVLDDLSARFI	5298
2QQD	BC	LYASE	B	2.3	4.6	2	20	KKEAEKTVREMAKIGFEMRG	5299
2QQP	CD	VIRUS	C	1.5	4.6	3	14	DEVVQLANRLQMEL	5300
2QQP	CD	VIRUS	D	2.3	4.6	2	12	PSVIKGIAQQAV	5301
2QQP	EF	VIRUS	F	1.5	4.6	3	16	TVSALASIGLGLLGKS	5302
2QRV	DC	TRANSFERASE/TRANSFERASE REGULATOR	C	2.3	4.6	2	15	PSWYLFQFHRLLQYA	5303
2R1T	AB	PROTEIN BINDING	B	1.5	4.6	3	11	TVIPVDVMRRA	5304
2UUN	AB	ELECTRON TRANSPORT	A	1.5	4.6	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	5305
2UUN	CD	ELECTRON TRANSPORT	C	1.5	4.6	3	27	STEIQVAFGRFRQAAAGLSAATALTSA	5306
2UUN	IJ	ELECTRON TRANSPORT	I	1.5	4.6	3	12	PLTDAVSTADSQ	5307
2UZ1	AB	LYASE	A	2.3	4.6	2	12	GATLHFQQLAVG	5308
2V4I	GH	TRANSFERASE	H	2.3	4.6	2	22	AGEFEEALHTAALALVKDIASD	5309
2V7Q	EG	HYDROLASE	G	1.5	4.6	3	75	ADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDK LTLTFNRTRQAVITKELIEIISGAAAL	5310
2VBN	AB	HYDROLASE	A	1.5	4.6	3	14	KEFLLYLAGFVDGD	5311
2VML	EF	PHOTOSYNTHESIS	E	1.5	4.6	3	27	NTELQAANGRFQRATASMEAARALTSN	5312
2VML	IJ	PHOTOSYNTHESIS	I	1.5	4.6	3	27	NTELQAANGRFQRATASMEAARALTSN	5313
2W9E	AL	IMMUNE SYSTEM	A	4.6	4.6	1	10	DYEDRYYREN	5314
2ZNL	AB	TRANSCRIPTION	A	2.3	4.6	2	19	PWVLLNASWFNSFLTHALS	5315
2ZT9	BH	PHOTOSYNTHESIS	H	1.5	4.6	3	25	AILTLGWVSLLVVFTWSIAMVVWGR	5316
3BUA	BF	DNA BINDING PROTEIN	B	4.6	4.6	1	17	YGDFRQIRDIMQALLVR	5317
3BUA	DH	DNA BINDING PROTEIN	D	1.5	4.6	3	17	YGDFRQIRDIMQALLVR	5318
3C1B	BD	STRUCTURAL PROTEIN/DNA	B	2.3	4.6	2	11	AMDVVYALKRQ	5319
3CHX	AB	MEMBRANE PROTEIN	A	2.3	4.6	2	6	IDRIYA	5320
3CJH	GH	PROTEIN TRANSPORT	H	2.3	4.6	2	20	KQKVQMSIHQFTNICFKKCV	5321
3CW2	FH	TRANSLATION	H	1.5	4.6	3	11	GVEKIKEVISK	5322
3CWB	CG	OXIDOREDUCTASE	G	1.5	4.6	3	23	KVAPPFLGAYLLYSWGTQEFERL	5323
3DCO	AB	MOTOR PROTEIN	A	2.3	4.6	2	6	VHWYVG	5324
3DRA	AB	TRANSFERASE	A	4.6	4.6	1	14	ERALHITELGINEL	5325
3EDL	AB	STRUCTURAL PROTEIN	A	2.3	4.6	2	6	VHWYVG	5326
3EIQ	AC	HYDROLASE/ANTITUMOR PROTEIN	A	4.6	4.6	1	11	KRTLRDIETFY	5327
3EUK	CE	CELL CYCLE	E	1.5	4.6	3	14	HFDVARIIVDQAVK	5328
3FWB	BC	CELL CYCLE, TRANSCRIPTION	C	1.5	4.6	3	15	WVDKVKDLTKSEMNI	5329
3FWC	EF	CELL CYCLE, TRANSCRIPTION	E	2.3	4.6	2	13	PLDEIKRAFQLFD	5330
3FWC	FH	CELL CYCLE, TRANSCRIPTION	H	1.5	4.6	3	16	TAQLKSQIQQYLVESG	5331
3GLI	FG	TRANSFERASE/DNA	F	1.5	4.6	3	15	LLALAQALERLSLLW	5332
3H0L	PR	LIGASE	R	2.3	4.6	2	5	QLKEL	5333
3H42	AB	HYDROLASE/IMMUNE SYSTEM	B	2.3	4.6	2	17	VSGTLIGLEFIRKSQLV	5334

3HRW	CD	OXYGEN TRANSPORT	C	2.3	4.6	2	19	PAVHASLDKFLASVSTVLT	5335
5CSC	AB	OXO-ACID-LYASE	A	2.3	4.6	2	7	TDGLIAL	5336
1A9W	CF	OXYGEN TRANSPORT	F	2.3	4.5	2	16	VEEAGGEALGRLLVVY	5337
1AOI	FH	DNA BINDING PROTEIN/DNA	F	2.3	4.5	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	5338
1AOI	GH	DNA BINDING PROTEIN/DNA	H	1.5	4.5	3	12	AIYVYKVLKQVH	5339
1APY	AB	HYDROLASE	A	4.5	4.5	1	13	KNATEAAWRALAS	5340
1AQD	GH	COMPLEX (MHC PROTEIN/ANTIGEN)	G	2.3	4.5	2	22	AQGALANIAVDKANLEIMTKRS	5341
1B33	CD	PHOTOSYNTHESIS	D	1.5	4.5	3	13	AITAVINSSDVQG	5342
1BCP	EF	TOXIN	F	1.5	4.5	3	16	TWFDTMLGFAISAYAL	5343
1BGY	EJ	ELECTRON TRANSPORT	E	1.5	4.5	3	35	EARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSA	5344
1CDL	AE	CALCIUM-BINDING PROTEIN	A	1.5	4.5	3	15	EEQIAEFKEAFSLFD	5345
1CDL	DH	CALCIUM-BINDING PROTEIN	D	1.5	4.5	3	15	EEQIAEFKEAFSLFD	5346
1CPC	KL	LIGHT HARVESTING PROTEIN	L	1.5	4.5	3	12	AFAKVVSQADAR	5347
1CUL	AB	LYASE/LYASE/SIGNALING PROTEIN	A	2.3	4.5	2	22	AQELVMTLNELFARFDKLAAEN	5348
1DCE	AB	TRANSFERASE	A	2.3	4.5	2	23	AAYLDDLRSKFLLENSVLKMEYA	5349
1DGH	AB	OXIDOREDUCTASE	A	2.3	4.5	2	12	VVFTDEMAHFDR	5350
1DIO	LM	LYASE	L	2.3	4.5	2	7	EPVFTDG	5351
1DIO	LM	LYASE	M	4.5	4.5	1	6	LENVLS	5352
1DOA	AB	CELL CYCLE	B	2.3	4.5	2	12	ESLRKYKEALLG	5353
1E7P	AB	OXIDOREDUCTASE	A	1.5	4.5	3	17	TGHTMLFAVANECLKLG	5354
1EJH	CG	TRANSLATION	C	2.3	4.5	2	11	VEDFWALYNHI	5355
1EYX	AB	PHOTOSYNTHESIS	A	1.5	4.5	3	27	SSDLESVQGNIQRASARLEAAEKLASN	5356
1F47	BA	CELL CYCLE	A	2.3	4.5	2	9	IPAFLRKQA	5357
1F66	GH	STRUCTURAL PROTEIN/DNA	H	1.5	4.5	3	12	AIYVYKVLKQVH	5358
1FNT	GN	HYDROLASE/HYDROLASE ACTIVATOR	N	2.3	4.5	2	20	ISDMQHIERLLKDLVTENAY	5359
1FYZ	AC	OXIDOREDUCTASE	C	2.3	4.5	2	13	KSARLAVEGLWQE	5360
1G20	AF	OXIDOREDUCTASE	A	2.3	4.5	2	7	EKDIVFG	5361
1G2C	IL	VIRAL PROTEIN	I	2.3	4.5	2	45	EVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	5362
1G2C	UX	VIRAL PROTEIN	U	2.3	4.5	2	48	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVN	5363
1G3I	FG	CHAPERONE/HYDROLASE	G	2.3	4.5	2	18	TADAFTLFELFERKLEMH	5364
1GCV	CD	OXYGEN STORAGE/TRANSPORT	D	2.3	4.5	2	16	MKTVVTQALDRMFKVY	5365
1GH0	QR	PHOTOSYNTHESIS	Q	1.5	4.5	3	12	PLTEAVSVADSQ	5366
1GO4	GB	CELL CYCLE	G	2.3	4.5	2	35	AEQSFLFSREEADTLRLKVEELEGERSRLEEEKRM	5367
1GXS	CD	LYASE	C	1.5	4.5	3	14	DHEDMIGMFESWWH	5368
1H2M	AS	TRANSCRIPTION ACTIVATOR/INHIBITOR	S	2.3	4.5	2	7	EELLRAL	5369
1I51	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.5	4.5	3	16	TDKDAEALFKCFRSLG	5370
1I7M	DC	LYASE	D	2.3	4.5	2	11	RSEWDILLKDV	5371
1IB1	DH	SIGNALING PROTEIN/TRANSFERASE	D	1.5	4.5	3	14	TLIMQLLRDNLTLW	5372

1IBL	JN	RIBOSOME	N	4.5	4.5	1	11	RICLRELAHKG	5373
1IRU	I1	HYDROLASE	1	1.5	4.5	3	19	LDRAMRLVKDVFISAAERD	5374
1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	4.5	4.5	1	9	YEEFVQMMT	5375
1JRO	CD	OXIDOREDUCTASE	D	2.3	4.5	2	13	PEAVLAAVRRAEG	5376
1K3Z	AD	TRANSCRIPTION	A	1.5	4.5	3	12	DRHRIEEKRKRT	5377
1K74	DE	TRANSCRIPTION	E	1.5	4.5	3	10	KILHRLLQEG	5378
1KFY	CD	OXIDOREDUCTASE	C	2.3	4.5	2	26	VIVIINLITLAAALLHTKTWFELAPK	5379
1KI1	CD	SIGNALING PROTEIN	C	2.3	4.5	2	7	LRPLSYP	5380
1KKL	AI	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN	A	1.5	4.5	3	17	ATKTFEKNLNHLIEHNE	5381
1KX4	EF	STRUCTURAL PROTEIN/DNA	E	1.5	4.5	3	14	KLPFQRLVREIAQD	5382
1LB1	CD	SIGNALING PROTEIN	C	2.3	4.5	2	25	AEDLQEALSSILGILKAVNDSMHLI	5383
1LNU	CD	SUGAR BINDING PROTEIN	C	4.5	4.5	1	7	PEFGQLA	5384
1LQB	BC	GENE REGULATION	B	2.3	4.5	2	11	ALELLMAANFL	5385
1M1Y	KL	OXIDOREDUCTASE	L	2.3	4.5	2	16	QGCVAYFRSYFNRHFR	5386
1MHY	BG	OXIDOREDUCTASE	G	4.5	4.5	1	15	KYEAEAIHIEFRQLY	5387
1MJG	AM	OXIDOREDUCTASE	M	2.3	4.5	2	9	EAVEQLLEE	5388
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	B	2.3	4.5	2	10	ARLAVEGLWQ	5389
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	2.3	4.5	2	10	PLWKGMKRVF	5390
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	1.5	4.5	3	16	AKEYARMEAVKDERQF	5391
1MTY	DB	MONOOXYGENASE	D	1.5	4.5	3	7	AQEVHRW	5392
1N4Q	IJ	TRANSFERASE	I	4.5	4.5	1	14	YHAWQHRQWVIQEF	5393
1N5W	AB	OXIDOREDUCTASE	B	4.5	4.5	1	6	RMENLS	5394
1NDO	AB	NON-HEME IRON DIOXYGENASE	A	1.5	4.5	3	19	FWESDDNDNMETASQNGKK	5395
1NDO	CD	NON-HEME IRON DIOXYGENASE	C	2.3	4.5	2	15	EDLKRRLADSVQRTF	5396
1OR0	CD	HYDROLASE	C	1.5	4.5	3	13	GDNILRLYGEARG	5397
1PD7	AB	TRANSCRIPTION	A	1.5	4.5	3	17	VEFNNAISYVNKIKTRF	5398
1QLE	AB	OXIDOREDUCTASE/IMMUNE SYSTEM	B	2.3	4.5	2	33	PLAHDQQWLDHFVLYIITAVTIFVCLLLLICIV	5399
1R1R	CF	OXIDOREDUCTASE	C	1.5	4.5	3	14	MQQLLKDLLTAYKF	5400
1R27	AB	OXIDOREDUCTASE	B	1.5	4.5	3	6	YPRIEA	5401
1R4P	AE	TOXIN	E	4.5	4.5	1	13	WNLQPLLQSAQLT	5402
1RH5	AB	PROTEIN TRANSPORT	A	1.5	4.5	3	19	TGVLLTVSIVYRMYEQLLR	5403
1S5R	AB	TRANSCRIPTION	B	1.5	4.5	3	17	VEFNHAINYVNKIKNRF	5404
1SDD	AB	BLOOD CLOTTING	B	2.3	4.5	2	5	EIQRA	5405
1T9G	DS	OXIDOREDUCTASE, ELECTRON TRANSPORT	D	1.5	4.5	3	21	EQQKEFQATARKFAREEIIPV	5406

1TME	13	VIRUS	3	4.5	4.5	1	6	LLELCK	5407
1TZN	Ii	TOXIN RECEPTOR/TOXIN	i	1.5	4.5	3	14	LVPSYAEKEAKISR	5408
1UF2	AD	VIRUS	D	1.5	4.5	3	14	GDFNALSNMFTQLS	5409
1UZH	RW	LYASE	R	2.3	4.5	2	6	WTDGLT	5410
1V54	AC	OXIDOREDUCTASE	A	2.3	4.5	2	9	PRMNNMSFW	5411
1V54	NO	OXIDOREDUCTASE	N	2.3	4.5	2	25	PAMMWALGFIFLFTVGGLTGIVLAN	5412
1VF5	AB	PHOTOSYNTHESIS	B	4.5	4.5	1	9	ATTIFLFGT	5413
1VF6	BD	PROTEIN BINDING/PROTEIN TRANSPORT	D	1.5	4.5	3	14	RDFQNAFKIHNAVT	5414
1VZJ	DI	HYDROLASE	D	4.5	4.5	1	10	HWKNQFDHYS	5415
1WCM	CJ	TRANSCRIPTION	J	1.5	4.5	3	7	LIEKFLR	5416
1WYU	AB	OXIDOREDUCTASE	B	1.5	4.5	3	15	FLALVRAWAYIRTLG	5417
1WYU	CD	OXIDOREDUCTASE	C	1.5	4.5	3	15	QLTALMGAMYLAALG	5418
1WYU	EF	OXIDOREDUCTASE	E	2.3	4.5	2	7	PVVQALA	5419
1XLS	EM	TRANSCRIPTION	E	1.5	4.5	3	7	PLLGEIC	5420
1YHU	KD	OXYGEN STORAGE/TRANSPORT	K	2.3	4.5	2	16	PDAWASCLAGIAAAIS	5421
1Z00	AB	HYDROLASE	B	2.3	4.5	2	9	PGPQDFLLK	5422
1ZLA	FH	PROTEIN BINDING/VIRUS/DNA	F	2.3	4.5	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	5423
2ACL	CD	TRANSCRIPTION	C	1.5	4.5	3	9	TFLMEMLEA	5424
2ACL	EF	TRANSCRIPTION	F	1.5	4.5	3	28	MFPRMLMKLVSLRTLSSVHSEQVFALRL	5425
2AFH	AD	OXIDOREDUCTASE	D	1.5	4.5	3	17	ASLTKERGRLVDMMTDS	5426
2B9S	AB	ISOMERASE/DNA	A	2.3	4.5	2	20	SVKGQSDMVKFEKARKLKDK	5427
2BG9	AB	ION CHANNEL/RECEPTOR	B	4.5	4.5	1	25	YLMFIMILVAFSVILSVVVLNLHHR	5428
2BR2	MN	HYDROLASE	N	1.5	4.5	3	29	PDEFRQAFDLAVKGINIIYNLEREALKSK	5429
2BSK	AD	PROTEIN TRANSPORT	D	4.5	4.5	1	6	KKLTEL	5430
2DD4	HI	HYDROLASE	H	2.3	4.5	2	18	LTELHNKIVEMRERVASG	5431
2DXB	JB	HYDROLASE	B	2.3	4.5	2	17	LTELHNKIVEMRERVAS	5432
2DXB	QR	HYDROLASE	R	2.3	4.5	2	13	AEDHRVWKDYVHT	5433
2DXB	WX	HYDROLASE	W	2.3	4.5	2	17	LTELHNKIVEMRERVAS	5434
2ERJ	BD	IMMUNE SYSTEM/CYTOKINE	D	1.5	4.5	3	26	SSSTKKTQLQLEHLLLDLQMILNGIN	5435
2GID	HK	TRANSLATION	K	1.5	4.5	3	17	HFAVTLEHFLESALDES	5436
2GJE	AD	TRANSLATION/RNA	D	4.5	4.5	1	12	HVDLAYLVGVCK	5437
2GUZ	KJ	CHAPERONE, PROTEIN TRANSPORT	J	1.5	4.5	3	15	MDKINNRFNYLFEVN	5438
2H0D	AB	METAL BINDING PROTEIN/LIGASE	A	1.5	4.5	3	7	ITELNPH	5439
2HDN	GH	TRANSLATION	H	1.5	4.5	3	18	AEWEAKILELAGFLDSYI	5440
2HHF	AB	TRANSFERASE	B	2.3	4.5	2	5	SSLHY	5441
2HPP	LH	HYDROLASE (SERINE PROTEINASE)	L	1.5	4.5	3	10	ERELLESYID	5442
2HUE	BC	DNA BINDING PROTEIN	C	2.3	4.5	2	11	KPAIRRLARRG	5443
2I2R	CF	TRANSPORT PROTEIN	F	2.3	4.5	2	15	KRELQVLYRGFKNEC	5444
2INP	AC	OXIDOREDUCTASE	C	1.5	4.5	3	25	YGAYVGNRAKMQESAETSFGFCEKR	5445

2ISS	BE	LYASE, TRANSFERASE	B	2.3	4.5	2	12	WIIKKGFAEMFK	5446
2J7A	QR	OXIDOREDUCTASE	Q	2.3	4.5	2	5	RNEMR	5447
2JIZ	CF	HYDROLASE	C	1.5	4.5	3	7	TELFYKG	5448
2NNA	AB	IMMUNE SYSTEM	A	1.5	4.5	3	22	PQFALTNIAVLKHNLNIVIKRS	5449
2NU9	AG	LIGASE	G	2.3	4.5	2	11	PYQGRELAFKL	5450
2O9I	BD	TRANSCRIPTION	D	1.5	4.5	3	9	KILHRLLQE	5451
2ODE	AB	SIGNALING PROTEIN	B	1.5	4.5	3	21	DQAQGKVHSLMEKDSYPRFLR	5452
2OM0	ef	HORMONE	f	1.5	4.5	3	18	NQHLCGSHLVEALYLVCG	5453
2OV2	AI	PROTEIN BINDING/TRANSFERASE	A	2.3	4.5	2	9	DRLRPLSYP	5454
2OZN	AB	TOXIN	B	2.3	4.5	2	10	IGDLAMVSKN	5455
2P58	AC	TRANSPORT PROTEIN/CHAPERONE	C	2.3	4.5	2	14	HEEANCIAEWLHLK	5456
2PL9	BE	SIGNALING PROTIEN	E	1.5	4.5	3	11	QDQVDDLLDSL	5457
2Q9Q	AG	REPLICATION	A	2.3	4.5	2	29	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	5458
2QRV	DC	TRANSFERASE/TRANSFERASE REGULATOR	D	2.3	4.5	2	16	TGRLFFEFYRLLHDAR	5459
2R17	AC	PROTEIN TRANSPORT	C	2.3	4.5	2	22	RIRFTLPPLVFAAYQLAFRYKE	5460
2R17	BD	PROTEIN TRANSPORT	D	2.3	4.5	2	20	PSLQVQLFIEILNRYIYFYE	5461
2RAO	AB	OXYGEN BINDING	A	4.5	4.5	1	19	PAVHASLDKFLANVSTVLT	5462
2RAO	CD	OXYGEN BINDING	D	2.3	4.5	2	16	VEEVGGEALGRLLVVY	5463
2RGN	DE	SIGNALING PROTEIN COMPLEX	D	1.5	4.5	3	10	RSERRKWIHC	5464
2RI4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	4.5	4.5	1	12	GAEALGRLLVVY	5465
2SIV	EF	ENVELOPE GLYCOPROTEIN	E	1.5	4.5	3	35	GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT	5466
2UW1	AB	OXIDOREDUCTASE	A	2.3	4.5	2	14	FEEQVRELRERAKE	5467
2UZ6	DN	RECEPTOR	N	2.3	4.5	2	7	PPCILNN	5468
2V4J	AB	OXIDOREDUCTASE	A	2.3	4.5	2	16	CPEDLLGVLELSYDEG	5469
2V7Q	BE	HYDROLASE	B	2.3	4.5	2	14	RSTVAQLVKRLTDA	5470
2WBJ	EF	IMMUNE SYSTEM	F	2.3	4.5	2	9	RPDAEYWNS	5471
2WHP	AB	HYDROLASE	A	2.3	4.5	2	16	AQTCAFWNRFLPKLLS	5472
2WME	DC	OXIDOREDUCTASE	D	2.3	4.5	2	11	LDRAADIAVMA	5473
2Z2L	AB	BIOSYNTHETIC PROTEIN	A	2.3	4.5	2	5	SSFIG	5474
2Z2L	DE	BIOSYNTHETIC PROTEIN	D	2.3	4.5	2	5	SSFIG	5475
2Z2T	AF	VIRAL PROTEIN/INHIBITOR	F	1.5	4.5	3	31	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK	5476
2ZME	AB	PROTEIN TRANSPORT	B	1.5	4.5	3	22	NISEAFEDLSKLMIKAKEMVEL	5477
2ZT9	AB	PHOTOSYNTHESIS	B	1.1	4.5	4	22	KLLGVLAMASVPLGLILVPFIE	5478
3A0B	AD	ELECTRON TRANSPORT	A	4.5	4.5	1	24	LHFFLAAWRVVGVWFAALGISTMA	5479
3BBN	CN	RIBOSOME	C	2.3	4.5	2	14	YAEGLQEDQKIRDC	5480
3BG4	BC	HYDROLASE/HYDROLASE INHIBITOR	C	1.5	4.5	3	11	LVNWVQQTLAA	5481
3C6L	BD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	D	2.3	4.5	2	13	PEILERTRAELDT	5482

3C72	AB	TRANSFERASE	A	2.3	4.5	2	15	YSSWHYRSCLLPQLH	5483
3CJB	AG	STRUCTURAL PROTEIN	G	1.5	4.5	3	18	QDESGAAAIFTVQLDDYL	5484
3CJT	EF	TRANSFERASE/RIBOSOMAL PROTEIN	E	2.3	4.5	2	9	WLEAWRRDL	5485
3CUE	BD	PROTEIN TRANSPORT	D	1.5	4.5	3	19	TELFTLTYGSIVAQLCQDY	5486
3CUE	HJ	PROTEIN TRANSPORT	J	1.5	4.5	3	19	TELFTLTYGSIVAQLCQDY	5487
3CUE	TV	PROTEIN TRANSPORT	V	1.5	4.5	3	19	TELFTLTYGSIVAQLCQDY	5488
3CUP	AB	IMMUNE SYSTEM	A	1.5	4.5	3	22	PQGGLQNIAAEKHNLGILTKRS	5489
3CW2	BD	TRANSLATION	D	1.5	4.5	3	10	VEKIKEVISK	5490
3D9A	CH	HYDROLASE/IMMUNE SYSTEM	C	4.5	4.5	1	12	TASVNCAKKIVS	5491
3EI4	EF	DNA BINDING PROTEIN	F	1.5	4.5	3	18	WPSVQQGLQQSFLHTLDS	5492
3ENO	BF	HYDROLASE/UNKNOWN FUNCTION	B	4.5	4.5	1	24	PLDAAVHHSEVIDTVISRALEKAK	5493
3EXG	CB	OXIDOREDUCTASE	B	1.5	4.5	3	6	KILEDN	5494
3EZQ	EF	APOPTOSIS	E	1.5	4.5	3	15	SDVDLSKYITTIAGV	5495
3F9K	AC	VIRAL PROTEIN, RECOMBINATION	A	1.5	4.5	3	12	IEPAQEEHEKYH	5496
3FBI	AB	TRANSCRIPTION	B	2.3	4.5	2	12	RFEVELEFIQSL	5497
3FH6	HI	TRANSPORT PROTEIN	I	1.5	4.5	3	19	QKARLFITHLLLLLFIAAI	5498
3G33	AD	CELL CYCLE	A	1.5	4.5	3	17	ISTVREVALLRRLEAFE	5499
3GFK	AB	TRANSCRIPTION/TRANSFERASE	A	2.3	4.5	2	11	LQDLYRLINEH	5500
3GHG	DE	BLOOD CLOTTING	E	1.5	4.5	3	24	RVLRSILENLRSKIQKLESDVSAQ	5501
3GLH	DE	TRANSFERASE	D	1.5	4.5	3	15	RRMGVEMTLLRALAF	5502
3GTU	AB	TRANSFERASE	B	1.5	4.5	3	27	EEEKIRVDIIENQVMDFRTQLIRLCYS	5503
3H0L	MO	LIGASE	M	1.5	4.5	3	24	YYDAYYLKAQKVRRLITNDFLKAF	5504
3HKZ	QR	TRANSFERASE	R	2.3	4.5	2	9	LQRTYDYLN	5505
3HOU	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	F	2.3	4.5	2	17	KYERARILGTRALQISM	5506
3PRO	AC	PRO REGION	C	1.5	4.5	3	10	QLKFAMQRDL	5507
7INS	CD	HORMONE	D	1.5	4.5	3	19	VNQHLCGSHLVEALYLVCG	5508
1A0O	CD	CHEMOTAXIS	D	2.2	4.4	2	12	EDDITAVLCFVI	5509
1AOI	CD	DNA BINDING PROTEIN/DNA	D	1.5	4.4	3	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	5510
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	A	1.5	4.4	3	8	APLDRVYH	5511
1AY7	AB	COMPLEX (ENZYME/INHIBITOR)	B	2.2	4.4	2	9	LDALWDCLT	5512
1AYY	CD	HYDROLASE	C	1.5	4.4	3	15	ALDAVEKGVRLVEDD	5513
1B33	AB	PHOTOSYNTHESIS	B	1.5	4.4	3	13	TAALEKLKSYFST	5514
1B4U	CB	DIOXYGENASE	B	1.5	4.4	3	14	PDLAWHIAQSLILD	5515
1B8D	AB	PHOTOSYNTHESIS	A	1.5	4.4	3	12	VITTTISAADAA	5516
1BPL	AB	GLYCOSYLTRANSFERASE	B	4.4	4.4	1	5	YGDMY	5517
1CB7	AB	ISOMERASE	A	1.5	4.4	3	6	GEIDCK	5518
1CDL	AE	CALCIUM-BINDING PROTEIN	A	1.5	4.4	3	16	DTDSEEEIREAFRVFD	5519
1DGH	AB	OXIDOREDUCTASE	B	2.2	4.4	2	12	VVFTDEMAHFDR	5520

1E7P	EF	OXIDOREDUCTASE	F	4.4	4.4	1	16	GDTTLWWIQAMTGFAM	5521
1F99	AB	PHOTOSYNTHESIS	A	1.5	4.4	3	27	NTELQVVNGRYNRATSSLEAAKALTAN	5522
1F9E	CD	APOPTOSIS	D	1.5	4.4	3	16	WYIQSLCQSLRERCPR	5523
1FHJ	AB	OXYGEN STORAGE/TRANSPORT	B	2.2	4.4	2	16	VDEVGGEALGRLLIVY	5524
1FSX	AB	OXYGEN STORAGE/TRANSPORT	B	2.2	4.4	2	16	VDEVGGEALGRLLVVY	5525
1FSX	CD	OXYGEN STORAGE/TRANSPORT	C	2.2	4.4	2	16	AAEYGAEALERMFLSF	5526
1G20	BE	OXIDOREDUCTASE	B	2.2	4.4	2	7	EDAAVFG	5527
1G2C	CD	VIRAL PROTEIN	D	2.2	4.4	2	30	DEFDASISQVNEKINQSLAFIRKSDELLHN	5528
1GCV	AB	OXYGEN STORAGE/TRANSPORT	B	2.2	4.4	2	16	MKTVVTQALDRMFKVY	5529
1GHQ	AB	IMMUNE SYSTEM/VIRAL PROTEIN RECEPTOR	A	1.5	4.4	3	15	SQVLCGAVKWLILEK	5530
1GK0	AB	HYDROLASE	A	1.5	4.4	3	10	EQTTVWLLTN	5531
1GK0	AB	HYDROLASE	A	4.4	4.4	1	11	VPERAQQWYAQ	5532
1H59	AB	INSULIN	B	2.2	4.4	2	7	PLHALLH	5533
1HBR	CD	OXYGEN STORAGE/TRANSPORT	D	2.2	4.4	2	16	VAECGAEALARLLIVY	5534
1I3Q	CJ	TRANSCRIPTION	J	2.2	4.4	2	7	LIEKFLR	5535
1I51	BE	HYDROLASE/HYDROLASE INHIBITOR	E	4.4	4.4	1	8	HADYLLRT	5536
1ID3	CD	STRUCTURAL PROTEIN/DNA	C	1.5	4.4	3	29	SGAPVYLTAVLEYLAAEILELAGNAARDN	5537
1IR2	AN	LYASE	A	2.2	4.4	2	6	WTDGLT	5538
1IR2	BI	LYASE	B	1.5	4.4	3	14	AKNYGRAVYECLRG	5539
1IR2	EN	LYASE	E	2.2	4.4	2	20	WRDRFLFVAEAIYKAQAETG	5540
1IWP	AG	LYASE	G	1.5	4.4	3	17	TVNAAFVRESAEVYQQR	5541
1JD2	RS	HYDROLASE	S	4.4	4.4	1	15	INSAARNIQHLLYGK	5542
1JD2	YR	HYDROLASE	R	1.5	4.4	3	22	AADCQFWETWLGSQCRLHELRE	5543
1JY2	NO	BLOOD CLOTTING	O	1.5	4.4	3	28	GCKLQDTLVRQERPIRKSIEDLRNTVDS	5544
1JY2	QR	BLOOD CLOTTING	R	1.5	4.4	3	27	GCKLQDTLVRQERPIRKSIEDLRNTVD	5545
1KFY	CD	OXIDOREDUCTASE	D	1.5	4.4	3	25	VFWGLFGAGGMWSAIIAPVMILLVG	5546
1KPE	AB	PROTEIN KINASE INHIBITOR	B	1.5	4.4	3	18	ESLLGHLMIVGKKCAADL	5547
1KYO	CG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	4.4	4.4	1	5	FDDLI	5548
1L4A	AD	ENDOCYTOSIS/EXOCYTOSIS	A	1.5	4.4	3	30	RLQQTQAQVEEVVDIMRVNVDKVLERDSKI	5549
1LQ8	CD	BLOOD CLOTTING	C	2.2	4.4	2	9	EKTLRKWLK	5550
1M1J	EF	BLOOD CLOTTING	E	2.2	4.4	2	34	NIPSSLRVLRAVIDSLHKKIQKLENAIATQTDYC	5551
1M2Z	AB	HORMONE/HORMONE ACTIVATOR	B	1.5	4.4	3	7	ALLRYLL	5552
1MDU	DE	STRUCTURAL PROTEIN	D	1.5	4.4	3	18	QDESGAAAIFTVQLDDYL	5553
1MIO	AD	MOLYBDENUM-IRON PROTEIN	D	1.5	4.4	3	17	ASIEEERGQLIDLMIDA	5554
1MJG	CO	OXIDOREDUCTASE	O	1.5	4.4	3	9	EAVEQLLEE	5555
1MMO	EH	OXIDOREDUCTASE (MONOOXYGENASE)	H	2.2	4.4	2	20	VNYFLDGERQLGTRLMELRN	5556
1N4Q	AB	TRANSFERASE	A	4.4	4.4	1	14	YHAWQHRQWVIQEF	5557

1NGM	AB	TRANSCRIPTION/DNA	A	2.2	4.4	2	6	RIIQKI	5558
1NIK	AB	TRANSCRIPTION	B	1.5	4.4	3	10	EMERDCMIAH	5559
1NU7	AB	HYDROLASE/PROTEIN BINDING	A	1.5	4.4	3	8	ERELLESY	5560
1O18	GI	CONTRACTILE PROTEIN	G	4.4	4.4	1	10	SAIPEGQFMD	5561
1O96	CD	ELECTRON TRANSFER	C	1.5	4.4	3	14	SEQAAKIIQIINEF	5562
1OCC	DK	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	1.5	4.4	3	14	EEWVAKQTKRMLDM	5563
1OR7	AC	TRANSCRIPTION	A	2.2	4.4	2	20	VGTVRSRIFRAREAIDNKVQ	5564
1PIV	13	VIRUS	1	2.2	4.4	2	5	IESFF	5565
1PMA	O2	PROTEASE	2	1.5	4.4	3	22	VGDAQVLVRYMKAELELYRLQR	5566
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	2.2	4.4	2	5	ERKYR	5567
1Q90	AR	PHOTOSYNTHESIS	R	1.5	4.4	3	31	MNKRNIMNLILAGGAGLPITTLALGYGAFFV	5568
1QPW	CD	OXYGEN TRANSPORT	C	4.4	4.4	1	16	AGAHGAEALERMFLGF	5569
1RCO	HC	LYASE	H	2.2	4.4	2	14	AKNYGRAVYECLRG	5570
1RCO	OI	LYASE	O	2.2	4.4	2	20	WRDRFLFCAEALYKAQAETG	5571
1RDT	AD	HORMONE/GROWTH FACTOR	D	1.5	4.4	3	29	LFAKLLQKMTDLRQIVTEHVQLLQVIKKT	5572
1RHI	13	VIRUS	1	2.2	4.4	2	5	VESFL	5573
1RM6	AB	OXIDOREDUCTASE	B	2.2	4.4	2	22	VKYRRRVLLAISRKVVDQLWEA	5574
1RP3	AB	TRANSCRIPTION	B	2.2	4.4	2	14	LEKKVKELKEKIEK	5575
1RYP	YL	MULTICATALYTIC PROTEINASE	L	2.2	4.4	2	11	QTFAYGVLDSN	5576
1S5L	dx	PHOTOSYNTHESIS	d	2.2	4.4	2	9	FDILDDWLK	5577
1SFC	EH	TRANSPORT PROTEIN	H	1.5	4.4	3	47	IGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKML	5578
1SQB	AB	OXIDOREDUCTASE	B	2.2	4.4	2	11	SFKITRGIEAV	5579
1SQB	EJ	OXIDOREDUCTASE	J	2.2	4.4	2	12	LTARLYSLLFRR	5580
1SQB	JK	OXIDOREDUCTASE	J	1.5	4.4	3	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	5581
1T0F	BD	DNA BINDING PROTEIN	D	2.2	4.4	2	7	LRYIYSQ	5582
1U9I	BC	CIRCADIAN CLOCK PROTEIN	B	1.5	4.4	3	11	PQDIIKNARSF	5583
1UKL	AD	PROTEIN TRANSPORT/DNA BINDING PROTEIN	A	2.2	4.4	2	30	DEVALQGIEFWSNVCDEEMDLAIEASEAAE	5584
1V54	RV	OXIDOREDUCTASE	R	2.2	4.4	2	9	IYPYVIQEL	5585
1W63	JR	ENDOCYTOSIS	J	2.2	4.4	2	10	WAQIFILDCL	5586
1XLS	DH	TRANSCRIPTION	H	1.5	4.4	3	25	LYAKLMGLLADLRSINNAYSYELQR	5587
1XV9	CD	DNA BINDING PROTEIN	D	1.5	4.4	3	23	LYAKLLGLLAELRSINEAYGYQI	5588
1Y14	AB	TRANSFERASE	A	2.2	4.4	2	13	KDLKNTMQYLTNF	5589
1Y8R	DE	LIGASE	E	2.2	4.4	2	14	GIGCELLKNLVLTG	5590
1YDI	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.5	4.4	3	25	TAPVAAVQAAVSNLVRVGKETVQTT	5591
1YFN	CG	PROTEIN BINDING	G	4.4	4.4	1	6	PHQWQK	5592
1Z7M	BG	TRANSFERASE	G	1.5	4.4	3	6	KSSFKF	5593

1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	E	1.5	4.4	3	11	TVALREIRRYQ	5594
1ZV8	KL	VIRAL PROTEIN	L	1.5	4.4	3	16	QKEIDRLNEVAKNLNE	5595
1ZVV	BP	TRANSCRIPTION/DNA	P	2.2	4.4	2	8	IMGLMSLA	5596
1ZY8	EM	OXIDOREDUCTASE	M	2.2	4.4	2	13	KEDALKLVQLKQT	5597
2ACL	GH	TRANSCRIPTION	G	1.5	4.4	3	23	PAEVEALREKVYASLEAYCKHKY	5598
2AFH	CD	OXIDOREDUCTASE	D	1.5	4.4	3	14	QDYKDMLAKKRDGF	5599
2AK4	AC	IMMUNE SYSTEM	A	2.2	4.4	2	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	5600
2AK4	QS	IMMUNE SYSTEM	Q	2.2	4.4	2	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	5601
2BA1	BG	RNA BINDING PROTEIN	G	1.1	4.4	4	19	PEDILVDIKRDYVLSKLRD	5602
2BE9	AB	TRANSFERASE	A	2.2	4.4	2	9	ASRFASEIS	5603
2BV8	ML	PHOTOSYNTHESIS	L	1.5	4.4	3	25	NRRMAACLRDMEIVLRYVSYAEIAG	5604
2C7J	AB	ELECTRON TRANSPORT	B	2.2	4.4	2	25	HRNQAACIRDLGFILRYVTYSVLAG	5605
2DD4	DF	HYDROLASE	F	4.4	4.4	1	8	PRQVLAEF	5606
2DF4	AC	LIGASE	C	1.5	4.4	3	21	ETEEMANTLESILDFAKQNDS	5607
2DFS	MQ	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	Q	4.4	4.4	1	10	AAELRHVMTN	5608
2DOQ	CD	CELL CYCLE	D	2.2	4.4	2	41	NDEAESFRNTWLLFRSFQQWITLTQTFKEQSRLADQAFLNK	5609
2EHO	AB	REPLICATION	B	2.2	4.4	2	12	WFNNYKRSLATY	5610
2EHO	IJ	REPLICATION	I	1.5	4.4	3	14	RIRYVLSSYLRCRL	5611
2F66	AE	TRANSPORT PROTEIN	A	1.5	4.4	3	29	DGLNQLYNLVAQDYALTDTIEALSRMLHR	5612
2FBW	BC	OXIDOREDUCTASE	C	2.2	4.4	2	14	AKEEMARFWEKNTK	5613
2FHX	AB	HYDROLASE, METAL BINDING PROTEIN	A	2.2	4.4	2	22	DLTKQLRLEENKKDRIKAAEFY	5614
2FJ7	AB	STRUCTURAL PROTEIN/DNA	B	2.2	4.4	2	13	NVIRDAVTYTEHA	5615
2FO1	AD	GENE REGULATION/SIGNALLING PROTEIN/DNA	D	2.2	4.4	2	17	ELHRQRSELARANYEKA	5616
2GTL	JO	OXYGEN STORAGE/TRANSPORT	J	4.4	4.4	1	18	HDREAFSQAIWRATFAQV	5617
2GV5	DF	CELL CYCLE	D	2.2	4.4	2	13	PLDEIKRAFQLFD	5618
2H9E	HL	HYDROLASE, BLOOD CLOTTING	H	4.4	4.4	1	10	RDWAESTLMT	5619
2HLD	JN	HYDROLASE	N	1.5	4.4	3	15	TREGNDLYREMKETG	5620
2HOD	GH	BLOOD CLOTTING	G	2.2	4.4	2	11	KNVRAQLVDMK	5621
2HTM	AE	BIOSYNTHETIC PROTEIN	A	2.2	4.4	2	16	AEEAVRLARLGRLLTG	5622
2HYI	IJ	HYDROLASE/RNA BINDING PROTEIN/RNA	I	2.2	4.4	2	11	FKEQIYDVYRY	5623
2I2R	IP	TRANSPORT PROTEIN	P	2.2	4.4	2	15	KRELQVLYRGFKNEC	5624
2IBZ	CF	OXIDOREDUCTASE	F	1.5	4.4	3	5	FDDLI	5625
2K2I	AB	CELL CYCLE	A	1.5	4.4	3	12	FKNLKRVAKELG	5626
2NPI	BD	TRANSCRIPTION	D	4.4	4.4	1	7	DSQWAAF	5627
2NS8	BH	TRANSCRIPTION	B	1.5	4.4	3	14	PLLRQAIELFDHQG	5628
2NTY	AC	SIGNALING PROTEIN	A	2.2	4.4	2	17	SALALSNAITNLAASIF	5629

2NZD	AB	STRUCTURAL PROTEIN/DNA	A	1.5	4.4	3	13	TVALREIRRYQKS	5630
2OCF	AD	HORMONE/GROWTH FACTOR	D	2.2	4.4	2	7	LRLMLAG	5631
2OM0	AB	HORMONE	B	1.5	4.4	3	18	NQHLCGSHLVEALYLVCG	5632
2OM0	EF	HORMONE	F	1.5	4.4	3	19	VNQHLCGSHLVEALYLVCG	5633
2P6A	AC	SIGNALING PROTEIN	C	1.5	4.4	3	9	TLFKWMIFN	5634
2PO6	AC	LIPID BINDING PROTEIN/IMMUNE SYSTEM	A	4.4	4.4	1	9	VNLAIQVLN	5635
2PV9	AB	HYDROLASE	A	2.2	4.4	2	6	EKELLD	5636
2Q8A	AL	IMMUNE SYSTEM	A	2.2	4.4	2	8	LDEMRHFY	5637
2QMB	CD	TRANSPORT PROTEIN	C	2.2	4.4	2	19	PEVHASLDKFLCAVGTVLT	5638
2QQD	AB	LYASE	A	2.2	4.4	2	13	PLNAFDGALLNAG	5639
2RII	BY	OXIDOREDUCTASE COMPLEX	Y	4.4	4.4	1	14	PAKVQSLVDTIRED	5640
2UZ6	CM	RECEPTOR	M	1.5	4.4	3	7	PPCILNN	5641
2VDN	AB	CELL ADHESION/IMMUNE SYSTEM	B	4.4	4.4	1	5	DGRLA	5642
2W19	AC	TRANSFERASE/ISOMERASE	C	1.5	4.4	3	11	HSREMKVIERY	5643
2Z2L	AB	BIOSYNTHETIC PROTEIN	B	2.2	4.4	2	19	SPLQSFMETQMDAFQEKVK	5644
2Z2L	EF	BIOSYNTHETIC PROTEIN	F	2.2	4.4	2	11	PGDLAEELRRN	5645
2ZCY	PQ	HYDROLASE	Q	2.2	4.4	2	13	FQVEYALEAVKRG	5646
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	A	1.5	4.4	3	15	RQEVKQMVVATLAES	5647
2ZHX	GH	HYDROLASE/HYDROLASE INHIBITOR	G	2.2	4.4	2	6	RDASTL	5648
2ZNV	AB	HYDROLASE/SIGNALING PROTEIN	A	2.2	4.4	2	10	EELFNVQDQH	5649
3BRT	CB	TRANSFERASE/TRANSCRIPTION	C	1.5	4.4	3	27	SEELVAEAHNLCTLLENAIQDTVREQG	5650
3BS5	AB	SIGNALING PROTEIN/MEMBRANE PROTEIN	A	2.2	4.4	2	7	GRALLRI	5651
3BZ1	BH	ELECTRON TRANSPORT	B	4.4	4.4	1	7	QRLYKAL	5652
3C1B	CD	STRUCTURAL PROTEIN/DNA	D	2.2	4.4	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	5653
3C1B	FH	STRUCTURAL PROTEIN/DNA	F	2.2	4.4	2	29	GLIYEETRGVLKVFLENVIRDAVTYTEHA	5654
3C7B	AB	OXIDOREDUCTASE	B	2.2	4.4	2	12	ASGIVKAVMDEL	5655
3C9A	AC	HORMONE/SIGNALING PROTEIN	C	2.2	4.4	2	8	ETFDAWYC	5656
3CFI	AB	PROTEIN TRANSPORT/IMMUNE SYSTEM	A	1.5	4.4	3	20	EQKMFAAMVADNQMAMVMLN	5657
3CHX	IJ	MEMBRANE PROTEIN	I	2.2	4.4	2	6	IDRIYA	5658
3CJT	CD	TRANSFERASE/RIBOSOMAL PROTEIN	C	4.4	4.4	1	5	DEDWL	5659
3CQX	BC	CHAPERONE	C	2.2	4.4	2	10	QKFQSIVIGC	5660
3CWB	EJ	OXIDOREDUCTASE	E	1.5	4.4	3	32	SEDRKGFSYLVTATACVATAYAAKNVVTQFIS	5661
3CWB	PT	OXIDOREDUCTASE	P	1.5	4.4	3	23	PLSQTLFWLLVANLLILTWIGSQ	5662
3D7W	AB	HYDROLASE	A	4.4	4.4	1	13	NPILWRARQYINS	5663
3DMT	BC	OXIDOREDUCTASE	C	4.4	4.4	1	5	WRGGR	5664
3DNL	AC	VIRAL PROTEIN	A	1.5	4.4	3	10	VEQMHEDIIS	5665
3DVE	AB	MEMBRANE PROTEIN	A	1.5	4.4	3	13	FPEFLTMMARKMK	5666

3EAB	DJ	CELL CYCLE	D	1.5	4.4	3	26	EQCERARRLQAKMMTNLVMAKDRLQL	5667
3EUB	KL	OXIDOREDUCTASE	K	2.2	4.4	2	23	IEFRRTLTLSFFFKFYLTVLKKL	5668
3F9K	MO	VIRAL PROTEIN, RECOMBINATION	M	1.5	4.4	3	12	IEPAQEEHEKYH	5669
3FKS	XY	HYDROLASE	X	4.4	4.4	1	7	QDIIAIL	5670
3FOE	AC	ISOMERASE/DNA	C	4.4	4.4	1	7	RPLVEAG	5671
3FWC	JK	CELL CYCLE, TRANSCRIPTION	K	1.5	4.4	3	17	DSTRETVLKQIREFLEE	5672
3FWC	NP	CELL CYCLE, TRANSCRIPTION	P	1.5	4.4	3	16	WVDKVKDLTKSEMNIN	5673
3GCG	AB	SIGNALING PROTEIN/TRANSCRIPTION	B	2.2	4.4	2	24	PITRFNTQTKMIEQVSQEIFERNF	5674
3GHG	HI	BLOOD CLOTTING	I	1.5	4.4	3	44	MIDAATLKSRKMLEEIMKYEASILTHDSSIRYLQEIYNSNNQKI	5675
3GJX	CA	PROTEIN TRANSPORT	C	1.5	4.4	3	6	VFHRKK	5676
3GLH	KO	TRANSFERASE	K	1.5	4.4	3	19	QTQLRQAVQLLTRTELTLK	5677
3H87	BC	TOXIN/ANTITOXIN	B	4.4	4.4	1	9	GEIARREFR	5678
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.5	4.4	3	13	YAAKLLFQELMAM	5679
3HOY	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	F	2.2	4.4	2	17	KYERARILGTRALQISM	5680
3MON	AB	SWEET-TASTING PROTEIN	B	2.2	4.4	2	16	FTQNLGKFAVDEENKI	5681
1A9W	CF	OXYGEN TRANSPORT	C	2.2	4.3	2	19	PAVHASLDKFLASVSTVLT	5682
1AHJ	CD	LYASE	C	2.2	4.3	2	9	PRKVLSEMG	5683
1AIP	FH	COMPLEX OF TWO ELONGATION FACTORS	H	4.3	4.3	1	6	DFVARN	5684
1AKH	AB	DNA BINDING PROTEIN/DNA	A	4.3	4.3	1	14	PQARAFLEEVFRRK	5685
1AOI	BD	DNA BINDING PROTEIN/DNA	D	2.2	4.3	2	12	SREIQTAVRLLL	5686
1AOI	FH	DNA BINDING PROTEIN/DNA	H	2.2	4.3	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	5687
1AYY	AB	HYDROLASE	A	2.2	4.3	2	16	NFGLHANVEAWKVLSK	5688
1BB1	AB	DE NOVO PROTEIN DESIGN	A	1.4	4.3	3	33	EIAAIEYEQAAIKEEIAAIKDKIAAIKEYIAAI	5689
1BCC	DJ	OXIDOREDUCTASE	D	1.4	4.3	3	35	DHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLKSR	5690
1BGY	OR	ELECTRON TRANSPORT	R	2.2	4.3	2	20	ENLYDDRVFRIKRALDLSMR	5691
1BI4	AB	DNA INTEGRATION	A	1.4	4.3	3	15	LKTAVQMAVFIHNHK	5692
1BPL	AB	GLYCOSYLTRANSFERASE	A	1.4	4.3	3	14	KGELQSAIKSLHSR	5693
1BXL	AB	COMPLEX (APOPTOSIS/PEPTIDE)	A	2.2	4.3	2	13	AYQSFEQVVNELF	5694
1CAX	EF	SEED STORAGE PROTEIN	F	2.2	4.3	2	7	SQLRDLD	5695
1CP9	AB	HYDROLASE	A	1.4	4.3	3	10	ISFDKEIRNN	5696
1DCE	AB	TRANSFERASE	A	2.2	4.3	2	12	QSAWFYHRWLLG	5697
1DEV	AB	SIGNALING PROTEIN	B	4.3	4.3	1	5	PAEYC	5698
1DFL	AY	CONTRACTILE PROTEIN	A	1.4	4.3	3	9	IRKWLVLRN	5699
1DFL	AZ	CONTRACTILE PROTEIN	Z	2.2	4.3	2	11	YEDFVKKVMAG	5700
1DGR	CN	PLANT PROTEIN	N	2.2	4.3	2	7	SQLRDLD	5701
1E1C	CD	ISOMERASE	D	2.2	4.3	2	14	EEQWEREVEKVLNR	5702
1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.2	4.3	2	12	VSQGMAVFNQLK	5703

1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.2	4.3	2	12	LFQMEMARRSTQ	5704
1E6V	BC	OXIDOREDUCTASE	C	2.2	4.3	2	12	PYIRARMYMWRY	5705
1E6V	EF	OXIDOREDUCTASE	F	2.2	4.3	2	12	PYIRARMYMWRY	5706
1EFP	CD	ELECTRON TRANSPORT	D	2.2	4.3	2	6	VDELVG	5707
1F66	AB	STRUCTURAL PROTEIN/DNA	A	1.4	4.3	3	11	TVALREIRRYQ	5708
1F66	FH	STRUCTURAL PROTEIN/DNA	H	1.4	4.3	3	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	5709
1F66	GH	STRUCTURAL PROTEIN/DNA	H	2.2	4.3	2	19	ELAKHAVSEGTKAVTKYTS	5710
1F9E	AB	APOPTOSIS	B	1.4	4.3	3	16	WYIQSLCQSLRERCPR	5711
1FN4	AB	IMMUNE SYSTEM	A	2.2	4.3	2	5	TEQLA	5712
1FS0	EG	HYDROLASE	G	2.2	4.3	2	39	ITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAH	5713
1G0U	PQ	HYDROLASE	P	1.4	4.3	3	18	VEILVRRLSDIKQGYTQH	5714
1G20	CD	OXIDOREDUCTASE	C	2.2	4.3	2	7	VGCGQYS	5715
1GGP	AB	SUGAR BINDING PROTEIN	A	2.2	4.3	2	5	RYIQN	5716
1GH0	WX	PHOTOSYNTHESIS	W	1.4	4.3	3	12	PLTEAVSVADSQ	5717
1H1L	CB	OXIDOREDUCTASE	B	2.2	4.3	2	17	DALTLERGRLVDMMLDS	5718
1H1L	CD	OXIDOREDUCTASE	C	4.3	4.3	1	6	LVEMEN	5719
1H6K	AX	NUCLEAR PROTEIN	X	2.2	4.3	2	12	RADAENAMRYIN	5720
1HH4	BE	SIGNALING PROTEIN/INHIBITOR	B	2.2	4.3	2	5	DRLRP	5721
1HH4	BE	SIGNALING PROTEIN/INHIBITOR	E	2.2	4.3	2	12	ESLRKYKEALLG	5722
1HV2	AB	SIGNALING PROTEIN	B	2.2	4.3	2	14	LKERCLQVVRSLVK	5723
1ID3	BD	STRUCTURAL PROTEIN/DNA	B	2.2	4.3	2	29	GLIYEEVRAVLKSFLESVIRDSVTYTEHA	5724
1IR2	W4	LYASE	W	2.2	4.3	2	6	WTDGLT	5725
1IRE	AB	LYASE	A	2.2	4.3	2	9	PRQLLKEEF	5726
1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.4	4.3	3	15	EEQIAEFKEAFSLFD	5727
1JMT	AB	RNA BINDING PROTEIN	B	1.4	4.3	3	8	PMQYKAMQ	5728
1K6L	LM	PHOTOSYNTHESIS	L	2.2	4.3	2	5	ERKYR	5729
1KAT	WX	CELL CYCLE, HORMONE/GROWTH FACTOR	X	2.2	4.3	2	6	WECFER	5730
1KBH	AB	TRANSCRIPTION	A	2.2	4.3	2	8	IPELVNQG	5731
1KF6	MN	OXIDOREDUCTASE	M	1.4	4.3	3	11	PFICELAKAYV	5732
1KVD	AB	TOXIN	B	1.4	4.3	3	17	KNDLQNMSADLAKNGFK	5733
1KYO	NO	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	2.2	4.3	2	29	GYILRYLHANGASFFFMVMFMHMAKGLYY	5734
1LNU	EF	SUGAR BINDING PROTEIN	E	4.3	4.3	1	7	PEFGQLA	5735
1M63	AB	HYDROLASE/ISOMERASE	B	1.4	4.3	3	13	NGELFQVLKMMVG	5736
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	4.3	4.3	1	7	GMLWDSA	5737
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	1.4	4.3	3	7	AQEVHRW	5738

1MO1	AB	TRANSPORT PROTEIN	B	1.4	4.3	3	13	EQEALEKLAAYVQ	5739
1MTY	EC	MONOOXYGENASE	E	1.4	4.3	3	10	PLWKGMKRVF	5740
1MVW	JK	CONTRACTILE PROTEIN	K	4.3	4.3	1	8	NICYVITH	5741
1N4Q	AB	TRANSFERASE	B	2.2	4.3	2	13	EKELNRIKRWCIM	5742
1NU7	EF	HYDROLASE/PROTEIN BINDING	E	2.2	4.3	2	8	ERELLESY	5743
1NU7	FH	HYDROLASE/PROTEIN BINDING	H	1.4	4.3	3	40	KDAKDKLMTRILGEDQYLLERKKVQYEEYKKLYKKYKEEN	5744
1NZY	AB	LYASE	B	2.2	4.3	2	13	PHFMPCLTRFLDG	5745
1OAO	AD	OXIDOREDUCTASE	D	2.2	4.3	2	9	EAVEQLLEE	5746
1OCC	CG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	G	1.4	4.3	3	10	ARTWRFLTFG	5747
1OCC	PT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	1.4	4.3	3	29	RKHMLQALFITITLGVYFTLLQASEYYEA	5748
1OCC	PW	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	W	1.4	4.3	3	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	5749
1OR0	AB	HYDROLASE	A	4.3	4.3	1	11	VPERAQQWYAQ	5750
1OR7	BF	TRANSCRIPTION	B	2.2	4.3	2	24	VGTVRSRIFRAREAIDNKVQPLIR	5751
1P9M	AB	SIGNALING PROTEIN/CYTOKINE	B	2.2	4.3	2	16	QARAVQMSTKVLIQFL	5752
1PHN	AB	ELECTRON TRANSPORT	A	1.4	4.3	3	27	NTELQAVNGRYQRAAASLEAARSLTSN	5753
1PSB	AC	METAL BINDING PROTEIN	A	1.4	4.3	3	12	QEVVDKVMETLD	5754
1Q5Q	BI	HYDROLASE	B	2.2	4.3	2	22	YNEFENLRRAGIVHADMRGYSY	5755
1Q5Q	GN	HYDROLASE	G	2.2	4.3	2	22	YNEFENLRRAGIVHADMRGYSY	5756
1Q5R	EL	HYDROLASE	L	2.2	4.3	2	23	AGIAIELVRLFAVELEHYEKIEG	5757
1Q7L	AB	HYDROLASE	A	2.2	4.3	2	12	PSVTLFRQYLRI	5758
1QGW	AC	PHOTOSYNTHESIS	A	2.2	4.3	2	12	ESDAAKKLQEFI	5759
1RKE	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	2.2	4.3	2	48	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVAE	5760
1S5L	BD	PHOTOSYNTHESIS	B	1.4	4.3	3	16	PRGWFTFAHAVFALLF	5761
1S9V	AB	IMMUNE SYSTEM	B	1.4	4.3	3	24	KDILERKRAAVDRVCRHNYQLELR	5762
1T0F	BD	DNA BINDING PROTEIN	B	1.4	4.3	3	17	ERTLEKLELERRYWQQK	5763
1T0Q	AB	OXIDOREDUCTASE	A	4.3	4.3	1	5	AHKAI	5764
1TN6	AB	TRANSFERASE	A	2.2	4.3	2	10	ESAWNYLKGI	5765
1TOC	DS	COMPLEX (HYDROLASE/INHIBITOR)	S	2.2	4.3	2	8	EVECQVAC	5766
1TTW	AB	CHAPERONE	B	2.2	4.3	2	7	RFAYAVL	5767
1TY4	BD	APOPTOSIS	B	1.4	4.3	3	13	FSPYQDVVRTVGN	5768
1U0S	YA	SIGNALING PROTEIN	Y	1.4	4.3	3	12	PSRVVEALNKVS	5769
1ULI	AB	OXIDOREDUCTASE	B	1.4	4.3	3	12	AQMMRGRLRKIT	5770
1UM9	CD	OXIDOREDUCTASE	D	4.3	4.3	1	16	EAAIVGAALGMAAHGL	5771
1UZD	RM	LYASE	M	2.2	4.3	2	14	DEQIAAQVDYIVAN	5772
1V54	QX	OXIDOREDUCTASE	Q	1.4	4.3	3	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	5773
1VCB	EF	TRANSCRIPTION	E	2.2	4.3	2	15	PEIALELLMAANFLD	5774

1VYW	CD	TRANSFERASE	D	1.4	4.3	3	15	KKQVLRMEHLVLKVL	5775
1VZJ	BI	HYDROLASE	B	4.3	4.3	1	9	HWKNQFDHY	5776
1WCM	AF	TRANSCRIPTION	F	2.2	4.3	2	17	KYERARILGTRALQISM	5777
1WDD	AS	LYASE	A	4.3	4.3	1	12	GNEIIRSACKWS	5778
1XFU	ES	LYASE/METAL BINDING PROTEIN	S	1.4	4.3	3	13	SEEEIREAFRVFD	5779
1XLS	HP	TRANSCRIPTION	H	2.2	4.3	2	11	MEDQISLLKGA	5780
1XXH	AE	TRANSFERASE	E	2.2	4.3	2	5	ELLIT	5781
1YE9	BF	OXIDOREDUCTASE	F	2.2	4.3	2	13	FHRRELWEAIEAG	5782
1YEW	IK	OXIDOREDUCTASE, MEMBRANE PROTEIN	I	2.2	4.3	2	10	IFIPRLLMVD	5783
1YQ3	CD	OXIDOREDUCTASE	C	2.2	4.3	2	10	FPHYVAVVKS	5784
1Z0J	AB	PROTEIN TRANSPORT	B	1.4	4.3	3	21	EELLLQQIDNIKAYIFDAKQC	5785
1Z0J	AB	PROTEIN TRANSPORT	B	1.4	4.3	3	22	LDEVEVLTENLRELKHTLAKQK	5786
1Z7Q	QR	HYDROLASE/HYDROLASE ACTIVATOR	R	2.2	4.3	2	13	FQVEYALEAVKRG	5787
1ZBB	FH	STRUCTURAL PROTEIN/DNA	H	2.2	4.3	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	5788
1ZL8	AB	PROTEIN BINDING	A	2.2	4.3	2	17	NLERDVQRILELMEHVQ	5789
1ZV8	GH	VIRAL PROTEIN	G	1.4	4.3	3	49	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS	5790
2ACL	CD	TRANSCRIPTION	D	1.4	4.3	3	25	MFPRMLMKLVSLRTLSSVHSEQVFA	5791
2BA1	FI	RNA BINDING PROTEIN	I	1.4	4.3	3	19	DENSIELARVVDRGIRESE	5792
2BEX	BD	HYDROLASE/INHIBITOR	D	1.4	4.3	3	9	WAQWFETQH	5793
2BSK	CF	PROTEIN TRANSPORT	C	2.2	4.3	2	19	KEFLGTYNKLTETCFLDCV	5794
2CZY	AB	GENE REGULATION	B	1.4	4.3	3	12	PQLIMLANVALT	5795
2D07	AB	HYDROLASE	B	4.3	4.3	1	12	LSKLMKAYCERQ	5796
2DD4	GI	HYDROLASE	I	4.3	4.3	1	8	PRQVLAEF	5797
2DWZ	CD	ONCOPROTEIN	D	2.2	4.3	2	12	RRQKRLIFSTIT	5798
2DXB	EF	HYDROLASE	F	2.2	4.3	2	10	PNYRRRLVRW	5799
2DXB	GI	HYDROLASE	I	4.3	4.3	1	8	PRQVLAEF	5800
2DXB	SU	HYDROLASE	U	4.3	4.3	1	8	PRQVLAEF	5801
2E9X	AD	REPLICATION	A	2.2	4.3	2	22	AEEMEWFNNYKRSLATYMRSLG	5802
2EHO	EG	REPLICATION	G	2.2	4.3	2	10	AAEVEFLAEK	5803
2EQ9	JL	OXIDOREDUCTASE	L	2.2	4.3	2	11	PAARKLARELG	5804
2F93	AB	MEMBRANE PROTEIN	B	2.2	4.3	2	27	AAAVQEAAVSAILGLIILLGINLGLVA	5805
2F95	AB	MEMBRANE PROTEIN	B	2.2	4.3	2	27	AAAVQEAAVSAILGLIILLGINLGLVA	5806
2FM8	BC	CHAPERONE/CELL INVASION	C	2.2	4.3	2	17	FPALIKQASLDALFKCG	5807
2FO1	DE	GENE REGULATION/SIGNALLING PROTEIN/DNA	D	2.2	4.3	2	17	ELHRQRSELARANYEKA	5808
2FUG	45	OXIDOREDUCTASE	5	1.4	4.3	3	11	EREVYDLFGIV	5809
2FUG	DE	OXIDOREDUCTASE	D	2.2	4.3	2	13	PSFVNLQSLPYAC	5810
2FUG	MN	OXIDOREDUCTASE	M	2.2	4.3	2	6	PSFVNL	5811

2IX7	CB	CONTRACTILE PROTEIN/METAL BINDING	B	1.4	4.3	3	11	EEEIREAFRVF	5812
2JBL	LM	ELECTRON TRANSPORT	L	1.4	4.3	3	28	GFWQAITVCALGAFISWMLREVEISRKL	5813
2JBL	LM	ELECTRON TRANSPORT	M	2.2	4.3	2	25	HIAWNFAAAIFFVLCIGCIHPTLVG	5814
2NQB	GH	STRUCTURAL PROTEIN/DNA	H	1.4	4.3	3	12	AIYIYTVLKQVH	5815
2NZD	EF	STRUCTURAL PROTEIN/DNA	E	1.4	4.3	3	13	TVALREIRRYQKS	5816
2OT3	AB	PROTEIN TRANSPORT	B	1.4	4.3	3	7	LGPIYYR	5817
2PF4	BF	HYDROLASE REGULATOR/VIRAL PROTEIN	F	4.3	4.3	1	8	FDCFRMWF	5818
2PVO	AD	ELECTRON TRANSPORT	A	2.2	4.3	2	17	KTLAAMKNFAEQYAKRT	5819
2Q9Q	AG	REPLICATION	G	2.2	4.3	2	37	IPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	5820
2Q9Q	EF	REPLICATION	E	2.2	4.3	2	7	LWLAINL	5821
2Q9Q	GH	REPLICATION	G	2.2	4.3	2	12	EKAMELIRELHR	5822
2QAR	AB	HYDROLASE REGULATOR	A	2.2	4.3	2	8	KEDFRYRS	5823
2QJK	GH	ELECTRON TRANSPORT	G	2.2	4.3	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	5824
2QJP	JK	ELECTRON TRANSPORT	J	2.2	4.3	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	5825
2QTV	BD	PROTEIN TRANSPORT	B	2.2	4.3	2	10	IQARRLWKDY	5826
2R1T	AB	PROTEIN BINDING	A	1.4	4.3	3	11	TVIPVDVMRRA	5827
2RII	BY	OXIDOREDUCTASE COMPLEX	B	4.3	4.3	1	9	TEIIAFSDR	5828
2UUN	AB	ELECTRON TRANSPORT	B	2.2	4.3	2	12	AFTKVAAQADTR	5829
2UZ1	DC	LYASE	D	2.2	4.3	2	12	GATLHFQQLAVG	5830
2V4J	AB	OXIDOREDUCTASE	B	1.4	4.3	3	12	ASGPVKAIMDEV	5831
2VAS	AB	MOTOR PROTEIN	B	1.4	4.3	3	11	DEEVDEMIREA	5832
2VDW	GH	TRANSFERASE	H	1.4	4.3	3	14	YFLQISRVNDLNRM	5833
2VT1	AB	MEMBRANE PROTEIN	A	2.2	4.3	2	9	EQTKSDIRN	5834
2W9E	AH	IMMUNE SYSTEM	A	2.2	4.3	2	10	DYEDRYYREN	5835
2WAX	CD	HYDROLASE	C	1.4	4.3	3	12	RFNLKSIEEQLG	5836
2WIN	AB	IMMUNE SYSTEM	B	4.3	4.3	1	5	KYELD	5837
2ZCY	AB	HYDROLASE	B	2.2	4.3	2	22	TADAEILINTARIHAQNYLKTY	5838
2ZCY	HZ	HYDROLASE	Z	2.2	4.3	2	19	VEEVIKLVRDSFTSATERH	5839
2ZCY	QX	HYDROLASE	X	1.4	4.3	3	22	AGDTVQFAEYIQANIQLYSIRE	5840
2ZFB	AB	METAL BINDING PROTEIN	B	2.2	4.3	2	16	VAECGAEALARLLIVY	5841
2ZIV	AB	HYDROLASE	A	1.4	4.3	3	16	ESTLQQAIVNTQVVDG	5842
2ZNW	BZ	IMMUNE SYSTEM/HYDROLASE	Z	4.3	4.3	1	11	TASVNCAKKIV	5843
2ZXE	AB	HYDROLASE/TRANSPORT PROTEIN	A	1.4	4.3	3	30	ERLISMAYGQIGMIQALGGFFSYFVILAEN	5844
3A0B	ai	ELECTRON TRANSPORT	a	1.4	4.3	3	23	WFGVIMIPTLLAATICFVIAFIA	5845
3BPO	AB	CYTOKINE/CYTOKINE RECEPTOR	A	2.2	4.3	2	10	EKTQRMLSGF	5846
3BVH	AC	BLOOD CLOTTING	A	4.3	4.3	1	8	QHIQLLQK	5847
3BZ1	AD	ELECTRON TRANSPORT	A	1.4	4.3	3	16	ISGTFNFMIVFQAEHN	5848
3BZ1	DX	ELECTRON TRANSPORT	D	2.2	4.3	2	10	WFDILDDWLK	5849

3BZL	AC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.4	4.3	3	13	AKALQIIKLAELY	5850
3C59	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	2.2	4.3	2	22	LWETVQKWREYRRQCQRSLTED	5851
3C5Z	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	G	4.3	4.3	1	7	PEFGQLA	5852
3C7B	DB	OXIDOREDUCTASE	D	2.2	4.3	2	9	AYTEELKKR	5853
3CFV	BE	HISTONE/CHAPERONE	E	1.4	4.3	3	9	KPAIRRLAR	5854
3CJT	KL	TRANSFERASE/RIBOSOMAL PROTEIN	K	4.3	4.3	1	5	DEDWL	5855
3CQG	AB	PROTEIN TRANSPORT	A	2.2	4.3	2	20	KEELRKLLQKLRESSLMLLD	5856
3CUQ	AB	PROTEIN TRANSPORT	A	1.4	4.3	3	19	QMSKQLDMFKTNLEEFASK	5857
3CWB	CG	OXIDOREDUCTASE	C	1.4	4.3	3	23	PLSQTLFWLLVANLLILTWIGSQ	5858
3DNL	GI	VIRAL PROTEIN	I	2.2	4.3	2	9	MRDNWRSEL	5859
3DUF	AB	OXIDOREDUCTASE/TRANSFERASE	A	4.3	4.3	1	13	GDFYEGINFAGAF	5860
3DUF	CD	OXIDOREDUCTASE/TRANSFERASE	D	1.4	4.3	3	5	IRYRT	5861
3DW8	DE	HYDROLASE	D	1.4	4.3	3	12	LYPIAVLIDELR	5862
3DW8	DE	HYDROLASE	D	2.2	4.3	2	9	PMVRRAAAS	5863
3E1Y	AF	TRANSLATION	A	4.3	4.3	1	9	QEGSQFVKG	5864
3EAB	CI	CELL CYCLE	C	2.2	4.3	2	28	SMEAERVRVFHKQAFEYISIALRIDEDE	5865
3EUB	JL	OXIDOREDUCTASE	J	4.3	4.3	1	17	FCTPGIVMSMYTLLRNQ	5866
3EX7	EH	HYDROLASE/RNA BINDING PROTEIN/RNA	H	2.2	4.3	2	9	RELYIHRIG	5867
3EXG	AB	OXIDOREDUCTASE	A	2.2	4.3	2	13	GQIFEAYNMAALW	5868
3EXG	GH	OXIDOREDUCTASE	H	4.3	4.3	1	14	EMGFAGIAVGAAMA	5869
3EXG	KL	OXIDOREDUCTASE	K	2.2	4.3	2	16	AQVPLGAGIALACKYN	5870
3EXH	HG	OXIDOREDUCTASE	G	2.2	4.3	2	16	AQVPLGAGIALACKYN	5871
3EXH	HG	OXIDOREDUCTASE	H	2.2	4.3	2	5	TYYMS	5872
3EZQ	IJ	APOPTOSIS	I	2.2	4.3	2	33	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	5873
3FH6	HI	TRANSPORT PROTEIN	H	1.4	4.3	3	12	SFISILIFKGLF	5874
3FKS	LM	HYDROLASE	L	2.2	4.3	2	12	VFYLHSRLLERA	5875
3FKS	SV	HYDROLASE	S	2.2	4.3	2	14	RSTVAQLVQTLEQH	5876
3FKU	EF	VIRAL PROTEIN/IMMUNE SYSTEM	F	2.2	4.3	2	14	NERTLDFHDSNVKN	5877
3FKU	IL	VIRAL PROTEIN/IMMUNE SYSTEM	I	1.4	4.3	3	10	YEELKHLLSR	5878
3FS4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	2.2	4.3	2	16	AEEYGAETLERMFITY	5879
3FWC	BD	CELL CYCLE, TRANSCRIPTION	D	1.4	4.3	3	16	FTQILSTVEPKALEMV	5880
3FXD	CD	UNKNOWN FUNCTION	C	1.4	4.3	3	18	DEQKETILKALNDAIEKG	5881
3G43	BE	METAL BINDING PROTEIN	B	2.2	4.3	2	15	EEQIAEFKEAFSLFD	5882
3G9V	CD	CYTOKINE/CYTOKINE RECEPTOR	D	1.1	4.3	4	12	LDLLFMSLRNAC	5883
3G9V	CD	CYTOKINE/CYTOKINE RECEPTOR	D	2.2	4.3	2	17	PYITNRTFMLAKEASLA	5884

3GHG	GI	BLOOD CLOTTING	G	2.2	4.3	2	29	GCRMKGLIDEVNQDFTNRINKLKNSLFEY	5885
3H0L	DF	LIGASE	D	2.2	4.3	2	6	PIEMYL	5886
3H87	BC	TOXIN/ANTITOXIN	B	2.2	4.3	2	11	GVTRLEVGFSA	5887
3HH2	AD	SIGNALING PROTEIN/CYTOKINE	D	4.3	4.3	1	12	ACHLRKATCLLG	5888
3HOY	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	2.2	4.3	2	13	LAMANSLRRVMIA	5889
5CSC	AB	OXO-ACID-LYASE	A	1.4	4.3	3	12	VSAHTSHLVGSA	5890
1AFV	AL	VIRAL PROTEIN/IMMUNE SYSTEM	A	4.2	4.2	1	6	GSDIAG	5891
1B33	LM	PHOTOSYNTHESIS	L	2.1	4.2	2	12	IVTKSIVNADAE	5892
1B4U	AB	DIOXYGENASE	A	1.4	4.2	3	10	YNLNQFAMSL	5893
1B4U	AD	DIOXYGENASE	D	1.4	4.2	3	14	PDLAWHIAQSLILD	5894
1BIQ	AB	OXIDOREDUCTASE	A	1.4	4.2	3	13	DIFEKLIEKQLSF	5895
1BR1	AH	MUSCLE PROTEIN	H	4.2	4.2	1	11	YEELVRMVLSG	5896
1CDL	AE	CALCIUM-BINDING PROTEIN	A	1.4	4.2	3	10	FPEFLTMMAR	5897
1CP9	AB	HYDROLASE	B	2.1	4.2	2	5	FDKWY	5898
1DFL	BX	CONTRACTILE PROTEIN	X	2.1	4.2	2	11	YEDFVKKVMAG	5899
1DFL	BX	CONTRACTILE PROTEIN	X	4.2	4.2	1	18	QDEIDDLKDVFELFDFWD	5900
1DX5	MI	SERINE PROTEINASE	I	2.1	4.2	2	5	ECENG	5901
1E6V	DF	OXIDOREDUCTASE	D	2.1	4.2	2	7	PAAMETH	5902
1ED3	AC	IMMUNE SYSTEM	A	2.1	4.2	2	11	YAERLRAYLEG	5903
1EF1	BD	MEMBRANE PROTEIN	B	4.2	4.2	1	15	KDQWEERIQVWHEEH	5904
1ES7	CB	CYTOKINE	B	2.1	4.2	2	7	SDFQCKD	5905
1FDH	AG	OXYGEN TRANSPORT	A	2.1	4.2	2	17	PVNFKLLSHCLLVTLAA	5906
1FDH	BH	OXYGEN TRANSPORT	B	2.1	4.2	2	17	PVNFKLLSHCLLVTLAA	5907
1FHJ	CD	OXYGEN STORAGE/TRANSPORT	D	2.1	4.2	2	16	VDEVGGEALGRLLIVY	5908
1FIQ	BC	OXIDOREDUCTASE	B	2.1	4.2	2	24	IEFRRTLTLSFFFKFYLTVLKKLG	5909
1FM6	UX	TRANSCRIPTION	U	2.1	4.2	2	23	PAEVEALREKVYASLEAYCKHKY	5910
1FM6	UX	TRANSCRIPTION	X	1.4	4.2	3	30	LFAKLLQKMTDLRQIVTEHVQLLQVIKKTE	5911
1FQ1	AB	HYDROLASE/TRANSFERASE	A	2.1	4.2	2	8	IKQYNYLH	5912
1FQV	KL	LIGASE	K	1.4	4.2	3	8	KRWYRLAS	5913
1G0U	BC	HYDROLASE	C	2.1	4.2	2	22	NADSRILIEKARVEAQSHRLTL	5914
1G2C	SV	VIRAL PROTEIN	S	2.1	4.2	2	48	LEGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	5915
1GH0	MN	PHOTOSYNTHESIS	M	1.4	4.2	3	12	PLTEAVSVADSQ	5916
1H1L	AD	OXIDOREDUCTASE	D	2.1	4.2	2	17	DALTLERGRLVDMMLDS	5917
1IHF	AB	TRANSCRIPTION/DNA	B	2.1	4.2	2	8	KELRDRAN	5918
1IR2	CP	LYASE	C	2.1	4.2	2	6	WTDGLT	5919
1IRU	EF	HYDROLASE	F	2.1	4.2	2	13	HQIEYAMEAVKQG	5920
1JD2	BI	HYDROLASE	I	1.4	4.2	3	22	ATDVTTLNEMFRYKTNLYKLKE	5921
1JD2	GN	HYDROLASE	G	1.4	4.2	3	23	IPDARNAALRAKAEAAEFRYKYG	5922

1JEY	AB	DNA BINDING PROTEIN/DNA	A	1.4	4.2	3	10 LVDEFKELVY	5923
1JR3	CD	TRANSFERASE	D	1.4	4.2	3	15 LLALAQALERLSLLW	5924
1JY2	OP	BLOOD CLOTTING	P	2.1	4.2	2	27 TCGIADFLNNYQTSVDKDLRTLEGILY	5925
1K6L	LM	PHOTOSYNTHESIS	L	2.1	4.2	2	29 GLWQIITICATGAFVSWALREVEICRKLG	5926
1KX4	BD	STRUCTURAL PROTEIN/DNA	B	2.1	4.2	2	27 IYEETRGVLKVFLENVIRDAVTYTEHA	5927
1L2W	GL	CHAPERONE	L	2.1	4.2	2	8 QYANNLAG	5928
1L9B	LM	PHOTOSYNTHESIS	M	2.1	4.2	2	28 GLWLIASFFMFVAVWSWWGRTYLRAQAL	5929
1L9J	LM	PHOTOSYNTHESIS	L	1.4	4.2	3	29 PAHMIAISFFFTNALALALHGALVLSAAN	5930
1L9J	RS	PHOTOSYNTHESIS	R	2.1	4.2	2	10 PDHEDTFFRD	5931
1LNU	AB	SUGAR BINDING PROTEIN	A	4.2	4.2	1	7 PEFGQLA	5932
1M1Y	AB	OXIDOREDUCTASE	A	2.1	4.2	2	8 VGCGQYSR	5933
1M1Y	KL	OXIDOREDUCTASE	K	2.1	4.2	2	12 DAWSSRILLEEM	5934
1MIO	AB	MOLYBDENUM-IRON PROTEIN	B	2.1	4.2	2	10 TYGKFIAREE	5935
1MJG	DP	OXIDOREDUCTASE	D	1.4	4.2	3	16 DLIYSILTQIASDVYG	5936
1MVW	GI	CONTRACTILE PROTEIN	I	4.2	4.2	1	10 ASQVGDIARA	5937
1N4Q	CD	TRANSFERASE	C	4.2	4.2	1	14 YHAWQHRQWVIQEF	5938
1N4Q	GH	TRANSFERASE	G	4.2	4.2	1	14 YHAWQHRQWVIQEF	5939
1N4Q	IJ	TRANSFERASE	I	2.1	4.2	2	13 KEYWRYIGRSLQS	5940
1N4Q	KL	TRANSFERASE	K	2.1	4.2	2	13 KEYWRYIGRSLQS	5941
1NI4	AB	OXIDOREDUCTASE	A	4.2	4.2	1	16 AQVPLGAGIALACKYN	5942
1NIK	CK	TRANSCRIPTION	C	2.1	4.2	2	14 LAMANSLRRVMIAE	5943
1NKP	DE	TRANSCRIPTION/DNA	E	2.1	4.2	2	23 AHHNALERKRRDHIKDSFHSLRD	5944
1NTK	CD	OXIDOREDUCTASE	C	2.1	4.2	2	29 GWIIRYMHANGASMFFICLYMHVGRGLYY	5945
1NX0	BD	HYDROLASE	D	2.1	4.2	2	9 AIDALSSDF	5946
1OCC	QX	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	1.4	4.2	3	14 EEWVAKQTKRMLDM	5947
1OQP	AB	PROTEIN BINDING	A	2.1	4.2	2	12 EEELQEMIAEAD	5948
1OR7	BF	TRANSCRIPTION	B	2.1	4.2	2	11 QKAFNLLVVRY	5949
1PID	CD	HORMONE	C	2.1	4.2	2	8 IVEQCCAS	5950
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	2.1	4.2	2	16 HIAWNFAAAIFFVLCI	5951
1Q90	AD	PHOTOSYNTHESIS	D	1.4	4.2	3	25 NDLLYMFPVVILGTFACVIGLSVLD	5952
1QVI	AY	CONTRACTILE PROTEIN	A	1.4	4.2	3	8 LYSKVKPL	5953
1R20	AD	HORMONE/GROWTH FACTOR RECEPTOR	D	4.2	4.2	1	23 PSLVEEIQRYYLNTLRVYILNQN	5954
1R4A	AE	PROTEIN TRANSPORT	E	2.1	4.2	2	15 TEFEYLRKVLFEYMM	5955
1RP3	AB	TRANSCRIPTION	A	1.4	4.2	3	21 NVEEEVIKRELTEKVKEAVSK	5956
1RP3	CD	TRANSCRIPTION	D	1.4	4.2	3	19 VEEKDLEKKVKELKEKIEK	5957
1RY1	CD	TRANSLATION	C	1.4	4.2	3	17 VKKIEKFHSQLMRLMVA	5958
1RYP	QR	MULTICATALYTIC PROTEINASE	R	2.1	4.2	2	12 FQVEYALEAVKR	5959
1S5L	bd	PHOTOSYNTHESIS	b	1.4	4.2	3	16 PRGWFTFAHAVFALLF	5960

1SB3	DF	OXIDOREDUCTASE	D	2.1	4.2	2	22	PLAVEGQTQGGVWMGMGQALSE	5961
1SQX	DG	OXIDOREDUCTASE	G	4.2	4.2	1	42	YFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQEFEKSK	5962
1T9G	RS	OXIDOREDUCTASE, ELECTRON TRANSPORT	R	1.4	4.2	3	15	AFGKNLLPRVAAKLE	5963
1TY4	BD	APOPTOSIS	D	2.1	4.2	2	6	DDFDAQ	5964
1UM9	AD	OXIDOREDUCTASE	A	1.4	4.2	3	14	WHLLRQEALLKEEL	5965
1USV	GH	CHAPERONE	G	1.4	4.2	3	22	KIMKVIRKNIVKKLIEAFNEIA	5966
1V54	AF	OXIDOREDUCTASE	A	2.1	4.2	2	5	LEWLN	5967
1V54	PT	OXIDOREDUCTASE	T	2.1	4.2	2	24	ARTWRFLTFGLALPSVALCTLNSW	5968
1VF6	AC	PROTEIN BINDING/PROTEIN TRANSPORT	A	1.4	4.2	3	15	LQVLDRLKMKLQEKG	5969
1VQP	FM	RIBOSOME	M	2.1	4.2	2	9	AYSYIRDAW	5970
1W1I	AF	HYDROLASE	F	1.4	4.2	3	19	PDEVVSLVNQGLQEGERDF	5971
1W1I	DH	HYDROLASE	H	1.4	4.2	3	19	PDEVVSLVNQGLQEGERDF	5972
1WYU	CD	OXIDOREDUCTASE	D	1.4	4.2	3	15	FLALVRAWAYIRTLG	5973
1XEW	XY	CELL CYCLE	Y	1.4	4.2	3	19	GGEKALTALAFVFAIQKFK	5974
1XLS	HP	TRANSCRIPTION	H	1.4	4.2	3	7	PLLGEIC	5975
1XTC	CF	TOXIN	C	2.1	4.2	2	32	NTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQS	5976
1YKE	AB	GENE REGULATION	A	1.4	4.2	3	22	MYERKVENIRTILVNIHHLLNE	5977
1YQ3	CD	OXIDOREDUCTASE	C	1.4	4.2	3	30	PALIYSAKFALVFPLSYHTWNGIRHLVWDM	5978
1YUC	AC	TRANSCRIPTION REGULATION	A	2.1	4.2	2	11	VDDQMKLLQNC	5979
1YYP	AB	REPLICATION/TRANSFERASE	B	4.2	4.2	1	6	PAFLPY	5980
1Z7Q	CD	HYDROLASE/HYDROLASE ACTIVATOR	D	2.1	4.2	2	13	FQVEYALEAVKRG	5981
1Z7Q	FG	HYDROLASE/HYDROLASE ACTIVATOR	G	2.1	4.2	2	22	IPDGRHLVNRGREEAASFKKLY	5982
1Z7Q	PQ	HYDROLASE/HYDROLASE ACTIVATOR	Q	2.1	4.2	2	10	QVEYALESIS	5983
1ZOQ	AC	TRANSCRIPTION/TRANSFERASE	C	2.1	4.2	2	13	PQQQQQVLNILKS	5984
1ZOQ	BD	TRANSCRIPTION/TRANSFERASE	D	1.4	4.2	3	13	PQQQQQVLNILKS	5985
2AK4	FH	IMMUNE SYSTEM	F	2.1	4.2	2	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	5986
2AK4	KM	IMMUNE SYSTEM	K	2.1	4.2	2	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	5987
2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	A	2.1	4.2	2	15	QGTLFELILAANYLD	5988
2BKY	AX	DNA BINDING PROTEIN	A	1.4	4.2	3	14	RAISKAVDTVEIVR	5989
2BL0	AC	MUSCLE PROTEIN	C	1.4	4.2	3	12	FPEFLSMMGRRM	5990
2BR2	MN	HYDROLASE	M	2.1	4.2	2	26	LQDIDQAENTARSTAVKLLEELKKHL	5991
2CZV	BD	HYDROLASE	B	4.2	4.2	1	11	KEAYELAKEWF	5992
2D74	AB	TRANSLATION	B	4.2	4.2	1	8	YEKLLEKA	5993
2DD4	AC	HYDROLASE	C	4.2	4.2	1	8	PRQVLAEF	5994
2DD4	BC	HYDROLASE	C	2.1	4.2	2	10	PNYRRRLVRW	5995
2DD4	EF	HYDROLASE	F	2.1	4.2	2	14	AEDHRVWKDYVHTL	5996
2DFK	CD	CELL CYCLE	C	2.1	4.2	2	13	IDGFLLTPVQKIC	5997

2DFS	AG	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	G	4.2	4.2	1	10	DEEVDEMIRE	5998
2DPP	AB	LYASE	B	2.1	4.2	2	14	PALVKLVEKALYDG	5999
2DXB	VX	HYDROLASE	X	4.2	4.2	1	8	PRQVLAEF	6000
2E1M	AC	OXIDOREDUCTASE	C	2.1	4.2	2	6	HLDVVR	6001
2EHO	EG	REPLICATION	E	4.2	4.2	1	14	RIRYVLSSYLRCRL	6002
2ES4	AD	HYDROLASE	A	2.1	4.2	2	17	RGEQLLAYVKQVLAATG	6003
2FBW	AB	OXIDOREDUCTASE	A	2.1	4.2	2	15	TGHSLLHTLYGRSLR	6004
2FHH	12	HYDROLASE	2	1.4	4.2	3	23	AAVAVEFARLYAVELEHYEKLEG	6005
2FJ7	BD	STRUCTURAL PROTEIN/DNA	B	2.1	4.2	2	13	NVIRDAVTYTEHA	6006
2FK0	GJ	VIRAL PROTEIN	G	2.1	4.2	2	8	YEELKHLL	6007
2FKW	MN	MEMBRANE PROTEIN, PHOTOSYNTHESIS	N	2.1	4.2	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	6008
2FUG	ST	OXIDOREDUCTASE	S	4.2	4.2	1	5	YICGE	6009
2GAG	AD	OXIDOREDUCTASE	A	1.4	4.2	3	16	AADVLDWLEEWLQTEW	6010
2GGM	AC	CELL CYCLE	A	2.1	4.2	2	16	EKDTKEEILKAFKLFD	6011
2GGM	BD	CELL CYCLE	B	2.1	4.2	2	16	EKDTKEEILKAFKLFD	6012
2GPP	BD	TRANSCRIPTION	B	2.1	4.2	2	25	DIKALTTLCDLADRELVVIIGWAKH	6013
2GPV	AG	TRANSCRIPTION	G	2.1	4.2	2	10	EAIIRKALMG	6014
2H0D	AB	METAL BINDING PROTEIN/LIGASE	B	2.1	4.2	2	5	LYELQ	6015
2H61	EC	METAL BINDING PROTEIN, SIGNALING PROTEIN	E	2.1	4.2	2	21	FQEFMAFVAMVTTACHEFFEH	6016
2HLD	CD	HYDROLASE	C	2.1	4.2	2	12	VFYLHSRLLERA	6017
2HLD	LM	HYDROLASE	M	1.4	4.2	3	15	TREGNDLYREMKETG	6018
2HUE	AB	DNA BINDING PROTEIN	B	2.1	4.2	2	11	PKDIQLARRIR	6019
2HWN	BE	TRANSFERASE	E	1.4	4.2	3	17	LAWKIAKMIVSDVMQQC	6020
2IBZ	DI	OXIDOREDUCTASE	I	2.1	4.2	2	27	VGTIFAGAFVFQTVFDTAITSWYENHN	6021
2J0Q	BF	HYDROLASE	B	2.1	4.2	2	9	RELYIHRIG	6022
2J0S	AC	HYDROLASE	A	4.2	4.2	1	9	RELYIHRIG	6023
2J59	AM	HYDROLASE	M	2.1	4.2	2	22	EEDTGVTNRDLISRRIKEYNNL	6024
2JIY	LH	PHOTOSYNTHESIS	L	2.1	4.2	2	5	ERKYR	6025
2NQB	EF	STRUCTURAL PROTEIN/DNA	E	2.1	4.2	2	13	TVALREIRRYQKS	6026
2O8F	AB	DNA BINDING PROTEIN/DNA	B	2.1	4.2	2	20	TFDGTAIANAVVKELAETIK	6027
2OBH	BD	CELL CYCLE	B	2.1	4.2	2	29	FGDFLTVMTQKMSEKDTKEEILKAFKLFD	6028
2OF5	DJ	APOPTOSIS	D	1.4	4.2	3	10	DRQINQLAQR	6029
2OF5	DK	APOPTOSIS	K	2.1	4.2	2	12	QDVAEEVRAVLE	6030
2P5T	EF	TRANSCRIPTION REGULATOR	E	2.1	4.2	2	19	PWILMSDDLSDLIHTNIYL	6031
2PBD	AP	STRUCTURAL PROTEIN	A	2.1	4.2	2	8	PSIVHRKC	6032
2QB0	AD	HYDROLASE REGULATOR	D	2.1	4.2	2	14	GDVLYELLQHILKQ	6033
2QKL	AB	HYDROLASE	B	2.1	4.2	2	23	VERLCFQIEQAHWFYEDFIRAQN	6034

2RAX	XY	CELL CYCLE	Y	1.4	4.2	3	38	FLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	6035
2RD0	AB	TRANSFERASE/ONCOPROTEIN	B	1.4	4.2	3	50	HEYNTQFQEKSREYDRLYEEYTRTSQEIQMKRTAIEAFNETIKIFEEQCQ	6036
2RF4	AD	TRANSFERASE	D	1.4	4.2	3	18	LSSSISQLKRIQRDFKGL	6037
2SIV	CB	ENVELOPE GLYCOPROTEIN	C	1.4	4.2	3	35	GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT	6038
2UW1	AB	OXIDOREDUCTASE	B	2.1	4.2	2	14	FEEQVRELRERAKE	6039
2V7Q	CD	HYDROLASE	C	2.1	4.2	2	12	VFYLHSRLLERA	6040
2V8W	AB	TRANSLATION	A	2.1	4.2	2	10	VEDFWALYNH	6041
2VGL	BM	PROTEIN TRANSPORT	B	2.1	4.2	2	14	EWGQIFILDCLSNY	6042
2VUS	AI	TRANSCRIPTION	A	2.1	4.2	2	16	MEEYAREVFPIEEEAN	6043
2W73	AL	METAL BINDING PROTEIN	A	1.4	4.2	3	15	EEQIAEFKEAFSLFD	6044
2Z3R	CJ	CYTOKINE/CYTOKINE RECEPTOR	C	2.1	4.2	2	19	ASIHDTVENLIILANNSLS	6045
2ZAL	AD	HYDROLASE	D	2.1	4.2	2	7	GEVFIRA	6046
2ZCY	PX	HYDROLASE	P	4.2	4.2	1	22	TADAEILINTARIHAQNYLKTY	6047
2ZCY	VW	HYDROLASE	W	2.1	4.2	2	18	PEDLFETISQALLNAADR	6048
3B9J	IJ	OXIDOREDUCTASE	J	2.1	4.2	2	7	KQVKSVA	6049
3BG0	DC	PROTEIN TRANSPORT, HYDROLASE	C	1.4	4.2	3	17	SQLIFNAQALKDRYEGN	6050
3BLH	AB	TRANSCRIPTION	A	1.4	4.2	3	13	ITALREIKILQLL	6051
3BO0	AB	RIBOSOME	A	1.4	4.2	3	25	GTGVLLTVSIVYRMYEQLLREKVSE	6052
3C7B	AB	OXIDOREDUCTASE	A	4.2	4.2	1	16	GARGLLKQLEISYKDK	6053
3C7B	AB	OXIDOREDUCTASE	B	2.1	4.2	2	5	YEYFT	6054
3CUE	TV	PROTEIN TRANSPORT	T	1.4	4.2	3	23	AGDFETKLSDYGHNIGIRLLELL	6055
3CXH	OS	OXIDOREDUCTASE	O	2.1	4.2	2	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	6056
3CXH	RS	OXIDOREDUCTASE	R	2.1	4.2	2	20	EDESYARAYRIIRAHQTELT	6057
3DRA	AB	TRANSFERASE	A	1.4	4.2	3	16	EDYKQIMGLLLALMKA	6058
3DTP	BF	CONTRACTILE PROTEIN	F	4.2	4.2	1	8	QVQEFKEA	6059
3DUF	AB	OXIDOREDUCTASE/TRANSFERASE	A	1.4	4.2	3	17	AQYIQAAGVALGLKMRG	6060
3E2Z	AB	TRANSFERASE, LYASE	A	2.1	4.2	2	12	AYGSLFNSIQGL	6061
3EA5	CD	TRANSPORT PROTEIN	D	1.4	4.2	3	13	LEGRILAALTLKN	6062
3EUB	24	OXIDOREDUCTASE	2	4.2	4.2	1	17	FCTPGIVMSMYTLLRNQ	6063
3EUH	BE	CELL CYCLE	E	1.4	4.2	3	15	ELDMMVGKILCYLYL	6064
3EXG	56	OXIDOREDUCTASE	5	2.1	4.2	2	16	AQVPLGAGIALACKYN	6065
3EZJ	EF	PROTEIN TRANSPORT	E	2.1	4.2	2	10	APILRQMIDS	6066
3EZQ	GH	APOPTOSIS	H	1.4	4.2	3	16	NLVADLVQEVQQARDL	6067
3EZQ	KL	APOPTOSIS	L	1.4	4.2	3	16	NLVADLVQEVQQARDL	6068
3FUB	CD	HORMONE	C	2.1	4.2	2	15	DTCKKYRSAYITPCT	6069
3FWC	EF	CELL CYCLE, TRANSCRIPTION	F	1.4	4.2	3	76	KQVITEQIANDLVKEVVNSSVISIVKREFSEANYRKDFIDTMTRELYDAF LHERLYLIYMDSRAELKRNSTLKKKF	6070
3G5O	DC	TOXIN/ANTITOXIN	D	1.4	4.2	3	14	IRESIAEADADIAS	6071
3GHG	HI	BLOOD CLOTTING	H	1.4	4.2	3	36	DETVNSNIPTNLRVLRSILENLRSKIQKLESDVSAQ	6072

3GTM	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.4	4.2	3	9	YCCRRMILT	6073
3H0L	SU	LIGASE	S	2.1	4.2	2	8	PIEMYLSD	6074
3HAY	CD	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	D	1.4	4.2	3	14	EEIVAHLPPLCEEK	6075
3HKZ	DL	TRANSFERASE	D	2.1	4.2	2	7	IRRASML	6076
3HS0	AB	IMMUNE SYSTEM	A	2.1	4.2	2	6	KAVYVL	6077
1A93	AB	LEUCINE ZIPPER	A	1.4	4.1	3	29	VQAEEQKLISEEDLLRKRREQLKHKLEQL	6078
1AHJ	EF	LYASE	E	2.1	4.1	2	10	FEYRARVVRE	6079
1AQD	AB	COMPLEX (MHC PROTEIN/ANTIGEN)	A	2.1	4.1	2	22	AQGALANIAVDKANLEIMTKRS	6080
1B33	CD	PHOTOSYNTHESIS	C	1.4	4.1	3	13	PGELDRIKSFVSS	6081
1B33	HI	PHOTOSYNTHESIS	I	2.1	4.1	2	13	TAALEKLKSYFST	6082
1B5F	CD	HYDROLASE	C	2.1	4.1	2	11	TAIVTQINHAI	6083
1BB1	AC	DE NOVO PROTEIN DESIGN	A	1.4	4.1	3	33	EIAAIEYEQAAIKEEIAAIKDKIAAIKEYIAAI	6084
1BBT	24	VIRUS	4	4.1	4.1	1	8	WFSKLASS	6085
1BCP	HL	TOXIN	H	1.4	4.1	3	13	YSRLRKMLYLIYV	6086
1BDJ	AB	COMPLEX (CHEMOTAXIS/TRANSFERASE)	B	2.1	4.1	2	15	WEDNVGEWIEEMKEE	6087
1DE4	DF	METAL TRANSPORT INHIBITOR/RECEPTOR	F	4.1	4.1	1	17	ERYNSQLLSFVRDLNQY	6088
1E6Y	BC	OXIDOREDUCTASE	C	2.1	4.1	2	12	PYFRSYFAAINF	6089
1EAY	AC	SIGNAL TRANSDUCTION COMPLEX	A	1.4	4.1	3	16	AATLEEKLNKIFEKLG	6090
1EER	AC	COMPLEX (CYTOKINE/RECEPTOR)	A	2.1	4.1	2	25	EPLQLHVDKAVSGLRSLTTLLRALG	6091
1EYX	AB	PHOTOSYNTHESIS	A	1.4	4.1	3	25	QEKINKCYRDIDHYMRLVNYSLVIG	6092
1FDH	AG	OXYGEN TRANSPORT	G	2.1	4.1	2	19	PEVQASWQKMVTGVASALS	6093
1G0U	AG	HYDROLASE	G	2.1	4.1	2	18	CDVLAKRMANLSQIYTQR	6094
1G20	CD	OXIDOREDUCTASE	D	2.1	4.1	2	16	QQNMKDGLQNCKATYK	6095
1H1L	AB	OXIDOREDUCTASE	B	2.1	4.1	2	13	DEYQELFRNKRQL	6096
1H2S	AB	MEMBRANE PROTEIN	B	2.1	4.1	2	30	AAAVQEAAVSAILGLIILLGINLGLVAATL	6097
1H3O	AB	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	B	2.1	4.1	2	12	KKKLQDLVREVD	6098
1HE1	BD	SIGNALING PROTEIN	B	2.1	4.1	2	5	LQQWG	6099
1HWM	AB	HYDROLASE	A	2.1	4.1	2	9	FEELYKITG	6100
1I7W	CD	CELL ADHESION	D	2.1	4.1	2	7	KKLADMY	6101
1IAK	BP	HISTOCOMPATIBILITY ANTIGEN I-AK	B	1.4	4.1	3	22	LERTRAELDTVCRHNYEKTETP	6102
1IBR	AB	CELL CYCLE, TRANSLATION	B	2.1	4.1	2	26	DEVALQGIEFWSNVCDEEMDLAIEAS	6103
1IR2	BO	LYASE	B	2.1	4.1	2	6	WTDGLT	6104
1IR2	CJ	LYASE	C	1.4	4.1	3	15	AKNYGRAVYECLRGG	6105
1IR2	DM	LYASE	D	2.1	4.1	2	6	WTDGLT	6106
1IR2	EL	LYASE	E	2.1	4.1	2	6	WTDGLT	6107

1IR2	FN	LYASE	F	2.1	4.1	2	21	NAPGAAANRVALEACTQARNE	6108
1IRU	12	HYDROLASE	2	2.1	4.1	2	18	PRAIHSWLTRAMYSRRSK	6109
1IRU	WX	HYDROLASE	W	4.1	4.1	1	23	AADTDMTTQLISSNLELHSLSTG	6110
1IZN	AB	PROTEIN BINDING	B	2.1	4.1	2	23	ARLRKLEVEANNAFDQYRDLYFE	6111
1J1D	EF	CONTRACTILE PROTEIN	F	2.1	4.1	2	37	SRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRA	6112
1JB0	AC	PHOTOSYNTHESIS	C	4.1	4.1	1	6	RCETAC	6113
1JD2	AH	HYDROLASE	H	1.4	4.1	3	22	AADTEAVTQLIGSNIELHSLYT	6114
1JD2	GN	HYDROLASE	N	1.4	4.1	3	22	AADTQAIADIVQYHLELYTSQY	6115
1JD2	HN	HYDROLASE	H	2.1	4.1	2	15	VVSALQMLKQHLFKY	6116
1JEB	AB	OXYGEN STORAGE/TRANSPORT	B	2.1	4.1	2	20	PENFRLLGNMIVIVLGHHLG	6117
1JPW	BE	CELL ADHESION	E	2.1	4.1	2	6	ADVKSS	6118
1K5D	AC	SIGNALING PROTEIN/SIGNALING ACTIVATOR	A	2.1	4.1	2	11	RVTYKNVPNWH	6119
1KDX	AB	TRANSCRIPTION REGULATION COMPLEX	B	1.4	4.1	3	11	RKILNDLSSDA	6120
1KF6	BD	OXIDOREDUCTASE	D	2.1	4.1	2	15	EPVFWGLFGAGGMWS	6121
1KKL	CH	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN	C	1.4	4.1	3	17	ATKTFEKNLNHLIEHNE	6122
1KYO	MG	OXIDOREDUCTASE/ELECTRON TRANSPORT	M	1.4	4.1	3	12	ALKLVRESELLG	6123
1L2W	AI	CHAPERONE	I	2.1	4.1	2	8	QYANNLAG	6124
1L4A	CD	ENDOCYTOSIS/EXOCYTOSIS	C	1.4	4.1	3	45	ELEEIQQQCNQVTDDSLESTRRMLNMCEESKEAGIRTLVMLDEQG	6125
1LB1	CD	SIGNALING PROTEIN	D	2.1	4.1	2	7	LRPLSYP	6126
1M56	GH	OXIDOREDUCTASE	H	2.1	4.1	2	35	PVATQIHWLDGFILVIIAAITIFVTLLILYAVWRF	6127
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	B	2.1	4.1	2	10	PEMAAVILKA	6128
1MO1	CD	TRANSPORT PROTEIN	D	1.4	4.1	3	13	EQEALEKLAAYVQ	6129
1N4Q	KL	TRANSFERASE	K	4.1	4.1	1	14	YHAWQHRQWVIQEF	6130
1N4Q	KL	TRANSFERASE	K	2.1	4.1	2	10	ESAWNYLKGI	6131
1N73	DF	BLOOD CLOTTING	F	1.4	4.1	3	39	EQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	6132
1NRJ	AB	PROTEIN TRANSPORT	A	2.1	4.1	2	14	EIQINSFISQLITS	6133
1OAO	AC	OXIDOREDUCTASE	C	2.1	4.1	2	14	LGDLPPILNRKRAQ	6134
1OCC	AL	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	2.1	4.1	2	30	HKDIGTLYLLFGAWAGMVGTALSLLIRAEL	6135
1OCC	DE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	4.1	4.1	1	12	ASQKALKEKEKA	6136
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.4	4.1	3	25	PAMMWALGFIFLFTVGGLTGIVLAN	6137

1OCC	NY	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.1	4.1	2	30	HKDIGTLYLLFGAWAGMVGTALSLLIRAEL	6138
1OQD	BL	IMMUNE RESPONSE	L	1.4	4.1	3	7	CQLRCSS	6139
1OQS	EF	HYDROLASE	E	2.1	4.1	2	14	ATDRCCFVHDCCYG	6140
1OR7	BF	TRANSCRIPTION	F	2.1	4.1	2	18	PEMQKTWESYHLIRDSMR	6141
1P0S	LH	HYDROLASE	H	4.1	4.1	1	11	RDWAESTLMTQ	6142
1PTO	GI	TOXIN	I	1.4	4.1	3	14	YDALRRLLYMIYMS	6143
1Q16	AC	OXIDOREDUCTASE	C	1.4	4.1	3	21	DIYPYIAGAVFLIGSWLRYDY	6144
1RH5	AB	PROTEIN TRANSPORT	B	1.4	4.1	3	13	KEFIEECRRVWLV	6145
1RM6	AB	OXIDOREDUCTASE	B	2.1	4.1	2	7	EWWRSGN	6146
1RM6	DE	OXIDOREDUCTASE	E	2.1	4.1	2	7	EWWRSGN	6147
1RP3	CD	TRANSCRIPTION	C	1.4	4.1	3	18	IRDLISYGVIGLIKAVDN	6148
1RUY	HM	VIRAL PROTEIN	H	2.1	4.1	2	10	YEELREQLSS	6149
1RUY	JI	VIRAL PROTEIN	J	2.1	4.1	2	10	YEELREQLSS	6150
1SCT	CD	OXYGEN TRANSPORT	C	2.1	4.1	2	19	SKLRGHAITLTYALNNFVD	6151
1SFC	FH	TRANSPORT PROTEIN	H	2.1	4.1	2	13	NEMDENLEQVSGI	6152
1SQB	DF	OXIDOREDUCTASE	F	2.1	4.1	2	20	ENLYDDRVFRIKRALDLSMR	6153
1SQX	EJ	OXIDOREDUCTASE	J	2.1	4.1	2	12	LTARLYSLLFRR	6154
1SXJ	DE	REPLICATION	D	2.1	4.1	2	15	FDEIKKYVNTFMKSG	6155
1T0Q	AB	OXIDOREDUCTASE	A	2.1	4.1	2	16	WAAIAARSFFDDMMMT	6156
1T0Q	AC	OXIDOREDUCTASE	A	1.4	4.1	3	18	WNDTWGQCWDVITDNLVN	6157
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	B	1.4	4.1	3	16	DTQLQQIVDKTIINAD	6158
1TIL	CD	TRANSCRIPTION	C	4.1	4.1	1	15	ESFARVTVAAFVAQL	6159
1TQE	PX	TRANSCRIPTION/PROTEIN BINDING/DNA	X	1.4	4.1	3	14	TEVKQKLQEFLLSK	6160
1U0S	YA	SIGNALING PROTEIN	Y	2.1	4.1	2	10	QAMVIEAIKA	6161
1U6G	AB	LIGASE	A	2.1	4.1	2	10	TFQMAILLQY	6162
1URQ	AD	TRANSPORT PROTEIN	A	1.4	4.1	3	56	EGVKGAASGVVGELARARLALDERGQKLSDLEERTAAMMSSADSFSKHAHEMMLKY	6163
1UZD	BT	LYASE	B	2.1	4.1	2	6	WTDGLT	6164
1V29	AB	LYASE	A	1.4	4.1	3	10	PAYRSRVVKE	6165
1V4U	AB	OXYGEN STORAGE/TRANSPORT	A	4.1	4.1	1	19	PDAHVSLDKFLASVALALA	6166
1V4U	AB	OXYGEN STORAGE/TRANSPORT	B	2.1	4.1	2	16	YEDIGPKALARCLIVY	6167
1V4U	CD	OXYGEN STORAGE/TRANSPORT	D	2.1	4.1	2	16	YEDIGPKALARCLIVY	6168
1V54	BD	OXIDOREDUCTASE	D	4.1	4.1	1	14	EEWVAKQTKRMLDM	6169
1V54	CG	OXIDOREDUCTASE	C	1.4	4.1	3	25	VPLLNTSVLLASGVSITWAHHSLME	6170
1VCB	BC	TRANSCRIPTION	B	2.1	4.1	2	15	PEIALELLMAANFLD	6171
1VF6	AC	PROTEIN BINDING/PROTEIN TRANSPORT	A	2.1	4.1	2	24	PLFNQILTLQQSIKQLKGQLNHIL	6172
1W63	BM	ENDOCYTOSIS	M	1.4	4.1	3	18	SLVFSFLYKVVQVFSEYF	6173

1W63	FO	ENDOCYTOSIS	O	1.4	4.1	3	18	SLVFSFLYKVVQVFSEYF	6174
1WDD	EW	LYASE	E	1.4	4.1	3	21	NAPGAAANRVALEACVQARNE	6175
1WDW	EF	LYASE	F	2.1	4.1	2	15	LKDAINEALRDWVAT	6176
1XD2	AC	SIGNALING PROTEIN	C	4.1	4.1	1	20	KAMKKWVESITKIIQRKKIA	6177
1YE9	DF	OXIDOREDUCTASE	D	2.1	4.1	2	12	FILREKITHFDH	6178
1YE9	IP	OXIDOREDUCTASE	P	2.1	4.1	2	13	FHRRELWEAIEAG	6179
1YE9	IP	OXIDOREDUCTASE	P	1.4	4.1	3	18	PLLQGRLFSYTDTQISRL	6180
1YV0	TI	CONTRACTILE PROTEIN	I	1.4	4.1	3	9	SQKLFDLRG	6181
1Z7Q	CJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.4	4.1	3	22	ATDVTTLNEMFRYKTNLYKLKE	6182
1ZA3	HR	IMMUNE SYSTEM/SIGNALING PROTEIN	H	1.4	4.1	3	8	YYSYYYSS	6183
1ZAV	AX	STRUCTURAL PROTEIN	X	1.4	4.1	3	15	VSELAELVKKLEDKF	6184
1ZGL	DE	IMMUNE SYSTEM	D	2.1	4.1	2	21	GALANIAVDKANLEIMTKRSN	6185
2A45	AB	BLOOD CLOTTING	A	2.1	4.1	2	8	ERELLESY	6186
2ADV	AC	HYDROLASE	A	1.4	4.1	3	12	GDNILRLYGEAR	6187
2ADV	AC	HYDROLASE	C	1.4	4.1	3	10	MLEQYFDMIT	6188
2AFH	CB	OXIDOREDUCTASE	B	1.4	4.1	3	17	ASLTKERGRLVDMMTDS	6189
2B8K	AB	TRANSFERASE	B	1.4	4.1	3	13	YAAKLLFQELMAM	6190
2BA0	BG	RNA BINDING PROTEIN	B	2.1	4.1	2	17	RRKVSIAEEAIYLIEQE	6191
2BCJ	BG	TRANSFERASE/HYDROLASE	G	2.1	4.1	2	15	VSKAAADLMAYCEAH	6192
2BL0	AB	MUSCLE PROTEIN	B	2.1	4.1	2	12	ADQIQECFQIFD	6193
2BYP	DI	RECEPTOR	I	4.1	4.1	1	6	PRCAWR	6194
2BZW	AB	TRANSCRIPTION	A	1.4	4.1	3	13	AYQSFEQVVNELF	6195
2C5I	TP	PROTEIN TRANSPORT	T	2.1	4.1	2	27	DDQEEEIQDILKDVEETIVDLDRSIIV	6196
2CCI	AB	CELL CYCLE	B	1.4	4.1	3	17	LQLVGTAAMLLASKFEE	6197
2D7D	AB	HYDROLASE/DNA	A	2.1	4.1	2	14	TLERIEIIRDLRLG	6198
2DBU	CD	TRANSFERASE	C	2.1	4.1	2	17	DALADDLKTYGSEVLPN	6199
2DOQ	BD	CELL CYCLE	B	2.1	4.1	2	13	PLDEIKRAFQLFD	6200
2E 74	BG	PHOTOSYNTHESIS	G	1.4	4.1	3	26	PLLDGLVLGLVFATLGGLFYAAYQQY	6201
2E 74	BH	PHOTOSYNTHESIS	H	2.1	4.1	2	24	IDVLGWVALLVVFTWSIAMVVWGR	6202
2E1M	BC	OXIDOREDUCTASE	B	2.1	4.1	2	12	EADWKRELDAIA	6203
2E9X	BC	REPLICATION	B	2.1	4.1	2	29	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	6204
2ERJ	CD	IMMUNE SYSTEM/CYTOKINE	D	4.1	4.1	1	20	IVEFLNRWITFAQSIISTLT	6205
2F9I	AB	TRANSFERASE	A	1.4	4.1	3	14	QSESIATNLIEMAS	6206
2FBW	AB	OXIDOREDUCTASE	B	2.1	4.1	2	8	IEDRQKLD	6207
2FHJ	CD	TRANSFERASE	C	2.1	4.1	2	12	HKWAMIAVKEAT	6208
2FKW	CD	MEMBRANE PROTEIN, PHOTOSYNTHESIS	D	2.1	4.1	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	6209
2FKW	IJ	MEMBRANE PROTEIN, PHOTOSYNTHESIS	J	2.1	4.1	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	6210

2FMM	ED	TRANSCRIPTION	E	2.1	4.1	2	27	RDECKRILRKLELEAYAGVISALRAQG	6211
2GTL	EH	OXYGEN STORAGE/TRANSPORT	E	1.4	4.1	3	16	LVLQSHLGHLADQHIQ	6212
2GTL	JK	OXYGEN STORAGE/TRANSPORT	K	1.4	4.1	3	19	PKFSAHALRILNGLDLAIN	6213
2GTL	MN	OXYGEN STORAGE/TRANSPORT	M	2.1	4.1	2	19	YLVKNQNLHIDYLAKKLHD	6214
2H0D	AB	METAL BINDING PROTEIN/LIGASE	A	1.4	4.1	3	11	KTLQDIVYKLV	6215
2HD5	AB	HYDROLASE	A	2.1	4.1	2	16	AQEFLRFLLDGLHNEV	6216
2HHF	AB	TRANSFERASE	A	2.1	4.1	2	16	GGNYGPTVLVQQEALK	6217
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	C	2.1	4.1	2	11	GTVALREIRRY	6218
2HLD	AD	HYDROLASE	A	4.1	4.1	1	14	RSTVAQLVQTLEQH	6219
2HNT	LE	SERINE PROTEASE	E	4.1	4.1	1	8	RETAASLL	6220
2HWN	AE	TRANSFERASE	E	2.1	4.1	2	17	LAWKIAKMIVSDVMQQC	6221
2HYB	AB	TRANSFERASE	A	1.4	4.1	3	11	LGQLVEAAIQA	6222
2HYB	EF	TRANSFERASE	F	2.1	4.1	2	9	SLESCLKFA	6223
2HZM	EF	TRANSCRIPTION	E	2.1	4.1	2	6	PALVFN	6224
2I2X	CB	TRANSFERASE	B	4.1	4.1	1	6	YNVALE	6225
2IBZ	CG	OXIDOREDUCTASE	C	1.4	4.1	3	36	VPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	6226
2ISS	AD	LYASE, TRANSFERASE	A	2.1	4.1	2	11	AEQAKIAEEAG	6227
2J3W	CF	TRANSPORT	C	2.1	4.1	2	21	EDGIKNFFTDVYDLYIKFAMN	6228
2JBL	LM	ELECTRON TRANSPORT	L	1.4	4.1	3	26	ALSIHRLGLFLASNIFLTGAFGTIAS	6229
2JIZ	BE	HYDROLASE	B	2.1	4.1	2	14	RSTVAQLVKRLTDA	6230
2JJ0	LM	PHOTOSYNTHESIS	M	2.1	4.1	2	7	ELEQIAD	6231
2NXX	AE	HORMONE/GROWTH FACTOR	A	2.1	4.1	2	23	VQEVEMLREKIYGVLEEYTRTTH	6232
2NXX	AE	HORMONE/GROWTH FACTOR	A	2.1	4.1	2	11	RLPALRSIGLK	6233
2OBH	AC	CELL CYCLE	A	2.1	4.1	2	29	FGDFLTVMTQKMSEKDTKEEILKAFKLFD	6234
2P1N	AB	SIGNALING PROTEIN	A	4.1	4.1	1	6	ENQWAF	6235
2P1N	DE	SIGNALING PROTEIN	D	2.1	4.1	2	14	EEEEEVRRENQWAF	6236
2P58	BC	TRANSPORT PROTEIN/CHAPERONE	C	1.4	4.1	3	14	LNVLLAEIALIGTG	6237
2PBD	AP	STRUCTURAL PROTEIN	P	2.1	4.1	2	18	GGLINKKCYEMASHLRRS	6238
2PBI	CD	SIGNALING PROTEIN	D	1.4	4.1	3	22	LASLKSEAESLKGKLEEERAKL	6239
2PJR	FG	HYDROLASE/DNA	F	1.4	4.1	3	13	EADEAQFVAGRIR	6240
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	V	2.1	4.1	2	15	IYDRLLEQQLQSINL	6241
2PL9	CF	SIGNALING PROTIEN	F	1.4	4.1	3	12	QDQVDDLLDSLG	6242
2PUK	AC	ELECTRON TRANSPORT	C	1.4	4.1	3	17	GPSKLIAPVIDELAKEY	6243
2QI9	AC	MEMBRANE PROTEIN	C	2.1	4.1	2	8	VWHYLTLH	6244
2QM6	AB	TRANSFERASE	A	2.1	4.1	2	7	SSSKKYF	6245
2QNA	AB	TRANSPORT PROTEIN	A	4.1	4.1	1	19	DGVVACAAGLIGDLCTAFG	6246
2QNA	AB	TRANSPORT PROTEIN	A	2.1	4.1	2	19	NKAKTLATWATKELRKLKN	6247
2QRV	DC	TRANSFERASE/TRANSFERASE REGULATOR	D	2.1	4.1	2	11	VSDKRDISRFL	6248

2QVS	EB	TRANSFERASE/TRANSFERASE REGULATOR	B	4.1	4.1	1	25	RVTFRRIIVKNNAKKRKMFESFIES	6249
2RD4	AB	HYDROLASE	B	4.1	4.1	1	6	WWDFAD	6250
2UUN	EF	ELECTRON TRANSPORT	E	2.1	4.1	2	12	PLTDAVSTADSQ	6251
2UUN	GH	ELECTRON TRANSPORT	H	2.1	4.1	2	12	AFTKVAAQADTR	6252
2UUN	UV	ELECTRON TRANSPORT	V	2.1	4.1	2	12	AFTKVAAQADTR	6253
2UZ1	AB	LYASE	B	2.1	4.1	2	12	GATLHFQQLAVG	6254
2V1S	DK	OXIDOREDUCTASE	K	4.1	4.1	1	9	LSRLLSYAG	6255
2VGO	BC	TRANSFERASE	C	2.1	4.1	2	5	LEELF	6256
2VN5	CD	CELL ADHESION	D	2.1	4.1	2	13	ALDFAGLKKYIMA	6257
2W2X	BC	SIGNALING PROTEIN/HYDROLASE	B	2.1	4.1	2	9	DRLRPLSYP	6258
2WAQ	AB	TRANSCRIPTION	A	1.4	4.1	3	20	PTELFFHAAGGREGLVDTAV	6259
2WBJ	FH	IMMUNE SYSTEM	F	2.1	4.1	2	12	YCRHNYGVVESF	6260
2WIN	CD	IMMUNE SYSTEM	D	4.1	4.1	1	5	KYELD	6261
2ZCY	HI	HYDROLASE	I	2.1	4.1	2	18	PEDLFETISQALLNAADR	6262
2ZCY	IY	HYDROLASE	Y	2.1	4.1	2	13	VGELFWKVKEEEG	6263
2ZCY	RS	HYDROLASE	S	2.1	4.1	2	13	FQVEYALEAIKQG	6264
2ZNL	AB	TRANSCRIPTION	A	2.1	4.1	2	22	PQLEGFSAESRKLLLIVQALRD	6265
3BLW	GH	OXIDOREDUCTASE	H	2.1	4.1	2	11	IDNSVLKVVTN	6266
3BO0	AC	RIBOSOME	A	4.1	4.1	1	7	IPILEKI	6267
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	B	2.1	4.1	2	22	FDNFISCLVRLDAMFRAFRSLD	6268
3BPN	AC	CYTOKINE/CYTOKINE RECEPTOR	A	2.1	4.1	2	19	LENFLERLKTIMREKYSKC	6269
3C01	AE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	A	2.1	4.1	2	9	EQVKSDIEN	6270
3CMA	FM	RIBOSOME	M	2.1	4.1	2	9	AYSYIRDAW	6271
3CWB	DJ	OXIDOREDUCTASE	D	1.4	4.1	3	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	6272
3DCG	DE	LIGASE/VIRAL PROTEIN	D	4.1	4.1	1	17	SHVLSKVCMYFTYKVRY	6273
3DHH	AB	OXIDOREDUCTASE	A	2.1	4.1	2	7	LFFPHEY	6274
3DHR	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	2.1	4.1	2	16	AGDLGGEALERLFITY	6275
3DHR	EF	OXYGEN STORAGE, OXYGEN TRANSPORT	F	2.1	4.1	2	16	VADCGAEALARLLIVY	6276
3DQV	DY	LIGASE	D	2.1	4.1	2	12	TFQLAVLFAWNQ	6277
3DUF	GF	OXIDOREDUCTASE/TRANSFERASE	G	2.1	4.1	2	13	FNLKEQYEIYKEK	6278
3DWL	BI	STRUCTURAL PROTEIN	I	1.4	4.1	3	19	FRNTLHFHIKASKAYMHQR	6279
3E3Q	HI	IMMUNE SYSTEM	H	2.1	4.1	2	24	AAEYYRAYLEGECVEWLHRYLKNG	6280
3EH3	AC	OXIDOREDUCTASE	C	2.1	4.1	2	14	LVFWLGVYAVFFAR	6281
3EZQ	GH	APOPTOSIS	G	2.1	4.1	2	33	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	6282
3F9K	IK	VIRAL PROTEIN, RECOMBINATION	I	1.4	4.1	3	12	IEPAQEEHEKYH	6283
3F9K	NO	VIRAL PROTEIN, RECOMBINATION	N	2.1	4.1	2	11	QEVKMVAWWIG	6284

3F9K	RS	VIRAL PROTEIN, RECOMBINATION	R	2.1	4.1	2	11	QEVKMVAWWIG	6285
3FAL	AD	SIGNALING PROTEIN	D	2.1	4.1	2	9	PLLSEIWDV	6286
3FGC	CD	OXIDOREDUCTASE	D	4.1	4.1	1	7	SADMRFF	6287
3FGC	CD	OXIDOREDUCTASE	D	4.1	4.1	1	11	PLTVAGFLLGM	6288
3FH9	AB	OXYGEN TRANSPORT	A	2.1	4.1	2	16	VGEYGAEALERMFLSF	6289
3FKS	JN	HYDROLASE	J	2.1	4.1	2	12	VFYLHSRLLERA	6290
3FKS	KO	HYDROLASE	K	4.1	4.1	1	7	VFYLHSR	6291
3FWC	AB	CELL CYCLE, TRANSCRIPTION	A	2.1	4.1	2	13	PLDEIKRAFQLFD	6292
3FWC	BC	CELL CYCLE, TRANSCRIPTION	C	1.4	4.1	3	14	WVDKVKDLTKSEMN	6293
3FWC	BD	CELL CYCLE, TRANSCRIPTION	D	1.4	4.1	3	16	WVDKVKDLTKSEMNIN	6294
3FWC	FG	CELL CYCLE, TRANSCRIPTION	G	1.4	4.1	3	13	WVDKVKDLTKSEM	6295
3FXD	AB	UNKNOWN FUNCTION	B	1.4	4.1	3	22	KDNTDAVEVLTELNTKVERAAL	6296
3GLI	FJ	TRANSFERASE/DNA	F	1.4	4.1	3	19	QTQLRQAVQLLTRTELTLK	6297
3H0L	VX	LIGASE	X	2.1	4.1	2	11	REWVLKIAKLA	6298
3HGK	CG	TRANSFERASE	C	4.1	4.1	1	7	PEYFIKG	6299
3HKZ	IJ	TRANSFERASE	I	4.1	4.1	1	6	FAYVMA	6300
3HPG	BG	TRANSFERASE	B	2.1	4.1	2	10	ESTQLLMKYL	6301
3HQR	AS	OXIDOREDUCTASE/TRANSCRIPTION	A	2.1	4.1	2	13	ADERAAAKVKYLT	6302
1A0O	AB	CHEMOTAXIS	A	2.0	4.0	2	14	AATLEEKLNKIFEK	6303
1AOI	EF	DNA BINDING PROTEIN/DNA	E	1.3	4.0	3	13	TVALREIRRYQKS	6304
1AOI	FH	DNA BINDING PROTEIN/DNA	H	2.0	4.0	2	12	SREIQTAVRLLL	6305
1B4U	CD	DIOXYGENASE	C	2.0	4.0	2	9	VHAYLAEFD	6306
1B5F	AB	HYDROLASE	A	2.0	4.0	2	11	TAIVTQINHAI	6307
1BGY	EJ	ELECTRON TRANSPORT	J	1.3	4.0	3	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	6308
1BR1	AB	MUSCLE PROTEIN	B	1.3	4.0	3	9	EEEVEQLVA	6309
1CDL	DH	CALCIUM-BINDING PROTEIN	D	1.3	4.0	3	9	FPEFLTMMA	6310
1CPC	KL	LIGHT HARVESTING PROTEIN	K	1.3	4.0	3	27	STEIQTAFGRFRQASASLAAAKALTEK	6311
1D2Z	CB	APOPTOSIS	C	2.0	4.0	2	7	HNAMRLI	6312
1DTD	AB	HYDROLASE/HYDROLASE INHIBITOR	B	2.0	4.0	2	7	PWCREGA	6313
1E3A	AB	ANTIBIOTIC RESISTANCE	A	1.3	4.0	3	22	PEDMSILQGYADGMNAWIDKVN	6314
1EQZ	FH	STRUCTURAL PROTEIN/DNA	H	2.0	4.0	2	11	AMDVVYALKRQ	6315
1FDH	BH	OXYGEN TRANSPORT	H	2.0	4.0	2	19	PEVQASWQKMVTGVASALS	6316
1FNT	AH	HYDROLASE/HYDROLASE ACTIVATOR	A	4.0	4.0	1	22	IPDARNAALRAKAEAAEFRYKY	6317
1FNT	DK	HYDROLASE/HYDROLASE ACTIVATOR	K	1.3	4.0	3	23	AGDTVQFAEYIQANIQLYSIRED	6318
1FNT	Za	HYDROLASE/HYDROLASE ACTIVATOR	a	4.0	4.0	1	15	INSAARNIQHLLYGK	6319
1FOE	CD	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	D	2.0	4.0	2	5	DRLRP	6320
1FYZ	BD	OXIDOREDUCTASE	B	2.0	4.0	2	21	AKEYARMEAVKDERQFGSLQD	6321
1G0U	AG	HYDROLASE	A	2.0	4.0	2	12	GQIDYALTAVKQ	6322
1G0U	HI	HYDROLASE	H	4.0	4.0	1	22	AADTEAVTQLIGSNIELHSLYT	6323

1G0U	VW	HYDROLASE	W	4.0	4.0	1	18	PEDLFETISQALLNAADR	6324
1G20	AE	OXIDOREDUCTASE	E	2.0	4.0	2	15	AGRGVITAINFLEEE	6325
1G3I	TM	CHAPERONE/HYDROLASE	M	4.0	4.0	1	13	ADAFTLFELFERK	6326
1G4Y	BR	SIGNALING PROTEIN	B	1.3	4.0	3	44	HAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQANTLVDLAKTQLH	6327
1H2S	AB	MEMBRANE PROTEIN	A	2.0	4.0	2	34	PTVDVALIVYLDLVTKVGFGFIALDAAATLRAEH	6328
1HR0	JN	RIBOSOME	N	1.3	4.0	3	11	RICLRELAHKG	6329
1HR8	CD	HYDROLASE	D	4.0	4.0	1	11	QQGIELEIENI	6330
1HT1	BF	CHAPERONE	B	1.3	4.0	3	12	TLFELFERKLEM	6331
1HXY	AB	IMMUNE SYSTEM/TOXIN	A	2.0	4.0	2	22	AQGALANIAVDKANLEIMTKRS	6332
1IK9	AC	GENE REGULATION/LIGASE	C	1.3	4.0	3	11	LNQLKEVFSGI	6333
1IR2	U2	LYASE	U	1.3	4.0	3	14	AKNYGRAVYECLRG	6334
1IR2	X1	LYASE	X	2.0	4.0	2	6	WTDGLT	6335
1IRU	QR	HYDROLASE	Q	2.0	4.0	2	15	CEQLVTALCDIKQAY	6336
1IW7	CF	TRANSFERASE	C	1.3	4.0	3	11	PEERLLRSIFG	6337
1IW7	NP	TRANSFERASE	P	2.0	4.0	2	16	STSDPVRQYLHEIGQV	6338
1J1D	BC	CONTRACTILE PROTEIN	C	2.0	4.0	2	18	REAEERRGEKGRALSTRA	6339
1JB0	AB	PHOTOSYNTHESIS	B	1.3	4.0	3	17	RGYWQELIETLVWAHER	6340
1JD2	2U	HYDROLASE	U	1.3	4.0	3	22	AADTQAIADIVQYHLELYTSQY	6341
1JEB	CB	OXYGEN STORAGE/TRANSPORT	B	4.0	4.0	1	6	PWTQRY	6342
1JJO	DF	SIGNALING PROTEIN	D	4.0	4.0	1	6	LIEEWA	6343
1JNR	CD	OXIDOREDUCTASE	C	1.3	4.0	3	10	VSQALLWACQ	6344
1JPW	BE	CELL ADHESION	B	1.3	4.0	3	18	DSVLFYAITTLHNLLLHQ	6345
1JR3	DE	TRANSFERASE	D	1.3	4.0	3	19	QTQLRQAVQLLTRTELTLK	6346
1JY2	OP	BLOOD CLOTTING	O	1.3	4.0	3	28	GCKLQDTLVRQERPIRKSIEDLRNTVDS	6347
1K3Z	AD	TRANSCRIPTION	D	2.0	4.0	2	9	ALHLAVIHQ	6348
1K6L	MH	PHOTOSYNTHESIS	M	2.0	4.0	2	7	TLLGWFG	6349
1KD8	AB	DE NOVO PROTEIN	A	1.3	4.0	3	34	VKQLEAEVEEIESEVWHLENEVARLEKENAECEA	6350
1KN1	AB	ELECTRON TRANSPORT	A	2.0	4.0	2	12	IVTKSIVNADAE	6351
1LTX	AB	TRANSFERASE/PROTEIN BINDING	A	2.0	4.0	2	13	YSSWHYRSCLLPQ	6352
1MIO	AB	MOLYBDENUM-IRON PROTEIN	A	2.0	4.0	2	8	IKEKFVIQ	6353
1MTY	DB	MONOOXYGENASE	B	2.0	4.0	2	11	PEMAAVILKAL	6354
1MTY	DB	MONOOXYGENASE	D	1.3	4.0	3	10	PLWKGMKRVF	6355
1MVW	JW	CONTRACTILE PROTEIN	W	1.3	4.0	3	9	QAVLSLYAS	6356
1MVW	P1	CONTRACTILE PROTEIN	1	1.3	4.0	3	9	QAVLSLYAS	6357
1MZN	EF	TRANSCRIPTION	E	2.0	4.0	2	8	TFLMEMLE	6358
1N1J	AB	DNA BINDING PROTEIN	A	2.0	4.0	2	29	KDAKECVQECVSEFISFITSEASERCHQE	6359
1N95	AB	TRANSFERASE	A	2.0	4.0	2	13	ESAWNYLKGILQD	6360
1NI4	CD	OXIDOREDUCTASE	D	4.0	4.0	1	13	IDQVINSAAKTYY	6361
1NMU	CB	SUGAR BINDING PROTEIN/RIBOSOME	B	1.3	4.0	3	11	KSELEYYAMLS	6362

1NTK	AB	OXIDOREDUCTASE	A	2.0	4.0	2	8	LEKEVESM	6363
1O18	MZ	CONTRACTILE PROTEIN	Z	1.3	4.0	3	9	QAVLSLYAS	6364
1OCC	EI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	E	4.0	4.0	1	11	KEIYPYVIQEL	6365
1OCC	PT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	T	1.3	4.0	3	10	ARTWRFLTFG	6366
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	R	2.0	4.0	2	16	FASAVRILEVVKDKAG	6367
1OCC	RV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	R	4.0	4.0	1	11	KEIYPYVIQEL	6368
1OR7	AC	TRANSCRIPTION	A	2.0	4.0	2	11	QKAFNLLVVRY	6369
1PIV	13	VIRUS	3	2.0	4.0	2	6	MMELAE	6370
1PK1	CD	TRANSCRIPTION REPRESSION	D	1.3	4.0	3	14	LGPALKICNLVNKV	6371
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.3	4.0	3	28	GLWLIASFFMFVAVWSWWGRTYLRAQAL	6372
1Q5Q	AH	HYDROLASE	A	2.0	4.0	2	22	YNEFENLRRAGIVHADMRGYSY	6373
1R27	CD	OXIDOREDUCTASE	D	1.3	4.0	3	6	YPRIEA	6374
1R4M	CD	CELL CYCLE	C	2.0	4.0	2	32	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS	6375
1RM6	DF	OXIDOREDUCTASE	D	2.0	4.0	2	22	PLAVEGQTQGGVWMGMGQALSE	6376
1RUY	LK	VIRAL PROTEIN	L	2.0	4.0	2	10	YEELREQLSS	6377
1RV6	VY	HORMONE/GROWTH FACTOR/RECEPTOR	V	2.0	4.0	2	8	FQEVWGRS	6378
1RYP	AG	MULTICATALYTIC PROTEINASE	A	1.3	4.0	3	22	IPDARNAALRAKAEAAEFRYKY	6379
1S5E	BM	TRANSERASE,TOXIN	M	2.0	4.0	2	20	DSQKKAIERMKDTLRIAYLT	6380
1S5L	LT	PHOTOSYNTHESIS	T	2.0	4.0	2	14	FACIIALFFFAIFF	6381
1SQB	AB	OXIDOREDUCTASE	A	1.3	4.0	3	19	ESEVLRGKNLLRNALVSHL	6382
1SUV	AE	METAL TRANSPORT	A	4.0	4.0	1	16	EEYNSQLLSFVRDLNQ	6383
1T3M	CB	HYDROLASE	B	2.0	4.0	2	7	GEVFIRA	6384
1TY4	AC	APOPTOSIS	A	4.0	4.0	1	13	AENFETFCEQLLA	6385
1U3H	CD	IMMUNE SYSTEM	C	2.0	4.0	2	6	VLTKRS	6386
1UPT	DC	HYDROLASE/PROTEIN-BINDING	D	4.0	4.0	1	13	TEFEYLRKVLFEY	6387
1UZD	HP	LYASE	H	2.0	4.0	2	6	WTDGLT	6388
1UZD	HW	LYASE	H	1.3	4.0	3	15	AKNYGRAVYECLRGG	6389
1V4U	CD	OXYGEN STORAGE/TRANSPORT	C	2.0	4.0	2	16	ADAIGADALGRMLAVY	6390
1V54	CJ	OXIDOREDUCTASE	J	1.3	4.0	3	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	6391
1V54	NS	OXIDOREDUCTASE	N	2.0	4.0	2	5	LEWLN	6392
1V54	OQ	OXIDOREDUCTASE	Q	4.0	4.0	1	14	EEWVAKQTKRMLDM	6393
1V54	PT	OXIDOREDUCTASE	P	1.3	4.0	3	25	VPLLNTSVLLASGVSITWAHHSLME	6394
1VYT	AE	TRANSPORT PROTEIN	A	2.0	4.0	2	12	PKVLQRLIRSRG	6395
1WDW	EF	LYASE	E	1.3	4.0	3	8	YNPIYRAG	6396
1WDW	KL	LYASE	L	2.0	4.0	2	19	ETLIEPLKELEKAYKRFKD	6397

1WYU	AB	OXIDOREDUCTASE	A	2.0	4.0	2	9	PVVQALAAR	6398
1WYU	EF	OXIDOREDUCTASE	E	1.3	4.0	3	15	EWKVLEELRRLAAQN	6399
1XME	AC	OXIDOREDUCTASE	A	2.0	4.0	2	36	PTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLR	6400
1XWJ	AB	CELL ADHESION/PROTEIN BINDING	A	1.3	4.0	3	21	RTIESILEPVAQQISHLVIMH	6401
1YA7	DK	HYDROLASE/HYDROLASE ACTIVATOR	K	2.0	4.0	2	23	VGDAQVLVRYMKAELELYRLQRR	6402
1YEW	FG	OXIDOREDUCTASE, MEMBRANE PROTEIN	G	2.0	4.0	2	9	QDGTWHQTI	6403
1YFN	AE	PROTEIN BINDING	E	2.0	4.0	2	5	PHQWQ	6404
1YHU	MO	OXYGEN STORAGE/TRANSPORT	M	1.3	4.0	3	20	PEFKAHIARVLGGLDRVISM	6405
1YNJ	CD	TRANSFERASE	D	2.0	4.0	2	9	PEKIRSWSY	6406
1YV0	TI	CONTRACTILE PROTEIN	I	1.3	4.0	3	19	KLHAKIDSVDEERYDTEVK	6407
1Z6O	BM	METAL BINDING PROTEIN	M	2.0	4.0	2	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	6408
1Z6O	FQ	METAL BINDING PROTEIN	Q	2.0	4.0	2	35	YHLVDYLTGDFLEEQYKGQRDLAGKASTLKKLMDR	6409
1ZAV	AW	STRUCTURAL PROTEIN	W	1.3	4.0	3	16	VSELAELVKKLEDKFG	6410
1ZBA	24	VIRUS	4	4.0	4.0	1	8	WFSKLASS	6411
1ZBB	AG	STRUCTURAL PROTEIN/DNA	A	1.3	4.0	3	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	6412
1ZOQ	BD	TRANSCRIPTION/TRANSFERASE	D	2.0	4.0	2	12	PQLMAAFIKQRT	6413
1ZV8	CD	VIRAL PROTEIN	C	1.3	4.0	3	45	KQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQ	6414
2ADV	AC	HYDROLASE	A	4.0	4.0	1	11	VPERAQQWYAQ	6415
2AFH	AB	OXIDOREDUCTASE	B	2.0	4.0	2	16	QGCVAYFRSYFNRHFR	6416
2BA0	CH	RNA BINDING PROTEIN	H	1.3	4.0	3	17	DILVDIKRDYVLSKLRD	6417
2BGN	CG	HYDROLASE	G	2.0	4.0	2	17	DAIKRIAYEFVEMKAKD	6418
2BYP	BG	RECEPTOR	G	4.0	4.0	1	6	PRCAWR	6419
2CZV	BD	HYDROLASE	D	2.0	4.0	2	10	VEYLRFALML	6420
2D7D	AB	HYDROLASE/DNA	B	1.3	4.0	3	19	ERQKVVEQMEHEMKEAAKA	6421
2DD4	HI	HYDROLASE	I	1.3	4.0	3	5	EWYRS	6422
2DFK	AB	CELL CYCLE	B	2.0	4.0	2	7	LRPLSYP	6423
2DFS	MN	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	1.3	4.0	3	38	QVAYLEKIRADKLRAACIRIQKTIRGWLMRKKYMRMRR	6424
2DXB	KL	HYDROLASE	K	2.0	4.0	2	16	YYGRWLLTAARILVDK	6425
2DXB	TU	HYDROLASE	U	1.3	4.0	3	5	EWYRS	6426
2DXB	VW	HYDROLASE	W	4.0	4.0	1	9	AEERRRKQN	6427
2E1M	AC	OXIDOREDUCTASE	A	2.0	4.0	2	11	TYEQLARELLL	6428
2E5L	JN	RIBOSOME	N	1.3	4.0	3	11	RICLRELAHKG	6429
2E9X	BC	REPLICATION	C	1.3	4.0	3	15	NADISQSLLQTFIGR	6430
2EHO	EG	REPLICATION	G	4.0	4.0	1	10	LWLAINLKQR	6431
2EHO	KL	REPLICATION	L	2.0	4.0	2	19	RGLFQTGQKGLNDFQCWEK	6432
2ES4	AD	HYDROLASE	D	2.0	4.0	2	35	PEAAARAAQMQQDDEAWQTRYQAYAAERDRIAAQG	6433
2FIF	EF	PROTEIN TURNOVER/ENDOCYTOSIS	F	1.3	4.0	3	35	SKCWREEYHKARQKQIQEDWELAERLQREEEEAFA	6434

2FK0	EF	VIRAL PROTEIN	F	1.3	4.0	3	23	KESTQKAIDGVTNKVNSIIDKMN	6435
2FKW	KL	MEMBRANE PROTEIN, PHOTOSYNTHESIS	L	2.0	4.0	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	6436
2G38	CD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	1.3	4.0	3	45	PVVMQLMEAAKPFVRWLTDLCVQLSEVERQIHEIVRAYEWAHHDM	6437
2GEZ	GH	HYDROLASE	G	2.0	4.0	2	22	RRKPREEGLRHCLQIGVEALKA	6438
2GWW	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.3	4.0	3	25	TAPVAAVQAAVSNLVRVGKETVQTT	6439
2HGR	GH	RIBOSOME	G	2.0	4.0	2	8	QLVIEFYS	6440
2HYB	JK	TRANSFERASE	J	1.3	4.0	3	11	LGQLVEAAIQA	6441
2I94	AB	PROTEIN BINDING	A	4.0	4.0	1	15	EEELSSWYQSFLKEC	6442
2INP	AC	OXIDOREDUCTASE	A	2.0	4.0	2	29	ARYVNALKLFISGISPLEHAAFQGYSKVG	6443
2J5G	AD	HYDROLASE	A	2.0	4.0	2	20	PREWDKTYWEGKKVLQNLLD	6444
2JBL	LM	ELECTRON TRANSPORT	M	2.0	4.0	2	28	GWWLMAGLFMTLSLGSWWIRVYSRARAL	6445
2JIZ	CD	HYDROLASE	C	2.0	4.0	2	12	VFYLHSRLLERA	6446
2NQB	AB	STRUCTURAL PROTEIN/DNA	A	1.3	4.0	3	13	TVALREIRRYQKS	6447
2ONL	AC	TRANSFERASE	A	2.0	4.0	2	21	DDHVQFLIYQILRGLKYIHSA	6448
2ONL	BD	TRANSFERASE	D	2.0	4.0	2	10	PLLLKRRKKA	6449
2OT3	AB	PROTEIN TRANSPORT	A	2.0	4.0	2	16	ADDFLPTLIYIVLKGN	6450
2P2C	AB	HYDROLASE	B	2.0	4.0	2	13	WYIEALAQVFSER	6451
2PK9	CD	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	C	1.3	4.0	3	13	STAIREISLMKEL	6452
2PMS	AC	METAL TRANSPORT, HYDROLASE	C	2.0	4.0	2	19	PQAKIAELENQVHRLEQEL	6453
2PQR	AC	APOPTOSIS	C	4.0	4.0	1	7	TTFRILA	6454
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	A	2.0	4.0	2	11	PIQIYEKIVSG	6455
2QEX	FM	RIBOSOME	M	2.0	4.0	2	9	AYSYIRDAW	6456
2QKM	GH	HYDROLASE	H	2.0	4.0	2	22	VERLCFQIEQAHWFYEDFIRAQ	6457
2QL5	AB	HYDROLASE	B	1.3	4.0	3	11	WFVQALCSILE	6458
2R1H	AB	OXYGEN BINDING	A	2.0	4.0	2	21	PEIHLSVDKFLQQLALALAEK	6459
2RHK	AC	VIRAL PROTEIN/NUCLEAR PROTEIN	C	2.0	4.0	2	6	YFYSKF	6460
2ROC	AB	APOPTOSIS	A	2.0	4.0	2	9	WDGFVEFFH	6461
2UUN	IJ	ELECTRON TRANSPORT	J	2.0	4.0	2	12	AFTKVAAQADTR	6462
2UUN	QR	ELECTRON TRANSPORT	R	2.0	4.0	2	12	AFTKVAAQADTR	6463
2UUN	WX	ELECTRON TRANSPORT	X	2.0	4.0	2	12	AFTKVAAQADTR	6464
2UVP	AB	UNKNOWN FUNCTION	B	2.0	4.0	2	12	HWFLNYILSNLN	6465
2V36	AB	TRANSFERASE	B	1.3	4.0	3	17	ATIISSVLQTILYHIEY	6466
2V4Z	AB	CELL CYCLE	B	1.3	4.0	3	21	TTAQKRVYSLMENDSYPRFLK	6467
2VE7	AC	CELL CYCLE	A	2.0	4.0	2	22	TWPHIVAALVWLIDCIKIHTAM	6468
2VL5	CD	IMMUNE SYSTEM	D	2.0	4.0	2	7	SEQLTSG	6469

2VOI	AB	APOPTOSIS	A	2.0	4.0	2	21	WGRIVTIFAFGGVLLKKLKQE	6470
2VPG	AB	GENE REGULATION	B	2.0	4.0	2	13	TEMANKAAEAVLK	6471
2VYR	AE	IMMUNE SYSTEM	A	2.0	4.0	2	15	VKEVMHYLGQYIMVK	6472
2W73	AL	METAL BINDING PROTEIN	L	2.0	4.0	2	16	IRNKIRAIGKMARVFS	6473
2W73	FO	METAL BINDING PROTEIN	F	4.0	4.0	1	11	AAELRHVMTNL	6474
2W85	AB	PROTEIN TRANSPORT	B	2.0	4.0	2	11	QEKFFQELFDS	6475
2WIN	GH	IMMUNE SYSTEM	G	2.0	4.0	2	7	KGVFVLN	6476
2ZAE	AB	HYDROLASE	B	1.3	4.0	3	18	PDLAKRYVELALEIQKKA	6477
2ZCY	JY	HYDROLASE	Y	2.0	4.0	2	10	QTFAYGVLDS	6478
3A0B	bd	ELECTRON TRANSPORT	b	2.0	4.0	2	9	VFALLFFFG	6479
3C1B	GH	STRUCTURAL PROTEIN/DNA	H	1.3	4.0	3	12	AIYVYKVLKQVH	6480
3C7B	DE	OXIDOREDUCTASE	D	2.0	4.0	2	6	HCINKM	6481
3C7B	DE	OXIDOREDUCTASE	D	4.0	4.0	1	16	GARGLLKQLEISYKDK	6482
3C91	CJ	HYDROLASE	C	1.3	4.0	3	23	VADARVLVDFARISAQQEKVTYG	6483
3CJH	GJ	PROTEIN TRANSPORT	G	2.0	4.0	2	25	DACIDQCLAKYMRSWNVISKAYISR	6484
3CJT	OP	TRANSFERASE/RIBOSOMAL PROTEIN	O	4.0	4.0	1	5	DEDWL	6485
3D24	CD	TRANSCRIPTION	C	2.0	4.0	2	22	VATLCDLFDREIVVTISWAKSI	6486
3D4U	AB	HYDROLASE/HYDROLASE INHIBITOR	A	2.0	4.0	2	11	VDGYDYTWKKD	6487
3D4X	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	4.0	4.0	1	19	ENFRLLGNVLVCVLAHHFG	6488
3DBJ	AB	PHOTOSYNTHESIS	A	2.0	4.0	2	12	VVTKSIVNADAE	6489
3DCG	BF	LIGASE/VIRAL PROTEIN	B	4.0	4.0	1	17	SHVLSKVCMYFTYKVRY	6490
3DHH	AB	OXIDOREDUCTASE	B	2.0	4.0	2	8	ERELWEKE	6491
3DHR	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	2.0	4.0	2	19	PEVHASLDKFVLAVGTVLT	6492
3DHT	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	4.0	4.0	1	17	HGGEYGEEALQRMFAAF	6493
3DXR	AB	PROTEIN TRANSPORT	B	1.3	4.0	3	30	QQKIQAAEAELDLVTDMFNKLVNNCYKKCI	6494
3EI4	AB	DNA BINDING PROTEIN	B	1.3	4.0	3	11	IVRTLHQHKLG	6495
3EXG	EF	OXIDOREDUCTASE	F	4.0	4.0	1	15	EMGFAGIAVGAAMAG	6496
3EXH	AC	OXIDOREDUCTASE	C	2.0	4.0	2	13	GQIFEAYNMAALW	6497
3EXH	DC	OXIDOREDUCTASE	D	4.0	4.0	1	14	EMGFAGIAVGAAMA	6498
3EZQ	CD	APOPTOSIS	C	2.0	4.0	2	33	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	6499
3FKU	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	2.0	4.0	2	17	FHDSNVKNLYDKVRLQL	6500
3FWB	BC	CELL CYCLE, TRANSCRIPTION	C	2.0	4.0	2	19	DSTRETVLKQIREFLEEIV	6501
3GCG	AB	SIGNALING PROTEIN/TRANSCRIPTION	A	1.3	4.0	3	9	DRLRPLSYP	6502
3GHG	AC	BLOOD CLOTTING	A	2.0	4.0	2	29	GCRMKGLIDEVNQDFTNRINKLKNSLFEY	6503
3GHG	AC	BLOOD CLOTTING	A	1.3	4.0	3	63	SSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVD MKRLEVDIDIKIRSC	6504
3GZD	DC	LYASE	D	2.0	4.0	2	14	PEVIQAMTKAMWEA	6505

3H0L	GI	LIGASE	I	2.0	4.0	2	11	REWVLKIAKLA	6506
3H2U	CD	CELL ADHESION	C	4.0	4.0	1	21	DIIAAAKRMALLMAEMSRLVR	6507
3HD7	AB	EXOCYTOSIS	A	1.3	4.0	3	44	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIIIIVY	6508
3HOU	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	2.0	4.0	2	14	LAMANSLRRVMIAE	6509
3HOU	DG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	2.0	4.0	2	13	KDLKNTMQYLTNF	6510
6RLX	AB	HORMONE (MUSCLE RELAXANT)	B	2.0	4.0	2	14	RELVRAQIAICGMS	6511
9PAI	AB	HYDROLASE INHIBITOR	A	2.0	4.0	2	22	PPSYVAHLASDFGVRVFQQVAQ	6512
1A4Y	DE	COMPLEX (INHIBITOR/NUCLEASE)	E	2.0	3.9	2	9	RYTHFLTQH	6513
1A9N	AB	RNA BINDING PROTEIN/RNA	B	2.0	3.9	2	12	KEELKRSLYALF	6514
1B33	EF	PHOTOSYNTHESIS	F	2.0	3.9	2	13	AITAVINSSDVQG	6515
1B33	LM	PHOTOSYNTHESIS	M	2.0	3.9	2	12	AITAVINSSDVQ	6516
1B9X	AB	SIGNALING PROTEIN	A	1.3	3.9	3	22	LDQLRQEAEQLKNQIRDARKAC	6517
1BP3	AB	HORMONE/GROWTH FACTOR	A	2.0	3.9	2	30	LSRLFDNAMLRAHRLHQLAFDTYQEFEEAY	6518
1DAN	TU	COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	U	2.0	3.9	2	5	PYLET	6519
1DCE	CD	TRANSFERASE	C	2.0	3.9	2	14	FHCWDYRRFVAAQA	6520
1DE4	GI	METAL TRANSPORT INHIBITOR/RECEPTOR	G	2.0	3.9	2	12	AWPTKLEWERHK	6521
1DGH	AD	OXIDOREDUCTASE	A	1.3	3.9	3	19	KMLQGRLFAYPDTHRHRLG	6522
1E0F	AD	COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B	A	2.0	3.9	2	11	KTERELLESYI	6523
1E6Y	EF	OXIDOREDUCTASE	E	2.0	3.9	2	23	VPKWNACAAVGTLAATLVNCGAG	6524
1EFP	AB	ELECTRON TRANSPORT	B	2.0	3.9	2	6	VDELVG	6525
1EIY	AB	LIGASE/RNA	A	2.0	3.9	2	14	MAHLKGAIYELAQA	6526
1FFT	AB	OXIDOREDUCTASE	A	1.3	3.9	3	14	AIPTGVKIFNWLFT	6527
1FNT	OV	HYDROLASE/HYDROLASE ACTIVATOR	O	3.9	3.9	1	22	IPDARNAALRAKAEAAEFRYKY	6528
1FPP	BA	PRENYLTRANSFERASE	A	3.9	3.9	1	16	EKFRDVYDYFRAVLQR	6529
1G3I	EK	CHAPERONE/HYDROLASE	K	2.0	3.9	2	13	LLKSAVELAKDWR	6530
1GH0	KL	PHOTOSYNTHESIS	K	2.0	3.9	2	25	QRGKDKCARDIGYYLRMVTYCLIAG	6531
1GOT	AB	COMPLEX (GTP-BINDING/TRANSDUCER)	A	2.0	3.9	2	8	RKKWIHCF	6532
1H0H	KL	DEHYDROGENASE	L	1.3	3.9	3	10	GCQVACKQWH	6533
1H2A	SL	OXIDOREDUCTASE	S	2.0	3.9	2	9	IDTLILDTL	6534
1HBR	CD	OXYGEN STORAGE/TRANSPORT	C	2.0	3.9	2	19	PEVHAAFDKFLSAVSAVLA	6535
1ICF	AB	HYDROLASE	A	2.0	3.9	2	12	MDYAFQYVQDNG	6536
1IR2	S1	LYASE	1	2.0	3.9	2	14	DEQIAAQVDYIVAN	6537
1IR2	V5	LYASE	V	2.0	3.9	2	6	WTDGLT	6538
1IR2	Y2	LYASE	Y	2.0	3.9	2	6	WTDGLT	6539

1IR2	Z3	LYASE	Z	2.0	3.9	2	6	WTDGLT	6540
1IRU	AG	HYDROLASE	A	2.0	3.9	2	14	YQVEYAFKAINQGG	6541
1IRU	AG	HYDROLASE	G	2.0	3.9	2	15	LKHLADRVAMYVHAY	6542
1IRU	AH	HYDROLASE	A	2.0	3.9	2	23	TADSRSQVQRARYEAANWKYKYG	6543
1IRU	CD	HYDROLASE	C	2.0	3.9	2	15	CEQLVTALCDIKQAY	6544
1IRU	CD	HYDROLASE	D	2.0	3.9	2	9	TADARIVIN	6545
1IRU	OV	HYDROLASE	O	2.0	3.9	2	23	TADSRSQVQRARYEAANWKYKYG	6546
1IRU	S1	HYDROLASE	1	2.0	3.9	2	22	HGDCLTLTKIIEARLKMYKHSN	6547
1IWA	AP	LYASE	P	2.0	3.9	2	14	DEQIKKQIDYMISK	6548
1IWA	OJ	LYASE	O	2.0	3.9	2	15	GKNYGRVVYEALKGG	6549
1J1D	DE	CONTRACTILE PROTEIN	E	2.0	3.9	2	46	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN	6550
1JD2	DL	HYDROLASE	L	1.3	3.9	3	15	INSAARNIQHLLYGK	6551
1JJO	CE	SIGNALING PROTEIN	C	3.9	3.9	1	6	LIEEWA	6552
1JYO	BE	CHAPERONE	B	2.0	3.9	2	22	TYHIISQLESFVNQQEALKNIL	6553
1JZD	BC	OXIDOREDUCTASE	B	2.0	3.9	2	9	GYSHKLHEQ	6554
1KG0	BC	VIRAL PROTEIN/IMMUNE SYSTEM	B	2.0	3.9	2	9	KDLLEQRRA	6555
1KTD	CD	IMMUNE SYSTEM	D	2.0	3.9	2	12	ELGRPDAENWNS	6556
1KXP	AD	CONTRACTILE PROTEIN/PROTEIN BINDING	D	2.0	3.9	2	11	NDEICEAFRKD	6557
1L9J	MH	PHOTOSYNTHESIS	H	2.0	3.9	2	24	LASLAIYSFWIFLAGLIYYLQTEN	6558
1L9J	RS	PHOTOSYNTHESIS	R	2.0	3.9	2	26	TLGIHRLGLLLSLSAVFFSALCMIIT	6559
1L9J	RS	PHOTOSYNTHESIS	S	2.0	3.9	2	27	PFHGLSIAFLYGSALLFAMHGATILAV	6560
1L9J	ST	PHOTOSYNTHESIS	S	2.0	3.9	2	27	PFHGLSIAFLYGSALLFAMHGATILAV	6561
1LB1	EF	SIGNALING PROTEIN	F	2.0	3.9	2	19	PDSLENIPEKWTPEVKHFC	6562
1LGH	AB	LIGHT HARVESTING COMPLEX	B	2.0	3.9	2	33	EEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWK	6563
1LGH	DE	LIGHT HARVESTING COMPLEX	E	2.0	3.9	2	33	EEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWK	6564
1LGH	GH	LIGHT HARVESTING COMPLEX	H	2.0	3.9	2	33	EEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWK	6565
1LGH	JK	LIGHT HARVESTING COMPLEX	K	2.0	3.9	2	33	EEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWK	6566
1M56	GI	OXIDOREDUCTASE	I	2.0	3.9	2	28	PWMGLIGLVVVLYTMFGWWSDVVTESLE	6567
1M8Q	D9	CONTRACTILE PROTEIN	9	1.3	3.9	3	9	QAVLSLYAS	6568
1M8Q	P0	CONTRACTILE PROTEIN	0	1.3	3.9	3	9	QAVLSLYAS	6569
1MHY	BD	OXIDOREDUCTASE	B	2.0	3.9	2	11	PERAAIIAAAV	6570
1MJG	DP	OXIDOREDUCTASE	P	2.0	3.9	2	30	VALFREVYHGAITATSYAEILLNQAIRTYG	6571
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	G	2.0	3.9	2	20	YLWIEAKLEEKVAVLKARAF	6572
1MT1	EF	LYASE	E	2.0	3.9	2	13	PLNAFDGALLNAG	6573
1MZN	CD	TRANSCRIPTION	C	2.0	3.9	2	7	TFLMEML	6574
1N4Q	IJ	TRANSFERASE	J	2.0	3.9	2	13	EKELNRIKRWCIM	6575
1N5W	BC	OXIDOREDUCTASE	B	2.0	3.9	2	11	AWRLWKVGEQL	6576

1NEX	CD	LIGASE, CELL CYCLE	D	3.9	3.9	1	5	LITSL	6577
1NKP	AB	TRANSCRIPTION/DNA	A	2.0	3.9	2	30	HMNVKRRTHNVLERQRRNELKRSFFALRDQ	6578
1NRL	BD	TRANSCRIPTION	B	2.0	3.9	2	21	LPHMADMSTYMFKGIISFAKV	6579
1NTK	DJ	OXIDOREDUCTASE	D	1.3	3.9	3	24	PEHDHRKRMGLKMLLMMGLLLPLV	6580
1NW9	AB	APOPTOSIS	A	3.9	3.9	1	9	PWEQHAKWY	6581
1NX0	AC	HYDROLASE	A	2.0	3.9	2	14	EVRQFRRLFAQLAG	6582
1OFU	YB	BACTERIAL CELL DIVISION INHIBITOR	Y	3.9	3.9	1	7	HEWLRRA	6583
1PCQ	FT	CHAPERONE	F	1.3	3.9	3	13	IREMLPVLEAVAK	6584
1PGR	CD	CYTOKINE	C	1.3	3.9	3	29	QSFLLKCLEQVRKIQGDGAALQEKLCATY	6585
1PMA	HU	PROTEASE	U	1.3	3.9	3	22	VGDAQVLVRYMKAELELYRLQR	6586
1POI	CD	TRANSFERASE	C	2.0	3.9	2	9	RRFRKWFEA	6587
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	2.0	3.9	2	25	HVPLAFCVPIFMFCVLQVFRPLLLG	6588
1PTO	JH	TOXIN	H	1.3	3.9	3	18	WSMYSRLRKMLYLIYVAG	6589
1Q5R	BJ	HYDROLASE	J	1.3	3.9	3	23	AGIAIELVRLFAVELEHYEKIEG	6590
1Q5R	CJ	HYDROLASE	J	1.3	3.9	3	23	AGIAIELVRLFAVELEHYEKIEG	6591
1QDL	AB	LYASE	A	2.0	3.9	2	21	EKDKAEHLMLVDLARNDLGKV	6592
1RD8	AD	VIRAL PROTEIN	A	2.0	3.9	2	8	YEELREQL	6593
1RYP	TU	MULTICATALYTIC PROTEINASE	T	2.0	3.9	2	15	VERAGHLLCDKAQKN	6594
1S5L	de	PHOTOSYNTHESIS	e	2.0	3.9	2	7	LAYDVFG	6595
1S5L	ef	PHOTOSYNTHESIS	f	2.0	3.9	2	27	TVRWVAVHTLAVPTIFFLGAIAAMQFI	6596
1SFC	FH	TRANSPORT PROTEIN	F	3.9	3.9	1	42	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID	6597
1SQK	AB	STRUCTURAL PROTEIN/PROTEIN BINDING	A	2.0	3.9	2	10	SVWIGGSILA	6598
1T0Q	AC	OXIDOREDUCTASE	A	3.9	3.9	1	22	WDQFMQDLDETHHGMHLGVWYW	6599
1TBG	CG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	2.0	3.9	2	5	PLVKG	6600
1TFO	AB	TOXIN/TOXIN INHIBITOR	B	3.9	3.9	1	17	PNILNCGEELFMAAERF	6601
1TO9	AB	BIOSYNTHETIC PROTEIN	A	2.0	3.9	2	15	ENFVISSYYEYQFWG	6602
1TQY	CD	TRANSFERASE	C	2.0	3.9	2	12	PSVMPAEVAWAV	6603
1UKL	AC	PROTEIN TRANSPORT/DNA BINDING PROTEIN	C	2.0	3.9	2	21	RKAIDYIKYLQQVNHKLRQEN	6604
1UZD	EI	LYASE	E	2.0	3.9	2	6	WTDGLT	6605
1UZD	KJ	LYASE	K	2.0	3.9	2	6	WTDGLT	6606
1UZH	HP	LYASE	H	2.0	3.9	2	6	WTDGLT	6607
1UZH	KJ	LYASE	K	2.0	3.9	2	6	WTDGLT	6608
1UZH	OC	LYASE	O	2.0	3.9	2	6	WTDGLT	6609
1UZH	VM	LYASE	V	2.0	3.9	2	6	WTDGLT	6610
1V4U	CD	OXYGEN STORAGE/TRANSPORT	C	3.9	3.9	1	21	PDAHVSLDKFLASVALALAER	6611
1V4U	CD	OXYGEN STORAGE/TRANSPORT	D	2.0	3.9	2	19	VETQCAFQKFLAVVVFALG	6612
1V9U	13	VIRUS/RECEPTOR	3	1.3	3.9	3	6	LVEICQ	6613

1VCB	KL	TRANSCRIPTION	K	2.0	3.9	2	15	PEIALELLMAANFLD	6614
1VF6	AC	PROTEIN BINDING/PROTEIN TRANSPORT	C	2.0	3.9	2	13	RDFQNAFKIHNAV	6615
1W2W	EF	ISOMERASE	E	2.0	3.9	2	14	DNGAKYLIDVLQKD	6616
1W5C	EF	PHOTOSYNTHESIS	F	2.0	3.9	2	25	VRWVAVHTLAVPTIFFLGAIAAMQF	6617
1W5C	KL	PHOTOSYNTHESIS	L	2.0	3.9	2	25	VRWVAVHTLAVPTIFFLGAIAAMQF	6618
1WYU	AB	OXIDOREDUCTASE	A	1.3	3.9	3	15	QLTALMGAMYLAALG	6619
1WYU	AB	OXIDOREDUCTASE	B	2.0	3.9	2	19	GAHGELTGILIIRAYHEDR	6620
1WYU	GH	OXIDOREDUCTASE	G	2.0	3.9	2	11	PEAVRRALAER	6621
1WYU	GH	OXIDOREDUCTASE	H	1.3	3.9	3	10	GSNPATASMA	6622
1X79	AB	PROTEIN TRANSPORT	B	1.3	3.9	3	88	TRDQVKKLQLMLRQANDQLEKTMKDKQELEDFIKQSSEDSSHQISALV LRAQASEILLEELQQGLSQAKRDVQEQMAVLMQSREQVSE	6623
1X79	AC	PROTEIN TRANSPORT	C	1.3	3.9	3	81	RDQVKKLQLMLRQANDQLEKTMKDKQELEDFIKQSSEDSSHQISALVL RAQASEILLEELQQGLSQAKRDVQEQMAVLMQS	6624
1XFV	DR	LYASE/METAL BINDING PROTEIN	R	3.9	3.9	1	13	SEEEIREAFRVFD	6625
1XV9	AB	DNA BINDING PROTEIN	B	2.0	3.9	2	21	RDEIDQLQEEMALTLQSYIKG	6626
1XXH	FG	TRANSFERASE	F	2.0	3.9	2	11	LLALAQALERL	6627
1XZP	AB	HYDROLASE	A	2.0	3.9	2	12	LTSAEAVRDLIE	6628
1YDI	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	2.0	3.9	2	20	RTIESILEPVAQQISHLVIM	6629
1YE9	CG	OXIDOREDUCTASE	G	2.0	3.9	2	17	LLQGRLFSYTDTQISRL	6630
1YE9	IM	OXIDOREDUCTASE	M	2.0	3.9	2	10	YSHPRLFWLS	6631
1YE9	LP	OXIDOREDUCTASE	P	2.0	3.9	2	17	PFEQRHIVDGFSFELSK	6632
1YKK	EF	OXIDOREDUCTASE	E	2.0	3.9	2	6	VHIGLA	6633
1YQ3	AB	OXIDOREDUCTASE	B	2.0	3.9	2	8	IEDRQKLD	6634
1YR5	AB	METAL BINDING PROTEIN/TRANSFERASE	A	2.0	3.9	2	15	EEQIAEFKEAFSLFD	6635
1Z7Q	AB	HYDROLASE/HYDROLASE ACTIVATOR	B	2.0	3.9	2	7	GQIDYAL	6636
1Z7Q	OP	HYDROLASE/HYDROLASE ACTIVATOR	P	2.0	3.9	2	7	GQIDYAL	6637
1ZT2	AB	REPLICATION, TRANSFERASE	B	2.0	3.9	2	8	FIDYLKYT	6638
2AA1	AB	OXYGEN STORAGE/TRANSPORT	A	3.9	3.9	1	19	PEAHVSLDKFLSGVALALA	6639
2ACM	AB	STRUCTURAL PROTEIN	A	2.0	3.9	2	18	DYYQELQRDISEMFLQIY	6640
2ADV	BC	HYDROLASE	C	3.9	3.9	1	9	LERFMALQL	6641
2AL2	AB	LYASE	B	1.3	3.9	3	23	FAEALRIGSEVYHNLKSLTKKRY	6642
2AXT	ad	ELECTRON TRANSPORT	a	2.0	3.9	2	12	VAAHGYFGRLIF	6643
2B8K	DG	TRANSFERASE	D	3.9	3.9	1	5	AQLGS	6644
2BA1	EH	RNA BINDING PROTEIN	E	1.3	3.9	3	35	RDEVKQAIELAKKGALQIYEMQREAILRRYIEVGE	6645
2C52	AB	TRANSFERASE	A	2.0	3.9	2	12	SALQDLLRTLKS	6646
2CCI	AB	CELL CYCLE	B	2.0	3.9	2	15	HEDIHTYLREMEVKC	6647

2DBU	AB	TRANSFERASE	B	2.0	3.9	2	7	IITTVLQ	6648
2DD4	AB	HYDROLASE	B	3.9	3.9	1	9	AEERRRKQN	6649
2DD4	DE	HYDROLASE	E	3.9	3.9	1	9	AEERRRKQN	6650
2DD4	HI	HYDROLASE	I	2.0	3.9	2	10	PNYRRRLVRW	6651
2DD4	JK	HYDROLASE	K	3.9	3.9	1	9	AEERRRKQN	6652
2DEN	AB	PROTEIN BINDING	A	2.0	3.9	2	11	IQAALELIFAG	6653
2DXB	DF	HYDROLASE	F	3.9	3.9	1	8	PRQVLAEF	6654
2DXB	JL	HYDROLASE	L	3.9	3.9	1	8	PRQVLAEF	6655
2DXB	NO	HYDROLASE	O	1.3	3.9	3	5	EWYRS	6656
2DXB	WX	HYDROLASE	W	2.0	3.9	2	16	YYGRWLLTAARILVDK	6657
2E 74	AG	PHOTOSYNTHESIS	G	2.0	3.9	2	26	PLLDGLVLGLVFATLGGLFYAAYQQY	6658
2EQ9	AC	OXIDOREDUCTASE	C	2.0	3.9	2	10	PAARKLAREL	6659
2EQ9	EF	OXIDOREDUCTASE	F	3.9	3.9	1	10	PAARKLAREL	6660
2ERJ	AD	IMMUNE SYSTEM/CYTOKINE	D	2.0	3.9	2	12	LKPLEEVLNLAQ	6661
2ERJ	FH	IMMUNE SYSTEM/CYTOKINE	H	2.0	3.9	2	26	SSSTKKTQLQLEHLLLDLQMILNGIN	6662
2F66	DB	TRANSPORT PROTEIN	D	2.0	3.9	2	29	DGLNQLYNLVAQDYALTDTIEALSRMLHR	6663
2F9I	CD	TRANSFERASE	C	1.3	3.9	3	14	QSESIATNLIEMAS	6664
2FK0	QR	VIRAL PROTEIN	R	2.0	3.9	2	24	YNAELLVLMENERTLDFHDSNVKN	6665
2FKW	GH	MEMBRANE PROTEIN, PHOTOSYNTHESIS	H	2.0	3.9	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	6666
2FOI	AC	OXIDOREDUCTASE	A	1.3	3.9	3	12	YGWGIAKELSKR	6667
2GEZ	AB	HYDROLASE	A	2.0	3.9	2	24	PERRKPREEGLRHCLQIGVEALKA	6668
2GW4	AB	LUMINESCENT PROTEIN	A	2.0	3.9	2	6	YDILTT	6669
2GZD	AC	PROTEIN TRANSPORT	C	1.3	3.9	3	19	KDTHIRELEDYIDNLLVRV	6670
2HPP	LH	HYDROLASE (SERINE PROTEINASE)	L	2.0	3.9	2	5	FEKKS	6671
2HTM	BF	BIOSYNTHETIC PROTEIN	B	2.0	3.9	2	16	AEEAVRLARLGRLLTG	6672
2HTM	DH	BIOSYNTHETIC PROTEIN	D	2.0	3.9	2	16	AEEAVRLARLGRLLTG	6673
2HZS	AB	TRANSCRIPTION	A	2.0	3.9	2	6	PALVFN	6674
2I2R	AE	TRANSPORT PROTEIN	E	2.0	3.9	2	12	EDTFKQIYAQFF	6675
2I2R	LP	TRANSPORT PROTEIN	P	1.3	3.9	3	12	EDTFKQIYAQFF	6676
2IAE	AB	HYDROLASE	A	2.0	3.9	2	9	WRVRYMVAD	6677
2IBX	AD	VIRAL PROTEIN	A	2.0	3.9	2	10	YEELKHLLSR	6678
2IBZ	DE	OXIDOREDUCTASE	D	1.3	3.9	3	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	6679
2IPK	BC	IMMUNE SYSTEM	B	3.9	3.9	1	9	RPDAEYWNS	6680
2J9U	CD	PROTEIN TRANSPORT	C	2.0	3.9	2	19	KDQLHPLLAELLISINRVT	6681
2JKR	LI	ENDOCYTOSIS	L	1.3	3.9	3	18	DSVKQSAALCLLRLYRTS	6682
2NNA	BC	IMMUNE SYSTEM	B	2.0	3.9	2	12	PLGPPAAEYWNS	6683
2NQB	CD	STRUCTURAL PROTEIN/DNA	D	1.3	3.9	3	12	AIYIYTVLKQVH	6684
2NQB	FH	STRUCTURAL PROTEIN/DNA	F	2.0	3.9	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	6685
2NUD	BD	TOXIN/PROTEIN BINDING	B	2.0	3.9	2	11	AKALKQHLQRY	6686

2OTJ	FM	RIBOSOME	M	2.0	3.9	2	9	AYSYIRDAW	6687
2OV2	CK	PROTEIN BINDING/TRANSFERASE	C	2.0	3.9	2	9	DRLRPLSYP	6688
2P1L	CD	APOPTOSIS	C	1.3	3.9	3	13	AYQSFEQVVNELF	6689
2P2C	HS	HYDROLASE	H	3.9	3.9	1	13	WYIEALAQVFSER	6690
2P4N	AB	TRANSPORT PROTEIN	A	2.0	3.9	2	6	VHWYVG	6691
2PMZ	QW	TRANSLATION, TRANSFERASE	Q	1.3	3.9	3	11	EEAIAEAKEIM	6692
2Q7N	AB	CYTOKINE RECEPTOR/CYTOKINE	B	3.9	3.9	1	23	VFQKKKLGCQLLGKYKQIIAVLA	6693
2Q9Q	EF	REPLICATION	E	1.3	3.9	3	10	AAEVEFLAEK	6694
2QBE	EL	RIBOSOME	E	2.0	3.9	2	6	EALVHQ	6695
2QBE	HZ	RIBOSOME	Z	3.9	3.9	1	9	GMRVIDKKG	6696
2QKM	CD	HYDROLASE	D	2.0	3.9	2	23	VERLCFQIEQAHWFYEDFIRAQN	6697
2QM6	AB	TRANSFERASE	A	1.3	3.9	3	13	QVAELIEKDMKKN	6698
2SIV	CD	ENVELOPE GLYCOPROTEIN	D	2.0	3.9	2	32	QEWERKVDFLEENITALLEEAQIQQEKNMYEL	6699
2SIV	EF	ENVELOPE GLYCOPROTEIN	F	1.3	3.9	3	31	QEWERKVDFLEENITALLEEAQIQQEKNMYE	6700
2UUN	IJ	ELECTRON TRANSPORT	J	2.0	3.9	2	13	VAQIDALSQMVAE	6701
2UUN	KL	ELECTRON TRANSPORT	K	2.0	3.9	2	27	STEIQVAFGRFRQAAAGLSAATALTSA	6702
2UY1	AB	RNA BINDING PROTEIN	A	1.3	3.9	3	17	MELFRELVDQKMDAIKA	6703
2UZ1	DB	LYASE	B	1.3	3.9	3	17	TEHIPRLVMQAIRAALS	6704
2UZ1	DC	LYASE	C	2.0	3.9	2	12	GATLHFQQLAVG	6705
2V8W	AB	TRANSLATION	B	1.3	3.9	3	7	RKFLMEC	6706
2VGO	AD	TRANSFERASE	D	2.0	3.9	2	5	LEELF	6707
2VJT	AB	PHOTOSYNTHESIS	B	2.0	3.9	2	12	AITAVINNYDVQ	6708
2W85	AB	PROTEIN TRANSPORT	A	2.0	3.9	2	12	LATRRAFLKKKG	6709
2WAX	AB	HYDROLASE	B	2.0	3.9	2	7	FEGNLAL	6710
2WJV	AD	HYDROLASE	D	2.0	3.9	2	19	DEDFIQALDKMMLENLQQR	6711
2Z2S	CD	TRANSCRIPTION	C	2.0	3.9	2	11	VATWIFTIARN	6712
2Z2S	GH	TRANSCRIPTION	H	2.0	3.9	2	5	SLASV	6713
2ZCY	AG	HYDROLASE	G	1.3	3.9	3	18	CDVLAKRMANLSQIYTQR	6714
2ZCY	CJ	HYDROLASE	J	1.3	3.9	3	22	AGDTVQFAEYIQANIQLYSIRE	6715
2ZCY	DK	HYDROLASE	K	2.0	3.9	2	22	AADCQFWETWLGSQCRLHELRE	6716
2ZCY	HI	HYDROLASE	H	3.9	3.9	1	23	AADTEAVTQLIGSNIELHSLYTS	6717
2ZCY	PX	HYDROLASE	X	3.9	3.9	1	22	AGDTVQFAEYIQANIQLYSIRE	6718
2ZET	BD	SIGNALING PROTEIN	D	3.9	3.9	1	9	EWYYQHVRA	6719
2ZNE	BD	APOPTOSIS	B	2.0	3.9	2	22	FSEFTGVWKYITDWQNVFRTYD	6720
2ZNW	AY	IMMUNE SYSTEM/HYDROLASE	Y	3.9	3.9	1	12	TASVNCAKKIVS	6721
2ZT9	EH	PHOTOSYNTHESIS	E	2.0	3.9	2	27	LAIVAYIGFLALFTGIAAGLLFGLRSA	6722
3B5N	BD	MEMBRANE PROTEIN	B	2.0	3.9	2	68	LAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVED AQLDVEQGVGHTDKAVKSAR	6723
3B8E	CD	HYDROLASE/TRANSPORT PROTEIN	D	2.0	3.9	2	19	FYVIFYGCLAGIFIGTIQV	6724
3BLW	KL	OXIDOREDUCTASE	L	2.0	3.9	2	11	IDNSVLKVVTN	6725

3BWN	DC	TRANSFERASE	D	2.0	3.9	2	15	KEVAKKMVEYIIVNS	6726
3BZ1	BD	ELECTRON TRANSPORT	D	2.0	3.9	2	28	KRWLHFFMLFVPVTGLWMSAIGVVGLAL	6727
3C01	DH	MEMBRANE PROTEIN, PROTEIN TRANSPORT	D	2.0	3.9	2	9	EQVKSDIEN	6728
3C1B	BD	STRUCTURAL PROTEIN/DNA	B	2.0	3.9	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	6729
3C60	EF	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	F	2.0	3.9	2	7	EAEISHT	6730
3C6L	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	C	1.3	3.9	3	19	GLQNIAVVKHNLGVLTKRS	6731
3C91	GN	HYDROLASE	N	1.3	3.9	3	22	VGDAQVLVRYMKAELELYRLQR	6732
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	B	1.3	3.9	3	15	HDMFMDMAMLVESQG	6733
3CJT	AB	TRANSFERASE/RIBOSOMAL PROTEIN	B	2.0	3.9	2	9	PVGPALGQH	6734
3CQC	AB	PROTEIN TRANSPORT	A	1.3	3.9	3	21	KEELRKLLQKLRESSLMLLDQ	6735
3DBH	EF	CELL CYCLE	F	2.0	3.9	2	9	NHVKKFLER	6736
3DBH	GH	CELL CYCLE	H	2.0	3.9	2	13	KAEVAAEFLNDRV	6737
3DCG	AB	LIGASE/VIRAL PROTEIN	B	2.0	3.9	2	17	SHVLSKVCMYFTYKVRY	6738
3DCT	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	B	1.3	3.9	3	9	QLLRYLLDK	6739
3DEG	CH	RIBOSOME	H	3.9	3.9	1	7	PALGQQG	6740
3DGE	BD	TRANSFERASE/SIGNALING PROTEIN	B	1.3	3.9	3	15	TPLTAIKAYAETIYN	6741
3DIN	FH	MEMBRANE PROTEIN, PROTEIN TRANSPORT	H	1.3	3.9	3	23	TIISVALIYMVQVQMSKFSELGG	6742
3DXA	DE	IMMUNE SYSTEM	E	1.3	3.9	3	7	EAEISHT	6743
3E2K	BC	HYDROLASE/HYDROLASE INHIBITOR	B	1.3	3.9	3	6	PISEKY	6744
3EA5	AB	TRANSPORT PROTEIN	B	1.3	3.9	3	13	LEGRILAALTLKN	6745
3EAB	CI	CELL CYCLE	C	2.0	3.9	2	28	EQCERARRLQAKMMTNLVMAKDRLQLLE	6746
3EIQ	AC	HYDROLASE/ANTITUMOR PROTEIN	A	2.0	3.9	2	9	RENYIHRIG	6747
3ENS	CD	HYDROLASE, BLOOD CLOTTING	D	3.9	3.9	1	10	RDWAESTLMT	6748
3EUB	AC	OXIDOREDUCTASE	A	3.9	3.9	1	17	FCTPGIVMSMYTLLRNQ	6749
3EXG	12	OXIDOREDUCTASE	1	3.9	3.9	1	17	AQVPLGAGIALACKYNG	6750
3EZQ	AB	APOPTOSIS	B	1.3	3.9	3	16	NLVADLVQEVQQARDL	6751
3EZQ	EF	APOPTOSIS	E	2.0	3.9	2	33	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	6752
3EZQ	IJ	APOPTOSIS	J	1.3	3.9	3	16	NLVADLVQEVQQARDL	6753
3F9K	BC	VIRAL PROTEIN, RECOMBINATION	B	2.0	3.9	2	11	QEVKMVAWWIG	6754
3F9K	de	VIRAL PROTEIN, RECOMBINATION	d	1.3	3.9	3	11	QEVKMVAWWIG	6755
3FAL	CD	SIGNALING PROTEIN	D	2.0	3.9	2	30	PLMFPRMLMKLVSLRTLSSVHSEQVFALRL	6756
3FDS	CD	TRANSFERASE	C	1.3	3.9	3	15	ESVLNVIAADVTLVG	6757
3FKS	BF	HYDROLASE	B	2.0	3.9	2	7	VFYLHSR	6758
3FKS	DG	HYDROLASE	D	1.3	3.9	3	8	QDIIAILG	6759
3FKU	EF	VIRAL PROTEIN/IMMUNE SYSTEM	F	1.3	3.9	3	26	ENLNKKMEDGFLDVWTYNAELLVLME	6760

3FLO	AB	TRANSFERASE	A	2.0	3.9	2	23	LQEASDVLDDQIESFTKIIQNHY	6761
3FWC	JK	CELL CYCLE, TRANSCRIPTION	K	3.9	3.9	1	16	FTQILSTVEPKALEMV	6762
3FWC	MN	CELL CYCLE, TRANSCRIPTION	M	3.9	3.9	1	10	EELRAMIEEF	6763
3GJX	ED	PROTEIN TRANSPORT	D	2.0	3.9	2	22	EEDEKRFLVTVIKDLLGLCEQK	6764
3GLH	DE	TRANSFERASE	E	1.3	3.9	3	21	PSRLQAILGDVCHIREQLMSV	6765
3GLH	KL	TRANSFERASE	K	1.3	3.9	3	15	LLALAQALERLSLLW	6766
3GM1	AE	TRANSFERASE	E	1.3	3.9	3	9	LDELMASLS	6767
3GTM	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.0	3.9	2	5	EIIQN	6768
3GZD	DC	LYASE	C	2.0	3.9	2	23	GTESNNLVIHSVVKHFHANQTSG	6769
3H9R	AB	ISOMERASE/PROTEIN KINASE	A	2.0	3.9	2	14	EKSWFRETELYNTV	6770
3HAX	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	2.0	3.9	2	12	SHEVVAWIKKIL	6771
3HKZ	OV	TRANSFERASE	V	2.0	3.9	2	11	HTLGNLIAGTL	6772
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	3.9	3.9	1	23	PQVCAKLFGNIQKVVNFWLLHNG	6773
3HOY	DG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	2.0	3.9	2	13	KDLKNTMQYLTNF	6774
3KIN	AB	MOTOR PROTEIN	B	2.0	3.9	2	6	KMTRIL	6775
1AFV	BM	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.9	3.8	2	21	QAAMQMLKETINEEAAEWDRL	6776
1B4U	AB	DIOXYGENASE	A	1.9	3.8	2	10	VHAYLAEFDD	6777
1BGY	DE	ELECTRON TRANSPORT	D	1.3	3.8	3	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	6778
1BGY	PV	ELECTRON TRANSPORT	V	1.9	3.8	2	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	6779
1DFL	AY	CONTRACTILE PROTEIN	A	1.3	3.8	3	9	WWKLYSKVK	6780
1DML	AF	DNA BINDING PROTEIN/TRANSFERASE	F	1.9	3.8	2	15	AEETRRMLHRAFDTL	6781
1EMU	AB	SIGNALING PROTEIN	B	1.9	3.8	2	11	DDLLQECISSA	6782
1EQZ	EF	STRUCTURAL PROTEIN/DNA	E	1.9	3.8	2	11	VGRVHRLLRKG	6783
1F93	DH	TRANSCRIPTION	H	1.9	3.8	2	13	QLQTELLAALLES	6784
1FDH	BH	OXYGEN TRANSPORT	H	1.9	3.8	2	16	VEDAGGETLGRLLVVY	6785
1FNT	LM	HYDROLASE/HYDROLASE ACTIVATOR	M	3.8	3.8	1	15	INSAARNIQHLLYGK	6786
1FS0	EG	HYDROLASE	E	1.3	3.8	3	18	QDLDEARAMEAKRKAEEH	6787
1FYZ	AC	OXIDOREDUCTASE	C	1.9	3.8	2	10	PEMAAVILKA	6788
1FYZ	BD	OXIDOREDUCTASE	B	1.3	3.8	3	10	PLWKGMKRVF	6789
1FYZ	BD	OXIDOREDUCTASE	D	1.9	3.8	2	11	PEMAAVILKAL	6790
1FYZ	BD	OXIDOREDUCTASE	D	1.9	3.8	2	7	EYEALTV	6791
1G0U	FG	HYDROLASE	G	1.9	3.8	2	14	YQVEYAFKATNQTN	6792
1G4Y	BR	SIGNALING PROTEIN	R	1.9	3.8	2	11	EAELQDMINEV	6793
1GK0	CD	HYDROLASE	C	1.9	3.8	2	10	EQTTVWLLTN	6794
1GO3	EF	TRANSFERASE	F	1.9	3.8	2	14	VSEAAEIMYNRAQI	6795

1GOT	AB	COMPLEX (GTP-BINDING/TRANSDUCER)	A	1.9	3.8	2	22	AEEKHSRELEKKLKEDAEKDAR	6796
1H3O	AB	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	A	1.3	3.8	3	14	QAPLQRRILEIGKK	6797
1HBM	AE	METHANOGENESIS	A	1.9	3.8	2	12	AATGDFAYAAKA	6798
1I7Q	CB	LYASE	C	1.9	3.8	2	13	LDLDSRIELEMRT	6799
1I7Y	AB	PHOTOSYNTHESIS	B	1.9	3.8	2	13	NAQFDALSNLVKE	6800
1IB1	AE	SIGNALING PROTEIN/TRANSFERASE	A	1.9	3.8	2	14	TLIMQLLRDNLTLW	6801
1IHF	AB	TRANSCRIPTION/DNA	A	1.9	3.8	2	9	QKLKSRVEN	6802
1IK9	BC	GENE REGULATION/LIGASE	C	3.8	3.8	1	11	LNQLKEVFSGI	6803
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.9	3.8	2	11	EEIREAFRVFD	6804
1IR2	AL	LYASE	A	1.3	3.8	3	14	AKNYGRAVYECLRG	6805
1IR2	CK	LYASE	K	1.9	3.8	2	14	DEQIAAQVDYIVAN	6806
1IR2	FI	LYASE	F	1.9	3.8	2	6	WTDGLT	6807
1IR2	GP	LYASE	G	1.3	3.8	3	14	AKNYGRAVYECLRG	6808
1IR2	HK	LYASE	H	1.9	3.8	2	6	WTDGLT	6809
1IR2	S6	LYASE	S	1.9	3.8	2	6	WTDGLT	6810
1IR2	T7	LYASE	T	1.9	3.8	2	6	WTDGLT	6811
1IR2	U8	LYASE	U	1.9	3.8	2	6	WTDGLT	6812
1IRU	EM	HYDROLASE	M	1.9	3.8	2	22	HGDCLTLTKIIEARLKMYKHSN	6813
1IRU	OU	HYDROLASE	O	1.9	3.8	2	14	YQVEYAFKAINQGG	6814
1IRU	WM	HYDROLASE	M	1.3	3.8	3	19	LDRAMRLVKDVFISAAERD	6815
1IW7	NP	TRANSFERASE	P	3.8	3.8	1	11	LRLVVSIAKKY	6816
1J8H	AB	IMMUNE SYSTEM	B	1.9	3.8	2	9	RPDAEYWNS	6817
1JB0	AJ	PHOTOSYNTHESIS	J	1.9	3.8	2	7	KHFLTYL	6818
1JB0	BF	PHOTOSYNTHESIS	F	1.9	3.8	2	11	SGQKRFERYSQ	6819
1JD2	CJ	HYDROLASE	J	1.3	3.8	3	22	AGDTVQFAEYIQANIQLYSIRE	6820
1JD2	FG	HYDROLASE	G	1.9	3.8	2	23	IPDARNAALRAKAEAAEFRYKYG	6821
1JD2	WP	HYDROLASE	P	1.3	3.8	3	22	ATDVTTLNEMFRYKTNLYKLKE	6822
1JJ2	FL	RIBOSOME	F	1.9	3.8	2	13	EEIVMHIPELADE	6823
1JMU	BG	VIRAL PROTEIN	G	3.8	3.8	1	9	VEKIRYALG	6824
1JOW	AB	CELL CYCLE/TRANSFERASE	A	1.9	3.8	2	21	EDLWPQLYEAASTTICKALIQ	6825
1K5D	AB	SIGNALING PROTEIN/SIGNALING ACTIVATOR	A	1.9	3.8	2	9	KTTFVKRHL	6826
1KF9	AB	HORMONE/GROWTH FACTOR	A	1.3	3.8	3	47	NVYDLLKDLEEGIQTLMGRLLLKNYGLLYCFNKDMSKVSTYLRTVQC	6827
1KX4	EF	STRUCTURAL PROTEIN/DNA	E	1.9	3.8	2	11	TVALREIRRYQ	6828
1L2W	DJ	CHAPERONE	J	1.9	3.8	2	8	QYANNLAG	6829
1L9B	MH	PHOTOSYNTHESIS	M	1.9	3.8	2	21	RWAIWMAVLVTLTGGIGILLS	6830

1M1Y	KL	OXIDOREDUCTASE	K	1.9	3.8	2	8	VGCGQYSR	6831
1M56	GI	OXIDOREDUCTASE	G	3.8	3.8	1	7	ITTFLNM	6832
1MHY	BD	OXIDOREDUCTASE	D	3.8	3.8	1	5	ADGFI	6833
1MHY	DG	OXIDOREDUCTASE	G	1.9	3.8	2	20	VNVFLRTDAALGTVLMEIRN	6834
1MJE	BA	GENE REGULATION/ANTITUMOR PROTEIN/DNA	B	1.9	3.8	2	5	DDFSN	6835
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	1.9	3.8	2	8	ARRTRTIG	6836
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	1.9	3.8	2	11	PEMAAVILKAL	6837
1MTY	DB	MONOOXYGENASE	B	1.9	3.8	2	13	KSARLAVEGLWQE	6838
1MXE	BF	METAL BINDING PROTEIN	B	1.9	3.8	2	12	DEEVDEMIREAD	6839
1N52	AB	RNA BINDING PROTEIN	A	3.8	3.8	1	10	RKTCAAQLVS	6840
1N5W	AB	OXIDOREDUCTASE	A	1.9	3.8	2	9	LIHFIREQQ	6841
1N5W	DE	OXIDOREDUCTASE	D	1.9	3.8	2	10	LIHFIREQQN	6842
1N5W	EF	OXIDOREDUCTASE	E	1.9	3.8	2	11	AWRLWKVGEQL	6843
1NEK	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	3.8	3.8	1	13	PEGFEQASAIMGS	6844
1NKP	AB	TRANSCRIPTION/DNA	B	1.9	3.8	2	27	KRAHHNALERKRRDHIKDSFHSLRDSV	6845
1NRL	BD	TRANSCRIPTION	B	3.8	3.8	1	11	IEDQISLLKGA	6846
1NVM	AB	LYASE/OXIDOREDUCTASE	B	3.8	3.8	1	5	PGTRA	6847
1NWD	AC	BINDING PROTEIN/HYDROLASE	C	1.9	3.8	2	20	DSEVQLEMITAWKKFVEEKK	6848
1NX0	AC	HYDROLASE	A	3.8	3.8	1	14	ATELMNILNKVVTR	6849
1NZY	CB	LYASE	B	3.8	3.8	1	7	YSLARIV	6850
1O94	EF	ELECTRON TRANSPORT	E	1.9	3.8	2	11	STGISVASYLN	6851
1OCC	AM	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	M	1.9	3.8	2	25	PKEQAIGLSVTFLSFLLPAGWVLYH	6852
1OUU	AB	OXYGEN TRANSPORT	A	1.3	3.8	3	17	NFKILSHNILVTLAIHF	6853
1OUU	CD	OXYGEN TRANSPORT	C	3.8	3.8	1	16	ADVVGAEALGRMLTAY	6854
1OVL	AB	TRANSCRIPTION	B	1.9	3.8	2	12	LISALVRAHVDS	6855
1OW3	AB	GENE REGULATION/SIGNALING PROTEIN	A	1.9	3.8	2	13	NTNLAVVFGPNLL	6856
1OW7	BE	TRANSFERASE	E	1.3	3.8	3	10	RELDELMASL	6857
1PRC	CL	PHOTOSYNTHETIC REACTION CENTER	L	1.9	3.8	2	15	ILSHLDWVNNFGYQY	6858
1Q16	AB	OXIDOREDUCTASE	B	1.9	3.8	2	14	EAQAQEMYRYLAIA	6859
1QLE	AC	OXIDOREDUCTASE/IMMUNE SYSTEM	A	1.9	3.8	2	30	SMDLAIFAVHVSGASSILGAINIITTFLNM	6860
1QPW	CB	OXYGEN TRANSPORT	B	3.8	3.8	1	6	PWTQRF	6861
1R27	CD	OXIDOREDUCTASE	C	1.9	3.8	2	7	LLMLTLG	6862
1R4M	CD	CELL CYCLE	D	3.8	3.8	1	7	VKKFLER	6863
1R5V	EB	SIGNALING PROTEIN	B	1.3	3.8	3	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	6864

1R5W	BE	SIGNALING PROTEIN	B	3.8	3.8	1	9	RPDAENWNS	6865
1R6O	AC	HYDROLASE	A	3.8	3.8	1	9	QAAYLLRKH	6866
1R6O	AD	HYDROLASE	D	1.3	3.8	3	15	VERATQLMLAVHYQG	6867
1RD8	AB	VIRAL PROTEIN	B	1.9	3.8	2	23	QKSTQNAIDGITNKVNSVIEKMN	6868
1RDT	AD	HORMONE/GROWTH FACTOR	A	1.9	3.8	2	23	PAEVEALREKVYASLEAYCKHKY	6869
1RH5	AB	PROTEIN TRANSPORT	A	1.9	3.8	2	17	GIGLFIAAGVSQTIFVG	6870
1RYP	CD	MULTICATALYTIC PROTEINASE	C	1.9	3.8	2	18	VEILVRRLSDIKQGYTQH	6871
1RYP	FM	MULTICATALYTIC PROTEINASE	M	1.9	3.8	2	22	AADGDALVKRFKNSVKWYHFDH	6872
1RYP	S1	MULTICATALYTIC PROTEINASE	1	1.9	3.8	2	15	INSAARNIQHLLYGK	6873
1S0Y	CF	LYASE	C	1.3	3.8	3	20	DEQKRALSAGLLRVISEATG	6874
1S5L	dl	PHOTOSYNTHESIS	l	1.3	3.8	3	24	RTSLYLGLLLILVLALLFSSYFFN	6875
1S5L	EF	PHOTOSYNTHESIS	F	1.9	3.8	2	27	TVRWVAVHTLAVPTIFFLGAIAAMQFI	6876
1S9V	AE	IMMUNE SYSTEM	E	1.3	3.8	3	24	KDILERKRAAVDRVCRHNYQLELR	6877
1S9V	DE	IMMUNE SYSTEM	D	1.9	3.8	2	21	PQFALTNIAVLKHNLNSLIKR	6878
1SQB	DE	OXIDOREDUCTASE	D	1.3	3.8	3	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	6879
1T0F	BD	DNA BINDING PROTEIN	D	1.9	3.8	2	5	MASLF	6880
1T3Q	DE	OXIDOREDUCTASE	E	1.9	3.8	2	22	PMIVEGQIRGGIAQAIGQTLLE	6881
1TEC	EI	COMPLEX (SERINE PROTEINASE-INHIBITOR)	E	3.8	3.8	1	14	WTAVANGITYAADQ	6882
1TI2	GH	OXIDOREDUCTASE	G	1.9	3.8	2	6	HTARLV	6883
1TI8	AB	VIRAL PROTEIN	B	1.3	3.8	3	19	YKSTQSAIDQITGKLNRLI	6884
1TIL	EF	TRANSCRIPTION	E	3.8	3.8	1	14	ESFARVTVAAFVAQ	6885
1TN6	AB	TRANSFERASE	B	3.8	3.8	1	15	QIVATDVCQFLELCQ	6886
1TQY	EF	TRANSFERASE	F	1.9	3.8	2	11	PWGWVSQIASG	6887
1TQY	GH	TRANSFERASE	H	1.9	3.8	2	11	PWGWVSQIASG	6888
1TUE	FG	REPLICATION	F	1.9	3.8	2	13	FITFLGALKSFLK	6889
1TUE	KL	REPLICATION	K	1.9	3.8	2	14	FITFLGALKSFLKG	6890
1TY4	AC	APOPTOSIS	A	1.9	3.8	2	17	YGRLIGLISFGGFVAAK	6891
1UM9	AB	OXIDOREDUCTASE	B	3.8	3.8	1	15	EAAIVGAALGMAAHG	6892
1UR6	AB	LIGASE	A	3.8	3.8	1	12	ALKRIHKELNDL	6893
1UZD	OC	LYASE	O	1.9	3.8	2	6	WTDGLT	6894
1UZD	RW	LYASE	R	1.9	3.8	2	6	WTDGLT	6895
1UZD	VM	LYASE	V	1.9	3.8	2	6	WTDGLT	6896
1UZH	AF	LYASE	A	1.9	3.8	2	6	WTDGLT	6897
1UZH	EI	LYASE	E	1.9	3.8	2	6	WTDGLT	6898
1V54	BI	OXIDOREDUCTASE	I	1.3	3.8	3	25	LLARRLRFHIVGAFMVSLGFATFYK	6899
1V54	DI	OXIDOREDUCTASE	D	3.8	3.8	1	8	PIQGFSAK	6900
1VCB	BC	TRANSCRIPTION	B	3.8	3.8	1	18	SHVLSKVCMYFTYKVRYT	6901
1VF6	BD	PROTEIN BINDING/PROTEIN TRANSPORT	D	1.9	3.8	2	13	VEDLFSSLKHIQH	6902

1VQN	FM	RIBOSOME	M	1.9	3.8	2	9	AYSYIRDAW	6903
1W1I	AF	HYDROLASE	F	1.9	3.8	2	18	RDAIKRIAYEFVEMKAKD	6904
1X86	GH	SIGNALING PROTEIN/MEMBRANE PROTEIN	G	1.9	3.8	2	13	EIKRQEVINELFY	6905
1XCG	AB	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	A	1.9	3.8	2	38	QREIDRQEVINELFVTEASHLRTLRVLDLIFYQRMKKE	6906
1XD2	BC	SIGNALING PROTEIN	B	1.9	3.8	2	8	RDQYMRTG	6907
1XFV	ES	LYASE/METAL BINDING PROTEIN	E	3.8	3.8	1	6	LTEIKK	6908
1XLT	HC	OXIDOREDUCTASE	C	3.8	3.8	1	10	AEDAAFIMKN	6909
1XXI	FJ	TRANSFERASE	J	1.9	3.8	2	17	RELLITDLLLRIEHYLQ	6910
1YEW	FG	OXIDOREDUCTASE, MEMBRANE PROTEIN	G	1.3	3.8	3	23	FTHLVWLVAYAWAIYWGASYFTE	6911
1Z5X	UE	HORMONE/GROWTH FACTOR RECEPTOR	U	3.8	3.8	1	23	TQQVENLREKVYAILEEYCRQTY	6912
1Z6O	BN	METAL BINDING PROTEIN	N	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6913
1Z6O	CO	METAL BINDING PROTEIN	O	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6914
1Z6O	DP	METAL BINDING PROTEIN	P	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6915
1Z6O	FR	METAL BINDING PROTEIN	R	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6916
1Z6O	GS	METAL BINDING PROTEIN	S	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6917
1Z6O	HO	METAL BINDING PROTEIN	H	1.9	3.8	2	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	6918
1Z6O	HT	METAL BINDING PROTEIN	T	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6919
1Z6O	IU	METAL BINDING PROTEIN	U	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6920
1Z6O	KW	METAL BINDING PROTEIN	W	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6921
1Z6O	LX	METAL BINDING PROTEIN	X	1.9	3.8	2	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	6922
1Z7Q	KZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.9	3.8	2	12	QTFAYGVLDSNY	6923
1Z8U	AB	ELECTRON TRANSPORT	B	1.3	3.8	3	12	PAVHASLDKFLA	6924
1ZAV	AW	STRUCTURAL PROTEIN	A	1.3	3.8	3	41	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK	6925
1ZE3	CD	CHAPERONE/STRUCTURAL/MEMBRANE PROTEIN	D	1.9	3.8	2	5	SRFEN	6926
1ZGL	AB	IMMUNE SYSTEM	A	3.8	3.8	1	5	EEFGR	6927
1ZOY	AB	OXIDOREDUCTASE	A	1.9	3.8	2	16	TGHSLLHTLYGRSLRY	6928
1ZV8	IH	VIRAL PROTEIN	H	1.3	3.8	3	17	QKEIDRLNEVAKNLNES	6929
2A1D	EF	HYDROLASE	E	1.3	3.8	3	9	EKELFESYI	6930
2A1J	AB	DNA BINDING PROTEIN	A	1.9	3.8	2	12	AANAKQLYDFIH	6931
2A7U	AB	HYDROLASE	A	1.9	3.8	2	14	STEISELIKQRIAQ	6932
2AA1	AD	OXYGEN STORAGE/TRANSPORT	D	1.9	3.8	2	6	PWTQRY	6933
2AK4	IJ	IMMUNE SYSTEM	J	1.9	3.8	2	7	EAEISHT	6934
2B87	AB	PROTEIN BINDING	A	1.9	3.8	2	14	GVQVKAFIDSLRDD	6935
2B8K	AE	TRANSFERASE	E	1.9	3.8	2	7	PVALYLG	6936
2BEQ	AD	VIRAL PROTEIN	A	1.3	3.8	3	35	QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	6937

2BEQ	AD	VIRAL PROTEIN	D	1.9	3.8	2	13	QKEIDRLNEVAKN	6938
2BL0	AC	MUSCLE PROTEIN	C	1.9	3.8	2	8	DNFINTMF	6939
2BR2	MN	HYDROLASE	M	1.9	3.8	2	17	NAIELARVVDRSLRDSK	6940
2BV8	KP	PHOTOSYNTHESIS	P	1.3	3.8	3	25	NRRMAACLRDMEIVLRYVSYAEIAG	6941
2D0O	AB	CHAPERONE	B	1.9	3.8	2	10	REVLLGIEEE	6942
2D0O	CD	CHAPERONE	D	1.9	3.8	2	17	SQAHRNTGNNAARLVKG	6943
2DBU	CD	TRANSFERASE	D	1.9	3.8	2	6	VNSIDY	6944
2DF4	AC	LIGASE	C	1.9	3.8	2	11	REEVEHIANLA	6945
2DXB	MN	HYDROLASE	N	3.8	3.8	1	9	AEERRRKQN	6946
2E9X	AC	REPLICATION	A	1.9	3.8	2	13	EKAMELIRELHRA	6947
2E9X	FH	REPLICATION	H	1.9	3.8	2	18	PAELIERLEQAWMNEKFA	6948
2EQB	AC	ENDOCYTOSIS/EXOCYTOSIS	A	1.9	3.8	2	6	FITTIG	6949
2F66	DE	TRANSPORT PROTEIN	E	1.3	3.8	3	29	SKDKEVIETLSEIYSIVITLDHVEKAYLK	6950
2F8N	HG	STRUCTURAL PROTEIN/DNA	H	1.9	3.8	2	21	GELAKHAVSEGTKAVTKYTSA	6951
2F9Y	AB	LIGASE	A	1.9	3.8	2	15	TEDLKNRRYQRLMSY	6952
2FBW	NO	OXIDOREDUCTASE	O	1.9	3.8	2	8	IEDRQKLD	6953
2FFD	AB	BLOOD CLOTTING	A	1.9	3.8	2	14	LKDYEDQQKQLEQV	6954
2FKW	AB	MEMBRANE PROTEIN, PHOTOSYNTHESIS	B	1.9	3.8	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	6955
2GTL	BM	OXYGEN STORAGE/TRANSPORT	B	3.8	3.8	1	18	HDREAFSQAIWRATFAQV	6956
2GTL	FG	OXYGEN STORAGE/TRANSPORT	F	1.9	3.8	2	19	PAFIAHADRVLGGLDIAIS	6957
2GUZ	IL	CHAPERONE, PROTEIN TRANSPORT	L	1.3	3.8	3	15	MDKINNRFNYLFEVN	6958
2HDN	AB	TRANSLATION	B	1.9	3.8	2	18	AEWEAKILELAGFLDSYI	6959
2HWN	AE	TRANSFERASE	A	1.3	3.8	3	16	LTELLQGYTVEVLRQQ	6960
2HZS	GH	TRANSCRIPTION	G	1.9	3.8	2	9	IDTILSSKL	6961
2I2X	AD	TRANSFERASE	D	3.8	3.8	1	5	YNVAL	6962
2IAE	EF	HYDROLASE	F	1.9	3.8	2	11	GFYDECLRKYG	6963
2IAN	BC	IMMUNE SYSTEM	B	1.9	3.8	2	10	RPDAEYWNSQ	6964
2IBZ	EI	OXIDOREDUCTASE	E	1.9	3.8	2	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	6965
2IBZ	EX	OXIDOREDUCTASE	E	3.8	3.8	1	5	DADRV	6966
2INP	BD	OXIDOREDUCTASE	B	1.9	3.8	2	29	ARYVNALKLFISGISPLEHAAFQGYSKVG	6967
2IY1	CD	HYDROLASE/NUCLEAR PROTEIN	C	3.8	3.8	1	9	FFFTKLKTA	6968
2JBL	LM	ELECTRON TRANSPORT	L	1.9	3.8	2	5	ERKYR	6969
2JJ0	LH	PHOTOSYNTHESIS	L	1.9	3.8	2	5	ERKYR	6970
2K2Q	AB	LIGASE/HYDROLASE	B	3.8	3.8	1	6	FLLSQT	6971
2NLA	AB	APOPTOSIS	A	1.9	3.8	2	21	WGRIVTLISFGAFVAKHLKTI	6972
2NXX	BF	HORMONE/GROWTH FACTOR	B	1.9	3.8	2	11	RLPALRSIGLK	6973
2NXX	DH	HORMONE/GROWTH FACTOR	D	1.9	3.8	2	23	VQEVEMLREKIYGVLEEYTRTTH	6974
2NZD	EF	STRUCTURAL PROTEIN/DNA	E	1.3	3.8	3	11	PKDIQLARRIR	6975
2O26	BY	CYTOKINE/SIGNALING PROTEIN	B	1.9	3.8	2	22	SHCWLRDMVIQLSLSLTTLLDK	6976

2OF5	EK	APOPTOSIS	E	1.9	3.8	2	16	VQSQVVEAFIRWRQRF	6977
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.9	3.8	2	5	LRGFL	6978
2OS8	AC	CONTRACTILE PROTEIN	C	1.9	3.8	2	15	QDEIDDLKEVFELFD	6979
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	A	1.9	3.8	2	8	PEEIRKTF	6980
2OZA	AB	SIGNALING PROTEIN/TRANSFERASE	A	3.8	3.8	1	9	PLLLKRRKK	6981
2P22	AD	TRANSPORT PROTEIN	A	1.3	3.8	3	34	MQESIARFHEIIAIDKNHLRAVEQAIEQTMHSLN	6982
2P2C	AB	HYDROLASE	A	1.9	3.8	2	6	PEFYQT	6983
2PBI	CD	SIGNALING PROTEIN	C	1.9	3.8	2	14	NLEAQNLGNFIVKY	6984
2PQ4	AB	CHAPERONE/OXIDOREDUCTASE	B	1.9	3.8	2	17	RRSFMKANAVAAAAAAA	6985
2PRG	BC	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	C	1.3	3.8	3	9	KILHRLLQE	6986
2PT7	EH	HYDROLASE/PROTEIN BINDING	H	1.9	3.8	2	19	YRYKALSYLLFNWIHPTYG	6987
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	B	1.9	3.8	2	6	ELALIY	6988
2QIE	ED	TRANSFERASE	E	1.9	3.8	2	19	IPMAEKKLAQIGDEINEKW	6989
2QJK	PQ	ELECTRON TRANSPORT	P	1.9	3.8	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	6990
2QJY	JK	OXIDOREDUCTASE	J	1.9	3.8	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	6991
2QJY	MN	OXIDOREDUCTASE	M	1.9	3.8	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	6992
2QM6	CD	TRANSFERASE	C	1.9	3.8	2	15	GGTHLIQILNVMENA	6993
2QMB	CD	TRANSPORT PROTEIN	D	1.9	3.8	2	16	VADCGAEALARLLIVY	6994
2QR1	CD	TRANSFERASE	D	1.9	3.8	2	6	AFLTSN	6995
2SIV	AB	ENVELOPE GLYCOPROTEIN	B	1.3	3.8	3	33	QEWERKVDFLEENITALLEEAQIQQEKNMYELQ	6996
2UUN	OP	ELECTRON TRANSPORT	O	1.9	3.8	2	27	STEIQVAFGRFRQAAAGLSAATALTSA	6997
2UUN	UV	ELECTRON TRANSPORT	U	1.9	3.8	2	12	PLTDAVSTADSQ	6998
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	B	1.9	3.8	2	15	TEEQLLAVQAIRKYG	6999
2V1S	AK	OXIDOREDUCTASE	K	1.9	3.8	2	9	LSRLLSYAG	7000
2V4I	GF	TRANSFERASE	F	1.3	3.8	3	11	WGRVAMAIGKC	7001
2V5P	AD	RECEPTOR/GLYCOPROTEIN	D	1.9	3.8	2	12	GELVDTLQFVCG	7002
2V6Q	AB	APOPTOSIS	A	1.9	3.8	2	21	LGRALAWMAWCMHACRTLCCN	7003
2V7Q	CF	HYDROLASE	C	1.9	3.8	2	14	RSTVAQLVKRLTDA	7004
2VDW	GH	TRANSFERASE	G	1.9	3.8	2	14	FATIIERSKKFING	7005
2VJH	AD	PHOTOSYNTHESIS	A	1.9	3.8	2	18	PQALTEFRSYLDYVINAL	7006
2VPG	CD	GENE REGULATION	D	1.9	3.8	2	13	TEMANKAAEAVLK	7007
2VRC	CD	OXIDOREDUCTASE	C	1.9	3.8	2	17	PLAHVHLATEYAIRTTN	7008
2VRC	CD	OXIDOREDUCTASE	C	1.3	3.8	3	18	NTLLIVQHANVVKAARDA	7009
2VRW	AB	SIGNALING PROTEIN	B	1.9	3.8	2	36	EYDKRCCCLREIQQTEEKYTDTLGSIQQHFMKPLQR	7010
2WB1	AB	TRANSCRIPTION	B	3.8	3.8	1	11	EMERDCLIGFG	7011
2WEL	AD	TRANSFERASE	D	1.3	3.8	3	15	EEQIAEFKEAFSLFD	7012

2WH2	X2	RIBOSOME	2	3.8	3.8	1	5	FQASI	7013
2WH4	UV	RIBOSOME	U	1.9	3.8	2	23	RKARETLFAAGNYAYAHRKRRKR	7014
2WIN	GH	IMMUNE SYSTEM	H	3.8	3.8	1	5	KYELD	7015
2ZDI	BC	CHAPERONE	B	3.8	3.8	1	43	PQVQAMLGQLDTYQQQLQLVIQQKQKVQADLNEAKKALEEIET	7016
2ZJQ	PZ	RIBOSOME	P	1.9	3.8	2	11	VQDAEDLLRFI	7017
2ZT9	AB	PHOTOSYNTHESIS	A	3.8	3.8	1	15	VAEAYSSVQYIMNEV	7018
3B71	BE	PROTEIN BINDING	E	1.9	3.8	2	10	MSQIKRLLSE	7019
3BCQ	AD	TRANSPORT PROTEIN/OXYGEN BINDING	D	1.9	3.8	2	7	PWTQRHF	7020
3CDG	CE	IMMUNE SYSTEM	C	1.3	3.8	3	29	SEYWDRETRSARDTAQIFRVNLRTLRGYY	7021
3CFI	JK	PROTEIN TRANSPORT/IMMUNE SYSTEM	K	1.9	3.8	2	25	LSQERTARLNELQRALVMMDSDFRQ	7022
3CJT	EF	TRANSFERASE/RIBOSOMAL PROTEIN	F	1.9	3.8	2	9	PVGPALGQH	7023
3CJT	IJ	TRANSFERASE/RIBOSOMAL PROTEIN	J	1.9	3.8	2	9	PVGPALGQH	7024
3CJT	MN	TRANSFERASE/RIBOSOMAL PROTEIN	M	1.9	3.8	2	8	LPGLFDGG	7025
3CW2	AC	TRANSLATION	C	1.3	3.8	3	14	GVEKIKEVISKALE	7026
3CXH	LN	OXIDOREDUCTASE	L	1.9	3.8	2	18	IDDLIHFTLKQWNRLTIS	7027
3D36	AC	TRANSFERASE/TRANSFERASE INHIBITOR	C	3.8	3.8	1	14	PEFIELIEKEIQRR	7028
3DBO	AB	TOXIN/ANTITOXIN	B	3.8	3.8	1	14	TDIRAQRLATLESV	7029
3DGE	AC	TRANSFERASE/SIGNALING PROTEIN	A	1.9	3.8	2	32	LSTLKEFLEVIIDQSNHLENLLNELLDFSRLE	7030
3DI2	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.9	3.8	2	16	DFDLHLLKVSEGTTIL	7031
3DTP	BF	CONTRACTILE PROTEIN	F	1.9	3.8	2	6	AFNLFD	7032
3E0J	EF	TRANSFERASE	F	1.9	3.8	2	14	GPLFNTDYDILKSN	7033
3E7S	AB	OXIDOREDUCTASE	B	1.9	3.8	2	20	WKDKAAVEINLAVLHSFQLA	7034
3EG5	AB	SIGNALING PROTEIN	A	1.9	3.8	2	19	PSSFENVKEKWVPEITHHC	7035
3EU7	AX	TRANSCRIPTION/ANTITUMOR PROTEIN	X	1.9	3.8	2	6	WFEELS	7036
3EUH	BE	CELL CYCLE	B	1.3	3.8	3	12	VFAQRLRQSVQT	7037
3EYJ	AB	VIRAL PROTEIN	B	1.9	3.8	2	24	NQHTIDVTDSEMNKLFERVRRQLR	7038
3EZQ	AB	APOPTOSIS	A	1.9	3.8	2	33	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	7039
3EZQ	EF	APOPTOSIS	F	1.3	3.8	3	16	NLVADLVQEVQQARDL	7040
3FGC	CD	OXIDOREDUCTASE	C	1.9	3.8	2	11	PYVAAAHLLGA	7041
3FGC	CD	OXIDOREDUCTASE	D	1.3	3.8	3	15	SDQVIEEMLDTAHYV	7042
3FLO	EF	TRANSFERASE	F	1.9	3.8	2	20	PLQLTSQIEHSIRAHISLYY	7043
3FWC	JL	CELL CYCLE, TRANSCRIPTION	L	1.3	3.8	3	16	FTQILSTVEPKALEMV	7044
3FXD	CD	UNKNOWN FUNCTION	C	1.9	3.8	2	21	NFLRVIGKKLIAIRDRFLKRI	7045
3G9K	DF	HYDROLASE	F	1.3	3.8	3	14	IPQILTPILDKYTH	7046
3GHG	KL	BLOOD CLOTTING	L	1.3	3.8	3	29	IRYLQEIYNSNNQKIVNLKEKVAQLEAQC	7047

3GJX	BA	PROTEIN TRANSPORT	A	1.9	3.8	2	22	EEDEKRFLVTVIKDLLGLCEQK	7048
3GTM	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	3.8	3.8	1	17	AQRDAVTLFCCLLRSRL	7049
3H0L	AC	LIGASE	A	1.9	3.8	2	6	PIEMYL	7050
3H0L	DE	LIGASE	D	1.9	3.8	2	13	IFEMYARTRDEGF	7051
3H0L	SU	LIGASE	U	1.9	3.8	2	11	REWVLKIAKLA	7052
3H4P	Ee	HYDROLASE	E	1.9	3.8	2	12	RARLEAQIYRLT	7053
3HAY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	C	1.9	3.8	2	13	GEYRRRWKREVLG	7054
3HHR	AB	HORMONE/RECEPTOR	A	3.8	3.8	1	6	REETQQ	7055
3HOY	BI	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.3	3.8	3	14	WQMLEMLKPCVEDG	7056
3MON	GH	SWEET-TASTING PROTEIN	H	1.9	3.8	2	17	PFTQNLGKFAVDEENKI	7057
1AWC	AB	TRANSCRIPTION/DNA	B	1.9	3.7	2	8	ALHWATEH	7058
1BCC	EJ	OXIDOREDUCTASE	J	1.9	3.7	2	23	IVVGALLFERAFDQGADAIYEHI	7059
1BGX	LH	COMPLEX (POLYMERASE/INHIBITOR)	L	1.9	3.7	2	7	SEQLTSG	7060
1CFF	AB	CALMODULIN	A	1.9	3.7	2	11	AELRHVMTNLG	7061
1CG5	AB	OXYGEN TRANSPORT	B	1.9	3.7	2	21	PKEHAAAYKFFRLVAEALSSN	7062
1DCE	CD	TRANSFERASE	D	3.7	3.7	1	10	SDLLGWWLCE	7063
1DE4	AC	METAL TRANSPORT INHIBITOR/RECEPTOR	A	1.9	3.7	2	12	AWPTKLEWERHK	7064
1DFK	AY	CONTRACTILE PROTEIN	A	1.2	3.7	3	13	QDQRIGLSVIQRN	7065
1DGH	AD	OXIDOREDUCTASE	D	1.2	3.7	3	19	KMLQGRLFAYPDTHRHRLG	7066
1E6V	BC	OXIDOREDUCTASE	B	1.9	3.7	2	14	VSATILYYNDLLEY	7067
1E6V	EF	OXIDOREDUCTASE	E	1.9	3.7	2	14	VSATILYYNDLLEY	7068
1E6Y	AE	OXIDOREDUCTASE	A	1.9	3.7	2	12	AAVADLSFAAKA	7069
1EAH	13	VIRUS	1	1.9	3.7	2	8	VQLRRKLE	7070
1EFU	CD	COMPLEX (TWO ELONGATION FACTORS)	C	3.7	3.7	1	11	TREHILLGRQV	7071
1EQZ	AB	STRUCTURAL PROTEIN/DNA	B	1.9	3.7	2	12	SIYVYKVLKQVH	7072
1F9E	EF	APOPTOSIS	F	1.2	3.7	3	16	WYIQSLCQSLRERCPR	7073
1FDH	AG	OXYGEN TRANSPORT	G	1.9	3.7	2	16	VEDAGGETLGRLLVVY	7074
1FFU	DE	HYDROLASE	D	3.7	3.7	1	17	FCTPGMLMRAYRFLQEN	7075
1FNT	AB	HYDROLASE/HYDROLASE ACTIVATOR	A	1.9	3.7	2	19	CDVLAKRMANLSQIYTQRA	7076
1FQV	IJ	LIGASE	J	1.9	3.7	2	14	QGTLFELILAANYL	7077
1G0U	GN	HYDROLASE	G	1.9	3.7	2	23	IPDARNAALRAKAEAAEFRYKYG	7078
1G0U	HI	HYDROLASE	I	1.9	3.7	2	12	SDQLFGMCESLY	7079
1GH0	GH	PHOTOSYNTHESIS	H	1.9	3.7	2	12	AFTKVVSQADTR	7080
1GH0	ST	PHOTOSYNTHESIS	T	1.9	3.7	2	13	TAQIDALSQMVAE	7081
1GPQ	AD	HYDROLASE/INHIBITOR	A	1.9	3.7	2	5	SLENH	7082

1GXS	AB	LYASE	A	1.9	3.7	2	14	DHEDMIGMFESWWH	7083
1H2A	SL	OXIDOREDUCTASE	S	3.7	3.7	1	6	FWDAMT	7084
1H3O	CD	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	D	1.9	3.7	2	10	KKKLQDLVRE	7085
1HBH	CD	OXYGEN CARRIER	D	1.9	3.7	2	16	YDDIGPKALSRCLIVY	7086
1HH4	AD	SIGNALING PROTEIN/INHIBITOR	D	1.9	3.7	2	12	ESLRKYKEALLG	7087
1I1Q	AB	LYASE	A	1.2	3.7	3	21	HKELSEHLMLVDLARNDLARI	7088
1I3Q	BC	TRANSCRIPTION	C	1.9	3.7	2	11	DEFIAHRLGLI	7089
1I51	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.2	3.7	3	13	WFVQALCSILEEH	7090
1I7M	BA	LYASE	A	1.9	3.7	2	12	LVPLLKLARDYS	7091
1I9R	HL	CYTOKINE/IMMUNE SYSTEM	L	1.9	3.7	2	5	DEQLK	7092
1IBC	AB	COMPLEX (HYDROLASE/PEPTIDE)	A	1.9	3.7	2	16	AEVDITGMTMLLQNLG	7093
1IBR	AB	CELL CYCLE, TRANSLATION	B	3.7	3.7	1	18	TRVRVAALQNLVKIMSLY	7094
1ICE	AB	CYTOKINE	A	1.9	3.7	2	15	AEVDITGMTMLLQNL	7095
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	3.7	3.7	1	12	DEEVDEMIREAD	7096
1IRU	QR	HYDROLASE	R	1.9	3.7	2	12	FQVEYAQEAVKK	7097
1IW7	AC	TRANSFERASE	A	1.9	3.7	2	11	VVEIILNLKEL	7098
1IW7	DE	TRANSFERASE	D	3.7	3.7	1	8	SFAQAEAR	7099
1J1E	AC	CONTRACTILE PROTEIN	C	1.2	3.7	3	10	ADAMMQALLG	7100
1JD2	12	HYDROLASE	2	3.7	3.7	1	10	YQVEYAFKAT	7101
1KCG	BC	IMMUNE SYSTEM	C	1.9	3.7	2	23	DAWGKQLEMLREVGQRLRLELAD	7102
1KF6	CD	OXIDOREDUCTASE	D	1.9	3.7	2	9	YERVLAFAQ	7103
1KF6	NO	OXIDOREDUCTASE	O	3.7	3.7	1	27	PVIVIINLITLAAALLHTKTWFELAPK	7104
1KMI	YZ	SIGNALING PROTEIN	Z	1.9	3.7	2	49	LADARELVTDTRQFLADVPAHTSFTNAQLLKIMMAQDFQDLTGQVIKRM	7105
1L2W	CJ	CHAPERONE	C	1.9	3.7	2	16	SLYTQLEMLVQGAERL	7106
1L2W	HL	CHAPERONE	H	1.9	3.7	2	16	SLYTQLEMLVQGAERL	7107
1L9J	RS	PHOTOSYNTHESIS	S	1.9	3.7	2	15	IFSHLDWTNNFSLVH	7108
1LB1	EF	SIGNALING PROTEIN	F	1.9	3.7	2	7	LRPLSYP	7109
1LNU	CD	SUGAR BINDING PROTEIN	C	1.2	3.7	3	21	PQGGLQNIAVVKHNLGVLTKR	7110
1MDY	AB	TRANSCRIPTION/DNA	A	1.9	3.7	2	26	DRRKAATMRERRRLSKVNEAFETLKR	7111
1MI5	DE	IMMUNE SYSTEM	E	1.9	3.7	2	7	EAEISHT	7112
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	B	1.9	3.7	2	15	SDYNRTVMRNWTGKW	7113
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	G	3.7	3.7	1	5	FRQAY	7114
1N5W	AC	OXIDOREDUCTASE	C	1.9	3.7	2	8	SLIPIMKT	7115
1NI4	AD	OXIDOREDUCTASE	D	1.9	3.7	2	6	KILEDN	7116

1NIW	EF	SIGNALING PROTEIN/OXIDOREDUCTASE	E	1.9	3.7	2	15	EEQIAEFKEAFSLFD	7117
1NTK	CF	OXIDOREDUCTASE	F	1.9	3.7	2	18	ASSRWLEGIRKWYYNAAG	7118
1OCC	CJ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	J	1.2	3.7	3	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	7119
1OR0	AB	HYDROLASE	A	1.9	3.7	2	10	EQTTVWLLTN	7120
1OR0	CD	HYDROLASE	D	1.9	3.7	2	7	REQVEAA	7121
1PID	CD	HORMONE	D	1.9	3.7	2	12	SHLVEALYLVCG	7122
1PMA	GT	PROTEASE	T	1.2	3.7	3	22	VGDAQVLVRYMKAELELYRLQR	7123
1POV	13	VIRUS	1	1.9	3.7	2	5	IESFF	7124
1QPW	CD	OXYGEN TRANSPORT	D	1.9	3.7	2	20	PENFRLLGNVIVVVLARRLG	7125
1QVF	FL	RIBOSOME	F	1.9	3.7	2	13	EEIVMHIPELADE	7126
1R27	AB	OXIDOREDUCTASE	B	1.9	3.7	2	14	EAQAQEMYRYLAIA	7127
1RCO	BC	LYASE	B	1.9	3.7	2	21	NAPGAVANRVALEACVQARNE	7128
1RCO	EF	LYASE	E	1.9	3.7	2	21	NAPGAVANRVALEACVQARNE	7129
1RCO	HI	LYASE	H	1.9	3.7	2	21	NAPGAVANRVALEACVQARNE	7130
1RCO	LS	LYASE	L	1.9	3.7	2	21	NAPGAVANRVALEACVQARNE	7131
1RCO	OP	LYASE	O	1.9	3.7	2	21	NAPGAVANRVALEACVQARNE	7132
1RCO	VW	LYASE	V	1.9	3.7	2	21	NAPGAVANRVALEACVQARNE	7133
1RM6	DF	OXIDOREDUCTASE	D	1.9	3.7	2	6	GVEKVT	7134
1RP3	GH	TRANSCRIPTION	H	1.9	3.7	2	10	TLSKIAQELS	7135
1RYP	EM	MULTICATALYTIC PROTEINASE	M	1.9	3.7	2	15	INSAARNIQHLLYGK	7136
1RYP	OV	MULTICATALYTIC PROTEINASE	O	1.2	3.7	3	22	IPDARNAALRAKAEAAEFRYKY	7137
1RYP	QR	MULTICATALYTIC PROTEINASE	Q	1.9	3.7	2	15	VEILVRRLSDIKQGY	7138
1RYP	WM	MULTICATALYTIC PROTEINASE	M	1.2	3.7	3	18	VEEVIKLVRDSFTSATER	7139
1RYP	WX	MULTICATALYTIC PROTEINASE	W	3.7	3.7	1	22	AADTEAVTQLIGSNIELHSLYT	7140
1S5L	ad	PHOTOSYNTHESIS	d	1.9	3.7	2	16	VAAIFRFLLFFQGFHN	7141
1S5L	EF	PHOTOSYNTHESIS	E	1.9	3.7	2	13	ALFIAGWLFVSTG	7142
1SEB	AB	COMPLEX (MHC II/PEPTIDE/TOXIN)	A	1.9	3.7	2	7	EEFGRFA	7143
1SQB	DJ	OXIDOREDUCTASE	J	1.9	3.7	2	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	7144
1SQB	DJ	OXIDOREDUCTASE	J	3.7	3.7	1	5	WKHIK	7145
1SVD	AM	LYASE	A	1.9	3.7	2	21	NAAGAAANRVALEACVEARNQ	7146
1T2V	BG	ANTITUMOR PROTEIN	B	3.7	3.7	1	9	LKYFLGIAG	7147
1TI2	EF	OXIDOREDUCTASE	F	1.2	3.7	3	12	NCFMGCMDEHEL	7148
1TU3	AF	PROTEIN TRANSPORT	F	1.2	3.7	3	33	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	7149
1U3H	GH	IMMUNE SYSTEM	H	1.9	3.7	2	33	RPDAEYYNKQYLERTRAELDTVCRYNYEETEVP	7150
1U7F	CB	SIGNALING PROTEIN	B	1.2	3.7	3	13	HRALQLLDEVLHT	7151
1UKL	AD	PROTEIN TRANSPORT/DNA BINDING PROTEIN	D	1.9	3.7	2	21	VLRKAIDYIKYLQQVNHKLRQ	7152
1V54	AC	OXIDOREDUCTASE	A	1.9	3.7	2	34	PILYQHLFWFFGHPEVYILILPGFGMISHIVTYY	7153

1V54	OV	OXIDOREDUCTASE	V	1.9	3.7	2	15	FAVAEKRKKAYADFY	7154
1V75	AB	OXYGEN STORAGE/TRANSPORT	B	3.7	3.7	1	16	VGEVGGEALARLLIVY	7155
1VCB	EF	TRANSCRIPTION	E	1.9	3.7	2	18	SHVLSKVCMYFTYKVRYT	7156
1VF5	OP	PHOTOSYNTHESIS	O	1.9	3.7	2	20	VFPVVIMGTFACIVALSVLD	7157
1VS5	CN	RIBOSOME	C	1.9	3.7	2	21	TKEFADNLDSDFKVRQYLTKE	7158
1W1I	BE	HYDROLASE	E	1.9	3.7	2	18	RDAIKRIAYEFVEMKAKD	7159
1W2W	IJ	ISOMERASE	I	1.9	3.7	2	16	VNLSNSLVEIKNILKS	7160
1W2W	IJ	ISOMERASE	I	1.9	3.7	2	14	DNGAKYLIDVLQKD	7161
1W63	HP	ENDOCYTOSIS	P	1.2	3.7	3	18	SLVFSFLYKVVQVFSEYF	7162
1W63	LV	ENDOCYTOSIS	V	1.2	3.7	3	18	SLVFSFLYKVVQVFSEYF	7163
1WCM	AB	TRANSCRIPTION	B	3.7	3.7	1	13	VAHLIECLLSKVA	7164
1WYU	GH	OXIDOREDUCTASE	G	1.9	3.7	2	5	LEDLF	7165
1WYU	GH	OXIDOREDUCTASE	H	1.9	3.7	2	18	GAHGELTGILIIRAYHED	7166
1X3Z	AB	HYDROLASE	B	1.9	3.7	2	12	VEDLLSLRQVVS	7167
1XFU	AO	LYASE/METAL BINDING PROTEIN	O	1.2	3.7	3	13	SEEEIREAFRVFD	7168
1XFU	BP	LYASE/METAL BINDING PROTEIN	P	1.2	3.7	3	13	SEEEIREAFRVFD	7169
1XFV	DR	LYASE/METAL BINDING PROTEIN	D	1.2	3.7	3	15	SLEKQKGVTNLLIKY	7170
1XTC	CE	TOXIN	C	1.9	3.7	2	8	THNRIKDE	7171
1XXI	AE	TRANSFERASE	E	1.9	3.7	2	17	RELLITDLLLRIEHYLQ	7172
1XXI	DE	TRANSFERASE	D	1.9	3.7	2	15	RRMGVEMTLLRALAF	7173
1Y8R	AB	LIGASE	A	1.2	3.7	3	20	APVCAVVGGILAQEIVKALS	7174
1Y8R	AB	LIGASE	B	1.9	3.7	2	20	ATTNAVIAGLIVLEGLKILS	7175
1Y8R	DE	LIGASE	D	1.9	3.7	2	21	APVCAVVGGILAQEIVKALSQ	7176
1YCP	JM	COMPLEX (SERINE PROTEASE/PEPTIDE)	J	1.2	3.7	3	10	EKELFESYIE	7177
1YE9	BG	OXIDOREDUCTASE	G	1.2	3.7	3	17	LLQGRLFSYTDTQISRL	7178
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.9	3.7	2	34	HAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT	7179
1YEW	AC	OXIDOREDUCTASE, MEMBRANE PROTEIN	A	1.2	3.7	3	10	IFIPRLLMVD	7180
1YHU	IK	OXYGEN STORAGE/TRANSPORT	I	1.9	3.7	2	20	PEFKAHIARVLGGLDRVISM	7181
1YQ3	BD	OXIDOREDUCTASE	B	1.9	3.7	2	15	PGKAIAEIKKMMATY	7182
1Z6O	FV	METAL BINDING PROTEIN	F	1.9	3.7	2	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	7183
1Z6O	IT	METAL BINDING PROTEIN	I	1.9	3.7	2	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	7184
1ZOQ	BD	TRANSCRIPTION/TRANSFERASE	B	1.9	3.7	2	13	TCLRALVEMARVG	7185
1ZOY	CD	OXIDOREDUCTASE	C	3.7	3.7	1	10	FESHLELVKS	7186
2A4J	AB	STRUCTURAL PROTEIN	A	3.7	3.7	1	12	DEELQEMIDEAD	7187
2B8K	AB	TRANSFERASE	B	3.7	3.7	1	13	VAHLIECLLSKVA	7188
2BCJ	AQ	TRANSFERASE/HYDROLASE	Q	1.2	3.7	3	9	RSERRKWIH	7189
2BEQ	AF	VIRAL PROTEIN	A	1.2	3.7	3	35	QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	7190

2BR2	EF	HYDROLASE	F	1.9	3.7	2	29	PDEFRQAFDLAVKGINIIYNLEREALKSK	7191
2BV8	OP	PHOTOSYNTHESIS	P	1.9	3.7	2	13	NTQLDALANMIAE	7192
2C1M	AB	PROTEIN TRANSPORT/MEMBRANE PROTEIN	A	3.7	3.7	1	15	PEVLADSCWAISYLT	7193
2DQT	LH	IMMUNE SYSTEM	L	1.9	3.7	2	6	SEQLTS	7194
2DXB	EF	HYDROLASE	E	1.9	3.7	2	16	YYGRWLLTAARILVDK	7195
2ES4	AD	HYDROLASE	D	1.2	3.7	3	10	EAIRAASLDR	7196
2F8N	AB	STRUCTURAL PROTEIN/DNA	A	1.9	3.7	2	16	KLPFQRLVREIAQDFK	7197
2FV4	AB	STRUCTURAL PROTEIN, PROTEIN BINDING	A	1.2	3.7	3	16	LAAFLVVARDMLLASL	7198
2FYN	PQ	OXIDOREDUCTASE	P	1.9	3.7	2	15	VDLAFASVEHIMRNV	7199
2G4D	AB	HYDROLASE/PROTEIN BINDING	A	3.7	3.7	1	10	FFFTKLKTAG	7200
2G77	AB	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	A	1.9	3.7	2	10	FQETITFLQN	7201
2GEZ	EF	HYDROLASE	E	1.9	3.7	2	24	PERRKPREEGLRHCLQIGVEALKA	7202
2GUZ	GH	CHAPERONE, PROTEIN TRANSPORT	H	1.9	3.7	2	15	MDKINNRFNYLFEVN	7203
2H4P	AB	HYDROLASE INHIBITOR	A	3.7	3.7	1	27	LEISMEQVSASIGNFTVDLFNKLNETN	7204
2HDN	CD	TRANSLATION	D	1.9	3.7	2	18	AEWEAKILELAGFLDSYI	7205
2HDN	IJ	TRANSLATION	J	1.9	3.7	2	18	AEWEAKILELAGFLDSYI	7206
2HGJ	FO	RIBOSOME	F	3.7	3.7	1	16	PHLLWEVVRWQLAKRR	7207
2HLD	LM	HYDROLASE	L	1.9	3.7	2	16	LKLFLAQYREVAAFAQ	7208
2HLD	SW	HYDROLASE	W	1.2	3.7	3	15	TREGNDLYREMKETG	7209
2HYB	MN	TRANSFERASE	M	1.2	3.7	3	11	LGQLVEAAIQA	7210
2HZM	AB	TRANSCRIPTION	A	1.9	3.7	2	6	PALVFN	7211
2HZM	EF	TRANSCRIPTION	E	1.9	3.7	2	9	IDTILSSKL	7212
2HZS	GH	TRANSCRIPTION	G	1.9	3.7	2	6	PALVFN	7213
2I2T	DP	RIBOSOME	P	1.9	3.7	2	6	QLEQEQ	7214
2IAE	AC	HYDROLASE	A	1.9	3.7	2	15	WRVRLAIIEYMPLLA	7215
2IAN	KM	IMMUNE SYSTEM	K	1.2	3.7	3	21	QGALANIAVDKANLEIMTKRS	7216
2IBZ	CF	OXIDOREDUCTASE	F	1.9	3.7	2	14	FTSIARIGDYILKS	7217
2INP	AC	OXIDOREDUCTASE	C	1.9	3.7	2	13	AALDESKAYWMDD	7218
2J59	FR	HYDROLASE	R	1.2	3.7	3	22	EEDTGVTNRDLISRRIKEYNNL	7219
2J5G	CD	HYDROLASE	D	1.9	3.7	2	27	QRLKRLVNEGIGYGLALEGITATDLRN	7220
2J8X	CD	HYDROLASE/INHIBITOR	D	1.9	3.7	2	9	PEEVEEVIG	7221
2K2I	AB	CELL CYCLE	A	1.9	3.7	2	13	TKEEILKAFKLFD	7222
2NUU	BH	TRANSPORT PROTEIN/SIGNALING PROTEIN	B	1.9	3.7	2	20	LLGACSGAIAGLVGVTPACG	7223
2OM0	ab	HORMONE	b	1.2	3.7	3	19	VNQHLCGSHLVEALYLVCG	7224
2ONK	FH	MEMBRANE PROTEIN	H	1.9	3.7	2	10	VRLEHVARTL	7225
2P5T	CD	TRANSCRIPTION REGULATOR	D	1.9	3.7	2	12	KTTIHRIKQKEF	7226

2PQR	AC	APOPTOSIS	A	1.9	3.7	2	14	IQSRFNYAWGLIKS	7227
2QAR	AB	HYDROLASE REGULATOR	B	1.9	3.7	2	30	GDVLYELLQHILKQRDLEAEAAAAEAAAKA	7228
2QYF	AB	CELL CYCLE	A	1.9	3.7	2	22	QKAIQDEIRSVIRQITATVTFL	7229
2UZ1	AB	LYASE	A	1.9	3.7	2	8	YHGVAAAF	7230
2V4I	AB	TRANSFERASE	B	1.9	3.7	2	14	PAEQDRLFRRVMDR	7231
2V4J	AE	OXIDOREDUCTASE	E	3.7	3.7	1	5	DPAYY	7232
2V7Q	HI	HYDROLASE	H	1.9	3.7	2	21	EATRAEIQIRIEANEALVKAL	7233
2VDW	AB	TRANSFERASE	B	1.9	3.7	2	13	YFLQISRVNDLNR	7234
2VPE	CD	GENE REGULATION	D	1.9	3.7	2	13	TEMANKAAEAVLK	7235
2W73	AL	METAL BINDING PROTEIN	A	1.9	3.7	2	29	FPEFLTMMARKMKDTDSEEEIREAFRVFD	7236
2WAQ	HQ	TRANSCRIPTION	Q	1.2	3.7	3	13	VDEAKRLFEDNYK	7237
2WB1	WR	TRANSCRIPTION	R	3.7	3.7	1	5	LPSRM	7238
2WH4	X2	RIBOSOME	2	3.7	3.7	1	5	FQASI	7239
2ZFB	AB	METAL BINDING PROTEIN	A	1.9	3.7	2	17	QADDYGAEALERMFVTY	7240
3A0B	DX	ELECTRON TRANSPORT	D	1.9	3.7	2	9	WFDILDDWL	7241
3B9J	AC	OXIDOREDUCTASE	A	3.7	3.7	1	17	FCTPGIVMSMYTLLRNQ	7242
3BOW	BC	HYDROLASE/HYDROLASE INHIBITOR	B	3.7	3.7	1	21	FEEFKYLWNNIKKWQGIYKRF	7243
3BPO	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.9	3.7	2	16	PSTALRELIEELVNIT	7244
3BRT	CB	TRANSFERASE/TRANSCRIPTION	B	1.2	3.7	3	60	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	7245
3BRT	CD	TRANSFERASE/TRANSCRIPTION	C	1.2	3.7	3	27	SEELVAEAHNLCTLLENAIQDTVREQG	7246
3C1B	CD	STRUCTURAL PROTEIN/DNA	D	1.9	3.7	2	12	SREIQTAVRLLL	7247
3C1B	FH	STRUCTURAL PROTEIN/DNA	H	3.7	3.7	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	7248
3C91	AH	HYDROLASE	H	1.2	3.7	3	22	VGDAQVLVRYMKAELELYRLQR	7249
3CJH	KH	PROTEIN TRANSPORT	K	1.9	3.7	2	16	TELVNKISENCFEKCL	7250
3CMA	FM	RIBOSOME	F	1.9	3.7	2	13	EEIVMHIPELADE	7251
3CQX	AD	CHAPERONE	D	1.9	3.7	2	9	QKFQSIVIG	7252
3CSY	KL	IMMUNE SYSTEM/VIRAL PROTEIN	L	1.2	3.7	3	23	LICGLRQLANETTQALQLFLRAT	7253
3CUQ	AB	PROTEIN TRANSPORT	B	1.9	3.7	2	11	LTEVYCLVNRA	7254
3CXH	AB	OXIDOREDUCTASE	B	1.2	3.7	3	12	ALKLVRESELLG	7255
3DHH	AB	OXIDOREDUCTASE	A	3.7	3.7	1	5	YELTR	7256
3DI2	CD	CYTOKINE/CYTOKINE RECEPTOR	C	1.9	3.7	2	17	KQYESVLMVSIDQLLDS	7257
3DIN	CD	MEMBRANE PROTEIN, PROTEIN TRANSPORT	D	1.9	3.7	2	32	FGVVLVILAVTSVYFFVLDFIFSGVVSAIFKA	7258
3DS3	BD	VIRAL PROTEIN	B	1.9	3.7	2	8	LEEMMTAC	7259
3DZU	AD	TRANSCRIPTION/DNA	A	3.7	3.7	1	11	RLPALRSIGLK	7260
3E2Z	AB	TRANSFERASE, LYASE	A	1.9	3.7	2	12	SYVKEELSKAAF	7261
3EAB	BH	CELL CYCLE	B	1.9	3.7	2	25	EQCERARRLQAKMMTNLVMAKDRLQ	7262
3EH3	AC	OXIDOREDUCTASE	A	1.9	3.7	2	7	TLDYVVH	7263
3EN1	AB	OXIDOREDUCTASE	B	1.9	3.7	2	11	ATMMKGRLRKI	7264

3EUB	AB	OXIDOREDUCTASE	B	1.9	3.7	2	7	KQVKSVA	7265
3EZB	AB	TRANSFERASE	B	1.2	3.7	3	14	TRPAAQFVKEAKGF	7266
3F02	AC	HYDROLASE INHIBITOR	A	1.9	3.7	2	8	LATLEPLV	7267
3F3P	FH	STRUCTURAL PROTEIN	H	1.9	3.7	2	7	IAELLPH	7268
3FGC	AB	OXIDOREDUCTASE	A	1.9	3.7	2	11	PYVAAAHLLGA	7269
3FWB	AB	CELL CYCLE, TRANSCRIPTION	A	1.9	3.7	2	13	PLDEIKRAFQLFD	7270
3GHG	DE	BLOOD CLOTTING	D	1.2	3.7	3	43	LRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIK	7271
3GLI	FJ	TRANSFERASE/DNA	J	1.9	3.7	2	17	RELLITDLLLRIEHYLQ	7272
3GZD	DC	LYASE	D	1.9	3.7	2	22	GTESNNLVIHSVVKHFHANQTS	7273
3H0L	JL	LIGASE	J	1.9	3.7	2	6	PIEMYL	7274
3H0L	JL	LIGASE	L	1.9	3.7	2	11	REWVLKIAKLA	7275
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	3.7	3.7	1	11	DTLCGIRKLTL	7276
3HRD	EH	OXIDOREDUCTASE	E	1.2	3.7	3	7	SLEKVMG	7277
3HUJ	GH	IMMUNE SYSTEM	H	1.9	3.7	2	5	EAEIS	7278
1AHJ	GH	LYASE	G	1.2	3.6	3	9	PRKVLSEMG	7279
1AOI	BD	DNA BINDING PROTEIN/DNA	B	1.8	3.6	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	7280
1AOI	GH	DNA BINDING PROTEIN/DNA	G	1.2	3.6	3	7	EELNKLL	7281
1B6C	AB	COMPLEX (ISOMERASE/PROTEIN KINASE)	B	1.8	3.6	2	14	ERSWFREAEIYQTV	7282
1BXR	GH	AMIDOTRANSFERASE	G	1.8	3.6	2	19	DKEYQIMRNASMAVLREIG	7283
1CIC	AB	IMMUNOGLOBULIN	A	1.8	3.6	2	6	SEQLTS	7284
1DCE	AB	TRANSFERASE	A	1.8	3.6	2	12	YGTWHHRCWLLS	7285
1FM6	UV	TRANSCRIPTION	U	1.8	3.6	2	6	TFLMEM	7286
1FOE	AB	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	B	1.8	3.6	2	5	DRLRP	7287
1FQJ	AC	SIGNALING PROTEIN	C	1.8	3.6	2	7	LHELAQY	7288
1FQV	GH	LIGASE	H	1.8	3.6	2	8	PEEIRKTF	7289
1G0U	H1	HYDROLASE	1	1.8	3.6	2	14	FGAHMANPLLRKVV	7290
1G0U	VW	HYDROLASE	V	3.6	3.6	1	22	AADTEAVTQLIGSNIELHSLYT	7291
1G2C	AB	VIRAL PROTEIN	A	1.8	3.6	2	45	EVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	7292
1GCV	AB	OXYGEN STORAGE/TRANSPORT	B	1.8	3.6	2	19	PGSFHLLTDCIIVELAYLR	7293
1GH0	EF	PHOTOSYNTHESIS	F	1.8	3.6	2	13	TAQIDALSQMVAE	7294
1GXS	AB	LYASE	B	1.8	3.6	2	10	LPVYRELIQA	7295
1GZS	DC	TOXIN/CELL CYCLE	D	1.8	3.6	2	30	PAYASQTREAILSAVYSKNKDQCCNLLISK	7296
1H6K	AX	NUCLEAR PROTEIN	X	1.8	3.6	2	11	EEQIYELFSKS	7297
1H6K	BY	NUCLEAR PROTEIN	Y	1.8	3.6	2	11	EEQIYELFSKS	7298
1HBM	DB	METHANOGENESIS	D	1.8	3.6	2	13	AATGDFAYAAKAE	7299
1HL6	AB	SIGNAL PROTEIN	B	1.2	3.6	3	15	QSVMEELKRIIIDSE	7300
1IB1	CG	SIGNALING PROTEIN/TRANSFERASE	C	1.8	3.6	2	14	TLIMQLLRDNLTLW	7301

1ID3	GH	STRUCTURAL PROTEIN/DNA	G	1.8	3.6	2	11	PRHLQLAIRND	7302
1IR2	GO	LYASE	O	1.8	3.6	2	14	DEQIAAQVDYIVAN	7303
1IRU	QR	HYDROLASE	R	1.8	3.6	2	9	TADARIVIN	7304
1IRU	YL	HYDROLASE	L	1.8	3.6	2	10	SVYAYGVMDR	7305
1IW7	MN	TRANSFERASE	N	3.6	3.6	1	8	PEKIRSWS	7306
1J1D	BC	CONTRACTILE PROTEIN	B	1.8	3.6	2	21	EREKKKKILAERRKVLAIDHL	7307
1J8H	AC	IMMUNE SYSTEM	A	1.2	3.6	3	22	AQGALANIAVDKANLEIMTKRS	7308
1JD2	HT	HYDROLASE	T	1.2	3.6	3	14	FGAHMANPLLRKVV	7309
1JJU	BC	ELECTRON TRANSPORT PROTEIN	C	3.6	3.6	1	7	LYGCADP	7310
1JNR	CB	OXIDOREDUCTASE	C	3.6	3.6	1	20	EKMLQRALELLAFLKEDLEK	7311
1JSU	BC	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.8	3.6	2	17	LQLVGTAAMLLASKFEE	7312
1K6L	LM	PHOTOSYNTHESIS	M	1.8	3.6	2	15	IFSHLDWTNNFSLVH	7313
1K7L	CD	TRANSCRIPTION	D	1.2	3.6	3	10	KILHRLLQEG	7314
1KF6	CD	OXIDOREDUCTASE	C	1.8	3.6	2	13	PEAWAGFVDFLQN	7315
1KF9	DE	HORMONE/GROWTH FACTOR	D	1.2	3.6	3	47	NVYDLLKDLEEGIQTLMGRLLLKNYGLLYCFNKDMSKVSTYLRTVQC	7316
1KFY	CD	OXIDOREDUCTASE	C	1.8	3.6	2	26	PEPIIKSLWAVTVVATIVILFVALYW	7317
1KN1	AB	ELECTRON TRANSPORT	A	1.2	3.6	3	12	PGELDRIKSFVL	7318
1KUP	AB	CELL ADHESION	A	1.8	3.6	2	5	FKRNR	7319
1KYO	DI	OXIDOREDUCTASE/ELECTRON TRANSPORT	I	3.6	3.6	1	7	WKDVKAK	7320
1KYO	NR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.8	3.6	2	21	EDESYARAYRIIRAHQTELTH	7321
1L2W	EK	CHAPERONE	E	1.8	3.6	2	16	SLYTQLEMLVQGAERL	7322
1LB1	CD	SIGNALING PROTEIN	D	1.8	3.6	2	19	PDSLENIPEKWTPEVKHFC	7323
1M1Y	IJ	OXIDOREDUCTASE	I	1.8	3.6	2	8	VGCGQYSR	7324
1M93	AC	VIRAL PROTEIN	A	3.6	3.6	1	10	DIFREIASSM	7325
1MJG	AM	OXIDOREDUCTASE	M	1.8	3.6	2	30	VALFREVYHGAITATSYAEILLNQAIRTYG	7326
1MJG	DP	OXIDOREDUCTASE	P	1.8	3.6	2	9	EAVEQLLEE	7327
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	1.8	3.6	2	7	EYEALTV	7328
1MUJ	BC	IMMUNE SYSTEM	B	1.8	3.6	2	12	ELGRPDAEYWNS	7329
1N4Q	GH	TRANSFERASE	G	1.8	3.6	2	14	YTVWHFRRVLLRSL	7330
1N5W	BC	OXIDOREDUCTASE	C	3.6	3.6	1	23	AEYRTKMAGVMLRRAVERAKARA	7331
1N5W	DF	OXIDOREDUCTASE	F	1.8	3.6	2	8	SLIPIMKT	7332
1NIW	CD	SIGNALING PROTEIN/OXIDOREDUCTASE	C	1.8	3.6	2	13	SEEEIREAFRVFD	7333
1NKP	DE	TRANSCRIPTION/DNA	D	1.8	3.6	2	28	NVKRRTHNVLERQRRNELKRSFFALRDQ	7334
1NRL	AC	TRANSCRIPTION	A	1.8	3.6	2	7	PLMQELF	7335

1NTK	DF	OXIDOREDUCTASE	F	1.8	3.6	2	20	ENLYDDRVFRIKRALDLSMR	7336
1OR0	AB	HYDROLASE	B	1.8	3.6	2	7	REQVEAA	7337
1ORS	BC	MEMBRANE PROTEIN	C	3.6	3.6	1	34	FRLVRLLRFLRILLIISRGSKFLSAIADAADKLV	7338
1OSV	BD	DNA BINDING PROTEIN	B	1.8	3.6	2	10	HEDQIALLKG	7339
1OXK	AB	SIGNALING PROTEIN	A	1.8	3.6	2	26	FSKGLIIQFIDQAQTTFAQMQRQLDG	7340
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.8	3.6	2	27	PWHGFSIGFAYGCGLLFAAHGATILAV	7341
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.8	3.6	2	24	HIPFAFAFAILAYLTLVLFRPVMM	7342
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.8	3.6	2	14	IFSHLDWTNNFSLV	7343
1Q5Q	EL	HYDROLASE	L	1.2	3.6	3	23	AGIAIELVRLFAVELEHYEKIEG	7344
1R27	AB	OXIDOREDUCTASE	A	1.8	3.6	2	7	LLMLTLG	7345
1R4M	EF	CELL CYCLE	E	1.2	3.6	3	11	DDYVHEFCRYG	7346
1RLD	AS	LYASE(CARBON-CARBON)	A	1.8	3.6	2	21	NAPGAVANRVALEACVKARNE	7347
1RM1	BC	TRANSCRIPTION/DNA	C	1.8	3.6	2	19	EQTLQDLKNIWQKKLTETK	7348
1RP3	AB	TRANSCRIPTION	A	1.8	3.6	2	14	LPLVKAIATNIKKH	7349
1RYP	KZ	MULTICATALYTIC PROTEINASE	K	3.6	3.6	1	14	YSGFYTFSLLDHHY	7350
1RYP	VN	MULTICATALYTIC PROTEINASE	V	1.2	3.6	3	6	PDEYEQ	7351
1S5E	AG	TRANSERASE,TOXIN	G	1.8	3.6	2	20	DSQKKAIERMKDTLRIAYLT	7352
1S5L	lt	PHOTOSYNTHESIS	t	1.8	3.6	2	13	FACIIALFFFAIF	7353
1SFC	KL	TRANSPORT PROTEIN	K	1.2	3.6	3	13	ADESLESTRRMLQ	7354
1T3Q	DE	OXIDOREDUCTASE	D	3.6	3.6	1	17	FCTAGMLATARSILAEN	7355
1TB6	LH	HYDROLASE/BLOOD CLOTTING	L	3.6	3.6	1	5	PRTFG	7356
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	B	1.8	3.6	2	10	FEEFCAVVGG	7357
1TIL	CD	TRANSCRIPTION	D	1.8	3.6	2	18	HHTAEELREQVTDVLENR	7358
1TUE	DE	REPLICATION	E	1.8	3.6	2	23	PKETLSERLSALQDKIIDHYEND	7359
1UM9	CD	OXIDOREDUCTASE	D	1.8	3.6	2	10	FDQLVSQVAK	7360
1UZD	AF	LYASE	A	1.8	3.6	2	6	WTDGLT	7361
1UZD	RM	LYASE	R	1.8	3.6	2	21	NAPGAAANRVALEACTQARNE	7362
1V75	AB	OXYGEN STORAGE/TRANSPORT	A	1.8	3.6	2	16	QEDFGAEALERMFIVY	7363
1VCB	HI	TRANSCRIPTION	H	1.8	3.6	2	15	PEIALELLMAANFLD	7364
1WYU	CD	OXIDOREDUCTASE	C	1.8	3.6	2	11	EEEIREMLRRV	7365
1WYU	GH	OXIDOREDUCTASE	G	1.8	3.6	2	15	EWKVLEELRRLAAQN	7366
1X86	AB	SIGNALING PROTEIN/MEMBRANE PROTEIN	A	1.8	3.6	2	10	TQMQRLTKYP	7367
1XDK	EF	HORMONE/GROWTH FACTOR RECEPTOR	E	1.8	3.6	2	7	RFAKLLL	7368
1XFU	CQ	LYASE/METAL BINDING PROTEIN	Q	1.2	3.6	3	13	SEEEIREAFRVFD	7369
1XTG	AB	TOXIN	A	3.6	3.6	1	9	EDNFVKFFK	7370
1XV9	CD	DNA BINDING PROTEIN	C	1.2	3.6	3	29	RFAKLLLRLPALRSIGLKCLEHLFFFKLI	7371
1XXH	IJ	TRANSFERASE	I	1.2	3.6	3	15	RRMGVEMTLLRALAF	7372
1XZP	AB	HYDROLASE	B	1.8	3.6	2	14	PLVVKKLLDLFLKS	7373

1Y8R	DE	LIGASE	E	1.8	3.6	2	21	ATTNAVIAGLIVLEGLKILSG	7374
1YA7	BH	HYDROLASE/HYDROLASE ACTIVATOR	H	1.2	3.6	3	23	VGDAQVLVRYMKAELELYRLQRR	7375
1YE9	AE	OXIDOREDUCTASE	E	1.8	3.6	2	17	LLQGRLFSYTDTQISRL	7376
1YE9	CG	OXIDOREDUCTASE	G	1.8	3.6	2	13	FHRRELWEAIEAG	7377
1YFN	AE	PROTEIN BINDING	E	3.6	3.6	1	6	PFWQKV	7378
1YFN	BF	PROTEIN BINDING	F	3.6	3.6	1	5	PHQWQ	7379
1YNJ	CD	TRANSFERASE	C	1.8	3.6	2	13	IEGRNAAYQAIIK	7380
1Z00	AB	HYDROLASE	A	1.8	3.6	2	7	LEQLIAA	7381
1Z0K	CD	PROTEIN TRANSPORT	D	1.8	3.6	2	19	PLLQQIHNITSFIRQAKAA	7382
1Z7Q	BC	HYDROLASE/HYDROLASE ACTIVATOR	C	3.6	3.6	1	10	QVEYALESIS	7383
1Z7Q	Rk	HYDROLASE/HYDROLASE ACTIVATOR	R	3.6	3.6	1	21	NADSRILIEKARVEAQSHRLT	7384
1ZBB	ag	STRUCTURAL PROTEIN/DNA	a	1.2	3.6	3	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	7385
1ZBB	FH	STRUCTURAL PROTEIN/DNA	F	1.8	3.6	2	11	AMDVVYALKRQ	7386
1ZGL	JK	IMMUNE SYSTEM	J	1.8	3.6	2	7	EEFGRFA	7387
1ZGL	KL	IMMUNE SYSTEM	K	1.8	3.6	2	13	AVDTYCRHNYGVG	7388
2AA1	CD	OXYGEN STORAGE/TRANSPORT	C	1.8	3.6	2	16	SDAIGNDALSRMIVVY	7389
2ACZ	BD	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	3.6	3.6	1	6	PSFWWN	7390
2ADV	AC	HYDROLASE	A	1.2	3.6	3	10	EQTTVWLLTN	7391
2ARP	AF	HORMONE/GROWTH FACTOR	F	3.6	3.6	1	12	ACHLRKATCLLG	7392
2AXT	AC	ELECTRON TRANSPORT	C	1.8	3.6	2	18	GPEASQAQAMTFLIRDQK	7393
2AXT	kz	ELECTRON TRANSPORT	z	3.6	3.6	1	27	DRSKQLIFLGSGLWIALVLVVGVLNFF	7394
2AXT	lm	ELECTRON TRANSPORT	m	1.8	3.6	2	25	GLIATALFVLVPSVFLIILYVQTES	7395
2AXT	LM	ELECTRON TRANSPORT	M	1.8	3.6	2	25	GLIATALFVLVPSVFLIILYVQTES	7396
2B5T	CD	BLOOD CLOTTING	C	1.2	3.6	3	7	ERELLES	7397
2BKI	AD	MOTOR PROTEIN/METAL-BINDING PROTEIN	D	3.6	3.6	1	7	RHVMTNL	7398
2C0L	AB	TRANSPORT PROTEIN/RECEPTOR	A	1.8	3.6	2	14	IRSRYNLGISCINL	7399
2C0L	AB	TRANSPORT PROTEIN/RECEPTOR	B	1.8	3.6	2	12	KANLVFKEIEKK	7400
2C1M	AB	PROTEIN TRANSPORT/MEMBRANE PROTEIN	A	3.6	3.6	1	12	ESVYKASLNLIE	7401
2D1P	DE	TRANSLATION	E	3.6	3.6	1	14	AGREGLDALLATSA	7402
2D1P	DF	TRANSLATION	D	3.6	3.6	1	16	QQASSAFQFAQALIAD	7403
2DFS	MP	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	P	1.8	3.6	2	8	DEEVDEMI	7404
2DOI	AB	HYDROLASE	B	3.6	3.6	1	21	ADAELQRLKNERHEEAELERL	7405
2DXB	KL	HYDROLASE	L	1.8	3.6	2	10	PNYRRRLVRW	7406
2E 74	CH	PHOTOSYNTHESIS	C	1.2	3.6	3	37	PNRVKWMIAFICLVMLAQLMLILKKKQVEKVQAAEMN	7407
2E2D	AC	HYDROLASE/HYDROLASE INHIBITOR	A	1.8	3.6	2	13	LFLVAAHEFGHSL	7408
2E9X	FH	REPLICATION	F	1.2	3.6	3	9	AAEVEFLAE	7409

2EHO	GH	REPLICATION	G	1.8	3.6	2	10	GTFLTQALNH	7410
2EHO	JL	REPLICATION	J	1.8	3.6	2	35	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW	7411
2ES4	BE	HYDROLASE	E	1.2	3.6	3	11	EAIRAASLDRG	7412
2F9Y	AB	LIGASE	A	1.8	3.6	2	6	VGAEER	7413
2FBW	BC	OXIDOREDUCTASE	B	3.6	3.6	1	6	PSYWWN	7414
2FBW	OP	OXIDOREDUCTASE	O	3.6	3.6	1	6	PSYWWN	7415
2FHH	WX	HYDROLASE	X	1.8	3.6	2	23	AAVAVEFARLYAVELEHYEKLEG	7416
2FK0	AB	VIRAL PROTEIN	B	1.2	3.6	3	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	7417
2FKW	RS	MEMBRANE PROTEIN, PHOTOSYNTHESIS	S	1.8	3.6	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	7418
2FOI	AC	OXIDOREDUCTASE	C	1.8	3.6	2	13	FIDYAIEYSEKYA	7419
2G38	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.8	3.6	2	35	KPFVRWLTDLCVQLSEVERQIHEIVRAYEWAHHDM	7420
2GUZ	EH	CHAPERONE, PROTEIN TRANSPORT	H	1.2	3.6	3	15	MDKINNRFNYLFEVN	7421
2HOD	BC	BLOOD CLOTTING	C	3.6	3.6	1	11	YNSNNQKIVNL	7422
2HY5	AB	TRANSFERASE	B	1.2	3.6	3	14	YAWEALEVVLIGAA	7423
2HZM	CD	TRANSCRIPTION	C	1.8	3.6	2	6	PALVFN	7424
2HZM	GH	TRANSCRIPTION	G	1.8	3.6	2	6	PALVFN	7425
2INP	BD	OXIDOREDUCTASE	D	1.8	3.6	2	30	EETQKQLLRLLVPLRHVELGANMNNAKIAG	7426
2J0Q	CD	HYDROLASE	C	1.8	3.6	2	25	PEGLRVFYYLVQDLKCLVFSLIGLH	7427
2J59	BN	HYDROLASE	N	1.8	3.6	2	22	EEDTGVTNRDLISRRIKEYNNL	7428
2J5G	ED	HYDROLASE	E	1.8	3.6	2	16	IGYGLALEGITATDLR	7429
2JGD	AB	OXIDOREDUCTASE	B	3.6	3.6	1	8	LERYLQLC	7430
2JIY	LM	PHOTOSYNTHESIS	L	1.8	3.6	2	28	GLWQIITICATGAFVSWALREVEICRKL	7431
2JJ0	LM	PHOTOSYNTHESIS	M	1.8	3.6	2	15	IFSHLDWTNNFSLVH	7432
2JKR	AB	ENDOCYTOSIS	B	3.6	3.6	1	16	PDLRDRGYIYWRLLST	7433
2JKR	AS	ENDOCYTOSIS	S	3.6	3.6	1	7	ELDLVFN	7434
2JTT	AC	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	A	1.8	3.6	2	22	SPLDQAIGLLIGIFHKYSGKEG	7435
2NOJ	CD	IMMUNE SYSTEM	D	1.8	3.6	2	14	VATHRKAQRAVNLI	7436
2NZ8	AB	SIGNALING PROTEIN, CELL CYCLE	A	1.8	3.6	2	9	DRLRPLSYP	7437
2NZ8	AB	SIGNALING PROTEIN, CELL CYCLE	B	1.2	3.6	3	25	ISSYLIKPVQRITKYQLLLKELLTC	7438
2NZD	BD	STRUCTURAL PROTEIN/DNA	D	1.8	3.6	2	12	SREIQTAVRLLL	7439
2O9I	AC	TRANSCRIPTION	A	1.8	3.6	2	22	LPHMADMSTYMFKGIISFAKVI	7440
2ONL	BD	TRANSFERASE	B	1.8	3.6	2	6	LNNIVK	7441
2P1L	GH	APOPTOSIS	G	1.2	3.6	3	16	PGTAYQSFEQVVNELF	7442
2P4N	AB	TRANSPORT PROTEIN	A	1.8	3.6	2	8	IYDICRRN	7443
2PBI	CD	SIGNALING PROTEIN	C	3.6	3.6	1	6	QFWDLN	7444
2PMZ	AK	TRANSLATION, TRANSFERASE	K	1.8	3.6	2	16	RYEIARVISARALQLA	7445

2POP	AB	SIGNALING PROTEIN/APOPTOSIS	A	3.6	3.6	1	11	EDELFRLSQLG	7446
2PQR	BD	APOPTOSIS	B	1.2	3.6	3	18	VNDERLGVKILTDIYKEA	7447
2Q3N	AB	PLANT PROTEIN	A	1.8	3.6	2	14	RYVSKLVVISLSNR	7448
2QJK	PQ	ELECTRON TRANSPORT	P	3.6	3.6	1	7	IEEDFNA	7449
2QM6	AB	TRANSFERASE	B	1.8	3.6	2	11	ADVKDNLTKMG	7450
2QR0	EF	IMMUNE SYSTEM	E	1.8	3.6	2	7	DEQLKSG	7451
2QSH	AX	DNA BINDING PROTEIN/DNA	X	1.2	3.6	3	10	PEVFVSMLLE	7452
2R00	AC	OXIDOREDUCTASE	C	1.2	3.6	3	14	GELSAKWAPIAAEA	7453
2R6C	CH	REPLICATION	C	1.8	3.6	2	11	LVTVTAELAAS	7454
2RI4	KL	OXYGEN STORAGE, OXYGEN TRANSPORT	L	1.8	3.6	2	15	DEVGAEALGRLLVVY	7455
2ROC	AB	APOPTOSIS	A	1.8	3.6	2	21	WGRIVTLISFGAFVAKHLKSV	7456
2UUN	CD	ELECTRON TRANSPORT	D	1.8	3.6	2	11	AFTKVAAQADT	7457
2UUN	KL	ELECTRON TRANSPORT	L	1.8	3.6	2	12	AFTKVAAQADTR	7458
2V4J	DE	OXIDOREDUCTASE	E	1.8	3.6	2	5	FEDFQ	7459
2V7Q	DJ	HYDROLASE	D	1.8	3.6	2	18	EEDKLTVSRARKIQRFLS	7460
2V8W	EF	TRANSLATION	F	1.8	3.6	2	9	RKFLMECRN	7461
2VAS	AB	MOTOR PROTEIN	B	1.8	3.6	2	14	DSEEEIREAFRVFD	7462
2VE7	AC	CELL CYCLE	C	3.6	3.6	1	8	QLYHQVSK	7463
2VGL	AB	PROTEIN TRANSPORT	A	3.6	3.6	1	10	STYIKFVNLF	7464
2VZD	BD	CELL ADHESION	B	1.8	3.6	2	15	LKSTLRVLYNLFTKY	7465
2W72	DC	OXYGEN TRANSPORT	C	3.6	3.6	1	16	AGEYGAEAYERMFLSF	7466
2WAQ	AC	TRANSCRIPTION	C	1.8	3.6	2	13	MRHILLVADVMTR	7467
2WH2	NU	RIBOSOME	U	3.6	3.6	1	14	DFRRLWIVRINAAC	7468
2WIN	BQ	IMMUNE SYSTEM	Q	1.8	3.6	2	24	FKKMSEAKYQLQKIYNEIDEALKS	7469
2WIN	DP	IMMUNE SYSTEM	P	1.8	3.6	2	24	FKKMSEAKYQLQKIYNEIDEALKS	7470
2Z2S	GH	TRANSCRIPTION	G	3.6	3.6	1	12	EAQRALIERAFF	7471
2ZAE	CD	HYDROLASE	C	1.8	3.6	2	7	GSYQEII	7472
2ZAL	CB	HYDROLASE	B	1.8	3.6	2	7	GEVFIRA	7473
2ZU0	AC	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	C	3.6	3.6	1	8	PEDRAGEG	7474
3A0B	ad	ELECTRON TRANSPORT	a	1.2	3.6	3	6	DIINRA	7475
3A0B	AI	ELECTRON TRANSPORT	A	1.8	3.6	2	20	WFGVIMIPTLLAATICFVIA	7476
3B4V	EH	HORMONE REGULATOR COMPLEX	H	1.8	3.6	2	9	KINLLGFLG	7477
3BG0	AB	PROTEIN TRANSPORT, HYDROLASE	B	1.8	3.6	2	17	SQLIFNAQALKDRYEGN	7478
3BIM	EN	TRANSCRIPTION REPRESSOR	E	1.2	3.6	3	15	HASDVLLNLNRLRSR	7479
3C1B	BD	STRUCTURAL PROTEIN/DNA	D	1.8	3.6	2	12	SREIQTAVRLLL	7480
3C72	AB	TRANSFERASE	A	1.8	3.6	2	16	ATLWNCRREVLQHLET	7481
3CHX	IJ	MEMBRANE PROTEIN	J	1.8	3.6	2	18	GATFAVSGLLIGEWINRY	7482
3CJH	AD	PROTEIN TRANSPORT	A	1.8	3.6	2	26	DACIDQCLAKYMRSWNVISKAYISRI	7483

3CJH	EB	PROTEIN TRANSPORT	E	1.8	3.6	2	16	TELVNKISENCFEKCL	7484
3CJT	EF	TRANSFERASE/RIBOSOMAL PROTEIN	E	1.8	3.6	2	10	DPILPGLFDG	7485
3CWB	OF	OXIDOREDUCTASE	F	1.2	3.6	3	20	YLEPYLKEVIRERLEREAWN	7486
3CXH	AB	OXIDOREDUCTASE	B	1.8	3.6	2	10	INYTKLKNAV	7487
3CXH	CG	OXIDOREDUCTASE	G	1.8	3.6	2	5	FDDLI	7488
3DBJ	AB	PHOTOSYNTHESIS	A	1.8	3.6	2	9	PGELDRIKN	7489
3DBJ	EF	PHOTOSYNTHESIS	E	1.8	3.6	2	9	PGELDRIKN	7490
3DD7	AB	RIBOSOME INHIBITOR	B	1.8	3.6	2	6	DSTNKE	7491
3DNL	AC	VIRAL PROTEIN	C	1.8	3.6	2	9	MRDNWRSEL	7492
3DVU	BD	VIRAL PROTEIN/APOPTOSIS	B	1.8	3.6	2	23	LVDVSKIITLTQEFRRHYDSVYR	7493
3E3Q	LM	IMMUNE SYSTEM	L	1.8	3.6	2	24	AAEYYRAYLEGECVEWLHRYLKNG	7494
3EAB	FL	CELL CYCLE	F	1.8	3.6	2	25	EQCERARRLQAKMMTNLVMAKDRLQ	7495
3EFF	BM	MEMBRANE PROTEIN	M	1.8	3.6	2	16	TTRALHERFDRLERML	7496
3ENO	BF	HYDROLASE/UNKNOWN FUNCTION	F	3.6	3.6	1	23	SSALRGTVNSYLRWIKAAIDVIE	7497
3ENS	AB	HYDROLASE, BLOOD CLOTTING	B	3.6	3.6	1	9	RDWAESTLM	7498
3EUB	BC	OXIDOREDUCTASE	B	1.8	3.6	2	23	IEFRRTLTLSFFFKFYLTVLKKL	7499
3FCS	AB	CELL ADHESION/BLOOD CLOTTING	B	1.8	3.6	2	5	DGRLA	7500
3FH9	AB	OXYGEN TRANSPORT	A	3.6	3.6	1	19	PAVHASLDKFLASVSTVLT	7501
3FWC	AB	CELL CYCLE, TRANSCRIPTION	A	1.8	3.6	2	9	ENEFIAICT	7502
3FWC	MN	CELL CYCLE, TRANSCRIPTION	M	1.8	3.6	2	11	IKNLRRVAKEL	7503
3GBM	BH	VIRAL PROTEIN / IMMUNE SYSTEM	B	1.2	3.6	3	22	KESTQKAIDGVTNKVNSIIDKM	7504
3GHG	BC	BLOOD CLOTTING	C	1.8	3.6	2	21	IYNSNNQKIVNLKEKVAQLEA	7505
3GLH	AE	TRANSFERASE	E	1.8	3.6	2	17	RELLITDLLLRIEHYLQ	7506
3H0L	AC	LIGASE	C	3.6	3.6	1	5	QLKEL	7507
3H0L	GI	LIGASE	G	1.8	3.6	2	6	PIEMYL	7508
3H0L	PR	LIGASE	P	1.8	3.6	2	13	IFEMYARTRDEGF	7509
3H0L	VX	LIGASE	V	1.8	3.6	2	13	IFEMYARTRDEGF	7510
3H11	AB	APOPTOSIS	B	1.2	3.6	3	14	ILTILTEVNYEVSN	7511
3HKZ	IM	TRANSFERASE	I	1.8	3.6	2	10	DVNRIFERVV	7512
3HRD	AB	OXIDOREDUCTASE	A	1.8	3.6	2	8	PIDIRILN	7513
3HUJ	AG	IMMUNE SYSTEM	A	3.6	3.6	1	11	LWVNLAIQVLN	7514
1A9W	AE	OXYGEN TRANSPORT	A	3.5	3.5	1	16	AGEYGAEALERMFLSF	7515
1AHJ	EF	LYASE	F	1.8	3.5	2	16	YYERYVIGVATLMVEK	7516
1AJS	AB	AMINOTRANSFERASE	B	1.2	3.5	3	17	PDSILRVLSQMQKIVRV	7517
1AYY	CD	HYDROLASE	C	3.5	3.5	1	13	AESEKEWKEWLKT	7518
1B33	AB	PHOTOSYNTHESIS	A	1.8	3.5	2	12	IVTKSIVNADAE	7519
1B8D	AB	PHOTOSYNTHESIS	B	1.8	3.5	2	12	AFSRVVVTSDAK	7520
1BCC	EJ	OXIDOREDUCTASE	E	1.8	3.5	2	35	SRESDPSRKGFSYLVTAVTTLGVAYAAKNVVTQFV	7521
1CDL	DG	CALCIUM-BINDING PROTEIN	G	1.8	3.5	2	17	RRKWQKTGHAVRAIGRL	7522
1CFF	AB	CALMODULIN	B	3.5	3.5	1	10	FRGLNRIQTQ	7523

1CPC	AB	LIGHT HARVESTING PROTEIN	A	1.2	3.5	3	27	STEIQTAFGRFRQASASLAAAKALTEK	7524
1D8D	AB	TRANSFERASE	A	1.8	3.5	2	15	ESAWNYLKGILQDRG	7525
1D9K	CD	IMMUNE SYSTEM	C	1.8	3.5	2	22	PQGGLQNIATGKHNLEILTKRS	7526
1E3D	AB	HYDROGENASE	B	1.2	3.5	3	29	PEANLVCTAHYLQALRAQVEVAKGMAVFG	7527
1E7P	BC	OXIDOREDUCTASE	C	1.2	3.5	3	15	YRQYLTFKTHKDLMR	7528
1E7P	EF	OXIDOREDUCTASE	F	1.2	3.5	3	15	YRQYLTFKTHKDLMR	7529
1E7P	HI	OXIDOREDUCTASE	I	1.2	3.5	3	15	YRQYLTFKTHKDLMR	7530
1E7P	KL	OXIDOREDUCTASE	L	1.2	3.5	3	15	YRQYLTFKTHKDLMR	7531
1EYS	LM	ELECTRON TRANSPORT	L	3.5	3.5	1	7	HVPFAFS	7532
1F5Q	AB	TRANSFERASE	B	1.8	3.5	2	20	EEDCRQMIYRSEREHDARMV	7533
1F5Q	CD	TRANSFERASE	D	1.8	3.5	2	20	EEDCRQMIYRSEREHDARMV	7534
1FHJ	CB	OXYGEN STORAGE/TRANSPORT	B	3.5	3.5	1	7	PWTQRFF	7535
1FM6	AD	TRANSCRIPTION	D	1.8	3.5	2	30	LFAKLLQKMTDLRQIVTEHVQLLQVIKKTE	7536
1FNT	DE	HYDROLASE/HYDROLASE ACTIVATOR	E	3.5	3.5	1	8	FQVEYSLE	7537
1FNT	RS	HYDROLASE/HYDROLASE ACTIVATOR	S	3.5	3.5	1	8	FQVEYSLE	7538
1FNT	YL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.8	3.5	2	12	QTFAYGVLDSNY	7539
1FPP	BA	PRENYLTRANSFERASE	A	3.5	3.5	1	14	YHAWQHRQWVIQEF	7540
1FQV	EF	LIGASE	E	3.5	3.5	1	9	PDVTGRLLS	7541
1FYZ	AE	OXIDOREDUCTASE	E	1.8	3.5	2	20	VNYFLDGERQLGTRLMELRN	7542
1FYZ	DF	OXIDOREDUCTASE	F	1.8	3.5	2	20	VNYFLDGERQLGTRLMELRN	7543
1G0U	EF	HYDROLASE	F	3.5	3.5	1	12	FQVEYAVKAVEN	7544
1G3I	SR	CHAPERONE/HYDROLASE	R	3.5	3.5	1	13	ADAFTLFELFERK	7545
1GCV	AD	OXYGEN STORAGE/TRANSPORT	D	3.5	3.5	1	7	PWTNRYF	7546
1GH0	ST	PHOTOSYNTHESIS	S	1.8	3.5	2	12	PLTEAVSVADSQ	7547
1H3O	CD	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	C	1.2	3.5	3	15	QAPLQRRILEIGKKH	7548
1HBH	CD	OXYGEN CARRIER	D	1.8	3.5	2	19	AETQGAFQKFLAVVVSALG	7549
1HE1	AC	SIGNALING PROTEIN	A	1.8	3.5	2	16	ALRSLSTALAGIRAGS	7550
1HE1	BD	SIGNALING PROTEIN	B	1.8	3.5	2	15	ALRSLSTALAGIRAG	7551
1I7W	CD	CELL ADHESION	C	1.2	3.5	3	10	AIPELTKLLN	7552
1I7Y	AB	PHOTOSYNTHESIS	A	1.2	3.5	3	12	PITEAIAAADTQ	7553
1IB1	BF	SIGNALING PROTEIN/TRANSFERASE	B	1.8	3.5	2	14	TLIMQLLRDNLTLW	7554
1IBT	AF	LYASE	A	1.2	3.5	3	12	LDGIVSYDRAET	7555
1ID3	EF	STRUCTURAL PROTEIN/DNA	F	1.8	3.5	2	16	FLESVIRDSVTYTEHA	7556
1IWP	LM	LYASE	M	1.2	3.5	3	13	RQTLEYQAQIAEQ	7557
1IYJ	CD	GENE REGULATION/ANTITUMOR PROTEIN	D	1.2	3.5	3	18	PERVLLQLKYRYDVEIDN	7558
1IZN	CD	PROTEIN BINDING	D	1.8	3.5	2	12	DQQLDCALDLMR	7559
1JB0	AB	PHOTOSYNTHESIS	A	1.8	3.5	2	14	SFGLYVHNDTMRAF	7560
1JD2	CD	HYDROLASE	D	1.8	3.5	2	13	FQVEYSLEAIKLG	7561

1JD2	XY	HYDROLASE	Y	1.8	3.5	2	13	FQVEYSLEAIKLG	7562
1JZD	AC	OXIDOREDUCTASE	A	3.5	3.5	1	9	GYSHKLHEQ	7563
1K6L	LM	PHOTOSYNTHESIS	M	1.8	3.5	2	7	ELEQIAD	7564
1KBH	AB	TRANSCRIPTION	A	1.8	3.5	2	14	SDERALLDQLHTLL	7565
1KDX	AB	TRANSCRIPTION REGULATION COMPLEX	A	1.8	3.5	2	16	QDLRSHLVHKLVQAIF	7566
1KFY	CD	OXIDOREDUCTASE	D	3.5	3.5	1	10	YERVLAFAQS	7567
1KFY	NO	OXIDOREDUCTASE	O	3.5	3.5	1	26	VIVIINLITLAAALLHTKTWFELAPK	7568
1KFY	NP	OXIDOREDUCTASE	P	1.8	3.5	2	27	EPVFWGLFGAGGMWSAIIAPVMILLVG	7569
1KG0	AB	VIRAL PROTEIN/IMMUNE SYSTEM	A	1.8	3.5	2	5	EEFGR	7570
1KX4	CD	STRUCTURAL PROTEIN/DNA	D	1.8	3.5	2	12	SREIQTAVRLLL	7571
1KYO	EH	OXIDOREDUCTASE/ELECTRON TRANSPORT	E	1.2	3.5	3	30	KGRSYAYFMVGAMGLLSSAGAKSTVETFIS	7572
1L1O	DF	DNA BINDING PROTEIN	D	1.8	3.5	2	14	LGLYNEAVKIIHDF	7573
1L2W	BI	CHAPERONE	B	1.8	3.5	2	16	SLYTQLEMLVQGAERL	7574
1LVC	AD	LYASE	D	1.8	3.5	2	7	EFKEAFS	7575
1LWU	AC	BLOOD CLOTTING	A	1.8	3.5	2	13	RIIHLQRRINMQL	7576
1LWU	KL	BLOOD CLOTTING	K	1.8	3.5	2	16	RSMKSVLEHLRAKMQR	7577
1M1Y	IJ	OXIDOREDUCTASE	I	1.8	3.5	2	6	FIFQKM	7578
1N4Q	AB	TRANSFERASE	B	3.5	3.5	1	15	RLTIAFFALSGLDML	7579
1N4Q	CD	TRANSFERASE	D	3.5	3.5	1	15	RLTIAFFALSGLDML	7580
1N4Q	EF	TRANSFERASE	E	1.8	3.5	2	14	YTVWHFRRVLLRSL	7581
1N4Q	EF	TRANSFERASE	E	3.5	3.5	1	14	YHAWQHRQWVIQEF	7582
1N4Q	IJ	TRANSFERASE	J	3.5	3.5	1	11	KDDIIEWIYSL	7583
1N4Q	KL	TRANSFERASE	L	3.5	3.5	1	11	KDDIIEWIYSL	7584
1N86	BC	BLOOD CLOTTING	C	1.8	3.5	2	14	VNLKEKVAQLEAQC	7585
1NF5	AB	TRANSFERASE/TRANSFERASE	B	3.5	3.5	1	7	RFDRIAH	7586
1NGM	EF	TRANSCRIPTION/DNA	E	3.5	3.5	1	18	REEIYQAFEAIYPVLSEF	7587
1NI4	AB	OXIDOREDUCTASE	B	3.5	3.5	1	13	IDQVINSAAKTYY	7588
1NRL	BD	TRANSCRIPTION	B	1.8	3.5	2	7	PLMQELF	7589
1NTK	DE	OXIDOREDUCTASE	D	1.2	3.5	3	24	PEHDHRKRMGLKMLLMMGLLLPLV	7590
1NTK	EJ	OXIDOREDUCTASE	J	1.2	3.5	3	30	TSTFALTIVVGALFFERAFDQGADAIYEHI	7591
1NVM	EF	LYASE/OXIDOREDUCTASE	F	1.8	3.5	2	17	IDEFTETTSKAIEVIGG	7592
1NW9	AB	APOPTOSIS	A	3.5	3.5	1	9	QEYINNIHL	7593
1O9U	AB	KINASE	A	3.5	3.5	1	5	PELIF	7594
1O9U	AB	KINASE	A	1.2	3.5	3	13	GVDQLVEIIKVLG	7595
1OC0	AB	HYDROLASE/INHIBITOR	A	1.8	3.5	2	15	VERARFIINDWVKTH	7596
1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.8	3.5	2	34	PILYQHLFWFFGHPEVYILILPGFGMISHIVTYY	7597
1OQS	GH	HYDROLASE	H	3.5	3.5	1	5	SVWNY	7598

1OXK	AB	SIGNALING PROTEIN	B	3.5	3.5	1	12	RPKLKTILTEFC	7599
1P22	AB	SIGNALING PROTEIN	B	1.2	3.5	3	8	PEEIRKTF	7600
1PNS	JN	RIBOSOME	N	1.8	3.5	2	11	RICLRELAHKG	7601
1QGW	AC	PHOTOSYNTHESIS	C	1.8	3.5	2	9	ADLQALKKF	7602
1QO0	BE	BINDING PROTEIN	B	1.8	3.5	2	17	IYPRESNHVMRHLYRQH	7603
1QPW	CD	OXYGEN TRANSPORT	C	1.8	3.5	2	19	PSVHASLDKFLANVSTVLT	7604
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	A	1.8	3.5	2	10	FPEFLNLMAR	7605
1QTY	VY	HORMONE/GROWTH FACTOR RECEPTOR	V	1.8	3.5	2	9	FMDVYQRSY	7606
1R27	CD	OXIDOREDUCTASE	D	1.8	3.5	2	14	EAQAQEMYRYLAIA	7607
1RCO	KM	LYASE	M	1.8	3.5	2	14	TDQLARQVDYLLNN	7608
1RZO	CD	HYDROLASE	C	1.8	3.5	2	6	VSILIP	7609
1SB3	DF	OXIDOREDUCTASE	D	1.8	3.5	2	6	GVEKVT	7610
1SB3	EF	OXIDOREDUCTASE	E	1.8	3.5	2	7	LEAIAEH	7611
1SFC	JK	TRANSPORT PROTEIN	K	1.8	3.5	2	13	ADESLESTRRMLQ	7612
1SQB	CF	OXIDOREDUCTASE	F	1.2	3.5	3	20	ENLYDDRVFRIKRALDLSMR	7613
1SQK	AB	STRUCTURAL PROTEIN/PROTEIN BINDING	B	1.8	3.5	2	13	PKVAENLKSQLEG	7614
1SQX	AB	OXIDOREDUCTASE	A	1.8	3.5	2	9	ALEKEVESM	7615
1T0F	BD	DNA BINDING PROTEIN	D	1.8	3.5	2	8	MHERLKGK	7616
1TN6	AB	TRANSFERASE	A	1.8	3.5	2	15	YQVWHHRRVLVEWLR	7617
1TO9	AB	BIOSYNTHETIC PROTEIN	B	1.8	3.5	2	15	ENFVISSYYEYQFWG	7618
1TQY	AB	TRANSFERASE	B	1.8	3.5	2	11	PWGWVSQIASG	7619
1TQY	CD	TRANSFERASE	C	1.8	3.5	2	10	PIVVACFDAI	7620
1TU3	DI	PROTEIN TRANSPORT	I	1.8	3.5	2	32	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIR	7621
1TYE	EF	CELL ADHESION	F	1.8	3.5	2	11	VNLYQNYSELI	7622
1UZD	AT	LYASE	A	1.8	3.5	2	15	AKNYGRAVYECLRGG	7623
1UZH	VC	LYASE	V	1.8	3.5	2	14	AKNYGRAVYECLRG	7624
1VS6	TX	RIBOSOME	X	3.5	3.5	1	5	ELLNL	7625
1WYU	CD	OXIDOREDUCTASE	C	1.8	3.5	2	8	PVVQALAA	7626
1X11	BD	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE)	D	1.8	3.5	2	6	PTYKFF	7627
1XCG	EF	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	E	1.2	3.5	3	38	SEHEKLCRARDQCREILKYVNEAVKQTENRHRLEGYQK	7628
1XFU	DR	LYASE/METAL BINDING PROTEIN	R	1.2	3.5	3	13	SEEEIREAFRVFD	7629
1Y76	CB	TRANSPORT PROTEIN	C	1.2	3.5	3	20	PLFNQILTLQQSIKQLKGQL	7630
1YCP	JK	COMPLEX (SERINE PROTEASE/PEPTIDE)	J	1.2	3.5	3	10	EKELFESYIE	7631
1YUC	BD	TRANSCRIPTION REGULATION	D	1.8	3.5	2	9	AILYALLSS	7632

1Z5X	UE	HORMONE/GROWTH FACTOR RECEPTOR	E	1.2	3.5	3	32	ATTIFAKLLSVLTELRTLGNMNSETCFSLKLK	7633
1Z6O	CN	METAL BINDING PROTEIN	C	1.8	3.5	2	16	LSLALYVFDEYLQKTV	7634
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	H	1.8	3.5	2	19	ELAKHAVSEGTKAVTKYTS	7635
1ZOY	BC	OXIDOREDUCTASE	B	3.5	3.5	1	6	PSYWWN	7636
1ZV8	IJ	VIRAL PROTEIN	J	1.2	3.5	3	16	QKEIDRLNEVAKNLNE	7637
1ZY8	EM	OXIDOREDUCTASE	E	1.8	3.5	2	6	CEDIAR	7638
2A4J	AB	STRUCTURAL PROTEIN	A	3.5	3.5	1	12	FKNLKRVAKELG	7639
2AA1	CD	OXYGEN STORAGE/TRANSPORT	C	3.5	3.5	1	19	PEAHVSLDKFLSGVALALA	7640
2AXT	ef	ELECTRON TRANSPORT	f	1.8	3.5	2	24	VRWVAVHTLAVPTIFFLGAIAAMQ	7641
2BCJ	BG	TRANSFERASE/HYDROLASE	B	1.8	3.5	2	14	QLKNQIRDARKACA	7642
2BEZ	CF	VIRAL PROTEIN	F	1.8	3.5	2	14	QKEIDRLNEVAKNL	7643
2BSK	EB	PROTEIN TRANSPORT	E	3.5	3.5	1	18	EFLGTYNKLTETCFLDCV	7644
2CCI	CD	CELL CYCLE	D	1.8	3.5	2	17	LQLVGTAAMLLASKFEE	7645
2CZV	AD	HYDROLASE	A	1.8	3.5	2	21	PYERANLLRFMMKAWKLVEKY	7646
2DD4	GH	HYDROLASE	H	3.5	3.5	1	9	AEERRRKQN	7647
2DPP	AB	LYASE	B	3.5	3.5	1	6	AEELWG	7648
2DSQ	CH	PROTEIN BINDING/HORMONE/GROWTH FACTOR	C	1.8	3.5	2	12	AELVDALQFVCG	7649
2DXB	EF	HYDROLASE	F	3.5	3.5	1	6	RDCLIG	7650
2DXB	JK	HYDROLASE	K	3.5	3.5	1	9	AEERRRKQN	7651
2E9X	FH	REPLICATION	F	1.8	3.5	2	10	LWLAINLKQR	7652
2EQ9	DF	OXIDOREDUCTASE	F	1.8	3.5	2	10	PAARKLAREL	7653
2ERJ	BD	IMMUNE SYSTEM/CYTOKINE	D	1.2	3.5	3	17	PRDLISNINVIVLELKG	7654
2EY4	BD	ISOMERASE/BIOSYNTHETIC PROTEIN	B	1.8	3.5	2	13	IRSLIHHIGLALG	7655
2F9I	AD	TRANSFERASE	D	1.8	3.5	2	12	MRQTLSEILKIH	7656
2FBW	AB	OXIDOREDUCTASE	B	3.5	3.5	1	10	SNFYAQYKSI	7657
2FBW	NO	OXIDOREDUCTASE	O	3.5	3.5	1	10	SNFYAQYKSI	7658
2FHJ	CD	TRANSFERASE	D	1.8	3.5	2	12	HKWAMIAVKEAT	7659
2FHO	AB	RNA BINDING PROTEIN	A	1.8	3.5	2	8	DEELDAMF	7660
2FSE	BE	IMMUNE SYSTEM, STRUCTURAL PROTEIN	B	1.8	3.5	2	22	KDLLEQRRAAVDTYCRHNYGVG	7661
2FUG	13	OXIDOREDUCTASE	3	3.5	3.5	1	17	DVVREAQAGMVEFTLLN	7662
2FUG	JK	OXIDOREDUCTASE	K	1.8	3.5	2	5	LSCKL	7663
2FYN	DE	OXIDOREDUCTASE	E	1.8	3.5	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	7664
2GL7	AB	TRANSCRIPTION	A	1.8	3.5	2	16	VKFLAITTDCLQILAY	7665
2GUZ	GB	CHAPERONE, PROTEIN TRANSPORT	B	1.8	3.5	2	23	FYLQSKVYRAAERLKWELAQREK	7666
2GWF	AB	HYDROLASE/LIGASE	B	1.8	3.5	2	7	LETRQMN	7667
2H0D	AB	METAL BINDING PROTEIN/LIGASE	B	1.8	3.5	2	11	PNFDALISKIY	7668

2H1L	BN	VIRAL PROTEIN	B	1.8	3.5	2	14	LSVYQKMKFNVAMG	7669
2HDN	EF	TRANSLATION	F	1.8	3.5	2	18	AEWEAKILELAGFLDSYI	7670
2HLD	EG	HYDROLASE	G	1.2	3.5	3	65	FEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYN RTRQAVITNELVDIITGA	7671
2HOD	GH	BLOOD CLOTTING	H	1.8	3.5	2	5	LRSKI	7672
2HYB	NO	TRANSFERASE	O	1.8	3.5	2	10	NSLESCLKFA	7673
2I2T	EL	RIBOSOME	E	3.5	3.5	1	6	PVSLIA	7674
2I2T	EL	RIBOSOME	E	3.5	3.5	1	8	QVVVAYAA	7675
2IBZ	AB	OXIDOREDUCTASE	A	1.2	3.5	3	20	DTEVERAKSLLKLQLGQLYE	7676
2IVF	AB	OXIDOREDUCTASE	B	3.5	3.5	1	6	YPRIEK	7677
2IVF	AB	OXIDOREDUCTASE	B	3.5	3.5	1	17	VKRVLAVLHTERENMRA	7678
2J8X	AB	HYDROLASE/INHIBITOR	A	3.5	3.5	1	5	PLAQN	7679
2JBL	HM	ELECTRON TRANSPORT	M	1.8	3.5	2	27	PWHGFSIGFAYGCGLLFAAHGATILAV	7680
2JDQ	BD	PROTEIN TRANSPORT	B	1.8	3.5	2	16	ESIKKEACWTISNITA	7681
2JF9	BQ	TRANSCRIPTION	B	1.8	3.5	2	22	MMGLLTNLADRELVHMINWAKR	7682
2JGD	AB	OXIDOREDUCTASE	B	3.5	3.5	1	12	AWYCSQHHFREV	7683
2JIZ	BF	HYDROLASE	B	1.8	3.5	2	12	VFYLHSRLLERA	7684
2JTT	BC	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	B	1.8	3.5	2	15	FQEYITFLGALAMIY	7685
2O02	AP	PROTEIN BINDING/TOXIN	A	3.5	3.5	1	21	AESKVFYLKMKGDYYRYLAEV	7686
2O60	AB	METAL BINDING PROTEIN	A	1.8	3.5	2	12	DEEVDEMIREAD	7687
2P1L	GH	APOPTOSIS	G	1.8	3.5	2	24	QMAAVKQALREAGDEFELRYRRAF	7688
2P22	AC	TRANSPORT PROTEIN	C	1.8	3.5	2	11	RHQLELYVTKF	7689
2P5T	CD	TRANSCRIPTION REGULATOR	C	3.5	3.5	1	18	PWILMSDDLSDLIHTNIY	7690
2PBD	AV	STRUCTURAL PROTEIN	V	1.8	3.5	2	7	LAAAIAG	7691
2PMZ	DP	TRANSLATION, TRANSFERASE	D	1.2	3.5	3	10	DEILAHRLAL	7692
2PQK	AB	APOPTOSIS	A	3.5	3.5	1	22	WGRIVTLISFGAFVAKHLKTIN	7693
2PSM	AF	CYTOKINE	A	1.2	3.5	3	19	KVTAMNCFLLELQVILHEY	7694
2QKM	AB	HYDROLASE	B	1.8	3.5	2	15	FSQVLDDLSARFILN	7695
2QLV	DE	TRANSFERASE/PROTEIN BINDING	D	1.2	3.5	3	19	AYPFLHLTTKLIMELAVNS	7696
2QM6	CD	TRANSFERASE	C	3.5	3.5	1	7	RERFLKY	7697
2R17	AC	PROTEIN TRANSPORT	C	1.8	3.5	2	20	PSLQVQLFIEILNRYIYFYE	7698
2R1H	CB	OXYGEN BINDING	B	3.5	3.5	1	6	PWTQRH	7699
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	A	3.5	3.5	1	26	KEKDEMVEQEFNRLLEATSYLSHQLD	7700
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	B	1.2	3.5	3	34	AATTVLRQLDMELVSVKRQIQNIKQTNSALKEKL	7701
2V1S	EJ	OXIDOREDUCTASE	J	1.8	3.5	2	10	RLSRLLSYAG	7702
2V36	CD	TRANSFERASE	C	1.8	3.5	2	7	QEKLSRT	7703
2V4I	CD	TRANSFERASE	D	1.8	3.5	2	14	PAEQDRLFRRVMDR	7704
2V4J	AB	OXIDOREDUCTASE	A	1.8	3.5	2	14	ADYLRQLCDIWDLR	7705
2V4J	AB	OXIDOREDUCTASE	B	1.8	3.5	2	5	FEDFQ	7706

2V4J	DE	OXIDOREDUCTASE	D	3.5	3.5	1	6	HCINTM	7707
2VDW	AB	TRANSFERASE	A	1.8	3.5	2	14	FATIIERSKKFING	7708
2VE7	AC	CELL CYCLE	C	3.5	3.5	1	5	QYKSS	7709
2VJM	AB	TRANSFERASE	A	1.8	3.5	2	9	MQDAVLNLV	7710
2VL2	BC	OXIDOREDUCTASE	C	1.8	3.5	2	11	AFVTGEWGRAH	7711
2VML	EF	PHOTOSYNTHESIS	F	1.8	3.5	2	12	AFTKAIVAADLR	7712
2WAQ	HQ	TRANSCRIPTION	H	1.8	3.5	2	12	IDEAYKILKELG	7713
2WB1	AB	TRANSCRIPTION	B	1.2	3.5	3	13	YAFKLLIQELMSM	7714
2WB1	WR	TRANSCRIPTION	R	3.5	3.5	1	11	EMERDCLIGFG	7715
2ZCY	VL	HYDROLASE	L	1.2	3.5	3	19	VEEVIKLVRDSFTSATERH	7716
2ZET	BD	SIGNALING PROTEIN	D	1.2	3.5	3	42	DEEAEHVWAVVQRDFDLRRREEERLQGLKGKIQKESSKRELL	7717
2ZHX	MN	HYDROLASE/HYDROLASE INHIBITOR	M	1.8	3.5	2	6	PLSASR	7718
3BBN	JN	RIBOSOME	N	1.8	3.5	2	10	GHILREMVHT	7719
3BCQ	AB	TRANSPORT PROTEIN/OXYGEN BINDING	A	3.5	3.5	1	21	PEVHVSMDKFLSLLSWSLSEK	7720
3BEJ	BF	TRANSCRIPTION REGULATOR	F	1.8	3.5	2	8	KILHRLLQ	7721
3BOW	AC	HYDROLASE/HYDROLASE INHIBITOR	A	3.5	3.5	1	22	LKEFYILWTKIQKYQKIYREID	7722
3BZ1	AC	ELECTRON TRANSPORT	A	1.8	3.5	2	26	SRSLHFFLAAWPVVGVWFTALGISTM	7723
3BZ1	LM	ELECTRON TRANSPORT	M	1.8	3.5	2	27	QLGLIATALFVLVPSVFLIILYVQTES	7724
3CFD	AB	IMMUNE SYSTEM	A	1.8	3.5	2	7	SEQLTSG	7725
3CHX	EF	MEMBRANE PROTEIN	E	1.8	3.5	2	6	IDRIYA	7726
3CI0	IK	PROTEIN TRANSPORT	K	3.5	3.5	1	30	RTRSQQEYQQALWYSASAESLALSALSLSL	7727
3CJT	GH	TRANSFERASE/RIBOSOMAL PROTEIN	G	3.5	3.5	1	5	DEDWL	7728
3CUE	BD	PROTEIN TRANSPORT	B	1.2	3.5	3	23	AGDFETKLSDYGHNIGIRLLELL	7729
3CWB	DE	OXIDOREDUCTASE	D	1.2	3.5	3	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	7730
3CWB	DJ	OXIDOREDUCTASE	J	3.5	3.5	1	7	WKHIKHK	7731
3CWB	OF	OXIDOREDUCTASE	O	1.8	3.5	2	11	SFRITRGIEAV	7732
3CWB	QU	OXIDOREDUCTASE	U	3.5	3.5	1	23	TEELFDFLHARDHCVAHKLFNKL	7733
3D7V	AB	APOPTOSIS	A	3.5	3.5	1	22	WGRIVTLISFGAFVAKHLKTIN	7734
3DBJ	GH	PHOTOSYNTHESIS	G	1.8	3.5	2	9	PGELDRIKN	7735
3DCG	CD	LIGASE/VIRAL PROTEIN	D	1.8	3.5	2	17	SHVLSKVCMYFTYKVRY	7736
3DHR	GH	OXYGEN STORAGE, OXYGEN TRANSPORT	G	3.5	3.5	1	16	AGDLGGEALERLFITY	7737
3DTP	AC	CONTRACTILE PROTEIN	A	3.5	3.5	1	26	KAFAKRQQQLTAMKVIQRNCAAYLKL	7738
3DTU	AB	OXIDOREDUCTASE	A	1.8	3.5	2	28	EWAGKLHFWMMFVGANLTFFPQHFLGRQ	7739
3DUH	BD	IMMUNE SYSTEM/CYTOKINE	D	1.8	3.5	2	26	RFKILRSLQAFVAVAARVFAHGAATL	7740
3DVU	AC	VIRAL PROTEIN/APOPTOSIS	A	1.8	3.5	2	25	SAVLVDVSKIITLTQEFRRHYDSVY	7741
3DVU	AC	VIRAL PROTEIN/APOPTOSIS	A	1.8	3.5	2	13	WKRDLSKLFTSLF	7742
3DW8	AB	HYDROLASE	A	1.8	3.5	2	16	PMVRRAAASKLGEFAK	7743
3E0J	EF	TRANSFERASE	E	1.2	3.5	3	16	GESLLGTQLLVDVVTG	7744

3E3Q	cd	IMMUNE SYSTEM	c	1.8	3.5	2	24	AAEYYRAYLEGECVEWLHRYLKNG	7745
3EAB	AG	CELL CYCLE	A	1.8	3.5	2	28	EQCERARRLQAKMMTNLVMAKDRLQLLE	7746
3EDX	EF	HYDROLASE	E	1.8	3.5	2	7	EKELLDS	7747
3EI4	CD	DNA BINDING PROTEIN	D	1.2	3.5	3	11	IVRTLHQHKLG	7748
3ENO	BF	HYDROLASE/UNKNOWN FUNCTION	B	1.8	3.5	2	19	APSLRVTATAARTISVLTG	7749
3ETR	LN	OXIDOREDUCTASE	L	3.5	3.5	1	17	FCTPGIVMSMYTLLRNQ	7750
3EXG	KL	OXIDOREDUCTASE	L	1.8	3.5	2	15	IDQVINSAAKTYYMS	7751
3EXH	EF	OXIDOREDUCTASE	F	3.5	3.5	1	14	EMGFAGIAVGAAMA	7752
3FDL	AB	APOPTOSIS	A	1.2	3.5	3	13	AYQSFEQVVNELF	7753
3FFD	BP	IMMUNE SYSTEM/HORMONE	P	1.8	3.5	2	16	IQDLRRRFFLHHLIAE	7754
3FKS	JM	HYDROLASE	J	1.8	3.5	2	14	RSTVAQLVQTLEQH	7755
3FKS	NP	HYDROLASE	P	1.8	3.5	2	29	MINRYSILYNRTRQAVITNELVDIITGAS	7756
3FMP	CD	ONCOPROTEIN/HYDROLASE	D	1.8	3.5	2	12	PGTVLDWCSKLK	7757
3FS4	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	3.5	3.5	1	6	PWTQRF	7758
3FWC	NO	CELL CYCLE, TRANSCRIPTION	O	3.5	3.5	1	8	FTQILSTV	7759
3FXD	AB	UNKNOWN FUNCTION	A	1.8	3.5	2	18	DEQKETILKALNDAIEKG	7760
3G33	CB	CELL CYCLE	B	1.8	3.5	2	15	DQRVLQSLLRLEERY	7761
3GM1	AF	TRANSFERASE	F	1.8	3.5	2	6	ELMASL	7762
3H0L	DF	LIGASE	F	1.8	3.5	2	11	REWVLKIAKLA	7763
3H0L	PR	LIGASE	R	1.8	3.5	2	11	REWVLKIAKLA	7764
3H4S	AE	MOTOR PROTEIN/CALCIUM BINDING PROTEIN	E	1.2	3.5	3	19	QTEFCVLMVRLSPEMMEDA	7765
3HKZ	IM	TRANSFERASE	M	1.8	3.5	2	12	IRHILLIADVMT	7766
3HPG	FK	TRANSFERASE	K	3.5	3.5	1	10	VNRCIEALDE	7767
5CSC	AB	OXO-ACID-LYASE	B	1.2	3.5	3	10	VSAHTSHLVG	7768
6RLX	CD	HORMONE (MUSCLE RELAXANT)	D	1.8	3.5	2	14	RELVRAQIAICGMS	7769
1B33	AB	PHOTOSYNTHESIS	A	1.7	3.4	2	13	PGELDRIKSFVSS	7770
1B33	HI	PHOTOSYNTHESIS	I	1.7	3.4	2	13	AITAVINSSDVQG	7771
1B4U	AD	DIOXYGENASE	A	1.1	3.4	3	10	VHAYLAEFDD	7772
1BCC	DJ	OXIDOREDUCTASE	J	3.4	3.4	1	9	WKHIKHKYE	7773
1BCP	HL	TOXIN	L	1.7	3.4	2	16	TWFDTMLGFAISAYAL	7774
1D4M	13	VIRUS	1	3.4	3.4	1	8	VQMRRKLE	7775
1D4M	13	VIRUS	1	1.7	3.4	2	6	VENFLG	7776
1D8D	AB	TRANSFERASE	A	1.7	3.4	2	15	YQVWHHRRVLVEWLK	7777
1DD4	BD	RIBOSOME	D	1.7	3.4	2	15	VSELAELVKKLEDKF	7778
1DE4	AC	METAL TRANSPORT INHIBITOR/RECEPTOR	C	3.4	3.4	1	18	YERYNSQLLSFVRDLNQY	7779
1DOA	AB	CELL CYCLE	A	1.7	3.4	2	19	PSSFENVKEKWVPEITHHC	7780
1E1C	CD	ISOMERASE	C	1.7	3.4	2	24	AYVEELTWDLARKAWGHIQEVEKV	7781

1E6Y	EF	OXIDOREDUCTASE	F	1.7	3.4	2	11	PYFRSYFAAIN	7782
1E7P	EF	OXIDOREDUCTASE	F	3.4	3.4	1	28	MWPLYLVLLFAVELHGSVGLYRLAVKWG	7783
1EF1	AC	MEMBRANE PROTEIN	A	3.4	3.4	1	15	KDQWEERIQVWHEEH	7784
1EF1	BD	MEMBRANE PROTEIN	D	3.4	3.4	1	10	TKQRIDEFES	7785
1EJR	CB	HYDROLASE	C	1.7	3.4	2	8	RQAYADMF	7786
1EV1	23	VIRUS	3	1.7	3.4	2	5	MEAYR	7787
1F2U	CD	REPLICATION	C	1.7	3.4	2	13	KSSLLDAILVGLY	7788
1F99	KL	PHOTOSYNTHESIS	K	1.7	3.4	2	12	PLTEAIAAADSQ	7789
1FFT	FH	OXIDOREDUCTASE	F	1.7	3.4	2	27	VDYWIWSLQLSGIGTTLTGINFFVTIL	7790
1FFU	DE	HYDROLASE	D	1.7	3.4	2	9	LIHFLREEL	7791
1FHJ	AD	OXYGEN STORAGE/TRANSPORT	D	3.4	3.4	1	7	PWTQRFF	7792
1FXK	BC	CHAPERONE	B	1.1	3.4	3	14	INETQKALEELSRA	7793
1FYZ	AC	OXIDOREDUCTASE	C	1.7	3.4	2	7	EYEALTV	7794
1G0U	AB	HYDROLASE	B	1.1	3.4	3	23	TADAEILINTARIHAQNYLKTYN	7795
1G0U	CD	HYDROLASE	D	3.4	3.4	1	12	FQVEYSLEAIKL	7796
1G0U	EL	HYDROLASE	L	1.7	3.4	2	21	AADGDALVKRFKNSVKWYHFD	7797
1G0U	IZ	HYDROLASE	I	1.7	3.4	2	12	SDQLFGMCESLY	7798
1G20	AD	OXIDOREDUCTASE	D	1.7	3.4	2	5	HTWLH	7799
1G2C	EF	VIRAL PROTEIN	E	1.7	3.4	2	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	7800
1G2C	GH	VIRAL PROTEIN	G	1.7	3.4	2	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	7801
1G2C	OP	VIRAL PROTEIN	P	1.7	3.4	2	30	SDEFDASISQVNEKINQSLAFIRKSDELLH	7802
1GCV	AB	OXYGEN STORAGE/TRANSPORT	A	1.7	3.4	2	19	PDTHCAVDKLLSAICQELS	7803
1GH0	IJ	PHOTOSYNTHESIS	J	1.7	3.4	2	12	AFTKVVSQADTR	7804
1GX7	AD	OXIDOREDUCTASE	A	1.7	3.4	2	11	PAVRYALGDAF	7805
1GZS	DC	TOXIN/CELL CYCLE	C	1.7	3.4	2	9	DRLRPLSYP	7806
1H2M	AS	TRANSCRIPTION ACTIVATOR/INHIBITOR	A	1.7	3.4	2	9	RKIVMDFLG	7807
1H59	AB	INSULIN	A	3.4	3.4	1	12	AELVDALQFVCG	7808
1HBR	AD	OXYGEN STORAGE/TRANSPORT	D	3.4	3.4	1	7	PWTQRFF	7809
1HEZ	CE	ANTIBODY	E	1.1	3.4	3	17	FEEATAEAYRYADLLAK	7810
1HV4	CD	OXYGEN STORAGE/TRANSPORT	D	1.7	3.4	2	16	VADCGAEALARLLIVY	7811
1I7Q	AB	LYASE	A	1.7	3.4	2	6	EDARLR	7812
1ID3	CD	STRUCTURAL PROTEIN/DNA	D	1.1	3.4	3	29	QKSMSILNSFVNDIFERIATEASKLAAYN	7813
1IR2	AI	LYASE	A	1.7	3.4	2	21	NAPGAAANRVALEACTQARNE	7814
1IRU	AB	HYDROLASE	B	3.4	3.4	1	12	VQIEYALAAVAG	7815
1IRU	CD	HYDROLASE	D	1.7	3.4	2	12	FQVEYAQEAVKK	7816
1IRU	OP	HYDROLASE	P	3.4	3.4	1	12	VQIEYALAAVAG	7817
1JB0	BI	PHOTOSYNTHESIS	B	3.4	3.4	1	33	EENLYQKIFASHFGHLAIIFLWVSGSLFHVAWQ	7818

1JNR	AB	OXIDOREDUCTASE	B	3.4	3.4	1	5	EEALK	7819
1KI6	AB	PHOSPHOTRANSFERASE	A	1.7	3.4	2	30	AGDAAVVMTSAQITMGMPYAVTDAVLAPHI	7820
1KI6	AB	PHOSPHOTRANSFERASE	B	1.7	3.4	2	9	MTYWRVLGA	7821
1KX4	FH	STRUCTURAL PROTEIN/DNA	H	1.7	3.4	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	7822
1KXP	AD	CONTRACTILE PROTEIN/PROTEIN BINDING	D	1.7	3.4	2	11	AMDVFVCTYFM	7823
1KYO	DI	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.7	3.4	2	32	PEHDERKRLGLKTVIILSSLYLLSIWVKKFKW	7824
1KYO	NP	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	3.4	3.4	1	24	NMGSLLGLCLVIQIVTGIFMAMHY	7825
1KYO	OP	OXIDOREDUCTASE/ELECTRON TRANSPORT	O	1.1	3.4	3	34	DERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	7826
1L2I	AC	TRANSCRIPTION RECEPTOR/COACTIVATOR	C	1.7	3.4	2	9	KILHRLLQD	7827
1L4A	BD	ENDOCYTOSIS/EXOCYTOSIS	D	1.1	3.4	3	15	AREDDMENNMKEVSS	7828
1LIA	KL	LIGHT HARVESTING PROTEIN	K	1.1	3.4	3	13	TSDLQSVQGNIQR	7829
1LTX	AR	TRANSFERASE/PROTEIN BINDING	R	1.7	3.4	2	16	MVEKRMLMKFLTFCVE	7830
1LWU	DF	BLOOD CLOTTING	D	1.7	3.4	2	13	RIIHLQRRINMQL	7831
1LYW	AD	ASPARTIC PROTEASE	A	1.7	3.4	2	6	IACWIH	7832
1M1J	DE	BLOOD CLOTTING	D	1.7	3.4	2	16	EGYDNIQKHLTQASSI	7833
1M1J	DE	BLOOD CLOTTING	D	3.4	3.4	1	15	IVETINILKPGLEGA	7834
1M1J	EF	BLOOD CLOTTING	F	1.7	3.4	2	19	IEQLTQKSKKIIEEIIRYE	7835
1MZN	AB	TRANSCRIPTION	A	1.7	3.4	2	11	LDDQVILLRAG	7836
1N5W	EF	OXIDOREDUCTASE	F	3.4	3.4	1	23	AEYRTKMAGVMLRRAVERAKARA	7837
1NFU	AB	HYDROLASE	A	3.4	3.4	1	9	RDWAESTLM	7838
1NHG	AC	OXIDOREDUCTASE	A	1.7	3.4	2	12	YGWGIAKELSKR	7839
1NI4	CB	OXIDOREDUCTASE	B	1.1	3.4	3	12	VKDIIFAIKKTL	7840
1NLW	DE	TRANSCRIPTION/DNA	E	1.7	3.4	2	22	HHNALERKRRDHIKDSFHSLRD	7841
1O96	CD	ELECTRON TRANSFER	D	1.7	3.4	2	12	IFDIEEELKAQL	7842
1OCC	LM	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	M	1.7	3.4	2	25	PKEQAIGLSVTFLSFLLPAGWVLYH	7843
1OCC	NP	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	3.4	3.4	1	33	VYGSTFFVATGFHGLHVIIGSTFLIVCFFRQLK	7844
1OCC	YZ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Z	1.7	3.4	2	25	PKEQAIGLSVTFLSFLLPAGWVLYH	7845
1OQS	AB	HYDROLASE	B	3.4	3.4	1	5	SVWNY	7846
1P8D	BD	MEMBRANE PROTEIN/PROTEIN BINDING	D	1.7	3.4	2	9	KILHRLLQE	7847
1PMA	FS	PROTEASE	S	1.1	3.4	3	22	VGDAQVLVRYMKAELELYRLQR	7848
1POI	CB	TRANSFERASE	B	1.7	3.4	2	15	NVRFVGFEINEYLHK	7849

1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.7	3.4	2	28	GLWQIITICATGAFVSWALREVEICRKL	7850
1Q7L	CD	HYDROLASE	C	1.7	3.4	2	17	KCVSIQYLEAVRRLKVE	7851
1QPW	CD	OXYGEN TRANSPORT	D	1.7	3.4	2	19	PDVQAAFQKVVAGVANALA	7852
1QVI	AZ	CONTRACTILE PROTEIN	Z	3.4	3.4	1	10	FADYMEAFKT	7853
1R1K	DA	HORMONE/GROWTH FACTOR RECEPTOR	D	1.7	3.4	2	30	PRCAVIFGKILGILTEIRTLGMQNSNMCIS	7854
1R4M	AB	CELL CYCLE	B	3.4	3.4	1	7	VKKFLER	7855
1RM6	AC	OXIDOREDUCTASE	A	1.7	3.4	2	6	GVEKVT	7856
1RM6	AC	OXIDOREDUCTASE	A	1.7	3.4	2	22	PLAVEGQTQGGVWMGMGQALSE	7857
1RP3	CD	TRANSCRIPTION	C	1.7	3.4	2	27	TEELFKTLDKINFSYILSLEEVFRDFA	7858
1RP3	GH	TRANSCRIPTION	G	1.7	3.4	2	14	LPLVKAIATNIKKH	7859
1RP3	GH	TRANSCRIPTION	G	1.7	3.4	2	18	IRDLISYGVIGLIKAVDN	7860
1RU7	AF	VIRAL PROTEIN	A	3.4	3.4	1	10	YEELREQLSS	7861
1S0Y	EB	LYASE	B	1.1	3.4	3	20	VARKQQLIRDVIDVTNKSIG	7862
1S0Y	GJ	LYASE	J	1.7	3.4	2	20	VARKQQLIRDVIDVTNKSIG	7863
1S5L	LM	PHOTOSYNTHESIS	M	1.7	3.4	2	26	QLGLIATALFVLVPSVFLIILYVQTE	7864
1SB3	AC	OXIDOREDUCTASE	A	1.7	3.4	2	6	GVEKVT	7865
1SQB	AJ	OXIDOREDUCTASE	J	3.4	3.4	1	12	LTARLYSLLFRR	7866
1SQB	CF	OXIDOREDUCTASE	F	3.4	3.4	1	18	ASSRWLEGIRKWYYNAAG	7867
1SQX	CF	OXIDOREDUCTASE	F	3.4	3.4	1	18	ASSRWLEGIRKWYYNAAG	7868
1T3Q	EF	OXIDOREDUCTASE	E	1.7	3.4	2	10	PERIFRSIQE	7869
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	1.1	3.4	3	16	EGVATYAAAVLFRMSE	7870
1U6G	AC	LIGASE	A	3.4	3.4	1	30	FEYTSKLQRMFQDIGVSKDLNEQFKKHLTN	7871
1ULI	AB	OXIDOREDUCTASE	A	1.7	3.4	2	17	VFEQDDGENWVEIQQVL	7872
1UZD	EJ	LYASE	E	1.7	3.4	2	14	AKNYGRAVYECLRG	7873
1UZH	BC	LYASE	B	1.7	3.4	2	21	NAPGAAANRVALEACTQARNE	7874
1V54	AD	OXIDOREDUCTASE	A	1.7	3.4	2	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	7875
1V54	AT	OXIDOREDUCTASE	A	1.7	3.4	2	33	LFVWSVMITAVLLLLSLPVLAAGITMLLTDRNL	7876
1V54	LM	OXIDOREDUCTASE	M	1.7	3.4	2	25	PKEQAIGLSVTFLSFLLPAGWVLYH	7877
1V54	NP	OXIDOREDUCTASE	N	1.7	3.4	2	34	PILYQHLFWFFGHPEVYILILPGFGMISHIVTYY	7878
1VCB	BC	TRANSCRIPTION	C	1.7	3.4	2	13	LKERCLQVVRSLV	7879
1VCB	HI	TRANSCRIPTION	H	3.4	3.4	1	18	SHVLSKVCMYFTYKVRYT	7880
1VCB	KL	TRANSCRIPTION	K	3.4	3.4	1	18	SHVLSKVCMYFTYKVRYT	7881
1VG9	AB	PROTEIN BINDING/PROTEIN TRANSPORT	A	1.7	3.4	2	15	QGELPQCFCRMCAVF	7882
1WYU	EF	OXIDOREDUCTASE	E	1.7	3.4	2	5	LEDLF	7883
1WYU	EF	OXIDOREDUCTASE	E	1.1	3.4	3	25	PEGLREVALKSVEMAHKLHALLLEV	7884
1WYW	AB	HYDROLASE	B	3.4	3.4	1	12	KKLKESYCQRQG	7885
1XFU	FT	LYASE/METAL BINDING PROTEIN	T	1.7	3.4	2	10	YEEFVQMMTA	7886

1XKM	AD	ANTIBIOTIC	A	1.7	3.4	2	15	PGFTALIKTLRKCKI	7887
1XME	AB	OXIDOREDUCTASE	A	1.7	3.4	2	6	TLDYVV	7888
1XME	AC	OXIDOREDUCTASE	A	1.7	3.4	2	6	TLDYVV	7889
1XV9	AB	DNA BINDING PROTEIN	B	1.7	3.4	2	23	LYAKLLGLLAELRSINEAYGYQI	7890
1XXH	AE	TRANSFERASE	A	1.7	3.4	2	19	QTQLRQAVQLLTRTELTLK	7891
1Y8R	AB	LIGASE	B	1.7	3.4	2	14	GIGCELLKNLVLTG	7892
1YDI	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.1	3.4	3	49	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVAEV	7893
1YE9	JN	OXIDOREDUCTASE	N	1.7	3.4	2	18	PLLQGRLFSYTDTQISRL	7894
1YE9	JN	OXIDOREDUCTASE	N	1.7	3.4	2	17	PFEQRHIVDGFSFELSK	7895
1YE9	JN	OXIDOREDUCTASE	N	1.7	3.4	2	13	PYIRERVVDQLAH	7896
1YHU	IK	OXYGEN STORAGE/TRANSPORT	K	1.7	3.4	2	20	PEFQGHVVRVMGGLDILINA	7897
1YHU	NP	OXYGEN STORAGE/TRANSPORT	P	3.4	3.4	1	18	GRRIAIAQAVFKDLFANV	7898
1YQ3	AB	OXIDOREDUCTASE	B	3.4	3.4	1	10	SNFYAQYKSI	7899
1YTZ	IC	CONTRACTILE PROTEIN	I	1.7	3.4	2	10	ADAMLRALLG	7900
1Z7Q	Rk	HYDROLASE/HYDROLASE ACTIVATOR	R	3.4	3.4	1	13	FQVEYALEAVKRG	7901
1Z7Q	YL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.7	3.4	2	12	QTFAYGVLDSNY	7902
1ZBB	bd	STRUCTURAL PROTEIN/DNA	b	1.7	3.4	2	11	AMDVVYALKRQ	7903
1ZBB	fh	STRUCTURAL PROTEIN/DNA	h	3.4	3.4	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	7904
1ZGL	HS	IMMUNE SYSTEM	H	3.4	3.4	1	13	AVDTYCRHNYGVG	7905
1ZLA	AB	PROTEIN BINDING/VIRUS/DNA	A	1.7	3.4	2	11	TVALREIRRYQ	7906
1ZOQ	AC	TRANSCRIPTION/TRANSFERASE	C	1.7	3.4	2	12	PQLMAAFIKQRT	7907
1ZV8	CD	VIRAL PROTEIN	D	1.7	3.4	2	17	QKEIDRLNEVAKNLNES	7908
1ZW3	AB	PROTEIN BINDING	A	1.7	3.4	2	22	RTIESILEPVAQQISHLVIMHE	7909
2A1J	AB	DNA BINDING PROTEIN	A	1.7	3.4	2	6	QDFLLK	7910
2A7U	AB	HYDROLASE	B	3.4	3.4	1	18	ITVARPYAKAAFDFAVEH	7911
2ACL	AB	TRANSCRIPTION	B	1.7	3.4	2	23	QLQVERLQHTYVEALHAYVSINH	7912
2AHM	AE	VIRAL PROTEIN, REPLICATION	E	1.7	3.4	2	12	DALNNIINNARD	7913
2AHM	DH	VIRAL PROTEIN, REPLICATION	D	1.7	3.4	2	18	TTEAFEKMVSLLSVLLSM	7914
2AYO	AB	HYDROLASE	A	1.7	3.4	2	16	ANECWIQMMRVLQQKL	7915
2BA0	BG	RNA BINDING PROTEIN	G	1.7	3.4	2	14	VDIKRDYVLSKLRD	7916
2BKY	BY	DNA BINDING PROTEIN	Y	1.1	3.4	3	16	ISKAVDVYNSLKDRLG	7917
2BTV	AF	VIRUS	F	1.7	3.4	2	17	ANVMEILGIAINRYNGL	7918
2BV8	AF	PHOTOSYNTHESIS	F	1.1	3.4	3	25	NRRMAACLRDMEIVLRYVSYAEIAG	7919
2CNW	BD	SIGNAL RECOGNITION	B	1.1	3.4	3	17	PAEVILATVYEALKEAL	7920
2D1P	AC	TRANSLATION	A	3.4	3.4	1	16	QQASSAFQFAQALIAD	7921
2DBU	CD	TRANSFERASE	C	1.1	3.4	3	14	ATATQVGVDILKEG	7922
2DD4	EF	HYDROLASE	F	3.4	3.4	1	6	RDCLIG	7923
2DF4	BC	LIGASE	B	3.4	3.4	1	8	KRAVDWAM	7924

2DFS	MR	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	1.7	3.4	2	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRDATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	7925
2E 74	AB	PHOTOSYNTHESIS	A	3.4	3.4	1	15	VTEAYASVQYIMNEV	7926
2E5L	DE	RIBOSOME	D	1.7	3.4	2	8	EQLVIEFY	7927
2EG4	AB	TRANSFERASE	B	1.7	3.4	2	8	MHEWLQEG	7928
2EHO	EF	REPLICATION	F	1.1	3.4	3	37	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY	7929
2EHO	KH	REPLICATION	H	3.4	3.4	1	10	EGWRTVFSAD	7930
2F66	AE	TRANSPORT PROTEIN	E	1.7	3.4	2	10	ASNAITRLER	7931
2F8N	DK	STRUCTURAL PROTEIN/DNA	K	1.7	3.4	2	7	EELNKLL	7932
2FBW	OP	OXIDOREDUCTASE	P	1.7	3.4	2	14	AKEEMARFWEKNTK	7933
2FHH	IJ	HYDROLASE	J	1.7	3.4	2	23	AAVAVEFARLYAVELEHYEKLEG	7934
2FHH	UV	HYDROLASE	V	1.1	3.4	3	23	AAVAVEFARLYAVELEHYEKLEG	7935
2FK0	CF	VIRAL PROTEIN	C	1.7	3.4	2	8	YEELKHLL	7936
2FO1	AD	GENE REGULATION/SIGNALLING PROTEIN/DNA	D	1.7	3.4	2	22	RPEMIANQRAVTAHLFNRYTED	7937
2FRV	IJ	OXIDOREDUCTASE	I	1.7	3.4	2	9	GCSESVLRT	7938
2FV4	AB	STRUCTURAL PROTEIN, PROTEIN BINDING	B	1.7	3.4	2	13	DFYKTKYIWERLG	7939
2FYN	AB	OXIDOREDUCTASE	B	1.7	3.4	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	7940
2G4D	AB	HYDROLASE/PROTEIN BINDING	A	1.7	3.4	2	7	RKDIQTL	7941
2GL7	DE	TRANSCRIPTION	D	1.7	3.4	2	17	DSVLFYAITTLHNLLLH	7942
2HLD	SV	HYDROLASE	S	1.7	3.4	2	15	LSKQAVAYRQLSLLL	7943
2HLD	TW	HYDROLASE	T	1.7	3.4	2	14	RSTVAQLVQTLEQH	7944
2HYB	AC	TRANSFERASE	A	3.4	3.4	1	16	QASDSAYQFAKAALEK	7945
2HYB	DF	TRANSFERASE	D	3.4	3.4	1	16	QASDSAYQFAKAALEK	7946
2HYB	GI	TRANSFERASE	G	3.4	3.4	1	16	QASDSAYQFAKAALEK	7947
2HZS	AB	TRANSCRIPTION	A	1.7	3.4	2	9	IDTILSSKL	7948
2I2X	GF	TRANSFERASE	F	3.4	3.4	1	6	YNVALE	7949
2IAN	ST	IMMUNE SYSTEM	T	1.7	3.4	2	7	EAEISHT	7950
2IBZ	DG	OXIDOREDUCTASE	D	1.7	3.4	2	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	7951
2JDQ	AE	PROTEIN TRANSPORT	A	3.4	3.4	1	16	ESIKKEACWTISNITA	7952
2JEA	AB	HYDROLASE	A	1.7	3.4	2	18	ENAIELARVVDRSLRDSK	7953
2JGZ	AB	TRANSFERASE	B	1.7	3.4	2	15	KHQIRQMEMKILRAL	7954
2JIY	LM	PHOTOSYNTHESIS	M	3.4	3.4	1	7	PAVFLRD	7955
2JIZ	BG	HYDROLASE	G	1.7	3.4	2	70	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFNRTRQAVITKELIEIISGAAAL	7956
2JM6	AB	APOPTOSIS	B	3.4	3.4	1	11	ETAFQGMLRKL	7957
2K2I	AB	CELL CYCLE	A	1.7	3.4	2	9	EQEFLRIMK	7958
2NPP	AC	SIGNALING PROTEIN,HYDROLASE	A	1.7	3.4	2	19	WRVRLAIIEYMPLLAGQLG	7959
2NPP	DF	SIGNALING PROTEIN,HYDROLASE	D	1.7	3.4	2	19	WRVRLAIIEYMPLLAGQLG	7960

2NPS	AB	TRANSPORT PROTEIN	A	1.1	3.4	3	52	QVDEVIDVMQENITKVIERGERLDELQDKSESLSDNATAFSNRSKQLRR QMW	7961
2NUU	CI	TRANSPORT PROTEIN/SIGNALING PROTEIN	C	1.7	3.4	2	15	LLGACSGAIAGLVGV	7962
2NVU	AB	PROTEIN TURNOVER, LIGASE	B	1.7	3.4	2	21	ASTNAVIAAVCATEVFKIATS	7963
2NZ0	AD	MEMBRANE PROTEIN	A	1.7	3.4	2	15	KRELQVLYRGFKNEC	7964
2O98	BQ	PROTEIN BINDING	B	1.7	3.4	2	34	VEERNLLSVAYKNVIGARRASWRIISSIEQKEES	7965
2OCF	AD	HORMONE/GROWTH FACTOR	A	1.7	3.4	2	9	DLLLEMLDA	7966
2OI9	AC	IMMUNE SYSTEM	A	1.1	3.4	3	29	PEYWERITQVAKGQEQWFRVNLRTLLGYY	7967
2OM0	cd	HORMONE	d	1.7	3.4	2	18	NQHLCGSHLVEALYLVCG	7968
2OM7	EL	RIBOSOME	L	1.7	3.4	2	5	ADQEK	7969
2P1L	CD	APOPTOSIS	C	1.7	3.4	2	24	QMAAVKQALREAGDEFELRYRRAF	7970
2P22	AB	TRANSPORT PROTEIN	B	1.7	3.4	2	28	SKDKEVIETLSEIYSIVITLDHVEKAYL	7971
2PF4	BF	HYDROLASE REGULATOR/VIRAL PROTEIN	B	3.4	3.4	1	10	WRVRYMVADK	7972
2PMZ	RY	TRANSLATION, TRANSFERASE	Y	1.7	3.4	2	6	INEVIH	7973
2QOY	CN	RIBOSOME	C	1.7	3.4	2	21	KEFADNLDSDFKVRQYLTKEL	7974
2QR0	KJ	IMMUNE SYSTEM	J	1.7	3.4	2	8	FMDVYQRS	7975
2QSH	AX	DNA BINDING PROTEIN/DNA	X	1.7	3.4	2	10	PQLREHIMAN	7976
2QVS	EB	TRANSFERASE/TRANSFERASE REGULATOR	B	3.4	3.4	1	11	MSERMKIVDVI	7977
2RAO	CD	OXYGEN BINDING	C	3.4	3.4	1	16	GGEYGAEAVERMFLGF	7978
2SEB	BE	COMPLEX (MHC CLASS II/SUPERANTIGEN)	B	1.7	3.4	2	9	RPDAEYWNS	7979
2UUN	EF	ELECTRON TRANSPORT	F	1.7	3.4	2	12	AFTKVAAQADTR	7980
2UUN	KL	ELECTRON TRANSPORT	K	1.7	3.4	2	12	PLTDAVSTADSQ	7981
2UUN	WX	ELECTRON TRANSPORT	W	1.7	3.4	2	12	PLTDAVSTADSQ	7982
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	A	3.4	3.4	1	25	KEKDEMVEQEFNRLLEATSYLSHQL	7983
2UY1	AB	RNA BINDING PROTEIN	B	1.7	3.4	2	14	SRMWDSMIEYEFMV	7984
2UZ6	AK	RECEPTOR	K	1.1	3.4	3	7	PPCILNN	7985
2V1C	AC	RECOMBINATION	A	3.4	3.4	1	17	VEGDATALYLQRLLEPL	7986
2V7Q	BG	HYDROLASE	G	1.7	3.4	2	75	ADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDK LTLTFNRTRQAVITKELIEIISGAAAL	7987
2VBN	AB	HYDROLASE	B	1.7	3.4	2	14	KEFLLYLAGFVDGD	7988
2VE7	BD	CELL CYCLE	D	3.4	3.4	1	20	EGFLPFSNLVTHLDSFLPIC	7989
2VGL	AS	PROTEIN TRANSPORT	A	1.1	3.4	3	16	TNLRYLALESMCTLAS	7990
2VH3	AB	UNKNOWN FUNCTION	B	1.7	3.4	2	12	LGSLCTLFQKLY	7991
2VJM	AB	TRANSFERASE	B	1.7	3.4	2	9	MQDAVLNLV	7992
2VML	GH	PHOTOSYNTHESIS	G	1.7	3.4	2	27	NTELQAANGRFQRATASMEAARALTSN	7993

2VPD	AB	GENE REGULATION	B	1.7	3.4	2	13	TEMANKAAEAVLK	7994
2VRC	CD	OXIDOREDUCTASE	D	3.4	3.4	1	17	PLAHVHLATEYATRTTN	7995
2VVC	AL	BLOOD CLOTTING	A	3.4	3.4	1	9	RDWAESTLM	7996
2WB1	AC	TRANSCRIPTION	C	1.7	3.4	2	8	HLLDAAAR	7997
2WB1	WY	TRANSCRIPTION	Y	1.7	3.4	2	12	MRHILLVADVMT	7998
2WD7	AB	OXIDOREDUCTASE	A	3.4	3.4	1	13	AEQIADAVIFLVS	7999
2WD7	AB	OXIDOREDUCTASE	B	3.4	3.4	1	13	AEQIADAVIFLVS	8000
2Z3R	KJ	CYTOKINE/CYTOKINE RECEPTOR	K	1.7	3.4	2	20	ASIHDTVENLIILANNSLSS	8001
2ZCY	M1	HYDROLASE	1	1.1	3.4	3	6	PDEYEQ	8002
2ZCY	OV	HYDROLASE	V	1.1	3.4	3	22	AADTEAVTQLIGSNIELHSLYT	8003
2ZCY	U1	HYDROLASE	1	1.7	3.4	2	22	AADTQAIADIVQYHLELYTSQY	8004
2ZCY	VW	HYDROLASE	W	1.1	3.4	3	12	SDQLFGMCESLY	8005
2ZJS	YE	PROTEIN TRANSPORT/IMMUNE SYSTEM	Y	1.7	3.4	2	13	GTSLIIFAGIVVE	8006
2ZPK	MI	IMMUNE SYSTEM	M	1.7	3.4	2	6	SEELET	8007
2ZSH	AB	HORMONE RECEPTOR	B	3.4	3.4	1	6	ELLAVL	8008
3A0B	ad	ELECTRON TRANSPORT	a	3.4	3.4	1	15	ISGTFNFMIVFQAEH	8009
3A0B	bh	ELECTRON TRANSPORT	b	1.7	3.4	2	26	LPKMFGIHLFLAGLLCFGFGAFHLTG	8010
3A0B	hx	ELECTRON TRANSPORT	x	3.4	3.4	1	25	PSLKGFFIGLLSGAVVLGLTFAVLI	8011
3B9J	BC	OXIDOREDUCTASE	B	1.7	3.4	2	10	TEIGIEMKFK	8012
3BLW	AB	OXIDOREDUCTASE	B	1.7	3.4	2	11	IDNSVLKVVTN	8013
3BMC	AB	OXIDOREDUCTASE	A	3.4	3.4	1	13	AEQIADAVIFLVS	8014
3BMC	AC	OXIDOREDUCTASE	A	1.7	3.4	2	27	VETQVAELIGTNAIAPFLLTMSFAQRQ	8015
3BPQ	CB	TOXIN	B	1.7	3.4	2	8	RKSIYDYF	8016
3BWU	CD	CHAPERONE, STRUCTURAL, MEMBRANE PROTEIN	D	3.4	3.4	1	10	AVADLSRFEN	8017
3BZ1	AD	ELECTRON TRANSPORT	D	1.7	3.4	2	28	KRWLHFFMLFVPVTGLWMSAIGVVGLAL	8018
3C01	AE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	E	1.7	3.4	2	13	QRALAVRAYAEKV	8019
3C5Z	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	C	3.4	3.4	1	7	PEFGQLA	8020
3C91	OW	HYDROLASE	O	3.4	3.4	1	23	VADARVLVDFARISAQQEKVTYG	8021
3CHX	JK	MEMBRANE PROTEIN	K	1.7	3.4	2	5	GTWHM	8022
3CUE	HJ	PROTEIN TRANSPORT	H	1.1	3.4	3	23	AGDFETKLSDYGHNIGIRLLELL	8023
3CWB	EJ	OXIDOREDUCTASE	J	1.7	3.4	2	10	LLRQAYSALF	8024
3CWB	QR	OXIDOREDUCTASE	Q	1.7	3.4	2	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	8025
3CWB	QW	OXIDOREDUCTASE	W	3.4	3.4	1	7	WKHIKHK	8026
3CXH	LM	OXIDOREDUCTASE	M	1.7	3.4	2	9	INYTKLKNA	8027
3D4X	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	3.4	3.4	1	7	PWTQRFF	8028

3DBJ	CD	PHOTOSYNTHESIS	C	1.7	3.4	2	9	PGELDRIKN	8029
3DF0	AB	HYDROLASE	B	3.4	3.4	1	9	IQEWLQLTM	8030
3DGG	CD	IMMUNE SYSTEM	C	1.7	3.4	2	6	SEQLTS	8031
3DHR	EF	OXYGEN STORAGE, OXYGEN TRANSPORT	E	3.4	3.4	1	16	AGDLGGEALERLFITY	8032
3DHR	GF	OXYGEN STORAGE, OXYGEN TRANSPORT	F	3.4	3.4	1	7	PWTQRFF	8033
3DNL	DF	VIRAL PROTEIN	F	1.7	3.4	2	9	MRDNWRSEL	8034
3DTP	AC	CONTRACTILE PROTEIN	C	1.7	3.4	2	9	EEEVEQLVA	8035
3DUF	DI	OXIDOREDUCTASE/TRANSFERASE	I	1.7	3.4	2	10	PSVRKYAREK	8036
3EA5	AB	TRANSPORT PROTEIN	A	1.7	3.4	2	5	DGYYI	8037
3EDQ	AB	HYDROLASE	B	1.7	3.4	2	13	WFIQSLCAMLKQY	8038
3EI4	CD	DNA BINDING PROTEIN	D	1.1	3.4	3	18	WPSVQQGLQQSFLHTLDS	8039
3ETR	AC	OXIDOREDUCTASE	A	3.4	3.4	1	17	FCTPGIVMSMYTLLRNQ	8040
3EXH	EC	OXIDOREDUCTASE	C	1.7	3.4	2	11	REEIQEVRSKS	8041
3EYM	CF	VIRAL PROTEIN	F	3.4	3.4	1	19	LKSTQAAIDQINGKLNRVI	8042
3FAL	AB	SIGNALING PROTEIN	A	1.7	3.4	2	18	GAIFDRVLTELVSKMRDM	8043
3FCU	AB	CELL ADHESION/BLOOD CLOTTING	B	1.7	3.4	2	5	DGRLA	8044
3FFD	AB	IMMUNE SYSTEM/HORMONE	B	1.7	3.4	2	5	SEELK	8045
3FGC	AB	OXIDOREDUCTASE	B	3.4	3.4	1	7	SADMRFF	8046
3FKS	UV	HYDROLASE	U	3.4	3.4	1	5	VFYLH	8047
3FPN	AB	DNA BINDING PROTEIN	B	3.4	3.4	1	11	RNALLRRLVDI	8048
3FWC	IJ	CELL CYCLE, TRANSCRIPTION	I	1.7	3.4	2	14	EEQKQEIYEAFSLF	8049
3G3A	AB	HYDROLASE/IMMUNE SYSTEM	B	3.4	3.4	1	8	VAWRNRCK	8050
3GE8	DF	OXIDOREDUCTASE	D	1.7	3.4	2	5	RQFDW	8051
3GHG	HI	BLOOD CLOTTING	I	1.7	3.4	2	13	VNLKEKVAQLEAQ	8052
3GTM	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	E	3.4	3.4	1	11	SDEKRELLKRY	8053
3GTM	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	3.4	3.4	1	5	DLYKL	8054
3H0L	PN	LIGASE	N	1.1	3.4	3	15	TKIGKEVIKEMVETG	8055
3HKZ	AB	TRANSFERASE	A	3.4	3.4	1	9	AQDYISGAY	8056
3HKZ	JW	TRANSFERASE	W	1.7	3.4	2	6	INEVIH	8057
3HRD	AD	OXIDOREDUCTASE	D	3.4	3.4	1	17	YCTPGMILTAKALLDKN	8058
3HRD	EF	OXIDOREDUCTASE	F	1.7	3.4	2	11	VGEPALIPMIP	8059
3HRD	EH	OXIDOREDUCTASE	H	3.4	3.4	1	15	YCTPGMILTAKALLD	8060
4RUB	CU	LYASE(CARBON-CARBON)	C	1.7	3.4	2	20	WRDRFLFCAEALYKAQAETG	8061
1AGR	DH	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	H	1.7	3.3	2	15	EENIDFWISCEEYKK	8062
1AHJ	AB	LYASE	B	1.7	3.3	2	17	YYERYVIGVATLMVEKG	8063

1B33	CD	PHOTOSYNTHESIS	D	3.3	3.3	1	13	TAALEKLKSYFST	8064
1CDL	BF	CALCIUM-BINDING PROTEIN	B	1.7	3.3	2	9	YEEFVQMMT	8065
1CXZ	AB	SIGNALING PROTEIN	B	1.7	3.3	2	27	GPVELLLRGSSRRLDLLHQQLQELHAH	8066
1E1C	AB	ISOMERASE	B	1.7	3.3	2	5	LAGDF	8067
1E6Y	AE	OXIDOREDUCTASE	E	1.7	3.3	2	10	APIVKSAVWG	8068
1EQZ	BD	STRUCTURAL PROTEIN/DNA	B	1.7	3.3	2	12	SREIQTAVRLLL	8069
1EYX	KL	PHOTOSYNTHESIS	K	1.1	3.3	3	27	SSDLESVQGNIQRASARLEAAEKLASN	8070
1F60	AB	TRANSLATION	A	1.7	3.3	2	15	YAWVLDKLKAERERG	8071
1F99	MN	PHOTOSYNTHESIS	N	1.1	3.3	3	13	NTQIDALLAIVSE	8072
1FFU	DE	HYDROLASE	D	1.7	3.3	2	9	AVQEGFYKE	8073
1FG9	AC	IMMUNE SYSTEM	A	1.7	3.3	2	13	PYVKEAENLKKYF	8074
1FNT	QR	HYDROLASE/HYDROLASE ACTIVATOR	R	1.7	3.3	2	13	FQVEYALEAVKRG	8075
1FS0	EG	HYDROLASE	G	1.1	3.3	3	17	LSELIGPVKVMLQAYDE	8076
1FYZ	AE	OXIDOREDUCTASE	A	1.7	3.3	2	33	PASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYG	8077
1FYZ	BD	OXIDOREDUCTASE	B	3.3	3.3	1	8	ARRTRTIG	8078
1G0U	OP	HYDROLASE	P	1.7	3.3	2	12	YQVEYALESISH	8079
1G0U	PW	HYDROLASE	P	1.7	3.3	2	23	TADAEILINTARIHAQNYLKTYN	8080
1G20	CB	OXIDOREDUCTASE	B	1.7	3.3	2	5	HTWLH	8081
1GH0	IJ	PHOTOSYNTHESIS	I	1.7	3.3	2	12	PLTEAVSVADSQ	8082
1GH0	OP	PHOTOSYNTHESIS	P	1.7	3.3	2	13	TAQIDALSQMVAE	8083
1GH0	ST	PHOTOSYNTHESIS	T	1.7	3.3	2	12	AFTKVVSQADTR	8084
1GH0	WX	PHOTOSYNTHESIS	X	1.7	3.3	2	13	TAQIDALSQMVAE	8085
1H1L	CB	OXIDOREDUCTASE	B	1.7	3.3	2	5	HTWLH	8086
1H2A	SL	OXIDOREDUCTASE	L	1.7	3.3	2	16	AADLKAVQDKLKTFVE	8087
1HBH	CD	OXYGEN CARRIER	C	3.3	3.3	1	21	PEAHVSLDKFLSGVALALAER	8088
1HR8	AB	HYDROLASE	B	3.3	3.3	1	19	DAEVNRAKAQLKAALLLSL	8089
1HR8	EF	HYDROLASE	F	3.3	3.3	1	19	DAEVNRAKAQLKAALLLSL	8090
1HV4	EH	OXYGEN STORAGE/TRANSPORT	H	1.7	3.3	2	6	PWTQRF	8091
1HX1	AB	CHAPERONE/CHAPERONE INHIBITOR	B	1.7	3.3	2	19	DRRVKATIEQFMKILEEID	8092
1I3O	AB	APOPTOSIS	A	1.7	3.3	2	15	TDVDAANLRETFRNL	8093
1I3Q	AB	TRANSCRIPTION	B	1.7	3.3	2	13	YAAKLLFQELMAM	8094
1I7W	AB	CELL ADHESION	A	1.7	3.3	2	17	QRLVQNCLWTLRNLSDA	8095
1IB1	AE	SIGNALING PROTEIN/TRANSFERASE	A	1.7	3.3	2	19	PIRLGLALNFSVFYYEILN	8096
1ID3	CD	STRUCTURAL PROTEIN/DNA	D	1.7	3.3	2	21	GELAKHAVSEGTRAVTKYSSS	8097
1IRU	GH	HYDROLASE	G	3.3	3.3	1	23	LADARSLADIAREEASNFRSNFG	8098
1IRU	UV	HYDROLASE	U	3.3	3.3	1	23	LADARSLADIAREEASNFRSNFG	8099
1IW7	NP	TRANSFERASE	P	3.3	3.3	1	24	KEHKRYLHIAREGEAARQHLIEAN	8100
1IWP	AG	LYASE	A	1.7	3.3	2	17	EDIASNILNMLRQRVTG	8101
1IZL	JN	PHOTOSYNTHESIS	N	3.3	3.3	1	7	FMLFVPV	8102
1JB0	BM	PHOTOSYNTHESIS	B	1.7	3.3	2	33	EENLYQKIFASHFGHLAIIFLWVSGSLFHVAWQ	8103

1JD2	OP	HYDROLASE	P	1.7	3.3	2	18	PEDLFETISQALLNAADR	8104
1JHL	HA	COMPLEX (ANTIBODY-ANTIGEN)	A	1.7	3.3	2	8	VAWRKHCK	8105
1JMU	BG	VIRAL PROTEIN	G	1.7	3.3	2	5	APIVL	8106
1JPW	BE	CELL ADHESION	B	1.7	3.3	2	16	VKFLAITTDCLQILAY	8107
1K6L	MH	PHOTOSYNTHESIS	H	1.7	3.3	2	22	LLEEDKICGYVAGGLMYAAPKR	8108
1KFY	OP	OXIDOREDUCTASE	P	1.7	3.3	2	30	FIGRVFLFLMIVLPLWCGLHRMHHAMHDLK	8109
1KI6	AB	PHOSPHOTRANSFERASE	A	1.7	3.3	2	9	MTYWRVLGA	8110
1KYO	OT	OXIDOREDUCTASE/ELECTRON TRANSPORT	T	3.3	3.3	1	7	WKDVKAK	8111
1KZ7	AB	SIGNALING PROTEIN	B	1.7	3.3	2	8	RLRPLSYP	8112
1L1O	AC	DNA BINDING PROTEIN	A	1.7	3.3	2	14	LGLYNEAVKIIHDF	8113
1L2W	BI	CHAPERONE	I	1.7	3.3	2	10	HSVIGFIQRM	8114
1L9B	LM	PHOTOSYNTHESIS	L	1.7	3.3	2	24	HIPFAFAFAILAYLTLVLFRPVMM	8115
1LB1	AB	SIGNALING PROTEIN	B	1.7	3.3	2	19	PDSLENIPEKWTPEVKHFC	8116
1LIA	AB	LIGHT HARVESTING PROTEIN	A	3.3	3.3	1	12	VITTTISAADAA	8117
1M1J	AB	BLOOD CLOTTING	A	1.7	3.3	2	27	GIIDDTDQNYSQRIDNIRQQLADSQNK	8118
1M1Y	AB	OXIDOREDUCTASE	B	1.7	3.3	2	16	QGCVAYFRSYFNRHFR	8119
1M8Q	DF	CONTRACTILE PROTEIN	D	3.3	3.3	1	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	8120
1MHM	BA	LYASE	B	1.7	3.3	2	11	KAQLDEILGPA	8121
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	B	1.7	3.3	2	9	AVPKAEWTN	8122
1MTY	BG	MONOOXYGENASE	G	3.3	3.3	1	15	KWEAEKIHIGFRQAY	8123
1MTY	EC	MONOOXYGENASE	C	1.7	3.3	2	7	EYEALTV	8124
1MTY	EC	MONOOXYGENASE	E	1.7	3.3	2	7	AQEVHRW	8125
1MXE	AE	METAL BINDING PROTEIN	A	1.7	3.3	2	15	EEQIAEFKEAFSLFD	8126
1N4Q	CD	TRANSFERASE	C	1.7	3.3	2	14	YTVWHFRRVLLRSL	8127
1NF5	CD	TRANSFERASE/TRANSFERASE	D	3.3	3.3	1	7	RFDRIAH	8128
1NIK	CK	TRANSCRIPTION	K	1.7	3.3	2	12	HTLGNLIRAELL	8129
1NTK	EJ	OXIDOREDUCTASE	J	1.7	3.3	2	12	LTARLYSLLFRR	8130
1OCC	DI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	3.3	3.3	1	7	PIQGFSA	8131
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	O	1.1	3.3	3	32	PIMEELLHFHDHTLMIVFLISSLVLYIISLML	8132
1OCC	PW	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	1.7	3.3	2	23	PWPLTGALSALLMTSGLTMWFHF	8133
1OCC	QV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	3.3	3.3	1	7	PIQGFSA	8134
1Q5Q	EL	HYDROLASE	E	1.7	3.3	2	22	YNEFENLRRAGIVHADMRGYSY	8135
1Q5Q	EM	HYDROLASE	M	1.7	3.3	2	23	AGIAIELVRLFAVELEHYEKIEG	8136
1QGW	AB	PHOTOSYNTHESIS	A	1.7	3.3	2	12	ESDAAKKLQEFI	8137

1QTY	ST	HORMONE/GROWTH FACTOR RECEPTOR	S	1.7	3.3	2	9	FMDVYQRSY	8138
1R4A	BF	PROTEIN TRANSPORT	F	3.3	3.3	1	15	TEFEYLRKVLFEYMM	8139
1R6O	BD	HYDROLASE	B	1.7	3.3	2	17	LSFQRVLQRAVFHVQSS	8140
1RKE	AB	CELL ADHESION, STRUCTURAL PROTEIN	B	3.3	3.3	1	32	EESEQATEMLVHNAQNLMQSVKETVREAEAAS	8141
1RM1	BC	TRANSCRIPTION/DNA	C	1.7	3.3	2	7	REDFENA	8142
1RP3	CD	TRANSCRIPTION	D	1.7	3.3	2	15	RIELSRLIGLLLETE	8143
1RYP	CJ	MULTICATALYTIC PROTEINASE	C	1.7	3.3	2	22	TADAEILINTARIHAQNYLKTY	8144
1RYP	HN	MULTICATALYTIC PROTEINASE	N	1.7	3.3	2	20	ISDMQHIERLLKDLVTENAY	8145
1RYP	KZ	MULTICATALYTIC PROTEINASE	Z	3.3	3.3	1	19	VEDALYLGKRSILAAAHRD	8146
1RYP	RY	MULTICATALYTIC PROTEINASE	Y	1.7	3.3	2	22	GDTVQFAEYIQANIQLYSIRED	8147
1RYP	TU	MULTICATALYTIC PROTEINASE	U	1.7	3.3	2	22	IPDGRHLVNRGREEAASFKKLY	8148
1S5L	BD	PHOTOSYNTHESIS	D	1.1	3.3	3	18	PYNAIAFSAPIAVFVSVF	8149
1S5L	CK	PHOTOSYNTHESIS	C	1.7	3.3	2	18	AHAGLIVFWAGAMTLFEL	8150
1S5L	ef	PHOTOSYNTHESIS	e	1.7	3.3	2	13	ALFIAGWLFVSTG	8151
1S5L	kz	PHOTOSYNTHESIS	z	1.7	3.3	2	26	TILFQLALAALVILSFVMVIGVPVAY	8152
1SEB	EF	COMPLEX (MHC II/PEPTIDE/TOXIN)	E	1.7	3.3	2	7	EEFGRFA	8153
1SVF	CD	VIRAL PROTEIN	C	1.7	3.3	2	59	AAVALVKANENAAAILNLKNAIQKTNAAVADVVQATQSLGTAVQAVQDHINSVVSPAIT	8154
1TIL	AB	TRANSCRIPTION	B	1.7	3.3	2	11	PAVKRLFDMSG	8155
1TX4	AB	COMPLEX (GTPASE ACTIVATN/PROTO-ONCOGENE)	B	1.7	3.3	2	9	DRLRPLSYP	8156
1UHL	AB	DNA BINDING PROTEIN	A	1.7	3.3	2	17	PSEVEVLREKVYASLET	8157
1UJW	AB	TRANSPORT PROTEIN/HYDROLASE	B	1.7	3.3	2	32	GHRMWQMAGLKAQRAQTDVNNKQAAFDAAAKE	8158
1USP	AB	OXIDOREDUCTASE	B	3.3	3.3	1	6	PYSAAT	8159
1UZD	KP	LYASE	K	1.1	3.3	3	21	NAPGAAANRVALEACTQARNE	8160
1UZD	VC	LYASE	V	1.7	3.3	2	14	AKNYGRAVYECLRG	8161
1V54	CJ	OXIDOREDUCTASE	C	1.7	3.3	2	23	PWPLTGALSALLMTSGLTMWFHF	8162
1V54	DE	OXIDOREDUCTASE	D	3.3	3.3	1	5	FAEMN	8163
1V54	NO	OXIDOREDUCTASE	N	3.3	3.3	1	37	DQIYNVVVTAHAFVMIFFMVMPIMIGGFGNWLVPLMI	8164
1VF6	AC	PROTEIN BINDING/PROTEIN TRANSPORT	A	3.3	3.3	1	13	NEKLSMFYETLKS	8165
1VF6	AC	PROTEIN BINDING/PROTEIN TRANSPORT	C	1.7	3.3	2	15	PDVEDLFSSLKHIQH	8166
1VRQ	BD	OXIDOREDUCTASE	B	1.7	3.3	2	9	SSVLAELAG	8167
1VZJ	AI	HYDROLASE	A	3.3	3.3	1	5	HWKNQ	8168
1W2W	AB	ISOMERASE	A	1.7	3.3	2	16	VNLSNSLVEIKNILKS	8169
1W2W	MN	ISOMERASE	M	1.7	3.3	2	16	VNLSNSLVEIKNILKS	8170
1WDD	AS	LYASE	S	1.1	3.3	3	14	VEDLLKQIEYLLRS	8171

1WYU	AB	OXIDOREDUCTASE	B	1.7	3.3	2	5	IFERS	8172
1WYU	CD	OXIDOREDUCTASE	C	1.7	3.3	2	15	EWKVLEELRRLAAQN	8173
1WYU	GF	OXIDOREDUCTASE	G	1.7	3.3	2	11	EEEIREMLRRV	8174
1XD2	AC	SIGNALING PROTEIN	A	1.1	3.3	3	11	SAMRDQYMRTG	8175
1XFV	CQ	LYASE/METAL BINDING PROTEIN	Q	1.7	3.3	2	11	AAELRHVMTNL	8176
1XLS	AE	TRANSCRIPTION	E	1.7	3.3	2	25	LYAKLMGLLADLRSINNAYSYELQR	8177
1Y14	CD	TRANSFERASE	C	3.3	3.3	1	13	KDLKNTMQYLTNF	8178
1Y56	AB	OXIDOREDUCTASE	A	1.7	3.3	2	8	LQIIKRLT	8179
1Y8H	AB	OXYGEN STORAGE/TRANSPORT	B	1.7	3.3	2	15	EEVGGEALGRLLVVY	8180
1YA7	DJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.1	3.3	3	23	VGDAQVLVRYMKAELELYRLQRR	8181
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	1.7	3.3	2	25	GATVCVLGLLLGEWINRYFNFWGWT	8182
1Z6O	JS	METAL BINDING PROTEIN	J	1.7	3.3	2	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	8183
1Z6O	KN	METAL BINDING PROTEIN	K	1.7	3.3	2	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	8184
1ZM2	CD	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	C	3.3	3.3	1	14	KDSVVAAFQWATKE	8185
1ZOY	CD	OXIDOREDUCTASE	C	1.7	3.3	2	30	LPMAMSICHRGTGIALSAGVSLFGLSALLL	8186
1ZRT	QR	OXIDOREDUCTASE/METAL TRANSPORT	Q	1.7	3.3	2	30	LVARKQMGLVAMVMLGLLSVMLYLTNKRLW	8187
2A45	GH	BLOOD CLOTTING	G	1.7	3.3	2	25	GCRMKGLIDEVNQDFTNRINKLKNS	8188
2AHM	AH	VIRAL PROTEIN, REPLICATION	H	1.7	3.3	2	68	EVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMADQAMTQMYKQARS EDKRAKVTSAMQTMLFTMLRKLD	8189
2AXT	BD	ELECTRON TRANSPORT	B	1.1	3.3	3	12	FFGHIWHGARTL	8190
2AXT	EF	ELECTRON TRANSPORT	F	1.7	3.3	2	24	VRWVAVHTLAVPTIFFLGAIAAMQ	8191
2BBM	AB	CALCIUM-BINDING PROTEIN	A	1.7	3.3	2	9	YEEFVTMMT	8192
2BGN	CG	HYDROLASE	G	1.7	3.3	2	19	PDEVVSLVNQGLQEGERDF	8193
2BR2	QR	HYDROLASE	R	1.7	3.3	2	28	PDEFRQAFDLAVKGINIIYNLEREALKS	8194
2BSK	EB	PROTEIN TRANSPORT	B	1.7	3.3	2	20	KGESVCLDRCVSKYLDIHER	8195
2C4F	TU	HYDROLASE	U	1.7	3.3	2	5	PYLET	8196
2C52	AB	TRANSFERASE	A	1.1	3.3	3	13	PQLMAAFIKQRTA	8197
2CCL	AB	CELL ADHESION	B	3.3	3.3	1	12	STDLTMLKRSVL	8198
2D0V	DE	OXIDOREDUCTASE	E	1.7	3.3	2	5	PKELN	8199
2DBU	CD	TRANSFERASE	D	1.7	3.3	2	7	IITTVLQ	8200
2DD4	KL	HYDROLASE	L	3.3	3.3	1	6	RDCLIG	8201
2DE5	AD	OXIDOREDUCTASE	A	3.3	3.3	1	7	EAILKRV	8202
2DS2	AB	PLANT PROTEIN	B	1.7	3.3	2	16	VCPVLRQAAQQVLQRQ	8203
2DXB	DE	HYDROLASE	E	3.3	3.3	1	9	AEERRRKQN	8204
2E9X	FG	REPLICATION	F	1.7	3.3	2	29	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	8205
2ESV	DE	IMMUNE SYSTEM	E	1.7	3.3	2	8	EAEISHTQ	8206
2F54	FL	IMMUNE SYSTEM	F	1.7	3.3	2	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	8207

2F8N	FH	STRUCTURAL PROTEIN/DNA	F	3.3	3.3	1	27	IYEETRGVLKVFLENVIRDAVTYTEHA	8208
2FHH	QZ	HYDROLASE	Q	3.3	3.3	1	18	RQLANVYAQTLGTIFTEQ	8209
2FK0	EB	VIRAL PROTEIN	E	1.7	3.3	2	8	YEELKHLL	8210
2FK0	KH	VIRAL PROTEIN	K	1.7	3.3	2	8	YEELKHLL	8211
2FKW	EF	MEMBRANE PROTEIN, PHOTOSYNTHESIS	F	1.7	3.3	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	8212
2G9H	BD	IMMUNE SYSTEM	B	1.7	3.3	2	22	KDLLEQRRAAVDTYCRHNYGVG	8213
2GO5	12	TRANSLATION/RNA	1	1.7	3.3	2	6	ALSLLN	8214
2GTL	EK	OXYGEN STORAGE/TRANSPORT	K	1.7	3.3	2	15	EEDHRIVQKQWDILW	8215
2GUZ	AP	CHAPERONE, PROTEIN TRANSPORT	P	1.1	3.3	3	15	MDKINNRFNYLFEVN	8216
2GV5	AC	CELL CYCLE	A	1.7	3.3	2	13	PLDEIKRAFQLFD	8217
2GV5	BC	CELL CYCLE	B	1.1	3.3	3	14	EEQKQEIYEAFSLF	8218
2GWF	CD	HYDROLASE/LIGASE	D	1.7	3.3	2	7	LETRQMN	8219
2H4C	EF	HYDROLASE	F	1.7	3.3	2	12	LFQFARLIDAKQ	8220
2H4M	AC	PROTEIN TRANSPORT	A	1.7	3.3	2	19	KRVQEAACSAFATLEEEAC	8221
2HLD	KO	HYDROLASE	K	1.7	3.3	2	12	VFYLHSRLLERA	8222
2HOD	JK	BLOOD CLOTTING	K	1.7	3.3	2	13	LRVLRSILENLRS	8223
2HQW	AB	METAL BINDING PROTEIN	A	1.7	3.3	2	12	DEEVDEMIREAD	8224
2HWZ	LH	IMMUNE SYSTEM	L	1.7	3.3	2	6	DEQLKS	8225
2HYB	MO	TRANSFERASE	M	3.3	3.3	1	17	QASDSAYQFAKAALEKG	8226
2HYB	PR	TRANSFERASE	P	3.3	3.3	1	16	QASDSAYQFAKAALEK	8227
2HYI	GI	HYDROLASE/RNA BINDING PROTEIN/RNA	I	3.3	3.3	1	9	RELYIHRIG	8228
2I2X	CD	TRANSFERASE	C	3.3	3.3	1	12	DKVLRDLMMLSD	8229
2ICW	EF	IMMUNE SYSTEM	E	3.3	3.3	1	9	RPDAEYWNS	8230
2INN	BD	OXIDOREDUCTASE	B	3.3	3.3	1	32	ARYVNALKLFISGISPLEHAAFQGYSKVGRQF	8231
2J03	FP	RIBOSOME	F	3.3	3.3	1	12	PHLLWEVVRWQL	8232
2J0Q	BD	HYDROLASE	D	1.7	3.3	2	12	YKEAQAAMEGLN	8233
2JBY	AB	APOPTOSIS	A	1.7	3.3	2	11	AKNYDTLYDIM	8234
2JDQ	BD	PROTEIN TRANSPORT	B	3.3	3.3	1	16	EDVQEQAVWALGNIAG	8235
2JIY	LM	PHOTOSYNTHESIS	M	1.7	3.3	2	28	GLWLIASFFMFVAVWSWWGRTYLRAQAL	8236
2JIZ	IL	HYDROLASE	I	1.7	3.3	2	14	RSTVAQLVKRLTDA	8237
2JKR	AB	ENDOCYTOSIS	A	1.7	3.3	2	17	VELQQRAVEYLRLSTVA	8238
2JZB	AB	TRANSFERASE/TRANSCRIPTION	A	1.7	3.3	2	14	KKSLTEIKDVLASR	8239
2K8F	AB	TRANSFERASE/TRANSCRIPTION	A	1.7	3.3	2	16	PSCQKMKRVVQHTKGC	8240
2KBR	AB	STRUCTURAL PROTEIN/CELL ADHESION	A	1.7	3.3	2	16	RKVAREFRHKVDFLIE	8241
2KBR	AB	STRUCTURAL PROTEIN/CELL ADHESION	B	1.7	3.3	2	14	RYLREAIQEYDNIA	8242
2NOJ	EF	IMMUNE SYSTEM	F	1.7	3.3	2	14	VATHRKAQRAVNLI	8243

2NVU	CJ	PROTEIN TURNOVER, LIGASE	C	1.7	3.3	2	14	INSIIYGLQYLFLE	8244
2NZ0	CD	MEMBRANE PROTEIN	C	1.7	3.3	2	11	EKLRWTFNLYD	8245
2NZD	BD	STRUCTURAL PROTEIN/DNA	B	1.7	3.3	2	11	AMDVVYALKRQ	8246
2O8F	AB	DNA BINDING PROTEIN/DNA	B	1.7	3.3	2	13	TFFVELSETASIL	8247
2O9I	AC	TRANSCRIPTION	A	1.7	3.3	2	7	PLMQELF	8248
2OTJ	FM	RIBOSOME	F	1.7	3.3	2	13	EEIVMHIPELADE	8249
2OZA	AB	SIGNALING PROTEIN/TRANSFERASE	A	1.1	3.3	3	19	KERWEDVKEEMTSALATMR	8250
2P7V	AB	TRANSCRIPTION	B	1.7	3.3	2	15	RERIRQIEAKALRKL	8251
2QI9	AC	MEMBRANE PROTEIN	A	3.3	3.3	1	7	EISARQL	8252
2QQD	DE	LYASE	D	3.3	3.3	1	13	PLNAFDGALLNAG	8253
2QRV	HG	TRANSFERASE/TRANSFERASE REGULATOR	H	1.7	3.3	2	11	VSDKRDISRFL	8254
2RHK	BD	VIRAL PROTEIN/NUCLEAR PROTEIN	B	3.3	3.3	1	18	IEDVKNAIGVLIGGLEWN	8255
2RIV	AB	SIGNALING PROTEIN	A	1.7	3.3	2	22	YKMSSINADFAFNLYRRFTVET	8256
2ROD	AB	APOPTOSIS	A	1.7	3.3	2	21	WGRIVTLISFGAFVAKHLKSV	8257
2SEB	AB	COMPLEX (MHC CLASS II/SUPERANTIGEN)	A	1.7	3.3	2	22	AQGALANIAVDKANLEIMTKRS	8258
2UUN	MN	ELECTRON TRANSPORT	N	1.7	3.3	2	13	VAQIDALSQMVAE	8259
2UUN	ST	ELECTRON TRANSPORT	T	1.7	3.3	2	12	AFTKVAAQADTR	8260
2V7Q	AD	HYDROLASE	D	1.1	3.3	3	28	SEHYDVARGVQKILQDYKSLQDIIAILG	8261
2VLH	AB	LYASE	B	1.7	3.3	2	16	DEMFSSAKELVVVYEG	8262
2VOY	CD	HYDROLASE	C	3.3	3.3	1	12	PVIGLDEILKFI	8263
2VRC	CD	OXIDOREDUCTASE	D	1.7	3.3	2	19	NTLLIVQHANVVKAARDAG	8264
2WBE	AB	STRUCTURAL PROTEIN	A	3.3	3.3	1	10	PTVIDEVRTG	8265
2WME	HE	OXIDOREDUCTASE	H	3.3	3.3	1	18	AMQRSRILRRAVDILRER	8266
2Z2S	GH	TRANSCRIPTION	G	1.7	3.3	2	11	ASQAEECAQDV	8267
2Z2Y	CD	HYDROLASE	C	1.7	3.3	2	12	YLYDMIIQAYNA	8268
2ZCY	GN	HYDROLASE	N	1.7	3.3	2	22	AADTQAIADIVQYHLELYTSQY	8269
2ZT9	BH	PHOTOSYNTHESIS	B	1.7	3.3	2	26	PNDLLYVFPIVIMGSFACIVALAVLD	8270
2ZU6	AB	HYDROLASE	A	3.3	3.3	1	9	PGRVFDMLN	8271
2ZXX	AC	CELL CYCLE/REPLICATION	A	1.7	3.3	2	44	YWKEVAEQRRKALYEALKENEKLHKEIEQKDSEIARLRKENKDL	8272
2ZXX	EF	CELL CYCLE/REPLICATION	E	3.3	3.3	1	55	SQYWKEVAEQRRKALYEALKENEKLHKEIEQKDSEIARLRKENKDLAE VAEHVQY	8273
3A0B	AD	ELECTRON TRANSPORT	A	1.7	3.3	2	15	ISGTFNFMIVFQAEH	8274
3A1G	CD	TRANSFERASE	C	1.7	3.3	2	11	ICSTIEELRRQ	8275
3B9J	IK	OXIDOREDUCTASE	I	3.3	3.3	1	17	FCTPGIVMSMYTLLRNQ	8276
3BL2	BD	VIRAL PROTEIN/APOPTOSIS	B	1.7	3.3	2	13	WKRDLSKLFTSLF	8277
3BLW	AB	OXIDOREDUCTASE	B	1.1	3.3	3	17	RLADGLFVNVAKELSKE	8278
3BLW	IJ	OXIDOREDUCTASE	J	1.7	3.3	2	11	IDNSVLKVVTN	8279

3BPN	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.7	3.3	2	26	AQQFHRHKQLIRFLKRLDRNLWGLAG	8280
3BUA	AE	DNA BINDING PROTEIN	A	1.7	3.3	2	17	YGDFRQIRDIMQALLVR	8281
3BZ1	DF	ELECTRON TRANSPORT	D	1.7	3.3	2	24	WSGILLFPCAYLALGGWLTGTTFV	8282
3C01	CG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	3.3	3.3	1	9	EQVKSDIEN	8283
3C4M	AC	MEMBRANE PROTEIN	A	1.7	3.3	2	21	KEEQIFLLHRAQAQCEKRLKE	8284
3C5W	AC	HYDROLASE	A	1.7	3.3	2	19	WRVRLAIIEYMPLLAGQLG	8285
3C5W	AC	HYDROLASE	A	1.7	3.3	2	17	YLHRMTTLFCINVLSEV	8286
3CDG	AJ	IMMUNE SYSTEM	A	1.7	3.3	2	29	SEYWDRETRSARDTAQIFRVNLRTLRGYY	8287
3CXH	NR	OXIDOREDUCTASE	R	1.7	3.3	2	14	FTSIARIGDYILKS	8288
3D5D	X2	RIBOSOME	2	1.7	3.3	2	25	PVELEKLVREKKRELMELRFQASIG	8289
3DBH	AB	CELL CYCLE	A	1.7	3.3	2	11	DDYVHEFCRYG	8290
3DWL	AD	STRUCTURAL PROTEIN	A	3.3	3.3	1	16	DHMERFWQQSLFKYLR	8291
3E0J	CD	TRANSFERASE	D	1.7	3.3	2	14	GPLFNTDYDILKSN	8292
3EDQ	BD	HYDROLASE	D	1.7	3.3	2	15	FMHILTRVNRKVATE	8293
3EI4	EF	DNA BINDING PROTEIN	F	1.1	3.3	3	11	IVRTLHQHKLG	8294
3EXG	34	OXIDOREDUCTASE	3	1.7	3.3	2	13	GQIFEAYNMAALW	8295
3EXH	AD	OXIDOREDUCTASE	D	1.7	3.3	2	6	KILEDN	8296
3EXH	AG	OXIDOREDUCTASE	G	1.7	3.3	2	11	REEIQEVRSKS	8297
3F1F	NU	RIBOSOME	U	1.7	3.3	2	42	FRKARETLFAAGNYAYAHRKRRKRDFRRLWIVRINAACRQHG	8298
3F9K	JK	VIRAL PROTEIN, RECOMBINATION	J	1.7	3.3	2	11	QEVKMVAWWIG	8299
3F9K	Ya	VIRAL PROTEIN, RECOMBINATION	Y	1.7	3.3	2	12	IEPAQEEHEKYH	8300
3FFD	AP	IMMUNE SYSTEM/HORMONE	P	1.7	3.3	2	16	IQDLRRRFFLHHLIAE	8301
3FWC	IJ	CELL CYCLE, TRANSCRIPTION	I	1.7	3.3	2	13	PLDEIKRAFQLFD	8302
3GE8	AB	OXIDOREDUCTASE	A	3.3	3.3	1	5	YELTR	8303
3GHG	DF	BLOOD CLOTTING	D	1.7	3.3	2	17	GCRMKGLIDEVNQDFTN	8304
3H6P	BD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.7	3.3	2	63	HTAFAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVA AAAKVNTLLDIAQANLG	8305
3H87	BC	TOXIN/ANTITOXIN	B	1.7	3.3	2	6	KSALVR	8306
3HKZ	IU	TRANSFERASE	U	1.7	3.3	2	16	RYEIARVISARALQLA	8307
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.1	3.3	3	13	YAAKLLFQELMAM	8308
3HPG	FK	TRANSFERASE	F	1.7	3.3	2	10	ESTQLLMKYL	8309
1A0H	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.1	3.2	3	9	KKWIQKVID	8310
1A0H	DE	COMPLEX (SERINE PROTEASE/INHIBITOR)	E	1.6	3.2	2	9	KKWIQKVID	8311
1AKH	AB	DNA BINDING PROTEIN/DNA	B	1.6	3.2	2	9	PELADLLSG	8312
1AOI	AG	DNA BINDING PROTEIN/DNA	A	1.1	3.2	3	13	TVALREIRRYQKS	8313
1B35	AC	VIRUS	A	1.6	3.2	2	7	QFDYYYY	8314

1B4U	CD	DIOXYGENASE	C	1.6	3.2	2	10	QEEYAQMMID	8315
1BCC	DJ	OXIDOREDUCTASE	J	1.6	3.2	2	23	IVVGALLFERAFDQGADAIYEHI	8316
1BCP	BF	TOXIN	B	1.6	3.2	2	13	YSRLRKMLYLIYV	8317
1BGX	TL	COMPLEX (POLYMERASE/INHIBITOR)	T	1.6	3.2	2	8	RDQLERVL	8318
1BIQ	AB	OXIDOREDUCTASE	A	1.6	3.2	2	11	PSVVFDDIVTN	8319
1CF4	AB	TRANSFERASE	A	3.2	3.2	1	13	KNVFDEAILAALE	8320
1CP9	AB	HYDROLASE	A	1.6	3.2	2	6	KQFIDY	8321
1E1C	CD	ISOMERASE	D	1.6	3.2	2	5	LAGDF	8322
1E6V	AC	OXIDOREDUCTASE	A	3.2	3.2	1	7	PAAMETH	8323
1ED3	AC	IMMUNE SYSTEM	A	1.6	3.2	2	13	FAAQITRNKWERA	8324
1EJH	BF	TRANSLATION	F	1.6	3.2	2	7	REFLLDF	8325
1F3M	AC	TRANSFERASE	A	3.2	3.2	1	16	PQAVLDVLEFYNSKKT	8326
1FCD	AC	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	C	1.6	3.2	2	13	TPYLQYAMSDFRE	8327
1FDH	BH	OXYGEN TRANSPORT	B	3.2	3.2	1	16	AGEYGAEALERMFLSF	8328
1FM6	UX	TRANSCRIPTION	U	1.6	3.2	2	7	RFAKLLL	8329
1FOE	EF	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	F	1.6	3.2	2	5	DRLRP	8330
1FQV	EF	LIGASE	F	3.2	3.2	1	10	EEEEAQVRKE	8331
1FYZ	AC	OXIDOREDUCTASE	A	3.2	3.2	1	8	ARRTRTIG	8332
1G0U	BJ	HYDROLASE	B	3.2	3.2	1	23	TADAEILINTARIHAQNYLKTYN	8333
1G0U	OU	HYDROLASE	O	3.2	3.2	1	13	GQIDYALTAVKQG	8334
1G0U	RS	HYDROLASE	S	3.2	3.2	1	12	FQVEYALEAIKQ	8335
1G0U	ST	HYDROLASE	S	3.2	3.2	1	15	VERAGHLLCDKAQKN	8336
1G20	AB	OXIDOREDUCTASE	A	1.6	3.2	2	16	KPEWEAVVAKYRPRLE	8337
1GCV	CD	OXYGEN STORAGE/TRANSPORT	D	1.6	3.2	2	17	SFHLLTDCIIVELAYLR	8338
1GH0	KL	PHOTOSYNTHESIS	K	1.6	3.2	2	12	PLTEAVSVADSQ	8339
1GLA	FG	PHOSPHOTRANSFERASE	G	1.6	3.2	2	16	RNYRYAGWKKAVKRAM	8340
1HBH	CD	OXYGEN CARRIER	C	1.6	3.2	2	16	ADAIGNDALSRMIVVY	8341
1HBR	CD	OXYGEN STORAGE/TRANSPORT	C	3.2	3.2	1	16	QEEFGAEALTRMFTTY	8342
1HE1	BD	SIGNALING PROTEIN	B	1.6	3.2	2	24	SAVVFKQMVLQQALPMTLKGLDKA	8343
1HR8	CD	HYDROLASE	D	3.2	3.2	1	19	DAEVNRAKAQLKAALLLSL	8344
1HR8	GH	HYDROLASE	H	3.2	3.2	1	19	DAEVNRAKAQLKAALLLSL	8345
1HV4	CD	OXYGEN STORAGE/TRANSPORT	D	1.6	3.2	2	19	PENFRLLGDILIIVLAAHF	8346
1HV4	GF	OXYGEN STORAGE/TRANSPORT	F	3.2	3.2	1	6	PWTQRF	8347
1I3O	CD	APOPTOSIS	C	1.6	3.2	2	15	TDVDAANLRETFRNL	8348
1I4D	AD	SIGNALING PROTEIN	A	1.6	3.2	2	50	ELELQIELLRETKRKYESVLQLGRALTAHLYSLLQTQHALGDAFADLSQK	8349
1IR2	X7	LYASE	X	1.6	3.2	2	14	AKNYGRAVYECLRG	8350
1IRU	AG	HYDROLASE	A	1.6	3.2	2	23	TADSRSQVQRARYEAANWKYKYG	8351

1IRU	J1	HYDROLASE	1	1.1	3.2	3	11	MLQPLLDNQVG	8352
1IRU	ST	HYDROLASE	T	3.2	3.2	1	13	HQIEYAMEAVKQG	8353
1IRU	V2	HYDROLASE	2	1.6	3.2	2	22	YADFQYLKQVLGQMVIDEELLG	8354
1IYJ	CD	GENE REGULATION/ANTITUMOR PROTEIN	C	1.6	3.2	2	5	AELEK	8355
1JD2	BI	HYDROLASE	B	1.6	3.2	2	22	TADAEILINTARIHAQNYLKTY	8356
1JEB	CD	OXYGEN STORAGE/TRANSPORT	D	1.6	3.2	2	20	PENFRLLGNMIVIVLGHHLG	8357
1JRO	AB	OXIDOREDUCTASE	A	1.6	3.2	2	20	AAYRMNAAQAMALRYVRELS	8358
1JRO	EF	OXIDOREDUCTASE	E	1.6	3.2	2	8	LLELLRAE	8359
1K7L	GH	TRANSCRIPTION	H	1.6	3.2	2	10	KILHRLLQEG	8360
1KEN	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.6	3.2	2	21	IQDLEKYVEDTKIDLWSYNAE	8361
1KF6	BD	OXIDOREDUCTASE	B	1.6	3.2	2	21	PAAAIQQGKVESSKDFLIATL	8362
1KF6	OP	OXIDOREDUCTASE	O	1.6	3.2	2	12	PEAWAGFVDFLQ	8363
1KI1	CD	SIGNALING PROTEIN	D	3.2	3.2	1	37	PTERKRQGYIHELIVTEENYVNDLQLVTEIFQKPLME	8364
1KKL	BJ	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN	B	1.6	3.2	2	14	ATKTFEKNLNHLIE	8365
1KUP	AB	CELL ADHESION	B	3.2	3.2	1	7	LITIHDR	8366
1KYO	CG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	1.6	3.2	2	20	EDESYARAYRIIRAHQTELT	8367
1KYO	MG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	1.6	3.2	2	21	YLLPYILEAEAAAKEKDELDN	8368
1L2W	CJ	CHAPERONE	J	1.6	3.2	2	10	HSVIGFIQRM	8369
1LO5	AB	IMMUNE SYSTEM/TOXIN	A	1.6	3.2	2	5	EEFGR	8370
1MMO	BD	OXIDOREDUCTASE (MONOOXYGENASE)	D	3.2	3.2	1	6	SDGFIS	8371
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	H	1.6	3.2	2	23	DNDYLWIEAKLEEKVAVLKARAF	8372
1MTY	DB	MONOOXYGENASE	B	1.6	3.2	2	7	EYEALTV	8373
1MTY	DB	MONOOXYGENASE	D	3.2	3.2	1	5	SDGFI	8374
1MXE	AE	METAL BINDING PROTEIN	A	1.6	3.2	2	10	YEEFVTMMTS	8375
1MXE	BF	METAL BINDING PROTEIN	B	1.6	3.2	2	12	EAELQDMINEVD	8376
1N4Q	AB	TRANSFERASE	A	1.6	3.2	2	14	YTVWHFRRVLLRSL	8377
1N4Q	AB	TRANSFERASE	A	1.6	3.2	2	16	EKFRDVYDYFRAVLQR	8378
1N4Q	CD	TRANSFERASE	D	3.2	3.2	1	11	KDDIIEWIYSL	8379
1N4Q	GH	TRANSFERASE	H	3.2	3.2	1	15	RLTIAFFALSGLDML	8380
1N4Q	IJ	TRANSFERASE	I	1.1	3.2	3	13	NSVWNQRHFVISN	8381
1N5W	AB	OXIDOREDUCTASE	B	1.6	3.2	2	22	PMIIEGQVHGGLTEAFAVAMGQ	8382
1N5W	DE	OXIDOREDUCTASE	E	1.6	3.2	2	22	PMIIEGQVHGGLTEAFAVAMGQ	8383
1N86	DE	BLOOD CLOTTING	D	3.2	3.2	1	9	LLQKNVRAQ	8384
1NVM	EF	LYASE/OXIDOREDUCTASE	F	3.2	3.2	1	6	PGTRAN	8385

1O96	QZ	ELECTRON TRANSFER	Z	1.6	3.2	2	14	VDSLGYASSLASKT	8386
1OVL	AB	TRANSCRIPTION	A	1.6	3.2	2	12	LISALVRAHVDS	8387
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.6	3.2	2	14	ALSIHRLGLFLASN	8388
1Q16	AB	OXIDOREDUCTASE	B	3.2	3.2	1	5	YEDRF	8389
1Q86	HN	RIBOSOME	H	1.1	3.2	3	11	TNETTKSIERG	8390
1Q90	AN	PHOTOSYNTHESIS	N	1.6	3.2	2	25	AIVQIGWAATCVMFSFSLSLVVWGR	8391
1R6O	BD	HYDROLASE	B	3.2	3.2	1	9	QAAYLLRKH	8392
1RP3	EF	TRANSCRIPTION	F	1.6	3.2	2	12	KVTLSKIAQELS	8393
1RP3	EF	TRANSCRIPTION	F	1.6	3.2	2	13	IELSRLIGLLLET	8394
1RSO	CD	NEUROPEPTIDE/MEMBRANE PROTEIN	C	1.6	3.2	2	12	NLFQALIDIQEF	8395
1RYP	IJ	MULTICATALYTIC PROTEINASE	I	3.2	3.2	1	22	AADTEAVTQLIGSNIELHSLYT	8396
1RYP	OW	MULTICATALYTIC PROTEINASE	W	1.6	3.2	2	22	AADTEAVTQLIGSNIELHSLYT	8397
1RYP	RS	MULTICATALYTIC PROTEINASE	S	3.2	3.2	1	11	FQVEYSLEAIK	8398
1RYP	RY	MULTICATALYTIC PROTEINASE	R	1.6	3.2	2	23	NADSRILIEKARVEAQSHRLTLE	8399
1RYP	T1	MULTICATALYTIC PROTEINASE	1	1.6	3.2	2	22	AADGDALVKRFKNSVKWYHFDH	8400
1RZO	AB	HYDROLASE	A	3.2	3.2	1	13	QYIEGEMRTRIRY	8401
1SB3	DE	OXIDOREDUCTASE	E	1.6	3.2	2	21	VKYRRRVLLAISRKVVDQLWE	8402
1SVF	AB	VIRAL PROTEIN	A	1.6	3.2	2	61	AAVALVKANENAAAILNLKNAIQKTNAAVADVVQATQSLGTAVQAV QDHINSVVSPAITAA	8403
1SXJ	CD	REPLICATION	D	3.2	3.2	1	11	ADAQSALRRTM	8404
1T0Q	AB	OXIDOREDUCTASE	B	1.6	3.2	2	10	KRERDVWEND	8405
1T3Q	DE	OXIDOREDUCTASE	E	3.2	3.2	1	8	REDTRLLT	8406
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.6	3.2	2	16	EGVATYAAAVLFRMSE	8407
1TQY	AB	TRANSFERASE	B	1.6	3.2	2	12	YAVNTGQISIRH	8408
1TQY	CD	TRANSFERASE	D	3.2	3.2	1	11	PWGWVSQIASG	8409
1U35	EF	STRUCTURAL PROTEIN/DNA	E	1.6	3.2	2	13	TVALREIRRYQKS	8410
1U3H	GH	IMMUNE SYSTEM	G	3.2	3.2	1	7	PEFAQLR	8411
1ULI	CD	OXIDOREDUCTASE	D	1.6	3.2	2	11	AQMMRGRLRKI	8412
1UM9	AB	OXIDOREDUCTASE	B	1.6	3.2	2	10	FDQLVSQVAK	8413
1UZH	KP	LYASE	P	3.2	3.2	1	14	DEQIAAQVDYIVAN	8414
1V54	NG	OXIDOREDUCTASE	N	1.6	3.2	2	16	YMGMVWAMMSIGFLGF	8415
1V54	OV	OXIDOREDUCTASE	V	3.2	3.2	1	12	SMKDFEEMRKAG	8416
1VZJ	AI	HYDROLASE	A	3.2	3.2	1	13	RQWKAEFHRWSSY	8417
1W5C	DE	PHOTOSYNTHESIS	D	1.6	3.2	2	8	FTRWCQLG	8418
1WYU	EF	OXIDOREDUCTASE	E	1.6	3.2	2	11	EEEIREMLRRV	8419
1XCG	EF	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	E	1.6	3.2	2	19	SEMQRLTKYPLLLESIIKH	8420
1XD2	AC	SIGNALING PROTEIN	C	3.2	3.2	1	28	AELKRFRKEYIQPVQLRVLNVCRHWVEH	8421
1XFU	CQ	LYASE/METAL BINDING PROTEIN	C	1.6	3.2	2	23	EKKRKISIFRGIQAYNEIENVLK	8422

1XFU	ES	LYASE/METAL BINDING PROTEIN	E	1.6	3.2	2	13	SAEFIKNLSSIRR	8423
1XKM	CD	ANTIBIOTIC	C	1.6	3.2	2	14	PGFTALIKTLRKCK	8424
1XM4	AB	HYDROLASE	B	1.6	3.2	2	18	KKQRQTLRKMVIDMVLAT	8425
1XTG	AB	TOXIN	A	1.1	3.2	3	15	KLKFDKLYKMLTEIY	8426
1XXH	FJ	TRANSFERASE	J	1.6	3.2	2	17	RELLITDLLLRIEHYLQ	8427
1Y3A	CG	SIGNALING PROTEIN	C	3.2	3.2	1	8	RKKWIHCF	8428
1YA7	EL	HYDROLASE/HYDROLASE ACTIVATOR	E	3.2	3.2	1	23	VADARVLVDFARISAQQEKVTYG	8429
1YE9	AF	OXIDOREDUCTASE	A	3.2	3.2	1	9	DTFWDYVSL	8430
1YE9	AG	OXIDOREDUCTASE	A	1.6	3.2	2	12	FILREKITHFDH	8431
1YE9	JO	OXIDOREDUCTASE	O	1.6	3.2	2	19	PLLQGRLFSYTDTQISRLG	8432
1YE9	KN	OXIDOREDUCTASE	N	3.2	3.2	1	13	FHRRELWEAIEAG	8433
1YOV	AB	SIGNALING PROTEIN	B	1.6	3.2	2	9	YRLTQGVVK	8434
1YOV	CD	SIGNALING PROTEIN	D	1.6	3.2	2	13	KAEVAAEFLNDRV	8435
1YQ3	AB	OXIDOREDUCTASE	A	1.6	3.2	2	15	TGHSLLHTLYGRSLR	8436
1YRT	AB	LAYSE, TOXIN	B	1.6	3.2	2	12	EEEIREAFRVFD	8437
1Z2C	AB	SIGNALING PROTEIN	A	1.6	3.2	2	13	IPEKWTPEVKHFC	8438
1Z6O	EP	METAL BINDING PROTEIN	E	1.6	3.2	2	16	LSLALYVFDEYLQKTV	8439
1Z7Z	34	VIRUS/RECEPTOR	3	1.6	3.2	2	5	KRLSH	8440
1ZNV	AB	HYDROLASE/PROTEIN BINDING	B	3.2	3.2	1	9	RNNNDRMKV	8441
1ZV8	ED	VIRAL PROTEIN	D	1.6	3.2	2	17	QKEIDRLNEVAKNLNES	8442
2A78	AB	PROTEIN BINDING/TRANSFERASE	B	1.6	3.2	2	16	SNLIKQVELLDKSFNK	8443
2ACL	AB	TRANSCRIPTION	A	1.6	3.2	2	23	PAEVEALREKVYASLEAYCKHKY	8444
2ACL	GH	TRANSCRIPTION	H	1.6	3.2	2	10	REDQIALLKT	8445
2AFH	AD	OXIDOREDUCTASE	D	1.6	3.2	2	5	HTWLH	8446
2AK4	KM	IMMUNE SYSTEM	K	3.2	3.2	1	13	TAAQITQRKWEAA	8447
2B5L	BD	PROTEIN BINDING/VIRALPROTEIN	D	1.6	3.2	2	11	VEYFTSQQVTG	8448
2BA0	CF	RNA BINDING PROTEIN	F	1.6	3.2	2	30	RDEVKQAIELAKKGALQIYEMQREAILRRY	8449
2BA0	FI	RNA BINDING PROTEIN	I	1.6	3.2	2	21	EKLFDELLDVSINCARKLREK	8450
2BA1	EH	RNA BINDING PROTEIN	E	1.6	3.2	2	18	RRSIEISKVSKEAFEAVI	8451
2BR2	ST	HYDROLASE	T	1.6	3.2	2	28	PDEFRQAFDLAVKGINIIYNLEREALKS	8452
2CCI	BF	CELL CYCLE	B	1.1	3.2	3	18	NSMRAILVDWLVEVGEEY	8453
2CG9	BY	CHAPERONE	B	1.1	3.2	3	23	KIMKVIRKNIVKKLIEAFNEIAE	8454
2CKF	CD	OXIDOREDUCTASE	D	1.6	3.2	2	12	FEELKQRVERLY	8455
2D1P	AB	TRANSLATION	A	1.6	3.2	2	11	LGALAEASLTC	8456
2D74	AB	TRANSLATION	B	3.2	3.2	1	14	PYLIANKLKKYIKE	8457
2DBU	CD	TRANSFERASE	C	3.2	3.2	1	14	EAEKYAYADRSEYL	8458
2DD4	HI	HYDROLASE	I	3.2	3.2	1	6	RDCLIG	8459
2DFS	AF	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	A	1.6	3.2	2	83	AAITIQRYVRGHQARCYATFLRRTRAAIIIQKFQRMYVVRKRYQCMRD ATIALQALLRGYLVRNKYQMMLREHKSIIIQKHVR	8460
2DXB	ST	HYDROLASE	T	3.2	3.2	1	9	AEERRRKQN	8461

2E 74	AB	PHOTOSYNTHESIS	B	3.2	3.2	1	22	PVATTIFLFGTLVTIWLGIGAT	8462
2E9X	AF	REPLICATION	A	1.6	3.2	2	6	NALRFH	8463
2F2F	BC	TOXIN	B	1.6	3.2	2	13	NESKWNINVRQLL	8464
2F2F	EF	TOXIN	E	1.6	3.2	2	13	NESKWNINVRQLL	8465
2FHW	BA	SIGNALING PROTEIN	B	1.6	3.2	2	12	REFIRAVIFTCG	8466
2FOI	BD	OXIDOREDUCTASE	D	3.2	3.2	1	13	STDIGSVASFLLS	8467
2FUG	45	OXIDOREDUCTASE	4	3.2	3.2	1	13	PSFVNLQSLPYAC	8468
2FUG	AB	OXIDOREDUCTASE	B	1.6	3.2	2	5	LSCKL	8469
2FUG	TU	OXIDOREDUCTASE	T	1.1	3.2	3	11	PTEVMGVASFY	8470
2FYN	GH	OXIDOREDUCTASE	G	1.6	3.2	2	15	VDLAFASVEHIMRNV	8471
2G2S	AB	LUMINESCENT PROTEIN	A	1.6	3.2	2	5	VTTLG	8472
2GSI	GH	IMMUNE SYSTEM	G	1.6	3.2	2	5	SEQLT	8473
2GW4	CD	LUMINESCENT PROTEIN	C	1.6	3.2	2	6	YDILTT	8474
2GWF	EF	HYDROLASE/LIGASE	F	1.6	3.2	2	7	LETRQMN	8475
2GYK	EF	ANTIBIOTIC/ANTIBIOTIC INHIBITOR	E	3.2	3.2	1	6	SALIYY	8476
2H1O	CG	GENE REGULATION/DNA COMPLEX	C	1.6	3.2	2	18	KKKNVLHERMEQSILPLF	8477
2HGR	GH	RIBOSOME	G	3.2	3.2	1	15	DYAVRLREKQKLRRI	8478
2HLD	CF	HYDROLASE	C	1.6	3.2	2	14	RSTVAQLVQTLEQH	8479
2HOD	GH	BLOOD CLOTTING	G	3.2	3.2	1	6	DQQKQL	8480
2HZM	AB	TRANSCRIPTION	A	1.6	3.2	2	9	IDTILSSKL	8481
2I2X	IL	TRANSFERASE	L	3.2	3.2	1	6	YNVALE	8482
2I2X	KL	TRANSFERASE	K	3.2	3.2	1	12	DKVLRDLMMLSD	8483
2I2X	ON	TRANSFERASE	N	3.2	3.2	1	6	YNVALE	8484
2IAE	DE	HYDROLASE	D	3.2	3.2	1	10	WRVRYMVADK	8485
2IBZ	AC	OXIDOREDUCTASE	A	1.6	3.2	2	18	IDDLIHFTLKQWNRLTIS	8486
2ICW	AG	IMMUNE SYSTEM	G	1.6	3.2	2	27	VEQIKRNIAILDEIMAKADNDLSYFIS	8487
2IHS	BD	PEPTIDE BINDINGPROTEIN	D	1.6	3.2	2	6	VERKRE	8488
2IVF	AB	OXIDOREDUCTASE	A	1.6	3.2	2	13	VSLIRELGRKVAK	8489
2IX7	CA	CONTRACTILE PROTEIN/METAL BINDING	A	1.6	3.2	2	11	EEEIREAFRVF	8490
2IZV	AC	TRANSCRIPTION	C	1.6	3.2	2	11	ALELLMAANFL	8491
2J7A	QR	OXIDOREDUCTASE	R	1.6	3.2	2	5	RPFCT	8492
2JBY	AB	APOPTOSIS	A	1.6	3.2	2	22	PSVKLATLTLLASVIKKLNKIQ	8493
2JDQ	AE	PROTEIN TRANSPORT	A	3.2	3.2	1	16	CTLQFESAWVLTNIAS	8494
2JIZ	JM	HYDROLASE	J	3.2	3.2	1	7	TELFYKG	8495
2JKR	AB	ENDOCYTOSIS	B	1.6	3.2	2	18	TQVQLTLLTAIVKLFLKK	8496
2JKR	LI	ENDOCYTOSIS	I	3.2	3.2	1	7	ELDLVFN	8497
2KBC	BA	HORMONE	B	3.2	3.2	1	16	LEYIRTVIYICASSRW	8498
2NUU	DJ	TRANSPORT PROTEIN/SIGNALING PROTEIN	D	3.2	3.2	1	20	LLGACSGAIAGLVGVTPACG	8499

2NV2	AB	LYASE/TRANSFERASE	A	1.6	3.2	2	10	ERVKRGMAEM	8500
2NV2	GH	LYASE/TRANSFERASE	G	1.6	3.2	2	10	ERVKRGMAEM	8501
2O97	AB	DNA BINDING PROTEIN	A	1.6	3.2	2	8	KALKDAVK	8502
2P24	AB	IMMUNE SYSTEM	A	3.2	3.2	1	5	PEFAQ	8503
2P2C	CD	HYDROLASE	D	3.2	3.2	1	15	VADMLVKVNALIKDR	8504
2P2C	HS	HYDROLASE	H	3.2	3.2	1	15	VADMLVKVNALIKDR	8505
2PBI	AB	SIGNALING PROTEIN	A	3.2	3.2	1	6	QFWDLN	8506
2PL9	AD	SIGNALING PROTIEN	A	1.6	3.2	2	10	KENIIAAAQA	8507
2Q9Q	AG	REPLICATION	G	3.2	3.2	1	5	NALRF	8508
2Q9Q	CD	REPLICATION	D	1.6	3.2	2	7	LDDILMS	8509
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	A	3.2	3.2	1	18	KAVDWWALGVLIYEMAAG	8510
2QJ9	AD	CYTOKINE/RECEPTOR	D	3.2	3.2	1	7	SDFQCRD	8511
2QJY	AB	OXIDOREDUCTASE	A	1.6	3.2	2	15	VDLAFASVEHIMRNV	8512
2QJY	MN	OXIDOREDUCTASE	M	1.6	3.2	2	15	VDLAFASVEHIMRNV	8513
2QM6	AB	TRANSFERASE	A	1.6	3.2	2	15	GGTHLIQILNVMENA	8514
2QM6	CD	TRANSFERASE	D	1.6	3.2	2	11	ADVKDNLTKMG	8515
2QMU	AC	TRANSLATION	C	3.2	3.2	1	13	EKEYVEMLDRLYS	8516
2QOU	CN	RIBOSOME	C	1.6	3.2	2	20	EFADNLDSDFKVRQYLTKEL	8517
2QR1	CD	TRANSFERASE	C	1.6	3.2	2	14	FLDLCAMLVCKLFS	8518
2QVS	EB	TRANSFERASE/TRANSFERASE REGULATOR	B	1.6	3.2	2	8	VQAFERLL	8519
2RGN	AB	SIGNALING PROTEIN COMPLEX	A	3.2	3.2	1	15	RMEESKALFRTIITY	8520
2V1S	AK	OXIDOREDUCTASE	A	1.6	3.2	2	19	AVQKFFLEEIQLGEELLAQ	8521
2V36	CD	TRANSFERASE	C	1.6	3.2	2	13	KFAKTLSDTVQDF	8522
2VGL	AB	PROTEIN TRANSPORT	B	3.2	3.2	1	11	TQVQLTLLTAI	8523
2VPE	AB	GENE REGULATION	A	1.6	3.2	2	10	ETAYGLLTAE	8524
2WB1	WR	TRANSCRIPTION	W	1.6	3.2	2	12	AQDYISGAYLLT	8525
2WB1	WR	TRANSCRIPTION	W	3.2	3.2	1	11	PTELFFHAAGG	8526
2WBJ	BD	IMMUNE SYSTEM	B	3.2	3.2	1	9	RPDAEYWNS	8527
2WH1	CN	RIBOSOME	C	1.6	3.2	2	18	KQYRHLLLEDQRIRGLLE	8528
2WH1	JN	RIBOSOME	N	1.6	3.2	2	7	LRELAHK	8529
2WHP	AB	HYDROLASE	B	1.6	3.2	2	12	DLAAEAVVLHYT	8530
2WIN	EF	IMMUNE SYSTEM	F	3.2	3.2	1	5	KYELD	8531
2WIN	LN	IMMUNE SYSTEM	N	1.6	3.2	2	8	LNVNELAT	8532
2WME	BC	OXIDOREDUCTASE	B	1.6	3.2	2	18	AMQRSRILRRAVDILRER	8533
2WME	DC	OXIDOREDUCTASE	C	1.6	3.2	2	11	LARAHRAIHRL	8534
2WME	DC	OXIDOREDUCTASE	D	1.6	3.2	2	11	LARAHRAIHRL	8535
2Z2S	AB	TRANSCRIPTION	A	1.6	3.2	2	11	ASQAEECAQDV	8536
2Z5C	BC	CHAPERONE/HYDROLASE	C	1.6	3.2	2	20	ARSMIEHARTAAVTHNLYYD	8537

2Z5C	EF	CHAPERONE/HYDROLASE	F	1.6	3.2	2	20	ARSMIEHARTAAVTHNLYYD	8538
2ZYZ	CD	SPLICING	C	1.1	3.2	3	14	IQTLLSVINMGETL	8539
3A0B	AD	ELECTRON TRANSPORT	A	3.2	3.2	1	6	DIINRA	8540
3A0B	HX	ELECTRON TRANSPORT	X	3.2	3.2	1	29	PSLKGFFIGLLSGAVVLGLTFAVLIAISQ	8541
3B4V	EH	HORMONE REGULATOR COMPLEX	E	1.6	3.2	2	13	FHSTVINHYRMRG	8542
3BCQ	CD	TRANSPORT PROTEIN/OXYGEN BINDING	D	1.6	3.2	2	13	IGPQALSRLLIVY	8543
3BGF	AB	VIRAL PROTEIN/IMMUNE SYSTEM	A	3.2	3.2	1	5	RNIDA	8544
3BLW	EF	OXIDOREDUCTASE	F	1.6	3.2	2	11	IDNSVLKVVTN	8545
3BLW	GH	OXIDOREDUCTASE	H	1.6	3.2	2	16	NLYGDILSDLNSGLSA	8546
3BMC	AB	OXIDOREDUCTASE	B	3.2	3.2	1	13	AEQIADAVIFLVS	8547
3BZ1	AD	ELECTRON TRANSPORT	A	1.6	3.2	2	13	IVAAHGYFGRLIF	8548
3BZ1	BM	ELECTRON TRANSPORT	M	1.6	3.2	2	27	QLGLIATALFVLVPSVFLIILYVQTES	8549
3C01	BF	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	3.2	3.2	1	13	QRALAVRAYAEKV	8550
3C1B	GH	STRUCTURAL PROTEIN/DNA	G	1.6	3.2	2	10	VGRVHRLLRK	8551
3C4M	BD	MEMBRANE PROTEIN	B	1.6	3.2	2	24	KEEQIFLLHRAQAQCEKRLKEVLQ	8552
3C60	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	G	3.2	3.2	1	7	PEFGQLA	8553
3C6L	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	G	1.1	3.2	3	22	PQGGLQNIAVVKHNLGVLTKRS	8554
3C7B	DE	OXIDOREDUCTASE	D	3.2	3.2	1	9	IGELIWRKG	8555
3CX6	AB	SIGNALING PROTEIN	A	3.2	3.2	1	23	FRPTIYSNVIKGMRVLVDAREKL	8556
3CXH	GH	OXIDOREDUCTASE	G	1.6	3.2	2	20	EDESYARAYRIIRAHQTELT	8557
3D3C	AK	TRANSCRIPTION	A	3.2	3.2	1	12	IADVEYQFLAEQ	8558
3D48	PR	HORMONE/HORMONE RECEPTOR	P	3.2	3.2	1	6	KEQAQQ	8559
3D5A	CN	RIBOSOME	N	1.6	3.2	2	11	RICLRELAHKG	8560
3DHH	AC	OXIDOREDUCTASE	A	3.2	3.2	1	22	WDLFLKDIDELHHSYHMGVWYW	8561
3DHH	AE	OXIDOREDUCTASE	E	1.6	3.2	2	7	MQELEIN	8562
3DHR	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	3.2	3.2	1	7	PWTQRFF	8563
3DHR	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	3.2	3.2	1	7	PWTQRFF	8564
3DHR	EH	OXYGEN STORAGE, OXYGEN TRANSPORT	H	3.2	3.2	1	7	PWTQRFF	8565
3DRA	AB	TRANSFERASE	A	1.6	3.2	2	14	SFALETLAKIYTQQ	8566
3DTP	AB	CONTRACTILE PROTEIN	B	1.6	3.2	2	20	EKEMASMKEEFTRLKEALEK	8567
3DVE	AB	MEMBRANE PROTEIN	A	1.6	3.2	2	15	EEQIAEFKEAFSLFD	8568
3E 20	DC	TRANSLATION	C	3.2	3.2	1	16	VKYVQEKKLIQRFFDE	8569
3E0J	CD	TRANSFERASE	C	1.1	3.2	3	16	GESLLGTQLLVDVVTG	8570

3E3Q	BC	IMMUNE SYSTEM	B	1.6	3.2	2	24	AAEYYRAYLEGECVEWLHRYLKNG	8571
3E8C	AG	TRANSFERASE	A	3.2	3.2	1	9	MFSHLRRIG	8572
3ETR	AC	OXIDOREDUCTASE	A	3.2	3.2	1	7	LLAYLRR	8573
3EUH	AC	CELL CYCLE	A	1.6	3.2	2	12	VFAQRLRQSVQT	8574
3F3P	BD	STRUCTURAL PROTEIN	D	1.6	3.2	2	14	PEIAKEIYTTLGNQ	8575
3FFC	AD	IMMUNE SYSTEM	A	3.2	3.2	1	24	VAEQDRAYLEGTCVEWLRRYLENG	8576
3FFC	FI	IMMUNE SYSTEM	F	3.2	3.2	1	24	VAEQDRAYLEGTCVEWLRRYLENG	8577
3FKS	GH	HYDROLASE	G	1.6	3.2	2	22	VPRDLFEYTLANQMLTAMAQGY	8578
3FKS	KX	HYDROLASE	X	3.2	3.2	1	11	IEDVVAKAEKL	8579
3FLO	EF	TRANSFERASE	E	3.2	3.2	1	23	LQEASDVLDDQIESFTKIIQNHY	8580
3G5O	DC	TOXIN/ANTITOXIN	C	1.6	3.2	2	10	TTARRDLHKL	8581
3GE8	DH	OXIDOREDUCTASE	H	1.6	3.2	2	8	MQELEINL	8582
3GHG	JK	BLOOD CLOTTING	J	1.6	3.2	2	113	GCRMKGLIDEVNQDFTNRINKLKNSLFEYQKNNKDSHSLTTNIMEILRG DFSSANNRDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQL VDMKRLEVDIDIKIRS	8583
3GHG	JK	BLOOD CLOTTING	K	1.6	3.2	2	27	RVLRSILENLRSKIQKLESDVSAQMEY	8584
3GLH	AB	TRANSFERASE	A	1.6	3.2	2	15	LLALAQALERLSLLW	8585
3H0L	JL	LIGASE	J	1.6	3.2	2	13	IFEMYARTRDEGF	8586
3H0L	MO	LIGASE	M	1.6	3.2	2	13	IFEMYARTRDEGF	8587
3H0L	MO	LIGASE	O	1.6	3.2	2	11	REWVLKIAKLA	8588
3H0L	VW	LIGASE	V	1.6	3.2	2	13	IFEMYARTRDEGF	8589
3H0L	VX	LIGASE	V	3.2	3.2	1	6	PIEMYL	8590
3HAY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	3.2	3.2	1	12	SHEVVAWIKKIL	8591
3HJW	AB	ISOMERASE/RNA	A	3.2	3.2	1	12	SHEVVAWIKKIL	8592
3HNS	HL	IMMUNE SYSTEM	L	1.6	3.2	2	6	SEQLTS	8593
3HOY	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.6	3.2	2	11	EETRAELSQLC	8594
3HRD	EF	OXIDOREDUCTASE	E	1.6	3.2	2	16	LIETLEKAREKAVEVM	8595
4RUB	CU	LYASE(CARBON-CARBON)	U	1.6	3.2	2	15	QEQLLSEVEYLLKNG	8596
4RUB	CV	LYASE(CARBON-CARBON)	C	1.6	3.2	2	15	CEEMIKRAVFARELG	8597
1A6A	AB	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)	A	3.1	3.1	1	7	EEFGRFA	8598
1AOK	AB	HYDROLASE	B	3.1	3.1	1	5	SVWNY	8599
1APY	CD	HYDROLASE	C	1.6	3.1	2	13	SASQALHSDWLAR	8600
1B33	KO	PHOTOSYNTHESIS	K	1.6	3.1	2	9	LKETYNSLG	8601
1B35	AC	VIRUS	A	1.6	3.1	2	8	SPQAMCIG	8602
1B4U	CD	DIOXYGENASE	C	1.6	3.1	2	11	VYFLSKLFSTD	8603
1B8D	KL	PHOTOSYNTHESIS	K	1.6	3.1	2	27	SSDLESIQGNIQRAAARLEAAQKLSGN	8604
1BEV	13	VIRUS	1	3.1	3.1	1	10	VQLRAKMSWF	8605

1BGY	AB	ELECTRON TRANSPORT	B	1.6	3.1	2	11	SFKITRGIEAV	8606
1BGY	CD	ELECTRON TRANSPORT	C	3.1	3.1	1	29	GWIIRYMHANGASMFFICLYMHVGRGLYY	8607
1BI4	AB	DNA INTEGRATION	B	1.6	3.1	2	14	LKTAVQMAVFIHNH	8608
1BVK	DF	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)	F	1.6	3.1	2	6	VQAWIR	8609
1D3B	CD	RNA BINDING PROTEIN	C	1.6	3.1	2	9	PIKVLHEAE	8610
1DFK	AZ	CONTRACTILE PROTEIN	Z	3.1	3.1	1	11	GAELRHVLTAL	8611
1DFL	AZ	CONTRACTILE PROTEIN	Z	3.1	3.1	1	11	GAELRHVLTAL	8612
1DFL	BX	CONTRACTILE PROTEIN	X	3.1	3.1	1	11	GAELRHVLTAL	8613
1E3D	AB	HYDROGENASE	A	3.1	3.1	1	12	EAAEEALQAAVN	8614
1E6Y	DB	OXIDOREDUCTASE	B	1.6	3.1	2	10	APIVKSAVWG	8615
1EAH	13	VIRUS	1	3.1	3.1	1	5	VESFF	8616
1F2U	AB	REPLICATION	B	3.1	3.1	1	19	GGERIALGLAFRLAMSLYL	8617
1F8V	AD	VIRUS/RNA	A	1.6	3.1	2	12	PLALECYHNLKM	8618
1F99	KL	PHOTOSYNTHESIS	L	3.1	3.1	1	13	AFAKVVAQADARG	8619
1FIQ	AC	OXIDOREDUCTASE	A	3.1	3.1	1	17	FCTPGIVMSMYTLLRNQ	8620
1FNT	CD	HYDROLASE/HYDROLASE ACTIVATOR	D	1.6	3.1	2	13	FQVEYALEAVKRG	8621
1FNT	FM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.6	3.1	2	7	VKWYHFD	8622
1FNT	GN	HYDROLASE/HYDROLASE ACTIVATOR	G	1.6	3.1	2	22	IPDGRHLVNRGREEAASFKKLY	8623
1FNT	KZ	HYDROLASE/HYDROLASE ACTIVATOR	K	3.1	3.1	1	14	YSGFYTFSLLDHHY	8624
1FNT	Sa	HYDROLASE/HYDROLASE ACTIVATOR	a	1.6	3.1	2	15	INSAARNIQHLLYGK	8625
1FS1	AB	LIGASE	A	1.6	3.1	2	9	DELLLGIFS	8626
1FYH	DE	IMMUNE SYSTEM	D	3.1	3.1	1	10	LNVQRKAIHE	8627
1FYZ	AC	OXIDOREDUCTASE	A	3.1	3.1	1	5	SDGFI	8628
1FYZ	BD	OXIDOREDUCTASE	B	1.6	3.1	2	7	AQEVHRW	8629
1G0U	HZ	HYDROLASE	Z	1.6	3.1	2	18	VEEVIKLVRDSFTSATER	8630
1G0U	PQ	HYDROLASE	Q	3.1	3.1	1	22	NADSRILIEKARVEAQSHRLTL	8631
1G3I	AH	CHAPERONE/HYDROLASE	H	3.1	3.1	1	18	TADAFTLFELFERKLEMH	8632
1G3N	EG	CELL CYCLE, SIGNALING PROTEIN	E	1.6	3.1	2	17	LSTIREVAVLRHLETFE	8633
1GG2	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	G	1.6	3.1	2	15	VSKAAADLMAYCEAH	8634
1GZL	BD	GLYCOPROTEIN	D	1.6	3.1	2	11	EEWDREIENYT	8635
1H1L	CD	OXIDOREDUCTASE	C	1.6	3.1	2	7	VGCGQYS	8636
1H6K	BY	NUCLEAR PROTEIN	B	3.1	3.1	1	11	FSHSFSALAKF	8637
1HV4	AB	OXYGEN STORAGE/TRANSPORT	B	1.6	3.1	2	16	VADCGAEALARLLIVY	8638
1HV4	GH	OXYGEN STORAGE/TRANSPORT	H	1.6	3.1	2	16	VADCGAEALARLLIVY	8639
1I51	CD	HYDROLASE/HYDROLASE INHIBITOR	D	1.6	3.1	2	13	WFVQALCSILEEH	8640
1IBR	AB	CELL CYCLE, TRANSLATION	A	3.1	3.1	1	5	FHRKK	8641
1IBR	AB	CELL CYCLE, TRANSLATION	B	1.6	3.1	2	18	EHMKESTLEAIGYICQDI	8642
1IBR	CD	CELL CYCLE, TRANSLATION	C	1.6	3.1	2	14	FEKPFLWLARKLIG	8643

1IBT	AB	LYASE	A	1.6	3.1	2	8	ELDAKLNK	8644
1ID3	AB	STRUCTURAL PROTEIN/DNA	A	1.6	3.1	2	10	KKEIKLARRL	8645
1IRU	DK	HYDROLASE	D	3.1	3.1	1	13	RARVECQSHRLTV	8646
1IRU	HN	HYDROLASE	N	1.6	3.1	2	22	YADFQYLKQVLGQMVIDEELLG	8647
1IRU	I2	HYDROLASE	2	1.6	3.1	2	19	QTEARDLVERCMRVLYYRD	8648
1IRU	OW	HYDROLASE	O	3.1	3.1	1	23	TADSRSQVQRARYEAANWKYKYG	8649
1IRU	RY	HYDROLASE	R	3.1	3.1	1	13	RARVECQSHRLTV	8650
1IWA	ON	LYASE	O	1.6	3.1	2	21	IQAGATANRVALEAMILARNE	8651
1IZN	AB	PROTEIN BINDING	A	3.1	3.1	1	13	FNEVFNDVRLLLN	8652
1J1D	AB	CONTRACTILE PROTEIN	B	1.6	3.1	2	45	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRIND	8653
1J1D	AC	CONTRACTILE PROTEIN	A	1.6	3.1	2	12	EDDIEELMKDGD	8654
1J1E	AC	CONTRACTILE PROTEIN	A	1.6	3.1	2	12	EDDIEELMKDGD	8655
1J1E	BC	CONTRACTILE PROTEIN	C	1.6	3.1	2	38	ASRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRA	8656
1JD2	12	HYDROLASE	2	1.6	3.1	2	22	IPDARNAALRAKAEAAEFRYKY	8657
1JD2	HI	HYDROLASE	I	3.1	3.1	1	15	PETFTQLVSSSLYER	8658
1JD2	ZS	HYDROLASE	S	1.6	3.1	2	21	AADGDALVKRFKNSVKWYHFD	8659
1JPW	AD	CELL ADHESION	A	1.6	3.1	2	18	DSVLFYAITTLHNLLLHQ	8660
1JRO	AB	OXIDOREDUCTASE	A	1.6	3.1	2	9	PVQQAMIDH	8661
1JRO	CD	OXIDOREDUCTASE	D	1.6	3.1	2	6	ARAHVT	8662
1JSU	BC	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	C	1.6	3.1	2	13	HEELTRDLEKHCR	8663
1K8I	AB	IMMUNE SYSTEM	B	1.6	3.1	2	6	WDVLTH	8664
1KEN	CD	VIRAL PROTEIN/IMMUNE SYSTEM	D	1.6	3.1	2	7	ENQHTID	8665
1KF6	AB	OXIDOREDUCTASE	A	1.0	3.1	3	15	TGFHMLHTLFQTSLQ	8666
1KF6	AB	OXIDOREDUCTASE	A	1.6	3.1	2	11	CPTEMTQLELW	8667
1KFU	LS	HYDROLASE	S	3.1	3.1	1	7	FRAFKSL	8668
1KFY	AB	OXIDOREDUCTASE	A	1.6	3.1	2	11	CPTEMTQLELW	8669
1KFY	CD	OXIDOREDUCTASE	C	1.6	3.1	2	12	PEAWAGFVDFLQ	8670
1KI6	AB	PHOSPHOTRANSFERASE	A	1.6	3.1	2	10	PQAVLAFVAL	8671
1KKQ	AE	TRANSCRIPTION	A	3.1	3.1	1	12	VETVTELTEFAK	8672
1KPE	AB	PROTEIN KINASE INHIBITOR	A	1.6	3.1	2	17	ESLLGHLMIVGKKCAAD	8673
1KX4	EF	STRUCTURAL PROTEIN/DNA	E	1.6	3.1	2	12	PKDIQLARRIRG	8674
1KYO	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.6	3.1	2	20	DTEVERAKSLLKLQLGQLYE	8675
1KYO	AC	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.6	3.1	2	18	IDDLIHFTLKQWNRLTIS	8676
1KYO	NR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.6	3.1	2	14	FTSIARIGDYILKS	8677
1KZ7	CD	SIGNALING PROTEIN	C	3.1	3.1	1	23	ELLDTERAYVEELLCVLEGYAAE	8678

1L9B	LH	PHOTOSYNTHESIS	L	1.6	3.1	2	5	ERKYR	8679
1L9B	LM	PHOTOSYNTHESIS	M	1.6	3.1	2	25	HTAWAFLSAIWLWMVLGFIRPILMG	8680
1L9J	LM	PHOTOSYNTHESIS	L	3.1	3.1	1	10	PDHEDTFFRD	8681
1LVC	AD	LYASE	A	1.0	3.1	3	18	SLEKQKGVTNLLIKYGIE	8682
1M56	AC	OXIDOREDUCTASE	A	1.6	3.1	2	9	PVLYQHILW	8683
1M63	EF	HYDROLASE/ISOMERASE	F	1.6	3.1	2	11	ELFQVLKMMVG	8684
1MFB	LH	IMMUNOGLOBULIN	L	3.1	3.1	1	6	SEELET	8685
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	G	3.1	3.1	1	6	EVDFRH	8686
1MO1	AB	TRANSPORT PROTEIN	A	1.6	3.1	2	13	EQEALEKLAAYVQ	8687
1MXE	BF	METAL BINDING PROTEIN	B	1.6	3.1	2	10	YEEFVTMMTS	8688
1N4M	BE	CELL CYCLE	B	1.6	3.1	2	13	IIVFYNSVFMQRL	8689
1N4Q	EF	TRANSFERASE	F	3.1	3.1	1	15	RLTIAFFALSGLDML	8690
1N4Q	EF	TRANSFERASE	F	3.1	3.1	1	11	KDDIIEWIYSL	8691
1N4Q	GH	TRANSFERASE	H	3.1	3.1	1	11	KDDIIEWIYSL	8692
1N4Q	KL	TRANSFERASE	K	1.6	3.1	2	14	YTVWHFRRVLLRSL	8693
1NT2	AB	RNA BINDING PROTEIN	A	3.1	3.1	1	13	QIEILKANAEFFL	8694
1NTK	AE	OXIDOREDUCTASE	A	1.6	3.1	2	20	DSQIEKERDVILQELQENDT	8695
1NVM	GH	LYASE/OXIDOREDUCTASE	H	3.1	3.1	1	6	PGTRAN	8696
1OAO	BC	OXIDOREDUCTASE	B	1.6	3.1	2	16	DLIYSILTQIASDVYG	8697
1OE9	AB	ATPASE/MYOSIN	B	1.6	3.1	2	11	YEDYLEGFRVF	8698
1ORS	AB	MEMBRANE PROTEIN	A	1.6	3.1	2	6	SEQLTS	8699
1PIV	13	VIRUS	1	3.1	3.1	1	8	VQLRRKLE	8700
1PRC	CM	PHOTOSYNTHETIC REACTION CENTER	M	1.6	3.1	2	15	IWPHIDWLTAFSIRY	8701
1PTO	BF	TOXIN	F	1.6	3.1	2	17	TWFDTMLGFAISAYALK	8702
1Q5Q	FM	HYDROLASE	M	1.6	3.1	2	23	AGIAIELVRLFAVELEHYEKIEG	8703
1QDL	AB	LYASE	B	1.6	3.1	2	12	FVYNIAQIVGEL	8704
1R6O	AC	HYDROLASE	A	1.6	3.1	2	17	LSFQRVLQRAVFHVQSS	8705
1RIW	BC	HYDROLASE/BLOOD CLOTTING	B	1.6	3.1	2	8	RETAASLL	8706
1RP3	AB	TRANSCRIPTION	A	3.1	3.1	1	31	TEELFKTLDKINFSYILSLEEVFRDFARDYS	8707
1RP3	CD	TRANSCRIPTION	D	1.6	3.1	2	13	KVTLSKIAQELSK	8708
1RP3	EF	TRANSCRIPTION	E	1.6	3.1	2	17	IRDLISYGVIGLIKAVD	8709
1RSO	AD	NEUROPEPTIDE/MEMBRANE PROTEIN	A	3.1	3.1	1	12	NLFQALIDIQEF	8710
1RTD	AB	TRANSFERASE/DNA	B	1.6	3.1	2	7	KETWETW	8711
1RZO	CD	HYDROLASE	C	1.6	3.1	2	13	QYIEGEMRTRIRY	8712
1S5E	BL	TRANSERASE,TOXIN	L	1.6	3.1	2	20	DSQKKAIERMKDTLRIAYLT	8713
1S9V	DE	IMMUNE SYSTEM	E	1.6	3.1	2	24	KDILERKRAAVDRVCRHNYQLELR	8714
1SA0	CB	CELL CYCLE	B	3.1	3.1	1	7	LHWYTGE	8715
1SCT	EF	OXYGEN TRANSPORT	E	1.6	3.1	2	18	PSRLKCVVEKFAVNHINR	8716

1SFC	EC	TRANSPORT PROTEIN	E	1.6	3.1	2	64	LQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFE TSAAKLKRKYWWKNLKM	8717
1SFC	EF	TRANSPORT PROTEIN	F	1.6	3.1	2	30	RIEYNVEHAVDYVERAVSDTKKAVKYQSKA	8718
1SQB	CE	OXIDOREDUCTASE	E	3.1	3.1	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	8719
1T0F	AC	DNA BINDING PROTEIN	C	3.1	3.1	1	8	MHERLKGK	8720
1T0Q	AB	OXIDOREDUCTASE	A	3.1	3.1	1	5	YDLTR	8721
1T3L	AB	TRANSPORT PROTEIN	A	1.6	3.1	2	18	EVTDMMQKALFDFLKHRF	8722
1TQY	GH	TRANSFERASE	G	3.1	3.1	1	11	SVMPAEVAWAV	8723
1TQY	GH	TRANSFERASE	H	1.6	3.1	2	18	QAGGLDALGHARRTIRRG	8724
1TUE	HJ	REPLICATION	J	3.1	3.1	1	24	IDSQIQYWQLIRWENAIFFAAREH	8725
1U54	AB	TRANSFERASE	A	3.1	3.1	1	8	LLDRLRKH	8726
1U5T	AB	TRANSPORT PROTEIN	B	1.6	3.1	2	9	PMEMREACE	8727
1U8T	AE	SIGNALING PROTEIN	E	1.6	3.1	2	9	QAEIDALLN	8728
1U9I	BC	CIRCADIAN CLOCK PROTEIN	B	3.1	3.1	1	11	RAQLLRNAYSW	8729
1UZH	KP	LYASE	K	1.6	3.1	2	21	NAPGAAANRVALEACTQARNE	8730
1V54	AB	OXIDOREDUCTASE	A	3.1	3.1	1	37	DQIYNVVVTAHAFVMIFFMVMPIMIGGFGNWLVPLMI	8731
1V54	CG	OXIDOREDUCTASE	C	1.0	3.1	3	29	RKHMLQALFITITLGVYFTLLQASEYYEA	8732
1VF5	NO	PHOTOSYNTHESIS	O	3.1	3.1	1	9	ATTIFLFGT	8733
1VF6	BD	PROTEIN BINDING/PROTEIN TRANSPORT	B	1.0	3.1	3	16	QVLQVLDRLKMKLQEK	8734
1W2B	FL	RIBOSOME	F	1.6	3.1	2	12	EIVMHIPELADE	8735
1W5C	AD	PHOTOSYNTHESIS	A	3.1	3.1	1	5	ICVAY	8736
1WCM	AE	TRANSCRIPTION	A	1.6	3.1	2	9	FIDIMEVLG	8737
1WYU	CD	OXIDOREDUCTASE	C	1.6	3.1	2	5	LEDLF	8738
1WYU	EF	OXIDOREDUCTASE	E	1.6	3.1	2	14	PEYRAVLRAYLEAV	8739
1XEW	XY	CELL CYCLE	X	1.6	3.1	2	7	DITKFIK	8740
1XFU	ES	LYASE/METAL BINDING PROTEIN	S	3.1	3.1	1	5	AFSLF	8741
1XTG	AB	TOXIN	A	1.6	3.1	2	13	DLGRMLLTSIVRG	8742
1XXI	DE	TRANSFERASE	E	1.6	3.1	2	21	PSRLQAILGDVCHIREQLMSV	8743
1YD8	VG	PROTEIN TRANSPORT, CHROMOSOMALPROTEIN	G	1.6	3.1	2	25	KVTKRLHTLEEVNNNVRLLSEMLLH	8744
1YE9	BF	OXIDOREDUCTASE	F	1.6	3.1	2	18	PLLQGRLFSYTDTQISRL	8745
1YE9	DE	OXIDOREDUCTASE	E	1.6	3.1	2	13	FHRRELWEAIEAG	8746
1YE9	DH	OXIDOREDUCTASE	H	3.1	3.1	1	17	PFEQRHIVDGFSFELSK	8747
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.6	3.1	2	7	YLWERYR	8748
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.6	3.1	2	25	GATVCVLGLLLGEWINRYFNFWGWT	8749
1YHU	MO	OXYGEN STORAGE/TRANSPORT	O	1.6	3.1	2	18	IPTLESMLDHLAGQHAVR	8750
1YOV	AB	SIGNALING PROTEIN	A	1.6	3.1	2	5	LVLPG	8751

1YUC	AC	TRANSCRIPTION REGULATION	A	1.0	3.1	3	22	TFGLMCKMADQTLFSIVEWARS	8752
1YV0	TI	CONTRACTILE PROTEIN	T	1.6	3.1	2	9	ELWDWLYQL	8753
1Z7Q	QX	HYDROLASE/HYDROLASE ACTIVATOR	X	1.6	3.1	2	22	ATDVTTLNEMFRYKTNLYKLKE	8754
1ZBB	BD	STRUCTURAL PROTEIN/DNA	B	1.6	3.1	2	11	AMDVVYALKRQ	8755
1ZBB	BD	STRUCTURAL PROTEIN/DNA	D	3.1	3.1	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	8756
1ZGL	BC	IMMUNE SYSTEM	B	1.6	3.1	2	10	GRPDAEYWNS	8757
1ZGL	EF	IMMUNE SYSTEM	E	1.6	3.1	2	8	RPDAEYWN	8758
1ZQ1	BD	LYASE	D	1.6	3.1	2	10	DDLKKKIKEN	8759
1ZRT	PQ	OXIDOREDUCTASE/METAL TRANSPORT	P	1.6	3.1	2	23	YFVIKDLFALALVLLGFFAVVAY	8760
2A40	DF	STRUCTURAL PROTEIN	F	1.6	3.1	2	12	ARSDLLSAIRQG	8761
2AA1	AB	OXYGEN STORAGE/TRANSPORT	A	1.6	3.1	2	16	SDAIGNDALSRMIVVY	8762
2AFH	AB	OXIDOREDUCTASE	B	3.1	3.1	1	9	KEYQELNFQ	8763
2AHM	AE	VIRAL PROTEIN, REPLICATION	A	1.6	3.1	2	20	SKMSDVKCTSVVLLSVLQQL	8764
2AK4	NP	IMMUNE SYSTEM	P	1.6	3.1	2	7	EAEISHT	8765
2AQ1	EF	IMMUNE SYSTEM	F	1.6	3.1	2	9	MGNMKYLYD	8766
2AXT	bh	ELECTRON TRANSPORT	b	3.1	3.1	1	6	RYQWDS	8767
2AXT	DE	ELECTRON TRANSPORT	E	1.6	3.1	2	12	AKQQVETFLEQL	8768
2AZE	AC	CELL CYCLE, TRANSCRIPTION	C	3.1	3.1	1	12	TSEKFQKINQMV	8769
2BA1	FI	RNA BINDING PROTEIN	I	1.6	3.1	2	24	EKLFDELLDVSINCARKLREKFKE	8770
2BL0	AC	MUSCLE PROTEIN	C	1.6	3.1	2	12	PAAFNEMFNEAD	8771
2BMO	AB	OXIDOREDUCTASE	A	1.6	3.1	2	19	FWESDDNENMETMSQNGKK	8772
2CLY	AB	HYDROLASE	B	3.1	3.1	1	7	WAYYKAN	8773
2D0O	CD	CHAPERONE	D	1.6	3.1	2	10	REVLLGIEEE	8774
2D0V	IJ	OXIDOREDUCTASE	J	1.6	3.1	2	5	PKELN	8775
2DBU	AB	TRANSFERASE	A	1.6	3.1	2	15	SGGIHIVQILNILEN	8776
2DSQ	IG	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	1.6	3.1	2	9	IVDECCFRS	8777
2DYM	EF	PROTEIN TURNOVER/PROTEIN TURNOVER	E	1.6	3.1	2	11	HMNDIKQLLWN	8778
2E 74	AB	PHOTOSYNTHESIS	B	1.6	3.1	2	26	PNDLLYVFPVVIMGTFACIVALSVLD	8779
2E 74	CE	PHOTOSYNTHESIS	C	1.6	3.1	2	37	PNRVKWMIAFICLVMLAQLMLILKKKQVEKVQAAEMN	8780
2EQ9	BC	OXIDOREDUCTASE	B	1.6	3.1	2	7	LTDLALT	8781
2F9I	CB	TRANSFERASE	B	1.6	3.1	2	12	MRQTLSEILKIH	8782
2FBW	OQ	OXIDOREDUCTASE	Q	1.6	3.1	2	27	PAVDYSLAAALTLHGHWGLGQVITDYV	8783
2FUG	12	OXIDOREDUCTASE	2	1.6	3.1	2	5	LSCKL	8784
2FYN	DE	OXIDOREDUCTASE	D	1.6	3.1	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	8785
2G4D	CD	HYDROLASE/PROTEIN BINDING	C	1.6	3.1	2	15	DEIINFYMNMLMERS	8786
2G9H	AB	IMMUNE SYSTEM	A	3.1	3.1	1	7	EEFGRFA	8787

2GAG	AB	OXIDOREDUCTASE	A	3.1	3.1	1	11	VADVLRATGAG	8788
2GL7	DE	TRANSCRIPTION	D	1.6	3.1	2	17	QRLVQNCLWTLRNLSDA	8789
2GTL	FG	OXYGEN STORAGE/TRANSPORT	G	1.6	3.1	2	19	PKFSAHALRILNGLDLAIN	8790
2GWW	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.6	3.1	2	20	RTIESILEPVAQQISHLVIM	8791
2H61	EC	METAL BINDING PROTEIN, SIGNALING PROTEIN	C	3.1	3.1	1	20	FQEFMAFVAMVTTACHEFFE	8792
2H67	AB	HORMONE/GROWTH FACTOR	A	3.1	3.1	1	6	LYQLEN	8793
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	C	1.6	3.1	2	10	KLPFQRLVRE	8794
2HLD	KP	HYDROLASE	P	1.6	3.1	2	46	SARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGASS	8795
2HOD	DE	BLOOD CLOTTING	D	1.0	3.1	3	38	KRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRS	8796
2HRK	AB	LIGASE/RNA BINDING PROTEIN	A	1.6	3.1	2	13	VNVSRWYTLLEMD	8797
2HYB	JL	TRANSFERASE	J	3.1	3.1	1	16	QASDSAYQFAKAALEK	8798
2HYI	AC	HYDROLASE/RNA BINDING PROTEIN/RNA	C	3.1	3.1	1	9	RELYIHRIG	8799
2HYI	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.6	3.1	2	13	KRKVDWLTEKMRE	8800
2HZS	EF	TRANSCRIPTION	E	1.6	3.1	2	6	PALVFN	8801
2I2R	AE	TRANSPORT PROTEIN	E	1.0	3.1	3	15	KRELQVLYRGFKNEC	8802
2I2X	MN	TRANSFERASE	M	3.1	3.1	1	12	DKVLRDLMMLSD	8803
2IBZ	AB	OXIDOREDUCTASE	B	1.6	3.1	2	8	INYTKLKN	8804
2IBZ	CE	OXIDOREDUCTASE	C	3.1	3.1	1	22	MGSLLGLCLVIQIVTGIFMAMH	8805
2ICW	GI	IMMUNE SYSTEM	G	1.6	3.1	2	28	EETKEVLKLFKLKVNQFYRHAFGIVNDY	8806
2ICW	GJ	IMMUNE SYSTEM	G	1.6	3.1	2	19	WWFRSLLVKGVYLIKRYYE	8807
2IO1	AB	PROTEIN BINDING, HYDROLASE	A	1.6	3.1	2	10	TFFYPKLKSG	8808
2JIZ	AD	HYDROLASE	D	3.1	3.1	1	9	PAPATTFAH	8809
2JIZ	CD	HYDROLASE	D	3.1	3.1	1	17	EDKLTVSRARKIQRFLS	8810
2JIZ	CF	HYDROLASE	F	1.6	3.1	2	20	SEHYDVARGVQKILQDYKSL	8811
2JKR	AS	ENDOCYTOSIS	S	1.6	3.1	2	20	NLAYLEAIHNFVEVLNEYFH	8812
2KIN	AB	MOTOR PROTEIN	B	1.0	3.1	3	16	KSLSALGNVISALAEG	8813
2NN6	EH	HYDROLASE/TRANSFERASE	H	3.1	3.1	1	20	LADREVISRLRNCIISLVTQ	8814
2NNA	BC	IMMUNE SYSTEM	B	1.6	3.1	2	24	KEVLERTRAELDTVCRHNYQLELR	8815
2NQB	CD	STRUCTURAL PROTEIN/DNA	C	1.6	3.1	2	10	PRHLQLAIRN	8816
2NQB	GH	STRUCTURAL PROTEIN/DNA	G	1.6	3.1	2	10	PRHLQLAIRN	8817
2O01	AB	PHOTOSYNTHESIS	A	1.6	3.1	2	6	SQVIQS	8818
2O97	AB	DNA BINDING PROTEIN	B	1.6	3.1	2	21	KAAAGRALDAIIASVTESLKE	8819
2OTJ	AZ	RIBOSOME	Z	1.6	3.1	2	15	RVSRRRVAEIESEMN	8820
2P2C	FR	HYDROLASE	F	3.1	3.1	1	15	VADMLVKVNALIKDR	8821

2P3F	HL	HYDROLASE	H	3.1	3.1	1	9	RDWAESTLM	8822
2P5T	AB	TRANSCRIPTION REGULATOR	A	1.6	3.1	2	14	PWILMSDDLSDLIH	8823
2PBI	AB	SIGNALING PROTEIN	A	1.6	3.1	2	21	DAAQTHIYMLMKKDSYARYLK	8824
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	H	3.1	3.1	1	5	NEVLQ	8825
2PKG	BC	HYDROLASE REGULATOR/VIRAL PROTEIN	C	1.6	3.1	2	6	WPECAK	8826
2PMZ	AC	TRANSLATION, TRANSFERASE	A	1.0	3.1	3	34	PTELFFHAAGGREGLVDTAVRTSQSGYMQRRLIN	8827
2PMZ	BD	TRANSLATION, TRANSFERASE	D	3.1	3.1	1	7	IRRASML	8828
2QE7	BF	HYDROLASE	F	3.1	3.1	1	11	TREGNDLYHEM	8829
2QJK	BC	ELECTRON TRANSPORT	B	1.0	3.1	3	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	8830
2QJK	DE	ELECTRON TRANSPORT	D	1.6	3.1	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	8831
2QJK	MN	ELECTRON TRANSPORT	M	1.6	3.1	2	11	FASVEHIMRNV	8832
2QKH	BA	SIGNALING PROTEIN/HORMONE	A	1.6	3.1	2	22	AGELYQRWERYRRECQETLAAA	8833
2QMB	AD	TRANSPORT PROTEIN	D	3.1	3.1	1	7	PWTQRFF	8834
2QQD	AE	LYASE	E	3.1	3.1	1	20	KKEAEKTVREMAKIGFEMRG	8835
2UZ1	DB	LYASE	D	1.6	3.1	2	17	TEHIPRLVMQAIRAALS	8836
2V36	AB	TRANSFERASE	A	1.6	3.1	2	13	KFAKTLSDTVQDF	8837
2V7Q	FJ	HYDROLASE	J	3.1	3.1	1	30	AFGKREQAEEERYFRARAKEQLAALKKHHE	8838
2V7Q	GI	HYDROLASE	G	1.6	3.1	2	75	ADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDK LTLTFNRTRQAVITKELIEIISGAAAL	8839
2V8W	EF	TRANSLATION	E	3.1	3.1	1	11	VEDFWALYNHI	8840
2VGL	AB	PROTEIN TRANSPORT	A	3.1	3.1	1	8	VPTRALLL	8841
2VML	KL	PHOTOSYNTHESIS	L	1.6	3.1	2	12	AFTKAIVAADLR	8842
2VXU	IM	IMMUNE SYSTEM	M	1.6	3.1	2	7	SEQLTSG	8843
2W73	EM	METAL BINDING PROTEIN	M	1.6	3.1	2	15	IRNKIRAIGKMARVF	8844
2WIU	AB	TRANSFERASE/TRANSCRIPTION	B	1.6	3.1	2	15	PTQLANAMKLVRQQN	8845
2WME	HE	OXIDOREDUCTASE	E	3.1	3.1	1	22	LAETRSVDIVTGADVLEYYAGL	8846
2Z5C	AC	CHAPERONE/HYDROLASE	C	1.0	3.1	3	20	ARSMIEHARTAAVTHNLYYD	8847
2ZCY	1	HYDROLASE	0	1.6	3.1	2	20	ISDMQHIERLLKDLVTENAY	8848
2ZCY	1	HYDROLASE	1	3.1	3.1	1	15	TETAASVFKELCYEN	8849
2ZCY	GH	HYDROLASE	G	3.1	3.1	1	18	CDVLAKRMANLSQIYTQR	8850
2ZCY	MN	HYDROLASE	N	3.1	3.1	1	15	TETAASVFKELCYEN	8851
2ZCY	OU	HYDROLASE	U	1.6	3.1	2	18	CDVLAKRMANLSQIYTQR	8852
2ZCY	SZ	HYDROLASE	Z	1.6	3.1	2	22	AADGDALVKRFKNSVKWYHFDH	8853
2ZCY	UV	HYDROLASE	U	3.1	3.1	1	18	CDVLAKRMANLSQIYTQR	8854
2ZCY	XK	HYDROLASE	K	1.6	3.1	2	10	QTFAYGVLDS	8855
2ZT9	AB	PHOTOSYNTHESIS	B	1.6	3.1	2	26	PNDLLYVFPIVIMGSFACIVALAVLD	8856
2ZT9	FH	PHOTOSYNTHESIS	F	1.6	3.1	2	28	SGELLNAALLSFGLIFVGWALGALLLKI	8857
2ZU6	AB	HYDROLASE	B	3.1	3.1	1	10	HHELVYEAII	8858
2ZXX	BF	CELL CYCLE/REPLICATION	F	1.6	3.1	2	30	ATCLLQRRQVFRQNLVERVKEQHKVFLASL	8859

2ZYZ	CB	SPLICING	C	1.6	3.1	2	14	DVLQEQVFKDLKSR	8860
3B5N	FH	MEMBRANE PROTEIN	F	1.6	3.1	2	67	LAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVED AQLDVEQGVGHTDKAVKSA	8861
3BBN	DE	RIBOSOME	E	1.6	3.1	2	11	GAVRTVLEMAG	8862
3BCQ	AB	TRANSPORT PROTEIN/OXYGEN BINDING	A	3.1	3.1	1	16	AEDIGADALARMLTVY	8863
3BCQ	AB	TRANSPORT PROTEIN/OXYGEN BINDING	B	1.6	3.1	2	20	PDNFRLLADCITVCVAMKFG	8864
3BJI	BC	SIGNALING PROTEIN	B	3.1	3.1	1	38	EYDKRCCCLREIQQTEEKYTDTLGSIQQHFLKPLQRFL	8865
3BL2	BD	VIRAL PROTEIN/APOPTOSIS	B	3.1	3.1	1	19	SGRIVGFFDVGRYVCEEVL	8866
3BZ1	EF	ELECTRON TRANSPORT	F	1.6	3.1	2	24	VRWVAVHTLAVPTIFFLGAIAAMQ	8867
3C1B	CD	STRUCTURAL PROTEIN/DNA	C	1.6	3.1	2	10	PRHLQLAVRN	8868
3C7B	AB	OXIDOREDUCTASE	A	3.1	3.1	1	9	IGELIWRKG	8869
3CJH	EB	PROTEIN TRANSPORT	E	1.6	3.1	2	24	DACIDQCLAKYMRSWNVISKAYIS	8870
3CJI	AB	VIRUS	A	1.6	3.1	2	5	VKFLF	8871
3CJT	AB	TRANSFERASE/RIBOSOMAL PROTEIN	A	3.1	3.1	1	8	LPGLFDGG	8872
3CUE	GJ	PROTEIN TRANSPORT	G	1.6	3.1	2	24	NLAIQIADNFLRKVYCLYSDYVMK	8873
3CW2	BL	TRANSLATION	B	1.6	3.1	2	15	KEEALSQYRQIKQFT	8874
3CWB	PQ	OXIDOREDUCTASE	P	1.6	3.1	2	12	AFSSVAHTCRNV	8875
3CWB	RW	OXIDOREDUCTASE	W	3.1	3.1	1	8	LLRQAYSA	8876
3CXH	NR	OXIDOREDUCTASE	R	1.6	3.1	2	5	FDDLI	8877
3D31	AC	TRANSPORT PROTEIN	C	1.6	3.1	2	10	PRLENAARSL	8878
3D54	CD	LIGASE	C	3.1	3.1	1	15	PRGETIERVLREEKG	8879
3D6N	AB	HYDROLASE/TRANSFERASE	B	3.1	3.1	1	13	RVFRSGAPLLNMF	8880
3DEP	AB	PROTEIN TRANSPORT, MEMBRANE PROTEIN	A	3.1	3.1	1	8	ALLFVAGL	8881
3DF0	BC	HYDROLASE	B	3.1	3.1	1	21	FEEFKYLWNNIKKWQGIYKRF	8882
3DHT	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.6	3.1	2	16	PDDVGGEALGRLLVVY	8883
3E0J	CD	TRANSFERASE	D	3.1	3.1	1	20	VNQAKQMLYDYVERKRKENS	8884
3E8C	AG	TRANSFERASE	G	3.1	3.1	1	8	TYADFIAS	8885
3EA5	AB	TRANSPORT PROTEIN	A	1.0	3.1	3	12	VPNWHRDLVRVC	8886
3EJB	GH	OXIDOREDUCTASE/LIPID TRANSPORT	G	3.1	3.1	1	7	DEEAEKI	8887
3EPD	12	VIRAL PROTEIN	2	3.1	3.1	1	5	YANAN	8888
3EQY	BD	ONCOPROTEIN	B	1.6	3.1	2	15	VKEVMHYLGQYIMVK	8889
3EQY	BD	ONCOPROTEIN	B	3.1	3.1	1	10	SPLYDMLRKN	8890
3EXG	KJ	OXIDOREDUCTASE	J	1.6	3.1	2	6	KILEDN	8891
3EXG	U6	OXIDOREDUCTASE	U	1.6	3.1	2	27	REDGLKYYRMMQTVRRMELKADQLYKQ	8892
3F9K	QS	VIRAL PROTEIN, RECOMBINATION	Q	1.6	3.1	2	12	IEPAQEEHEKYH	8893
3FH6	FB	TRANSPORT PROTEIN	B	1.6	3.1	2	7	FGLKLAG	8894

3FHI	AB	TRANSFERASE	A	1.6	3.1	2	11	PIQIYEKIVSG	8895
3FS4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.6	3.1	2	19	PEVHASLDKFLCAVGAVLT	8896
3FS4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.6	3.1	2	16	VADCGAEALARLLIVY	8897
3FWC	AB	CELL CYCLE, TRANSCRIPTION	A	1.6	3.1	2	14	EEQKQEIYEAFSLF	8898
3G43	BE	METAL BINDING PROTEIN	B	1.6	3.1	2	14	FPEFLTMMARKMKD	8899
3GE8	DF	OXIDOREDUCTASE	D	3.1	3.1	1	6	AWRAYH	8900
3GHG	AB	BLOOD CLOTTING	B	1.6	3.1	2	29	SNIPTNLRVLRSILENLRSKIQKLESDVS	8901
3GLH	AB	TRANSFERASE	B	1.6	3.1	2	13	EHVLTALANGLSL	8902
3GMW	CD	PROTEIN BINDING	C	1.6	3.1	2	5	PVTEK	8903
3GTM	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.6	3.1	2	13	LAMANSLRRVMIA	8904
3GZD	DC	LYASE	C	1.6	3.1	2	14	PEVIQAMTKAMWEA	8905
3H87	AD	TOXIN/ANTITOXIN	A	3.1	3.1	1	5	KSALV	8906
3HD7	FG	EXOCYTOSIS	G	1.6	3.1	2	52	TRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAE KNLKD	8907
3HHZ	CM	VIRAL PROTEIN/RNA	M	1.6	3.1	2	11	VVEWLGWFEDQ	8908
3HKZ	IV	TRANSFERASE	I	1.6	3.1	2	7	KEEAQQI	8909
3HOU	MD	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	1.6	3.1	2	15	DDELERILKELSNLE	8910
3HRD	AB	OXIDOREDUCTASE	B	3.1	3.1	1	14	SGTAMAQIAAEELG	8911
3HUJ	AG	IMMUNE SYSTEM	A	1.6	3.1	2	29	DQQWETLQHIFRVYRSSFTRDVKEFAKML	8912
12 E8	LH	IMMUNOGLOBULIN	L	1.5	3.0	2	6	SEQLTS	8913
1A2Y	AC	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)	C	3.0	3.0	1	5	VQAWI	8914
1A6A	AB	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)	A	3.0	3.0	1	22	AQGALANIAVDKANLEIMTKRS	8915
1AOI	BH	DNA BINDING PROTEIN/DNA	H	1.5	3.0	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	8916
1AOI	EF	DNA BINDING PROTEIN/DNA	E	3.0	3.0	1	12	PKDIQLARRIRG	8917
1B8D	KL	PHOTOSYNTHESIS	L	1.5	3.0	2	12	AFSRVVVTSDAK	8918
1BCC	AB	OXIDOREDUCTASE	B	1.5	3.0	2	17	ENVQAAKNKLKAKYLMS	8919
1BGY	PT	ELECTRON TRANSPORT	T	1.5	3.0	2	13	ERLELCDERVSSR	8920
1BPL	AB	GLYCOSYLTRANSFERASE	B	1.5	3.0	2	13	KHKIEPILKARKQ	8921
1BXN	AL	LYASE	A	1.0	3.0	3	14	GRNYGRVVYEGLKG	8922
1CAX	CF	SEED STORAGE PROTEIN	C	3.0	3.0	1	9	KNFLEASYD	8923
1CB7	AB	ISOMERASE	A	1.5	3.0	2	15	AVGNKILDHAFTNAG	8924
1CDL	BF	CALCIUM-BINDING PROTEIN	B	1.5	3.0	2	15	EEQIAEFKEAFSLFD	8925
1CDL	DG	CALCIUM-BINDING PROTEIN	D	3.0	3.0	1	12	EAELQDMINEVD	8926
1D2Z	CB	APOPTOSIS	C	1.5	3.0	2	15	LPVRAQLCAHLDALD	8927

1D9K	GH	IMMUNE SYSTEM	G	1.5	3.0	2	22	PQGGLQNIATGKHNLEILTKRS	8928
1DCE	AB	TRANSFERASE	A	1.5	3.0	2	16	ATLWNCRREVLQHLET	8929
1DCE	AB	TRANSFERASE	B	3.0	3.0	1	14	PFHTLFGIAGLSLL	8930
1DGH	AD	OXIDOREDUCTASE	D	1.5	3.0	2	11	PDMVWDFWSLR	8931
1DGR	CY	PLANT PROTEIN	Y	1.5	3.0	2	8	RQVSDLTF	8932
1DIO	LM	LYASE	L	1.5	3.0	2	10	EATELKLGML	8933
1E6V	AE	OXIDOREDUCTASE	A	3.0	3.0	1	14	AAVSDFAFASKHAE	8934
1E6V	DB	OXIDOREDUCTASE	D	3.0	3.0	1	14	AAVSDFAFASKHAE	8935
1EAH	12	VIRUS	2	3.0	3.0	1	5	YENAN	8936
1EF1	BD	MEMBRANE PROTEIN	B	1.5	3.0	2	17	PETAVLLASYAVQSKYG	8937
1EQZ	CD	STRUCTURAL PROTEIN/DNA	C	1.5	3.0	2	12	PKDIQLARRIRG	8938
1EQZ	FH	STRUCTURAL PROTEIN/DNA	H	1.5	3.0	2	27	IYEETRGVLKVFLENVIRDAVTYTEHA	8939
1EYS	LM	ELECTRON TRANSPORT	M	3.0	3.0	1	15	IFPHLDWTAAFSIRY	8940
1F66	EF	STRUCTURAL PROTEIN/DNA	E	1.5	3.0	2	12	TVALREIRRYQK	8941
1F66	GH	STRUCTURAL PROTEIN/DNA	G	1.5	3.0	2	10	VGRIHRHLKS	8942
1F80	AE	TRANSFERASE	E	1.5	3.0	2	7	DEDAEKI	8943
1FDH	AG	OXYGEN TRANSPORT	A	3.0	3.0	1	16	AGEYGAEALERMFLSF	8944
1FFU	DF	HYDROLASE	F	1.5	3.0	2	8	SLLPMMKL	8945
1FNT	JK	HYDROLASE/HYDROLASE ACTIVATOR	K	3.0	3.0	1	17	PQAVSSFVRQELAKSIR	8946
1FPP	BA	PRENYLTRANSFERASE	A	1.5	3.0	2	13	NSVWNQRHFVISN	8947
1FS2	AD	LIGASE	A	3.0	3.0	1	9	VSTLHGILS	8948
1FSX	CD	OXYGEN STORAGE/TRANSPORT	D	1.5	3.0	2	20	PENFKLLGNVLVVVLARNFG	8949
1G0U	AB	HYDROLASE	B	3.0	3.0	1	12	YQVEYALESISH	8950
1G0U	OP	HYDROLASE	O	1.5	3.0	2	18	TKLLVSEVAKIMQEATQS	8951
1GG2	AB	COMPLEX (GTP-BINDING/TRANSDUCER)	A	1.5	3.0	2	23	KAAVERSKMIDRNLREDGEKAAR	8952
1GH0	AB	PHOTOSYNTHESIS	B	1.5	3.0	2	13	TAQIDALSQMVAE	8953
1GH0	GH	PHOTOSYNTHESIS	H	1.5	3.0	2	13	TAQIDALSQMVAE	8954
1GH6	AB	ANTITUMOR PROTEIN	B	1.5	3.0	2	11	FKIIVTAYKDL	8955
1GO3	EF	TRANSFERASE	E	3.0	3.0	1	14	LKETVKKILMEKYE	8956
1H1L	AB	OXIDOREDUCTASE	B	3.0	3.0	1	15	NNNMNLGLQNASALY	8957
1H4L	BE	KINASE/KINASE ACTIVATOR	B	1.5	3.0	2	14	VPSSALREICLLKE	8958
1H6K	BY	NUCLEAR PROTEIN	Y	1.5	3.0	2	12	RADAENAMRYIN	8959
1HLU	AP	COMPLEX (ACETYLATION/ACTIN-BINDING)	A	1.5	3.0	2	5	VHRKC	8960
1HR0	DE	RIBOSOME	D	3.0	3.0	1	8	ENLVIEFY	8961
1HV4	EF	OXYGEN STORAGE/TRANSPORT	F	1.5	3.0	2	16	VADCGAEALARLLIVY	8962
1I7Q	AD	LYASE	A	3.0	3.0	1	13	LDLDSRIELEMRT	8963
1I7W	CD	CELL ADHESION	C	3.0	3.0	1	15	QVVVNKAAVMVHQLS	8964
1IB1	BF	SIGNALING PROTEIN/TRANSFERASE	B	1.5	3.0	2	19	PIRLGLALNFSVFYYEILN	8965

1IB1	DH	SIGNALING PROTEIN/TRANSFERASE	D	1.5	3.0	2	19	PIRLGLALNFSVFYYEILN	8966
1IBT	CD	LYASE	C	1.5	3.0	2	8	ELDAKLNK	8967
1IHF	AB	TRANSCRIPTION/DNA	B	1.5	3.0	2	12	KSELIERLATQQ	8968
1IRU	BC	HYDROLASE	C	3.0	3.0	1	11	YQVEYAMEAIG	8969
1IRU	IJ	HYDROLASE	J	3.0	3.0	1	14	PYTLMSMVANLLYE	8970
1IRU	KZ	HYDROLASE	Z	1.5	3.0	2	19	VEQAYDLARRAIYQATYRD	8971
1IRU	WX	HYDROLASE	X	3.0	3.0	1	14	PYTLMSMVANLLYE	8972
1IWP	LM	LYASE	M	1.5	3.0	2	7	LEKVLSG	8973
1IZN	CD	PROTEIN BINDING	D	3.0	3.0	1	23	ARLRKLEVEANNAFDQYRDLYFE	8974
1J1D	DF	CONTRACTILE PROTEIN	D	1.5	3.0	2	12	EEELSDLFRMFD	8975
1J3I	AD	OXIDOREDUCTASE, TRANSFERASE	D	3.0	3.0	1	7	EDDFVYF	8976
1JB0	AB	PHOTOSYNTHESIS	B	3.0	3.0	1	5	YLWLN	8977
1JB0	IL	PHOTOSYNTHESIS	I	1.5	3.0	2	26	FLPWIFIPVVCWLMPTVVMGLLFLYI	8978
1JD2	BC	HYDROLASE	C	1.5	3.0	2	13	FQVEYALEAVKRG	8979
1JEB	AD	OXYGEN STORAGE/TRANSPORT	D	3.0	3.0	1	6	PWTQRY	8980
1JFI	AB	TRANSCRIPTION/DNA	B	1.5	3.0	2	12	RAAINKMIKETL	8981
1JNR	AD	OXIDOREDUCTASE	A	3.0	3.0	1	19	EKMLQRALELLAFLKEDLE	8982
1JRO	GH	OXIDOREDUCTASE	G	3.0	3.0	1	20	AAYRMNAAQAMALRYVRELS	8983
1JSU	BC	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.5	3.0	2	18	NSMRAILVDWLVEVGEEY	8984
1K7L	EF	TRANSCRIPTION	E	3.0	3.0	1	23	LNDQVTLLKYGVYEAIFAMLSSV	8985
1KEN	EF	VIRAL PROTEIN/IMMUNE SYSTEM	F	3.0	3.0	1	12	LLVALENQHTID	8986
1KF6	CD	OXIDOREDUCTASE	D	1.5	3.0	2	29	FIGRVFLFLMIVLPLWCGLHRMHHAMHDL	8987
1KIL	AE	MEMBRANE PROTEIN	A	1.5	3.0	2	50	VDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKY	8988
1KKQ	DH	TRANSCRIPTION	H	1.5	3.0	2	6	EAIIRK	8989
1KQF	AB	OXIDOREDUCTASE	A	3.0	3.0	1	6	LLDYVN	8990
1KVD	CD	TOXIN	C	3.0	3.0	1	7	EVNWHNG	8991
1KXV	BD	HYDROLASE, IMMUNE SYSTEM	B	3.0	3.0	1	7	PYQVRDC	8992
1KYO	CG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	1.5	3.0	2	14	FTSIARIGDYILKS	8993
1LB1	AB	SIGNALING PROTEIN	A	3.0	3.0	1	13	LDSYLLKPVQRIT	8994
1LIA	AB	LIGHT HARVESTING PROTEIN	B	1.5	3.0	2	12	AFSRVVVNSDSK	8995
1LNU	EF	SUGAR BINDING PROTEIN	E	1.5	3.0	2	21	PQGGLQNIAVVKHNLGVLTKR	8996
1LO5	AB	IMMUNE SYSTEM/TOXIN	A	1.5	3.0	2	22	AQGALANIAVDKANLEIMTKRS	8997
1LQS	RM	IMMUNE SYSTEM	M	1.5	3.0	2	15	LDTLFSRLEEYLHSR	8998
1LWU	DE	BLOOD CLOTTING	E	1.5	3.0	2	15	VKIRIESTVAGSLRS	8999
1M56	AB	OXIDOREDUCTASE	B	1.5	3.0	2	9	SLPVLFNQQ	9000
1N34	GK	RIBOSOME	K	1.5	3.0	2	17	PYAAQLAALDAAKKAMA	9001
1N4Q	AB	TRANSFERASE	B	3.0	3.0	1	11	KDDIIEWIYSL	9002

1N4Q	IJ	TRANSFERASE	I	1.5	3.0	2	10	ESAWNYLKGI	9003
1ND0	GH	IMMUNE SYSTEM	G	1.5	3.0	2	6	SEQLTS	9004
1NEK	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.5	3.0	2	8	PEQREKLD	9005
1NIK	CJ	TRANSCRIPTION	J	1.5	3.0	2	7	LIEKFLR	9006
1NIW	GH	SIGNALING PROTEIN/OXIDOREDUCTASE	G	3.0	3.0	1	11	EEIREAFRVFD	9007
1NLW	AB	TRANSCRIPTION/DNA	B	1.5	3.0	2	24	RAHHNALERKRRDHIKDSFHSLRD	9008
1NRO	LH	SERINE PROTEINASE/RECEPTOR	L	1.5	3.0	2	10	TERELLESYI	9009
1OAO	AD	OXIDOREDUCTASE	A	1.5	3.0	2	31	PVNLVFSAIRVALADYTGEHIATDFSDILFG	9010
1OCC	AD	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.5	3.0	2	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	9011
1OFU	YB	BACTERIAL CELL DIVISION INHIBITOR	B	1.5	3.0	2	15	LGEYSDVGNIIEQFA	9012
1PCQ	GU	CHAPERONE	G	3.0	3.0	1	13	EALATLVVNTMRG	9013
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.5	3.0	2	5	GWWLD	9014
1Q90	BD	PHOTOSYNTHESIS	D	3.0	3.0	1	22	PIATILFLLGTLVAVWLGIGST	9015
1QGW	BD	PHOTOSYNTHESIS	D	1.5	3.0	2	14	GNKRLDSVNSIVSN	9016
1QVI	AZ	CONTRACTILE PROTEIN	Z	1.5	3.0	2	11	YEDFVKKVMAG	9017
1R3I	LH	MEMBRANE PROTEIN	L	1.5	3.0	2	6	SEQLTS	9018
1RCO	LW	LYASE	L	1.5	3.0	2	6	WTDGLT	9019
1RM6	AC	OXIDOREDUCTASE	A	3.0	3.0	1	8	REETFIAH	9020
1RP3	AB	TRANSCRIPTION	A	1.5	3.0	2	18	IRDLISYGVIGLIKAVDN	9021
1RP3	AB	TRANSCRIPTION	B	1.5	3.0	2	11	IELSRLIGLLL	9022
1RP3	GH	TRANSCRIPTION	H	1.5	3.0	2	15	LEKKVKELKEKIEKG	9023
1RUY	HM	VIRAL PROTEIN	M	1.5	3.0	2	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	9024
1RUY	JI	VIRAL PROTEIN	I	1.5	3.0	2	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	9025
1RYP	H2	MULTICATALYTIC PROTEINASE	H	1.5	3.0	2	6	PDEYEQ	9026
1RYP	HN	MULTICATALYTIC PROTEINASE	H	3.0	3.0	1	15	TETAASVFKELCYEN	9027
1RYP	OV	MULTICATALYTIC PROTEINASE	V	1.5	3.0	2	22	AADTQAIADIVQYHLELYTSQY	9028
1RYP	YL	MULTICATALYTIC PROTEINASE	L	3.0	3.0	1	19	VEDALYLGKRSILAAAHRD	9029
1S1C	AX	SIGNALING PROTEIN	X	1.5	3.0	2	30	NLKAAFEKNINTERTLKTQAVNKLAEIMNR	9030
1SB3	DF	OXIDOREDUCTASE	D	3.0	3.0	1	8	REETFIAH	9031
1SCT	GH	OXYGEN TRANSPORT	G	3.0	3.0	1	19	SKLRGHAITLTYALNNFVD	9032
1SQX	CF	OXIDOREDUCTASE	F	3.0	3.0	1	5	RDDTI	9033
1SQX	CG	OXIDOREDUCTASE	C	1.5	3.0	2	33	HPYITIGQLASVLYFLLILVLMPTAGTIENKLL	9034
1TQE	SY	TRANSCRIPTION/PROTEIN BINDING/DNA	Y	1.5	3.0	2	14	TEVKQKLQEFLLSK	9035
1TU3	EJ	PROTEIN TRANSPORT	E	1.5	3.0	2	8	HSLAPMYY	9036

1U35	EF	STRUCTURAL PROTEIN/DNA	E	1.5	3.0	2	14	KLPFQRLVREIAQD	9037
1U35	EF	STRUCTURAL PROTEIN/DNA	E	1.5	3.0	2	12	PKDIQLARRIRG	9038
1U9I	BC	CIRCADIAN CLOCK PROTEIN	C	1.5	3.0	2	19	SSVVRRELFRLVARLKQIG	9039
1UB4	AC	DNA BINDING PROTEIN	A	1.5	3.0	2	15	PEELQLIKAKINVLI	9040
1UEA	CD	COMPLEX (METALLOPROTEASE/INHIBITOR)	C	1.5	3.0	2	13	LFLVAAHEIGHSL	9041
1UPT	FE	HYDROLASE/PROTEIN-BINDING	E	3.0	3.0	1	7	RPYWRCY	9042
1UVQ	AB	IMMUNOLOGY	B	1.5	3.0	2	28	KEVLEGTRAELDTVCRHNYEVAFRGILQ	9043
1UZD	AI	LYASE	A	1.5	3.0	2	21	NAPGAAANRVALEACTQARNE	9044
1UZH	VW	LYASE	W	3.0	3.0	1	14	DEQIAAQVDYIVAN	9045
1V4U	CB	OXYGEN STORAGE/TRANSPORT	B	3.0	3.0	1	6	PWTQRY	9046
1V54	BI	OXIDOREDUCTASE	I	3.0	3.0	1	12	SMKDFEEMRKAG	9047
1VCB	EF	TRANSCRIPTION	F	1.5	3.0	2	13	LKERCLQVVRSLV	9048
1VSA	HO	RIBOSOME	O	3.0	3.0	1	13	RKRRKRDFRRLWI	9049
1W63	LV	ENDOCYTOSIS	L	1.5	3.0	2	18	VDFVRKAVRAIGRCAIKV	9050
1W72	AH	IMMUNE SYSTEM	A	1.5	3.0	2	29	PEYWDQETRNMKAHSQTDRANLGTLRGYY	9051
1WDD	AS	LYASE	A	1.5	3.0	2	21	NAPGAAANRVALEACVQARNE	9052
1WEJ	LF	COMPLEX (ANTIBODY/ELECTRON TRANSPORT)	F	3.0	3.0	1	15	KTEREDLIAYLKKAT	9053
1WX5	AB	OXIDOREDUCTASE/METAL TRANSPORT	A	1.5	3.0	2	10	LHNRVHVWVG	9054
1WYU	AB	OXIDOREDUCTASE	A	1.5	3.0	2	14	PEYRAVLRAYLEAV	9055
1WYU	AB	OXIDOREDUCTASE	A	1.5	3.0	2	5	LEDLF	9056
1WYU	AB	OXIDOREDUCTASE	A	1.5	3.0	2	15	EWKVLEELRRLAAQN	9057
1X79	AB	PROTEIN TRANSPORT	A	3.0	3.0	1	10	MRPTLFRLAS	9058
1XFU	CQ	LYASE/METAL BINDING PROTEIN	Q	3.0	3.0	1	5	AFSLF	9059
1XFV	AO	LYASE/METAL BINDING PROTEIN	O	3.0	3.0	1	13	SEEEIREAFRVFD	9060
1XFV	CQ	LYASE/METAL BINDING PROTEIN	C	1.5	3.0	2	24	QEKKRKISIFRGIQAYNEIENVLK	9061
1XFV	CQ	LYASE/METAL BINDING PROTEIN	Q	1.5	3.0	2	9	VDQMIREAD	9062
1XPK	DC	TRANSFERASE	C	1.5	3.0	2	16	YAATPAIQLAKDYLAT	9063
1XPK	DC	TRANSFERASE	D	1.5	3.0	2	15	AATPAIQLAKDYLAT	9064
1XQ5	AD	OXYGEN STORAGE/TRANSPORT	D	1.5	3.0	2	7	PWTQRYF	9065
1XTC	AC	TOXIN	C	1.5	3.0	2	32	NTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQS	9066
1XXI	IJ	TRANSFERASE	J	1.5	3.0	2	20	APARLHWLATLLMDALKRHH	9067
1XZP	AB	HYDROLASE	A	1.5	3.0	2	12	ETSLKLSLRNLK	9068
1Y8X	AB	LIGASE	B	1.5	3.0	2	6	TSIEER	9069
1YKE	AB	GENE REGULATION	B	1.5	3.0	2	16	RLTQLQICLDQMTEQF	9070
1Z2C	CD	SIGNALING PROTEIN	C	1.5	3.0	2	7	LRPLSYP	9071
1Z7Q	SZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.5	3.0	2	23	AADCQFWETWLGSQCRLHELREK	9072
1ZGL	BC	IMMUNE SYSTEM	B	1.5	3.0	2	13	AVDTYCRHNYGVG	9073

1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	E	1.5	3.0	2	12	PKDIQLARRIRG	9074
1ZOY	AB	OXIDOREDUCTASE	A	3.0	3.0	1	22	QDAIHYMTEQAPASVVELENYG	9075
1ZV8	EF	VIRAL PROTEIN	E	1.5	3.0	2	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	9076
1ZV8	IJ	VIRAL PROTEIN	I	1.5	3.0	2	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	9077
1ZY8	DL	OXIDOREDUCTASE	L	1.5	3.0	2	10	PAARNILEKH	9078
2A45	GI	BLOOD CLOTTING	G	1.5	3.0	2	25	GCRMKGLIDEVNQDFTNRINKLKNS	9079
2ACZ	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.5	3.0	2	12	GPEAILELEHMG	9080
2AHM	CG	VIRAL PROTEIN, REPLICATION	C	1.5	3.0	2	20	SKMSDVKCTSVVLLSVLQQL	9081
2AXT	ac	ELECTRON TRANSPORT	c	1.5	3.0	2	18	GPEASQAQAMTFLIRDQK	9082
2AXT	bd	ELECTRON TRANSPORT	d	3.0	3.0	1	13	IFRFLLFFQGFHN	9083
2BA0	EH	RNA BINDING PROTEIN	E	1.5	3.0	2	16	RRSIEISKVSKEAFEA	9084
2BA0	EH	RNA BINDING PROTEIN	H	1.5	3.0	2	22	EKLFDELLDVSINCARKLREKF	9085
2BEQ	AF	VIRAL PROTEIN	F	1.5	3.0	2	13	QKEIDRLNEVAKN	9086
2BGN	DH	HYDROLASE	H	3.0	3.0	1	18	RDAIKRIAYEFVEMKAKD	9087
2BL0	AB	MUSCLE PROTEIN	B	1.5	3.0	2	10	SSEVEELMKE	9088
2C2V	EF	CHAPERONE	F	3.0	3.0	1	15	RNFRLLEELEEGQKG	9089
2D26	AB	HYDROLASE/HYDROLASE INHIBITOR	A	3.0	3.0	1	6	LQHLEN	9090
2DFK	CD	CELL CYCLE	C	3.0	3.0	1	37	RDQMRANVINEIMSTERHYIKHLKDICEGYLKQCRKR	9091
2DS2	AB	PLANT PROTEIN	A	3.0	3.0	1	7	CQRQFLQ	9092
2DS2	CD	PLANT PROTEIN	C	3.0	3.0	1	10	WRCQRQFLQH	9093
2DXB	HI	HYDROLASE	I	3.0	3.0	1	6	RDCLIG	9094
2DXB	KL	HYDROLASE	L	3.0	3.0	1	6	RDCLIG	9095
2DZN	CD	PROTEIN BINDING	C	1.5	3.0	2	8	PLHWSVSF	9096
2E 74	EH	PHOTOSYNTHESIS	E	1.5	3.0	2	27	ILGAVFYIVFIALFFGIAVGIIFAIKS	9097
2E5L	FR	RIBOSOME	R	3.0	3.0	1	17	GKEQRILAKTIKRARIL	9098
2EHO	AC	REPLICATION	A	1.5	3.0	2	7	LKVSIHQ	9099
2EKV	AC	CONTRACTILE PROTEIN	C	1.5	3.0	2	11	ADEFMEAFKTF	9100
2ERJ	EH	IMMUNE SYSTEM/CYTOKINE	H	1.5	3.0	2	7	KLTRMLT	9101
2ES4	AD	HYDROLASE	D	1.5	3.0	2	26	PDERAQQAALHAQQDAVTKIADLQKA	9102
2EY4	AC	ISOMERASE/BIOSYNTHETIC PROTEIN	A	1.5	3.0	2	12	IRSLIHHIGLAL	9103
2F5Z	EM	OXIDOREDUCTASE/PROTEIN BINDING	E	1.5	3.0	2	6	CEDIAR	9104
2FBW	BD	OXIDOREDUCTASE	D	1.5	3.0	2	27	PAVDYSLAAALTLHGHWGLGQVITDYV	9105
2FFD	DE	BLOOD CLOTTING	D	1.5	3.0	2	10	LKDYEDQQKQ	9106
2FHO	AB	RNA BINDING PROTEIN	B	3.0	3.0	1	9	AEEMYDIFG	9107
2GUZ	EF	CHAPERONE, PROTEIN TRANSPORT	F	1.5	3.0	2	8	LDESCKIL	9108
2GUZ	GH	CHAPERONE, PROTEIN TRANSPORT	H	1.5	3.0	2	8	LDESCKIL	9109
2H1L	FR	VIRAL PROTEIN	R	1.5	3.0	2	5	PHHER	9110

2HII	YZ	REPLICATION	Z	3.0	3.0	1	5	ILKVA	9111
2HJ9	AC	SIGNALING PROTEIN	C	3.0	3.0	1	10	FALMEKLKSE	9112
2HLD	BE	HYDROLASE	B	1.5	3.0	2	14	RSTVAQLVQTLEQH	9113
2HLD	GI	HYDROLASE	G	1.5	3.0	2	16	FQESALIADKLLSVMK	9114
2HLD	JM	HYDROLASE	J	1.5	3.0	2	15	LSKQAVAYRQLSLLL	9115
2I2X	OP	TRANSFERASE	O	3.0	3.0	1	12	DKVLRDLMMLSD	9116
2IAN	AB	IMMUNE SYSTEM	A	3.0	3.0	1	6	EEFGRF	9117
2IBZ	DE	OXIDOREDUCTASE	E	3.0	3.0	1	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	9118
2ICW	BC	IMMUNE SYSTEM	B	3.0	3.0	1	9	RPDAEYWNS	9119
2IE3	AC	SIGNALING PROTEIN,HYDROLASE	A	3.0	3.0	1	17	YLHRMTTLFCINVLSEV	9120
2IK8	AB	SIGNALING PROTEIN	B	1.0	3.0	3	13	HETRELTRMNLQT	9121
2INP	AC	OXIDOREDUCTASE	A	3.0	3.0	1	13	SVPKSFFDDARSA	9122
2IO5	AB	CHAPERONE/STRUCTURAL PROTEIN	B	1.5	3.0	2	12	PKDIQLARRIRG	9123
2IOF	AK	HYDROLASE	K	3.0	3.0	1	11	WMCYKNAMELG	9124
2ISS	CF	LYASE, TRANSFERASE	C	1.5	3.0	2	12	WIIKKGFAEMFK	9125
2J0Q	AC	HYDROLASE	A	3.0	3.0	1	9	RELYIHRIG	9126
2J8X	AB	HYDROLASE/INHIBITOR	B	3.0	3.0	1	10	LSDIIEKETG	9127
2JIY	LM	PHOTOSYNTHESIS	M	1.5	3.0	2	24	HTAWWFLSAIWLWMVLGFIRPILM	9128
2JIZ	HK	HYDROLASE	H	3.0	3.0	1	14	RSTVAQLVKRLTDA	9129
2JQ9	AB	PROTEIN TRANSPORT	A	1.5	3.0	2	26	DKAKESIRAKCVQYLDRAEKLKDYLR	9130
2NNU	AB	TRANSCRIPTION	A	1.5	3.0	2	23	LAVSKNKALQAIELQLTLETIYN	9131
2NUU	EJ	TRANSPORT PROTEIN/SIGNALING PROTEIN	E	1.5	3.0	2	7	EEQEREG	9132
2NXX	BF	HORMONE/GROWTH FACTOR	B	3.0	3.0	1	23	VQEVEMLREKIYGVLEEYTRTTH	9133
2NYL	AC	HYDROLASE	A	1.5	3.0	2	14	ANVRFNVAKSLQKI	9134
2NZ0	CD	MEMBRANE PROTEIN	C	1.5	3.0	2	12	EDTFKQIYAQFF	9135
2NZD	GH	STRUCTURAL PROTEIN/DNA	H	1.5	3.0	2	12	SREIQTAVRLLL	9136
2O5X	LH	IMMUNE SYSTEM	L	1.5	3.0	2	6	DEQLKS	9137
2OF5	EJ	APOPTOSIS	J	1.5	3.0	2	11	YREVQRIRHEF	9138
2OOB	AB	LIGASE	A	1.5	3.0	2	11	VDAKIAKLMGE	9139
2OS8	AB	CONTRACTILE PROTEIN	B	3.0	3.0	1	11	ETIRNAFGMFD	9140
2OV2	GO	PROTEIN BINDING/TRANSFERASE	G	1.5	3.0	2	14	LKTVFDEAIRAVLG	9141
2P2C	GH	HYDROLASE	H	1.5	3.0	2	13	WYIEALAQVFSER	9142
2PMZ	AB	TRANSLATION, TRANSFERASE	A	3.0	3.0	1	5	LEDVS	9143
2PMZ	GW	TRANSLATION, TRANSFERASE	W	3.0	3.0	1	7	NEVFISL	9144
2PMZ	QR	TRANSLATION, TRANSFERASE	Q	3.0	3.0	1	8	PDEIRKMS	9145
2PMZ	QW	TRANSLATION, TRANSFERASE	W	1.5	3.0	2	16	RYEIARVISARALQLA	9146
2PQA	AB	REPLICATION	B	3.0	3.0	1	14	LGLYNEAVKIIHDF	9147
2PXY	CD	IMMUNE SYSTEM	C	3.0	3.0	1	7	PEFAQLR	9148
2Q9Q	AB	REPLICATION	A	1.5	3.0	2	7	LWLAINL	9149

2QJ9	BC	CYTOKINE/RECEPTOR	C	3.0	3.0	1	6	SDFQCR	9150
2QLV	AB	TRANSFERASE/PROTEIN BINDING	A	1.5	3.0	2	19	AYPFLHLTTKLIMELAVNS	9151
2QLV	AC	TRANSFERASE/PROTEIN BINDING	A	3.0	3.0	1	19	AYPFLHLTTKLIMELAVNS	9152
2QM6	AB	TRANSFERASE	B	1.5	3.0	2	5	EMDDF	9153
2QQP	GH	VIRUS	G	1.5	3.0	2	14	DEVVQLANRLQMEL	9154
2QR0	AC	IMMUNE SYSTEM	C	1.5	3.0	2	8	FMDVYQRS	9155
2QRV	EF	TRANSFERASE/TRANSFERASE REGULATOR	E	3.0	3.0	1	16	TGRLFFEFYRLLHDAR	9156
2R6G	AG	HYDROLASE/TRANSPORT PROTEIN	G	1.5	3.0	2	13	PWQAFRLVLLPLS	9157
2RAX	XY	CELL CYCLE	Y	1.5	3.0	2	5	WLDYF	9158
2RFK	AB	ISOMERASE/RNA	B	1.5	3.0	2	12	GEYRRRWKREVL	9159
2RII	AY	OXIDOREDUCTASE COMPLEX	A	1.5	3.0	2	17	VDETLRLVQAFQFTDKH	9160
2RIV	AB	SIGNALING PROTEIN	A	1.5	3.0	2	7	MESVEAA	9161
2UUN	AB	ELECTRON TRANSPORT	B	1.5	3.0	2	13	VAQIDALSQMVAE	9162
2UUN	EF	ELECTRON TRANSPORT	F	1.5	3.0	2	13	VAQIDALSQMVAE	9163
2V1D	AC	OXIDOREDUCTASE/REPRESSOR	A	3.0	3.0	1	5	LKHWD	9164
2V4I	CD	TRANSFERASE	D	3.0	3.0	1	22	AGEFEEALHTAALALVKDIASD	9165
2V4I	EF	TRANSFERASE	F	3.0	3.0	1	22	AGEFEEALHTAALALVKDIASD	9166
2V4J	AB	OXIDOREDUCTASE	B	3.0	3.0	1	9	LGEWAERIG	9167
2V4Z	AB	CELL CYCLE	A	1.5	3.0	2	10	RSERKKWIHC	9168
2V7H	AB	IMMUNE SYSTEM	A	1.5	3.0	2	6	SEQLTS	9169
2V7Q	CF	HYDROLASE	C	1.5	3.0	2	15	LSKQAVAYRQMSLLL	9170
2VDA	AB	PROTEIN TRANSPORT	B	1.5	3.0	2	7	LAVAVAA	9171
2VGL	AS	PROTEIN TRANSPORT	A	1.5	3.0	2	18	DSVKQSAALCLLRLYRTS	9172
2VGL	AS	PROTEIN TRANSPORT	S	1.5	3.0	2	14	QTKVLKQLLMLQSL	9173
2VGL	BM	PROTEIN TRANSPORT	M	1.5	3.0	2	12	FVLIYELLDEIL	9174
2VGO	AD	TRANSFERASE	D	1.5	3.0	2	8	VDRMYGTI	9175
2VML	GJ	PHOTOSYNTHESIS	G	1.5	3.0	2	8	LREVNRTF	9176
2VPE	AB	GENE REGULATION	B	1.5	3.0	2	13	TEMANKAAEAVLK	9177
2VPE	CD	GENE REGULATION	C	1.5	3.0	2	10	ETAYGLLTAE	9178
2VUS	EM	TRANSCRIPTION	M	1.5	3.0	2	11	NACGLFLKLHG	9179
2VXQ	HL	ALLERGEN	L	1.5	3.0	2	6	DEQLKS	9180
2W72	AB	OXYGEN TRANSPORT	A	3.0	3.0	1	19	PAVHASLDKFLASVSTVLT	9181
2W72	DC	OXYGEN TRANSPORT	C	3.0	3.0	1	19	PAVHASLDKFLASVSTVLT	9182
2WAQ	AC	TRANSCRIPTION	C	3.0	3.0	1	16	IGIVAAQSVGEPGTQL	9183
2WB1	WY	TRANSCRIPTION	Y	1.5	3.0	2	8	HLLDAAAR	9184
2WB1	YR	TRANSCRIPTION	R	3.0	3.0	1	11	EMERDCLIGFG	9185
2WBJ	BD	IMMUNE SYSTEM	B	1.5	3.0	2	12	YCRHNYGVVESF	9186
2WD7	AC	OXIDOREDUCTASE	C	3.0	3.0	1	26	VETQVAELIGTNAIAPFLLTMSFAQR	9187
2WH4	NU	RIBOSOME	U	3.0	3.0	1	14	DFRRLWIVRINAAC	9188

2WME	DC	OXIDOREDUCTASE	D	3.0	3.0	1	15	TSTGKKVMASASSSS	9189
2WME	FE	OXIDOREDUCTASE	E	1.5	3.0	2	10	LARAHRAIHR	9190
2Z91	AB	IMMUNE SYSTEM	B	1.5	3.0	2	5	SEQLT	9191
2ZCY	0N	HYDROLASE	0	3.0	3.0	1	6	WDFAKD	9192
2ZT9	AB	PHOTOSYNTHESIS	A	1.5	3.0	2	23	ELTWVSGVILAVITVSFGVTGYS	9193
2ZT9	BG	PHOTOSYNTHESIS	G	1.5	3.0	2	28	PLLSGIVLGLIVVTLAGLFYAAYKQYKR	9194
3A0B	bd	ELECTRON TRANSPORT	d	3.0	3.0	1	8	FLIYPLGQ	9195
3A0B	lt	ELECTRON TRANSPORT	l	1.5	3.0	2	18	RTSLYLGLLLILVLALLF	9196
3B9J	BC	OXIDOREDUCTASE	C	1.5	3.0	2	9	PEHAERAAH	9197
3BCQ	CB	TRANSPORT PROTEIN/OXYGEN BINDING	B	3.0	3.0	1	6	WTQRHF	9198
3BCQ	CD	TRANSPORT PROTEIN/OXYGEN BINDING	C	1.0	3.0	3	19	PANFKILSHNLLVVLAQQF	9199
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.5	3.0	2	9	CQLHQVIVA	9200
3BTP	AB	DNA BINDING PROTEIN, CHAPERONE	A	1.5	3.0	2	8	PPLAFERI	9201
3BVH	DF	BLOOD CLOTTING	F	1.0	3.0	3	23	QEIYNSNNQKIVNLKEKVAQLEA	9202
3BZ1	AD	ELECTRON TRANSPORT	D	1.5	3.0	2	12	IFRFLLFFQGFH	9203
3C03	BC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.5	3.0	2	13	AKALQIIKLAELY	9204
3C5J	AB	MEMBRANE PROTEIN	A	1.5	3.0	2	22	AQGALANIAVDKANLEIMTKRS	9205
3C5Z	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	D	3.0	3.0	1	10	RPDAEYWNSQ	9206
3C5Z	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	H	3.0	3.0	1	10	RPDAEYWNSQ	9207
3C7B	AE	OXIDOREDUCTASE	E	1.5	3.0	2	9	WERFFELTG	9208
3C91	U2	HYDROLASE	2	1.5	3.0	2	22	VGDAQVLVRYMKAELELYRLQR	9209
3CJH	KH	PROTEIN TRANSPORT	K	1.5	3.0	2	26	DACIDQCLAKYMRSWNVISKAYISRI	9210
3CJT	GH	TRANSFERASE/RIBOSOMAL PROTEIN	G	3.0	3.0	1	7	LPGLFDG	9211
3CQX	BC	CHAPERONE	C	1.5	3.0	2	24	LEDQKKIKRRLETLLRNIDNSDKA	9212
3CXH	EI	OXIDOREDUCTASE	E	1.5	3.0	2	33	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSMT	9213
3CXH	LT	OXIDOREDUCTASE	T	1.5	3.0	2	27	VGTIFAGAFVFQTVFDTAITSWYENHN	9214
3D4X	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	3.0	3.0	1	6	PWTQRF	9215
3D69	AB	IMMUNE SYSTEM	A	1.5	3.0	2	6	SEELQA	9216
3DHR	GH	OXYGEN STORAGE, OXYGEN TRANSPORT	G	1.5	3.0	2	19	PVNFKLLGHCFLVVVAVHF	9217
3DKN	AC	PROTEIN TRANSPORT/RNA	C	1.5	3.0	2	20	PEHVIGVTVAFVIIEAILTY	9218
3DOE	AB	SIGNALING PROTEIN/HYDROLASE	A	1.5	3.0	2	8	LLTILKKM	9219
3DUF	GH	OXIDOREDUCTASE/TRANSFERASE	H	1.5	3.0	2	5	IRYRT	9220
3DW8	AB	HYDROLASE	A	3.0	3.0	1	6	ELLPFL	9221

3DWL	FG	STRUCTURAL PROTEIN	G	1.5	3.0	2	10	IGCIVRVLNS	9222
3DWL	KL	STRUCTURAL PROTEIN	L	1.5	3.0	2	10	IGCIVRVLNS	9223
3E1Y	BE	TRANSLATION	B	3.0	3.0	1	9	QEGSQFVKG	9224
3E2Z	AB	TRANSFERASE, LYASE	B	1.5	3.0	2	12	AYGSLFNSIQGL	9225
3E8C	CI	TRANSFERASE	I	3.0	3.0	1	7	YADFIAS	9226
3E8C	FL	TRANSFERASE	L	3.0	3.0	1	5	DFIAS	9227
3EA5	AB	TRANSPORT PROTEIN	A	1.0	3.0	3	14	FEKPFLWLARKLIG	9228
3EHU	AC	MEMBRANE PROTEIN	C	1.5	3.0	2	15	LAQQAHSNRKLMEII	9229
3EI4	AB	DNA BINDING PROTEIN	B	3.0	3.0	1	18	WPSVQQGLQQSFLHTLDS	9230
3EPF	12	VIRAL PROTEIN	2	3.0	3.0	1	5	YENAN	9231
3EQY	AC	ONCOPROTEIN	A	1.5	3.0	2	15	VKEVMHYLGQYIMVK	9232
3EQY	AC	ONCOPROTEIN	A	3.0	3.0	1	10	SPLYDMLRKN	9233
3EXG	QR	OXIDOREDUCTASE	Q	3.0	3.0	1	16	AQVPLGAGIALACKYN	9234
3F02	BD	HYDROLASE INHIBITOR	B	1.5	3.0	2	8	LATLEPLV	9235
3F5C	AC	TRANSCRIPTION	A	1.5	3.0	2	18	LRAISKQAEDYLYYKHVN	9236
3F9K	UW	VIRAL PROTEIN, RECOMBINATION	W	1.5	3.0	2	10	TEMITTLKKI	9237
3FH6	FG	TRANSPORT PROTEIN	G	1.5	3.0	2	19	QKARLFITHLLLLLFIAAI	9238
3FKS	UX	HYDROLASE	U	1.5	3.0	2	14	RSTVAQLVQTLEQH	9239
3FKU	EF	VIRAL PROTEIN/IMMUNE SYSTEM	F	3.0	3.0	1	22	KESTQKAIDGVTNKVNSIIDKM	9240
3FWC	BC	CELL CYCLE, TRANSCRIPTION	C	1.5	3.0	2	16	NYELISNELKARLLQE	9241
3G4S	FM	RIBOSOME	F	1.0	3.0	3	11	TNETTKSIERG	9242
3GJX	FD	PROTEIN TRANSPORT	F	1.5	3.0	2	6	VFHRKK	9243
3GLH	NO	TRANSFERASE	N	1.5	3.0	2	15	RRMGVEMTLLRALAF	9244
3GTM	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.5	3.0	2	7	QSSIDRG	9245
3H0L	GI	LIGASE	G	1.5	3.0	2	13	IFEMYARTRDEGF	9246
3H87	AD	TOXIN/ANTITOXIN	A	3.0	3.0	1	9	GEIARREFR	9247
3HKZ	CK	TRANSFERASE	K	3.0	3.0	1	10	HFNEVFISLW	9248
3HRW	CD	OXYGEN TRANSPORT	D	3.0	3.0	1	16	PAAQAAFQKVVAGVAT	9249
1AFV	BM	VIRAL PROTEIN/IMMUNE SYSTEM	B	2.9	2.9	1	6	GSDIAG	9250
1AHJ	EF	LYASE	E	1.5	2.9	2	9	PRKVLSEMG	9251
1AVF	PA	ASPARTIC PROTEASE	P	1.5	2.9	2	8	IRETMKEK	9252
1AWC	AB	TRANSCRIPTION/DNA	A	1.5	2.9	2	10	LWQFLLELLT	9253
1AYY	AB	HYDROLASE	A	2.9	2.9	1	14	AESEKEWKEWLKTS	9254
1B33	JK	PHOTOSYNTHESIS	J	1.5	2.9	2	12	IVTKSIVNADAE	9255
1BGY	OP	ELECTRON TRANSPORT	O	2.9	2.9	1	8	FSSVTHIC	9256
1BGY	PR	ELECTRON TRANSPORT	R	1.5	2.9	2	20	ENLYDDRVFRIKRALDLSMR	9257
1BM3	LH	IMMUNE SYSTEM	L	1.5	2.9	2	6	SEQLTS	9258
1BX2	DE	IMMUNE SYSTEM	D	1.5	2.9	2	23	AQGALANIAVDKANLEIMTKRSN	9259
1C0G	SA	CONTRACTILE PROTEIN	A	2.9	2.9	1	12	SVWIGGSILASL	9260

1CB7	CD	ISOMERASE	C	1.5	2.9	2	14	AVGNKILDHAFTNA	9261
1CM1	AB	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	A	1.5	2.9	2	9	YEEFVQMMT	9262
1D2Z	CD	APOPTOSIS	C	1.5	2.9	2	13	ASNEFLNIWGGQY	9263
1DGR	AW	PLANT PROTEIN	W	1.5	2.9	2	8	RQVSDLTF	9264
1DX5	CO	SERINE PROTEINASE	O	1.5	2.9	2	11	KKWIQKVIDQF	9265
1E7P	DE	OXIDOREDUCTASE	D	1.5	2.9	2	8	QEICEYFA	9266
1E7P	JK	OXIDOREDUCTASE	J	1.5	2.9	2	9	QEICEYFAG	9267
1EBD	BC	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)	C	1.5	2.9	2	10	PSVRKYAREK	9268
1EM8	AB	GENE REGULATION	A	2.9	2.9	1	14	EKQAYRLDEALWAR	9269
1EQZ	AB	STRUCTURAL PROTEIN/DNA	A	1.5	2.9	2	10	PRHLQLAIRN	9270
1EYS	LM	ELECTRON TRANSPORT	L	1.5	2.9	2	12	SEHENTFFRDIV	9271
1EYX	KL	PHOTOSYNTHESIS	K	2.9	2.9	1	12	VITTVISAADSA	9272
1F66	EF	STRUCTURAL PROTEIN/DNA	E	1.5	2.9	2	12	PKDIQLARRIRG	9273
1F6F	AC	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR	A	2.9	2.9	1	28	LQSLFDRATTVANYNSKLAGEMVNRFDE	9274
1F80	CF	TRANSFERASE	C	1.5	2.9	2	9	QKRFAERIL	9275
1FBV	AC	LIGASE	A	2.9	2.9	1	10	TSCLTSWQES	9276
1FIQ	AC	OXIDOREDUCTASE	A	1.5	2.9	2	9	LLAYLRRKL	9277
1FJ1	AB	IMMUNE SYSTEM	A	1.5	2.9	2	7	SEQLTSG	9278
1FNT	QY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.5	2.9	2	23	AGDTVQFAEYIQANIQLYSIRED	9279
1FQV	AB	LIGASE	B	1.5	2.9	2	8	PEEIRKTF	9280
1FQV	CD	LIGASE	C	1.5	2.9	2	8	KRWYRLAS	9281
1G0U	VM	HYDROLASE	M	1.5	2.9	2	14	FGAHMANPLLRKVV	9282
1G73	BC	APOPTOSIS/APOPTOSIS INHIBITOR	C	2.9	2.9	1	9	PWEQHAKWY	9283
1GCV	CB	OXYGEN STORAGE/TRANSPORT	C	1.5	2.9	2	19	PQNFPMLSECIIVTLATHL	9284
1GH0	CD	PHOTOSYNTHESIS	C	1.5	2.9	2	12	PLTEAVSVADSQ	9285
1GH0	CD	PHOTOSYNTHESIS	D	1.5	2.9	2	13	TAQIDALSQMVAE	9286
1GH0	KB	PHOTOSYNTHESIS	K	1.5	2.9	2	17	DAAVEANSYLDYAINAL	9287
1GH0	KL	PHOTOSYNTHESIS	L	1.5	2.9	2	13	TAQIDALSQMVAE	9288
1HBM	BC	METHANOGENESIS	C	2.9	2.9	1	9	PYVRSRAYL	9289
1I3R	CD	IMMUNE SYSTEM	C	2.9	2.9	1	5	EEFAK	9290
1I3R	GH	IMMUNE SYSTEM	H	2.9	2.9	1	9	RPDAENWNS	9291
1I4O	BD	APOPTOSIS/HYDROLASE	D	2.9	2.9	1	8	HADYLLRT	9292
1IB1	CG	SIGNALING PROTEIN/TRANSFERASE	C	1.5	2.9	2	19	PIRLGLALNFSVFYYEILN	9293
1IBT	EF	LYASE	E	1.5	2.9	2	8	ELDAKLNK	9294
1IJD	AB	PHOTOSYNTHESIS	B	1.5	2.9	2	30	SEQAEELHKHVIDGTRVFLVIAAIAHFLAF	9295
1IJD	CD	PHOTOSYNTHESIS	D	1.5	2.9	2	30	SEQAEELHKHVIDGTRVFLVIAAIAHFLAF	9296
1IJD	EF	PHOTOSYNTHESIS	F	1.5	2.9	2	30	SEQAEELHKHVIDGTRVFLVIAAIAHFLAF	9297

1IR2	BJ	LYASE	B	2.9	2.9	1	21	NAPGAAANRVALEACTQARNE	9298
1IR2	EM	LYASE	E	2.9	2.9	1	21	NAPGAAANRVALEACTQARNE	9299
1IRU	JK	HYDROLASE	J	2.9	2.9	1	22	ATDVQTVAQRLKFRLNLYELKE	9300
1IRU	OW	HYDROLASE	W	2.9	2.9	1	23	AADTDMTTQLISSNLELHSLSTG	9301
1IWA	GD	LYASE	G	1.5	2.9	2	15	GKNYGRVVYEALKGG	9302
1J34	AB	PROTEIN BINDING/BLOOD CLOTTING	A	1.5	2.9	2	10	WDDAERFCTE	9303
1JB0	BX	PHOTOSYNTHESIS	B	2.9	2.9	1	10	VFAQFIQAAH	9304
1JB0	FJ	PHOTOSYNTHESIS	F	2.9	2.9	1	11	SGQKRFERYSQ	9305
1JD2	AG	HYDROLASE	A	2.9	2.9	1	13	GQIDYALTAVKQG	9306
1JD2	PK	HYDROLASE	K	1.5	2.9	2	13	VGELFWKVKEEEG	9307
1JD2	VO	HYDROLASE	O	1.5	2.9	2	22	AADTEAVTQLIGSNIELHSLYT	9308
1JD2	XQ	HYDROLASE	Q	1.5	2.9	2	22	AGDTVQFAEYIQANIQLYSIRE	9309
1JNR	CD	OXIDOREDUCTASE	D	2.9	2.9	1	5	EEALK	9310
1JR3	BE	TRANSFERASE	B	1.5	2.9	2	15	RRMGVEMTLLRALAF	9311
1KF6	BC	OXIDOREDUCTASE	B	2.9	2.9	1	6	YCSEVC	9312
1KF6	CD	OXIDOREDUCTASE	D	1.5	2.9	2	15	EPVFWGLFGAGGMWS	9313
1KFU	LS	HYDROLASE	L	1.5	2.9	2	9	CQLHQVIVA	9314
1KQF	AB	OXIDOREDUCTASE	A	2.9	2.9	1	5	RTASV	9315
1KYO	GH	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	1.5	2.9	2	20	EDESYARAYRIIRAHQTELT	9316
1KYO	LM	OXIDOREDUCTASE/ELECTRON TRANSPORT	L	1.5	2.9	2	20	DTEVERAKSLLKLQLGQLYE	9317
1L1O	EF	DNA BINDING PROTEIN	E	1.5	2.9	2	19	NEFTTHILEVINAHMVLSK	9318
1L2W	HL	CHAPERONE	L	1.5	2.9	2	10	HSVIGFIQRM	9319
1LKY	CD	TRANSCRIPTION	C	2.9	2.9	1	7	GKALLLL	9320
1LQ8	EF	BLOOD CLOTTING	E	1.5	2.9	2	6	MQQVEN	9321
1LWU	AB	BLOOD CLOTTING	A	1.5	2.9	2	12	QQLTLLQHNIKT	9322
1LWU	DE	BLOOD CLOTTING	D	1.5	2.9	2	12	QQLTLLQHNIKT	9323
1M1J	AB	BLOOD CLOTTING	A	1.5	2.9	2	15	GYDNIQKHLTQASSI	9324
1M2Z	AB	HORMONE/HORMONE ACTIVATOR	A	1.5	2.9	2	10	LDDQMTLLQY	9325
1M93	BC	VIRAL PROTEIN	B	1.5	2.9	2	6	LESIEQ	9326
1MF8	AB	HYDROLASE, LIGASE	B	2.9	2.9	1	5	IHKKM	9327
1MHY	BD	OXIDOREDUCTASE	B	2.9	2.9	1	7	SSVGRDC	9328
1MJG	BN	OXIDOREDUCTASE	B	1.5	2.9	2	30	PVNLVFSAIRVALADYTGEHIATDFSDILF	9329
1MJG	CO	OXIDOREDUCTASE	C	1.5	2.9	2	30	PVNLVFSAIRVALADYTGEHIATDFSDILF	9330
1MJG	DO	OXIDOREDUCTASE	O	1.5	2.9	2	30	VALFREVYHGAITATSYAEILLNQAIRTYG	9331
1MZN	AB	TRANSCRIPTION	A	1.5	2.9	2	22	PVTNICQAADKQLFTLVEWAKR	9332
1N4Q	IJ	TRANSFERASE	I	1.5	2.9	2	14	YTVWHFRRVLLRSL	9333
1N5W	AB	OXIDOREDUCTASE	A	1.5	2.9	2	9	ALQEGFRMM	9334
1N5W	BC	OXIDOREDUCTASE	B	1.5	2.9	2	11	RYVAADAIELV	9335

1N5W	DE	OXIDOREDUCTASE	E	2.9	2.9	1	6	RMENLS	9336
1N86	BC	BLOOD CLOTTING	C	1.5	2.9	2	20	THDSSIRYLQEIYNSNNQKI	9337
1ND0	EF	IMMUNE SYSTEM	E	1.5	2.9	2	6	SEQLTS	9338
1NF5	AB	TRANSFERASE/TRANSFERASE	A	1.5	2.9	2	12	LLEWACVLFHTS	9339
1NHG	BD	OXIDOREDUCTASE	B	1.5	2.9	2	12	YGWGIAKELSKR	9340
1NTK	CG	OXIDOREDUCTASE	C	2.9	2.9	1	34	HPYITIGQLASVLYFLLILVLMPTAGTIENKLLK	9341
1PMA	CP	PROTEASE	P	1.5	2.9	2	22	VGDAQVLVRYMKAELELYRLQR	9342
1POI	CD	TRANSFERASE	D	1.5	2.9	2	5	LRFMA	9343
1PTO	LH	TOXIN	L	1.5	2.9	2	17	TWFDTMLGFAISAYALK	9344
1QHH	BD	HYDROLASE	D	1.5	2.9	2	5	LHAAK	9345
1R27	AB	OXIDOREDUCTASE	B	2.9	2.9	1	5	YEDRF	9346
1R4M	AI	CELL CYCLE	I	1.5	2.9	2	13	VERIKERVEEKEG	9347
1R5W	DF	SIGNALING PROTEIN	D	2.9	2.9	1	9	RPDAENWNS	9348
1R8Q	AF	PROTEIN TRANSPORT/EXCHANGE FACTOR	F	1.5	2.9	2	14	EELLRNLYDSIRNE	9349
1RIO	HB	TRANSCRIPTION/DNA	H	1.5	2.9	2	15	RERIRQIENKALRKL	9350
1RM6	DF	OXIDOREDUCTASE	D	2.9	2.9	1	8	REETFIAH	9351
1RP3	EF	TRANSCRIPTION	F	1.5	2.9	2	14	LEKKVKELKEKIEK	9352
1RYP	AI	MULTICATALYTIC PROTEINASE	A	2.9	2.9	1	18	CDVLAKRMANLSQIYTQR	9353
1RYP	PX	MULTICATALYTIC PROTEINASE	P	1.5	2.9	2	16	TKLLVSEVAKIMQEAT	9354
1RYP	YL	MULTICATALYTIC PROTEINASE	Y	2.9	2.9	1	13	YSGFYTFSLLDHH	9355
1S0Y	KH	LYASE	H	1.5	2.9	2	19	VARKQQLIRDVIDVTNKSI	9356
1S6C	AB	TRANSPORT PROTEIN	B	2.9	2.9	1	11	LPFARAAAIGW	9357
1SA0	CD	CELL CYCLE	D	1.5	2.9	2	8	RKLAVNMV	9358
1SB3	AB	OXIDOREDUCTASE	B	1.5	2.9	2	21	VKYRRRVLLAISRKVVDQLWE	9359
1SB3	AC	OXIDOREDUCTASE	A	2.9	2.9	1	8	REETFIAH	9360
1SKR	AB	TRANSFERASE/ELECTRON TRANSPORT/DNA	B	1.5	2.9	2	6	GPCKMI	9361
1SQB	CD	OXIDOREDUCTASE	D	2.9	2.9	1	5	YRHLV	9362
1T3Q	AB	OXIDOREDUCTASE	B	2.9	2.9	1	7	RQENFLG	9363
1T3Q	DE	OXIDOREDUCTASE	E	2.9	2.9	1	7	RQENFLG	9364
1TBG	AE	COMPLEX (GTP-BINDING/TRANSDUCER)	A	1.5	2.9	2	5	LSQIT	9365
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.5	2.9	2	18	DSVLFYAITTLHNLLLHQ	9366
1TI2	KL	OXIDOREDUCTASE	K	1.5	2.9	2	6	HTARLV	9367
1TIL	CD	TRANSCRIPTION	D	1.5	2.9	2	8	PAVKRLFD	9368
1TO9	AB	BIOSYNTHETIC PROTEIN	B	2.9	2.9	1	9	PTAYSYTSH	9369
1TQY	AB	TRANSFERASE	A	2.9	2.9	1	11	SVMPAEVAWAV	9370
1TZN	Hh	TOXIN RECEPTOR/TOXIN	h	1.5	2.9	2	14	LVPSYAEKEAKISR	9371

1U35	CD	STRUCTURAL PROTEIN/DNA	C	1.5	2.9	2	10	PRHILLAVAN	9372
1U35	FH	STRUCTURAL PROTEIN/DNA	H	2.9	2.9	1	29	SKAMGIMNSFVNDIFERIASEASRLAHYN	9373
1U35	GH	STRUCTURAL PROTEIN/DNA	H	1.5	2.9	2	11	SIYVYKVLKQV	9374
1UUZ	AD	HYDROLASE/INHIBITOR	D	2.9	2.9	1	6	VQAWIR	9375
1UZD	HJ	LYASE	H	1.5	2.9	2	21	NAPGAAANRVALEACTQARNE	9376
1UZD	HJ	LYASE	J	2.9	2.9	1	14	DEQIAAQVDYIVAN	9377
1V54	DK	OXIDOREDUCTASE	K	2.9	2.9	1	5	FHDKY	9378
1VF6	BD	PROTEIN BINDING/PROTEIN TRANSPORT	B	2.9	2.9	1	13	NEKLSMFYETLKS	9379
1W5C	HJ	PHOTOSYNTHESIS	H	1.5	2.9	2	10	FAHAVFALLF	9380
1WDW	CD	LYASE	C	1.5	2.9	2	8	YNPIYRAG	9381
1WMI	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.5	2.9	2	12	EEEIAELLELAR	9382
1WQ9	AB	TOXIN	A	2.9	2.9	1	9	FLDVYQRSA	9383
1WYU	AB	OXIDOREDUCTASE	A	1.5	2.9	2	11	PEAVRRALAER	9384
1WYU	CD	OXIDOREDUCTASE	C	1.5	2.9	2	14	PEYRAVLRAYLEAV	9385
1X3Z	AB	HYDROLASE	B	1.5	2.9	2	10	LAPLLENISA	9386
1X86	AB	SIGNALING PROTEIN/MEMBRANE PROTEIN	B	1.5	2.9	2	9	DRLRPLSYP	9387
1XD2	BC	SIGNALING PROTEIN	B	2.9	2.9	1	18	TKSFEDIHQYREQIKRVK	9388
1XFU	BP	LYASE/METAL BINDING PROTEIN	P	2.9	2.9	1	5	AFSLF	9389
1XFV	DR	LYASE/METAL BINDING PROTEIN	R	2.9	2.9	1	7	KEAFSLF	9390
1XFV	ES	LYASE/METAL BINDING PROTEIN	S	2.9	2.9	1	7	KEAFSLF	9391
1XGP	AB	IMMUNE SYSTEM	A	1.5	2.9	2	6	SEQLTS	9392
1XLS	AE	TRANSCRIPTION	A	1.5	2.9	2	23	PAEVEALREKVYASLEAYCKHKY	9393
1XQS	BD	CHAPERONE	D	1.5	2.9	2	18	KRAVRRLRTACERAKRTL	9394
1XWJ	AB	CELL ADHESION/PROTEIN BINDING	B	1.5	2.9	2	20	ELIESARKVSEKVSHVLAAL	9395
1YE9	BE	OXIDOREDUCTASE	B	1.5	2.9	2	9	DTFWDYVSL	9396
1YE9	BG	OXIDOREDUCTASE	G	2.9	2.9	1	13	FHRRELWEAIEAG	9397
1YE9	CH	OXIDOREDUCTASE	C	1.5	2.9	2	9	DTFWDYVSL	9398
1YHU	NP	OXYGEN STORAGE/TRANSPORT	P	2.9	2.9	1	20	NEFKAHCIRVVNGLDSSIGL	9399
1YSL	AB	LYASE	B	1.5	2.9	2	9	AAVVLHRLM	9400
1Z7Q	KZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	2.9	2.9	1	19	VEDALYLGKRSILAAAHRD	9401
1ZBB	EF	STRUCTURAL PROTEIN/DNA	E	1.5	2.9	2	12	PKDIQLARRIRG	9402
1ZY3	AB	APOPTOSIS	B	1.5	2.9	2	16	KNIARHLAQVGDSMDR	9403
2A1D	BD	HYDROLASE	D	1.5	2.9	2	20	LKGRLTSLESQFINALDILE	9404
2A6Q	AE	TOXIN INHIBITOR/TOXIN	E	2.9	2.9	1	12	EESWDDYLYWQE	9405
2AA1	AB	OXYGEN STORAGE/TRANSPORT	B	1.5	2.9	2	19	GEVQAAFQKFMAVVVSSLG	9406
2AA1	CB	OXYGEN STORAGE/TRANSPORT	B	1.5	2.9	2	6	PWTQRY	9407
2AA1	CD	OXYGEN STORAGE/TRANSPORT	D	1.5	2.9	2	19	GEVQAAFQKFMAVVVSSLG	9408
2AAI	AB	GLYCOSIDASE	A	2.9	2.9	1	13	QYIEGEMRTRIRY	9409

2ACL	AB	TRANSCRIPTION	A	1.5	2.9	2	7	RFAKLLL	9410
2ACZ	BD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.5	2.9	2	27	GVHDFILVRATAIVLTLYIIYMVGFFA	9411
2AK4	TU	IMMUNE SYSTEM	U	1.5	2.9	2	7	EAEISHT	9412
2AXT	AI	ELECTRON TRANSPORT	I	1.5	2.9	2	24	ETLKITVYIVVTFFVLLFVFGFLS	9413
2AXT	BD	ELECTRON TRANSPORT	D	2.9	2.9	1	13	IFRFLLFFQGFHN	9414
2B8K	AF	TRANSFERASE	F	2.9	2.9	1	17	KYERARILGTRALQISM	9415
2B8K	CJ	TRANSFERASE	J	1.5	2.9	2	7	LIEKFLR	9416
2BA0	BE	RNA BINDING PROTEIN	E	1.5	2.9	2	30	RDEVKQAIELAKKGALQIYEMQREAILRRY	9417
2CKF	EF	OXIDOREDUCTASE	E	2.9	2.9	1	11	GENMSSATYVN	9418
2DD4	BC	HYDROLASE	C	2.9	2.9	1	6	RDCLIG	9419
2DD4	KL	HYDROLASE	K	2.9	2.9	1	9	AEERRRKQN	9420
2DWZ	CD	ONCOPROTEIN	D	1.5	2.9	2	6	LEDYVA	9421
2DXB	BC	HYDROLASE	C	2.9	2.9	1	6	RDCLIG	9422
2DXB	GH	HYDROLASE	H	2.9	2.9	1	9	AEERRRKQN	9423
2E 74	AB	PHOTOSYNTHESIS	A	2.9	2.9	1	9	IQALADDVT	9424
2E 74	CD	PHOTOSYNTHESIS	C	1.5	2.9	2	37	PNRVKWMIAFICLVMLAQLMLILKKKQVEKVQAAEMN	9425
2EFC	CD	TRANSPORT PROTEIN	D	1.5	2.9	2	8	HSLAPMYY	9426
2EQ9	GI	OXIDOREDUCTASE	I	1.5	2.9	2	10	PAARKLAREL	9427
2F8N	AB	STRUCTURAL PROTEIN/DNA	A	1.5	2.9	2	12	PKDIQLARRIRG	9428
2F8N	HG	STRUCTURAL PROTEIN/DNA	H	2.9	2.9	1	12	SREIQTAVRLLL	9429
2F93	AB	MEMBRANE PROTEIN	B	1.5	2.9	2	22	GALTVLFGAIAYGEVTAAAATG	9430
2F9I	AB	TRANSFERASE	A	1.5	2.9	2	6	KAAEER	9431
2F9I	CD	TRANSFERASE	C	1.5	2.9	2	6	KAAEER	9432
2FF6	GA	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	A	2.9	2.9	1	12	SVWIGGSILASL	9433
2FIF	AB	PROTEIN TURNOVER/ENDOCYTOSIS	B	1.5	2.9	2	36	SKCWREEYHKARQKQIQEDWELAERLQREEEEAFAS	9434
2FK0	GJ	VIRAL PROTEIN	J	1.5	2.9	2	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	9435
2FKW	OP	MEMBRANE PROTEIN, PHOTOSYNTHESIS	P	1.5	2.9	2	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	9436
2FUG	69	OXIDOREDUCTASE	6	2.9	2.9	1	13	PEALIYAVMQLQK	9437
2FUG	OP	OXIDOREDUCTASE	O	2.9	2.9	1	13	PEALIYAVMQLQK	9438
2FUG	XY	OXIDOREDUCTASE	X	2.9	2.9	1	13	PEALIYAVMQLQK	9439
2FYN	MN	OXIDOREDUCTASE	M	1.5	2.9	2	15	VDLAFASVEHIMRNV	9440
2GPP	BD	TRANSCRIPTION	B	1.5	2.9	2	8	KLFLEMLE	9441
2GTL	BC	OXYGEN STORAGE/TRANSPORT	B	1.5	2.9	2	19	PAFIAHADRVLGGLDIAIS	9442
2GUZ	IJ	CHAPERONE, PROTEIN TRANSPORT	J	1.5	2.9	2	8	LDESCKIL	9443
2GUZ	KL	CHAPERONE, PROTEIN TRANSPORT	L	1.5	2.9	2	8	LDESCKIL	9444
2GYK	AB	ANTIBIOTIC/ANTIBIOTIC INHIBITOR	A	2.9	2.9	1	6	SALIYY	9445

2H4C	GH	HYDROLASE	H	1.5	2.9	2	11	LFQFARLIDAK	9446
2H4Q	AB	HYDROLASE INHIBITOR	A	2.9	2.9	1	32	RWGSELEISMEQVSASIGNFTVDLFNKLNETN	9447
2HHF	AB	TRANSFERASE	B	1.5	2.9	2	17	GGNYGPTVLVQQEALKR	9448
2HHH	CE	RIBOSOME	C	1.5	2.9	2	15	VRRAIKQAVQRVMES	9449
2HIO	BD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	B	1.5	2.9	2	12	SREIQTAVRLLL	9450
2HRK	AB	LIGASE/RNA BINDING PROTEIN	B	2.9	2.9	1	10	LDQLNLVLRD	9451
2HUE	AB	DNA BINDING PROTEIN	B	2.9	2.9	1	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	9452
2I2R	BF	TRANSPORT PROTEIN	F	1.5	2.9	2	8	HVDVFFQK	9453
2I2X	EF	TRANSFERASE	E	2.9	2.9	1	12	DKVLRDLMMLSD	9454
2I3S	CD	CELL CYCLE	D	1.5	2.9	2	5	FNLIY	9455
2IDO	AB	TRANSFERASE	A	2.9	2.9	1	8	PEAFGVHG	9456
2IK8	CD	SIGNALING PROTEIN	D	1.5	2.9	2	21	DAAQGKTRTLMEKDSYPRFLK	9457
2INN	AF	OXIDOREDUCTASE	A	2.9	2.9	1	7	PVHQIYQ	9458
2INN	BD	OXIDOREDUCTASE	D	1.5	2.9	2	13	RLGIGQYLSRIAL	9459
2J0Q	BI	HYDROLASE	B	1.5	2.9	2	14	KRKVDWLTEKMREA	9460
2JBL	CM	ELECTRON TRANSPORT	C	1.5	2.9	2	18	LSDAYATFALMMSISDSL	9461
2JIZ	IM	HYDROLASE	M	2.9	2.9	1	15	TREGNDLYHEMIESG	9462
2JIZ	JK	HYDROLASE	K	1.5	2.9	2	15	TREGNDLYHEMIESG	9463
2JJ0	LM	PHOTOSYNTHESIS	M	2.9	2.9	1	7	TLLGWFG	9464
2JKI	CU	CHAPERONE	C	2.9	2.9	1	8	KSDLVNNL	9465
2JKR	AS	ENDOCYTOSIS	A	1.5	2.9	2	12	RGLAVFISDIRN	9466
2JKR	LI	ENDOCYTOSIS	L	1.5	2.9	2	12	RGLAVFISDIRN	9467
2JKR	LI	ENDOCYTOSIS	L	1.5	2.9	2	14	YTEKQIGYLFISVL	9468
2K2I	AB	CELL CYCLE	A	1.5	2.9	2	10	EELQEMIDEA	9469
2K7W	AB	APOPTOSIS	B	1.5	2.9	2	16	IWIAQELRRIGDEFNA	9470
2NPP	DF	SIGNALING PROTEIN,HYDROLASE	D	2.9	2.9	1	17	YLHRMTTLFCINVLSEV	9471
2NS8	DF	TRANSCRIPTION	D	1.5	2.9	2	14	PLLRQAIELFDHQG	9472
2NV2	MN	LYASE/TRANSFERASE	N	1.5	2.9	2	11	STTMRRLIDTY	9473
2NV2	WX	LYASE/TRANSFERASE	W	1.5	2.9	2	10	ERVKRGMAEM	9474
2NV2	WX	LYASE/TRANSFERASE	X	1.5	2.9	2	11	STTMRRLIDTY	9475
2NVU	BC	PROTEIN TURNOVER, LIGASE	B	1.5	2.9	2	10	ESLQFLLDTC	9476
2NYL	BC	HYDROLASE	C	2.9	2.9	1	9	FYDECLRKY	9477
2NZD	GH	STRUCTURAL PROTEIN/DNA	H	1.5	2.9	2	12	AIYVYKVLKQVH	9478
2NZU	GL	TRANSCRIPTION	L	1.5	2.9	2	8	IMGVMSLG	9479
2O9I	AC	TRANSCRIPTION	A	2.9	2.9	1	10	IEDQISLLKG	9480
2P1L	GH	APOPTOSIS	G	2.9	2.9	1	21	WGRIVAFFSFGGALCVESVDK	9481
2P1N	AB	SIGNALING PROTEIN	B	2.9	2.9	1	7	VLEHVFS	9482
2P2C	GH	HYDROLASE	H	2.9	2.9	1	15	VADMLVKVNALIKDR	9483
2P5T	AB	TRANSCRIPTION REGULATOR	B	1.5	2.9	2	12	KTTIHRIKQKEF	9484

2PJR	AB	HYDROLASE/DNA	A	1.5	2.9	2	9	FVAGRIREA	9485
2PKG	BC	HYDROLASE REGULATOR/VIRAL PROTEIN	B	1.5	2.9	2	6	KEWAHA	9486
2PVG	AC	ELECTRON TRANSPORT	A	1.5	2.9	2	17	ATLAAMKNFAEQYAKRT	9487
2Q9Q	BC	REPLICATION	C	1.5	2.9	2	38	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG	9488
2QA4	FM	RIBOSOME	F	1.5	2.9	2	13	EEIVMHIPELADE	9489
2QAR	DE	HYDROLASE REGULATOR	E	1.5	2.9	2	20	GDVLYELLQHILKQRDLEAE	9490
2QJP	GH	ELECTRON TRANSPORT	G	2.9	2.9	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	9491
2QKM	EF	HYDROLASE	F	1.5	2.9	2	15	FSQVLDDLSARFILN	9492
2QL2	CD	TRANSCRIPTION/DNA	D	1.5	2.9	2	25	RMKANARERNRMHGLNAALDNLRKV	9493
2QR1	CD	TRANSFERASE	C	1.5	2.9	2	15	APEILLAVYRALQRA	9494
2QYF	CD	CELL CYCLE	D	1.5	2.9	2	14	STAACLRRLFRAIF	9495
2R5C	AB	TRANSFERASE	A	2.9	2.9	1	12	AYEALYATIQGH	9496
2UUN	ST	ELECTRON TRANSPORT	S	1.5	2.9	2	12	PLTDAVSTADSQ	9497
2UUN	UV	ELECTRON TRANSPORT	V	1.5	2.9	2	13	VAQIDALSQMVAE	9498
2UY1	AB	RNA BINDING PROTEIN	B	1.5	2.9	2	17	MELFRELVDQKMDAIKA	9499
2V7H	LH	IMMUNE SYSTEM	L	2.9	2.9	1	5	SEQLT	9500
2V7Q	BE	HYDROLASE	B	1.5	2.9	2	15	LSKQAVAYRQMSLLL	9501
2V7Q	BF	HYDROLASE	B	1.5	2.9	2	12	VFYLHSRLLERA	9502
2VJT	AB	PHOTOSYNTHESIS	B	2.9	2.9	1	13	GAALDKLKAYFTT	9503
2VML	GH	PHOTOSYNTHESIS	H	1.5	2.9	2	12	AFTKAIVAADLR	9504
2VT1	AB	MEMBRANE PROTEIN	B	2.9	2.9	1	13	QCALAVRKYANEV	9505
2W83	AC	PROTEIN TRANSPORT	C	1.5	2.9	2	64	PEFMGREVENLILENTQLLETKNALNIVKNDLIAKVDELTCEKDVLQGELEAVKQAKLKLEEKN	9506
2WBJ	EF	IMMUNE SYSTEM	E	2.9	2.9	1	5	EEFGR	9507
2WIN	HQ	IMMUNE SYSTEM	Q	1.5	2.9	2	21	TYYKRTIKISGQKAMYALKSK	9508
2Z2L	DE	BIOSYNTHETIC PROTEIN	E	1.5	2.9	2	19	SPLQSFMETQMDAFQEKVK	9509
2Z2S	AB	TRANSCRIPTION	B	1.5	2.9	2	17	DECRARAGALDAVGGSL	9510
2ZCY	M1	HYDROLASE	M	2.9	2.9	1	6	WDFAKD	9511
2ZFB	AB	METAL BINDING PROTEIN	A	1.5	2.9	2	19	PVNFKLLGQCFLVVVAIHN	9512
2ZT9	CD	PHOTOSYNTHESIS	C	1.5	2.9	2	35	ANRVGWLIAFVALVMLAQVMLVLKKKQVEKVQAAE	9513
3B9J	IK	OXIDOREDUCTASE	I	1.5	2.9	2	9	RPILQGFRT	9514
3BL2	AC	VIRAL PROTEIN/APOPTOSIS	A	1.5	2.9	2	9	LSKLFTSLF	9515
3BZ1	AI	ELECTRON TRANSPORT	A	1.5	2.9	2	7	WELSYRL	9516
3BZL	BD	MEMBRANE PROTEIN, PROTEIN TRANSPORT	B	2.9	2.9	1	7	LANNIKK	9517
3C1B	AB	STRUCTURAL PROTEIN/DNA	A	1.5	2.9	2	12	PKDIQLARRIRG	9518
3C60	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	C	2.9	2.9	1	7	PEFGQLA	9519
3C7B	DE	OXIDOREDUCTASE	D	2.9	2.9	1	12	TLELCYDLTMTY	9520

3C8G	CB	TRANSCRIPTION REGULATOR	C	1.5	2.9	2	11	IDVALRLIYAL	9521
3C91	OW	HYDROLASE	W	2.9	2.9	1	15	IEAVATLLSNMLNQV	9522
3CFV	BE	HISTONE/CHAPERONE	B	2.9	2.9	1	22	TVEERVINEEYKIWKKNTPFLY	9523
3CIP	AG	STRUCTURAL PROTEIN	A	2.9	2.9	1	12	SVWIGGSILASL	9524
3CJH	GJ	PROTEIN TRANSPORT	G	1.5	2.9	2	16	TELVNKISENCFEKCL	9525
3CJT	GH	TRANSFERASE/RIBOSOMAL PROTEIN	H	1.5	2.9	2	9	PVGPALGQH	9526
3CJT	KL	TRANSFERASE/RIBOSOMAL PROTEIN	K	2.9	2.9	1	11	DPILPGLFDGG	9527
3CSY	KL	IMMUNE SYSTEM/VIRAL PROTEIN	L	1.5	2.9	2	13	ILNRKAIDFLLQR	9528
3CW2	EM	TRANSLATION	E	2.9	2.9	1	15	KEEALSQYRQIKQFT	9529
3D4X	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	2.9	2.9	1	16	AGEYGAEALERTFCSF	9530
3D5B	W5	RIBOSOME	W	1.5	2.9	2	11	PRKVRLVVDLI	9531
3D5D	I1	RIBOSOME	1	1.5	2.9	2	13	IPKVYELVERAKG	9532
3D5D	W5	RIBOSOME	W	1.5	2.9	2	11	PRKVRLVVDLI	9533
3DCT	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	A	1.5	2.9	2	26	HEDQIALLKGSAVEAMFLRSAEIFNK	9534
3DHR	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	1.5	2.9	2	19	PVNFKLLGHCFLVVVAVHF	9535
3DKN	AC	PROTEIN TRANSPORT/RNA	A	1.5	2.9	2	21	FKEKLKWTGIVLVLYFIMGCI	9536
3DL8	AG	PROTEIN TRANSPORT	A	1.5	2.9	2	28	REYQMEGFAMFEHMIESIEDEVAKFVMK	9537
3DNL	DF	VIRAL PROTEIN	D	1.5	2.9	2	10	VEQMHEDIIS	9538
3DOE	AB	SIGNALING PROTEIN/HYDROLASE	B	1.5	2.9	2	10	DIFDMLLTFT	9539
3DTP	AC	CONTRACTILE PROTEIN	C	2.9	2.9	1	15	EEQTAEFKEAFQLFD	9540
3DTU	CD	OXIDOREDUCTASE	C	2.9	2.9	1	28	EWAGKLHFWMMFVGANLTFFPQHFLGRQ	9541
3DVU	BD	VIRAL PROTEIN/APOPTOSIS	B	1.5	2.9	2	13	WKRDLSKLFTSLF	9542
3DZU	AD	TRANSCRIPTION/DNA	D	1.5	2.9	2	29	LFAKLLQKMTDLRQIVTEHVQLLQVIKKT	9543
3E8C	AG	TRANSFERASE	A	2.9	2.9	1	18	KAVDWWALGVLIYEMAAG	9544
3ESW	AB	HYDROLASE	B	1.5	2.9	2	12	LAPLLENISARY	9545
3ETR	LN	OXIDOREDUCTASE	L	1.5	2.9	2	9	RPILQGFRT	9546
3EUH	AC	CELL CYCLE	A	1.5	2.9	2	40	LVFDLQSKLDRIISWGQQSIDLWIGYDRHVHKFIRTAIDM	9547
3EX7	AC	HYDROLASE/RNA BINDING PROTEIN/RNA	C	2.9	2.9	1	9	RELYIHRIG	9548
3EX7	EH	HYDROLASE/RNA BINDING PROTEIN/RNA	H	1.5	2.9	2	11	IRILRDIEQYY	9549
3EXG	56	OXIDOREDUCTASE	6	2.9	2.9	1	5	TYYMS	9550
3F5C	AB	TRANSCRIPTION	B	2.9	2.9	1	5	PCFQI	9551
3FCS	CD	CELL ADHESION/BLOOD CLOTTING	D	1.5	2.9	2	5	DGRLA	9552
3FKS	WY	HYDROLASE	Y	1.5	2.9	2	62	LANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTR QAVITNELVDIITGAS	9553
3FWB	AB	CELL CYCLE, TRANSCRIPTION	A	2.9	2.9	1	11	DEELRAMIEEF	9554

3FWC	MN	CELL CYCLE, TRANSCRIPTION	M	1.5	2.9	2	10	ENEFIAICTD	9555
3FWC	NP	CELL CYCLE, TRANSCRIPTION	P	1.5	2.9	2	16	FTQILSTVEPKALEMV	9556
3FWC	NP	CELL CYCLE, TRANSCRIPTION	P	1.5	2.9	2	20	DSTRETVLKQIREFLEEIVD	9557
3G43	CE	METAL BINDING PROTEIN	C	1.5	2.9	2	12	DEEVDEMIREAD	9558
3GE8	AE	OXIDOREDUCTASE	E	2.9	2.9	1	8	TLADQALH	9559
3GJX	CA	PROTEIN TRANSPORT	A	1.5	2.9	2	20	DEQNFIQNLSLFLCTFLKEH	9560
3GLH	DE	TRANSFERASE	E	1.5	2.9	2	20	APARLHWLATLLMDALKRHH	9561
3GLI	IJ	TRANSFERASE/DNA	I	1.5	2.9	2	14	RRMGVEMTLLRALA	9562
3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	1.5	2.9	2	16	YVTKRQSLKLLGELLL	9563
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.5	2.9	2	11	EMERDCMIAHG	9564
3GTU	CD	TRANSFERASE	C	1.5	2.9	2	12	SNAILRYIARKH	9565
3H4P	Aa	HYDROLASE	a	1.5	2.9	2	6	LYKMRT	9566
3H4P	Ll	HYDROLASE	l	1.5	2.9	2	6	LYKMRT	9567
3HOU	MW	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.5	2.9	2	11	LDQVLNMLYWV	9568
3HOY	CJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.5	2.9	2	7	LIEKFLR	9569
6RLX	CD	HORMONE (MUSCLE RELAXANT)	C	2.9	2.9	1	7	KRSLARF	9570
7INS	AB	HORMONE	B	1.5	2.9	2	19	VNQHLCGSHLVEALYLVCG	9571
7INS	EF	HORMONE	F	1.5	2.9	2	19	VNQHLCGSHLVEALYLVCG	9572
1AHJ	GH	LYASE	G	2.8	2.8	1	6	KDCLIG	9573
1AIP	FH	COMPLEX OF TWO ELONGATION FACTORS	H	2.8	2.8	1	13	VKELIQQAIAKIG	9574
1AOI	BD	DNA BINDING PROTEIN/DNA	D	2.8	2.8	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	9575
1B4U	AB	DIOXYGENASE	A	1.4	2.8	2	11	VYFLSKLFSTD	9576
1BCC	GH	OXIDOREDUCTASE	H	1.4	2.8	2	23	TEELFDFLHARDHCVAHKLFNSL	9577
1BGY	QV	ELECTRON TRANSPORT	V	1.4	2.8	2	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	9578
1BXN	EK	LYASE	K	1.4	2.8	2	14	DEQITKQLEYCLNQ	9579
1CDL	AE	CALCIUM-BINDING PROTEIN	A	1.4	2.8	2	12	DEEVDEMIREAD	9580
1CIC	CD	IMMUNOGLOBULIN	C	1.4	2.8	2	7	SEQLTSG	9581
1CUL	BC	LYASE/LYASE/SIGNALING PROTEIN	B	1.4	2.8	2	19	LECLRLLNEIIADFDDLLS	9582
1DE4	DF	METAL TRANSPORT INHIBITOR/RECEPTOR	D	2.8	2.8	1	12	AWPTKLEWERHK	9583
1DEE	CD	IMMUNE SYSTEM	C	1.4	2.8	2	6	DEQLKS	9584
1DFL	BW	CONTRACTILE PROTEIN	B	1.4	2.8	2	9	WWKLYSKVK	9585
1DGH	CD	OXIDOREDUCTASE	C	1.4	2.8	2	19	KMLQGRLFAYPDTHRHRLG	9586
1DGR	AW	PLANT PROTEIN	W	1.4	2.8	2	8	GEEVEELL	9587
1DGR	BM	PLANT PROTEIN	M	1.4	2.8	2	8	RQVSDLTF	9588

1DKD	CG	CHAPERONE	C	1.4	2.8	2	15	IREMLPVLEAVAKAG	9589
1DS6	AB	SIGNALING PROTEIN	B	2.8	2.8	1	7	LKELQEM	9590
1E6Y	BC	OXIDOREDUCTASE	B	1.4	2.8	2	15	MFERHQLLGLAYQGL	9591
1E7P	GH	OXIDOREDUCTASE	G	1.4	2.8	2	9	QEICEYFAG	9592
1EJO	LH	IMMUNE SYSTEM	L	1.4	2.8	2	6	SEQLTS	9593
1EQZ	GH	STRUCTURAL PROTEIN/DNA	G	1.4	2.8	2	11	TVALREIRRYQ	9594
1F3U	CD	TRANSCRIPTION	C	2.8	2.8	1	9	KYLSQQWAK	9595
1F3U	GH	TRANSCRIPTION	G	2.8	2.8	1	9	KYLSQQWAK	9596
1F66	AB	STRUCTURAL PROTEIN/DNA	A	1.4	2.8	2	12	PKDIQLARRIRG	9597
1FNT	EM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.4	2.8	2	15	INSAARNIQHLLYGK	9598
1FNT	GH	HYDROLASE/HYDROLASE ACTIVATOR	G	2.8	2.8	1	22	IPDGRHLVNRGREEAASFKKLY	9599
1FNT	Ub	HYDROLASE/HYDROLASE ACTIVATOR	U	1.4	2.8	2	22	IPDGRHLVNRGREEAASFKKLY	9600
1FPP	BA	PRENYLTRANSFERASE	A	1.4	2.8	2	14	YQVWHHRRVLVEWL	9601
1FQV	MN	LIGASE	N	1.4	2.8	2	8	PEEIRKTF	9602
1FS2	CD	LIGASE	D	1.4	2.8	2	8	PEEIRKTF	9603
1FSX	CD	OXYGEN STORAGE/TRANSPORT	C	2.8	2.8	1	19	PVNFKLLSHSLLVTLASHL	9604
1G0U	DL	HYDROLASE	L	1.4	2.8	2	15	INSAARNIQHLLYGK	9605
1G0U	IY	HYDROLASE	Y	1.4	2.8	2	13	VGELFWKVKEEEG	9606
1G1E	AB	TRANSCRIPTION	A	1.4	2.8	2	13	IQMLLEAADYLER	9607
1G1X	FB	RIBOSOME	B	1.4	2.8	2	11	KEEKQKVIQEF	9608
1G20	CD	OXIDOREDUCTASE	C	2.8	2.8	1	6	DAWSSR	9609
1GPW	AB	LYASE/TRANSFERASE	B	2.8	2.8	1	12	IMNLYRGVKRAS	9610
1H0H	AB	DEHYDROGENASE	A	2.8	2.8	1	5	RTSTK	9611
1H1L	CD	OXIDOREDUCTASE	C	2.8	2.8	1	12	SYELEAFVKALK	9612
1H1L	CD	OXIDOREDUCTASE	D	2.8	2.8	1	12	LWHFRSLMFTRQ	9613
1HBM	AB	METHANOGENESIS	B	1.4	2.8	2	12	KVEGTAVGFSFF	9614
1HBM	EC	METHANOGENESIS	C	2.8	2.8	1	20	VEAVEIMQRIHVLRSQGGFN	9615
1HV4	CD	OXYGEN STORAGE/TRANSPORT	C	1.4	2.8	2	19	PVNFKFLGHCFLVVVAIHH	9616
1I2M	AB	CELL CYCLE	A	2.8	2.8	1	5	QEKFG	9617
1I9R	XY	CYTOKINE/IMMUNE SYSTEM	Y	1.4	2.8	2	5	DEQLK	9618
1IBR	AB	CELL CYCLE, TRANSLATION	B	1.4	2.8	2	18	RLELEAAQKFLERAAVEN	9619
1II8	AB	REPLICATION	B	1.4	2.8	2	11	ERVKKEIKDLE	9620
1IR2	T1	LYASE	T	1.4	2.8	2	14	AKNYGRAVYECLRG	9621
1IRU	PQ	HYDROLASE	Q	2.8	2.8	1	11	YQVEYAMEAIG	9622
1IRU	U2	HYDROLASE	2	1.4	2.8	2	22	YADFQYLKQVLGQMVIDEELLG	9623
1IRU	XY	HYDROLASE	X	2.8	2.8	1	22	ATDVQTVAQRLKFRLNLYELKE	9624
1IW7	CD	TRANSFERASE	C	1.4	2.8	2	13	IEGRNAAYEAIIK	9625
1IW7	MN	TRANSFERASE	M	1.4	2.8	2	13	ESFRVLVKELQAL	9626
1IYJ	AB	GENE REGULATION/ANTITUMOR PROTEIN	A	1.4	2.8	2	5	AELEK	9627

1J1D	DF	CONTRACTILE PROTEIN	D	1.4	2.8	2	11	DDIEELMKDGD	9628
1J1E	DE	CONTRACTILE PROTEIN	E	1.4	2.8	2	46	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN	9629
1JD2	OM	HYDROLASE	O	1.4	2.8	2	11	SLAAMAVLESH	9630
1JD2	PK	HYDROLASE	K	1.4	2.8	2	19	VEDALYLGKRSILAAAHRD	9631
1JD2	V2	HYDROLASE	V	2.8	2.8	1	13	GQIDYALTAVKQG	9632
1JEB	CB	OXYGEN STORAGE/TRANSPORT	C	1.4	2.8	2	19	PVNFKLLSHCLLVTLAARF	9633
1JEB	CD	OXYGEN STORAGE/TRANSPORT	C	2.8	2.8	1	19	AEAHAAWDKFLSVVSSVLT	9634
1JRO	EF	OXIDOREDUCTASE	F	1.4	2.8	2	9	HRAARIAAR	9635
1KF6	AB	OXIDOREDUCTASE	B	1.4	2.8	2	10	THFIESLEAI	9636
1KIL	AB	MEMBRANE PROTEIN	B	1.4	2.8	2	17	RIEYNVEHAVDYVERAV	9637
1KIL	BC	MEMBRANE PROTEIN	B	1.4	2.8	2	17	RIEYNVEHAVDYVERAV	9638
1KQF	BC	OXIDOREDUCTASE	B	2.8	2.8	1	8	TSVSLWKG	9639
1KX4	EC	STRUCTURAL PROTEIN/DNA	E	1.4	2.8	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	9640
1KXV	AC	HYDROLASE, IMMUNE SYSTEM	A	2.8	2.8	1	7	PYQVRDC	9641
1KYO	CE	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	2.8	2.8	1	22	NMGSLLGLCLVIQIVTGIFMAM	9642
1L9J	LM	PHOTOSYNTHESIS	L	1.4	2.8	2	10	WVDWWQWWVK	9643
1LK3	BM	IMMUNE SYSTEM	B	1.4	2.8	2	10	EKGIYKAMSE	9644
1LUJ	AB	STRUCTURAL PROTEIN	B	2.8	2.8	1	10	ASEEEFLRTY	9645
1LWU	EF	BLOOD CLOTTING	E	2.8	2.8	1	23	SVLEHLRAKMQRMEEAIKTQKEL	9646
1M2O	CD	PROTEIN TRANSPORT/SIGNALING PROTEIN	D	1.4	2.8	2	6	RLWKDY	9647
1M56	AC	OXIDOREDUCTASE	A	1.4	2.8	2	28	DLAIFAVHLSGASSILGAINMITTFLNM	9648
1M56	GI	OXIDOREDUCTASE	G	2.8	2.8	1	7	FFTRWFM	9649
1MIO	CD	MOLYBDENUM-IRON PROTEIN	C	1.4	2.8	2	6	IGCSFY	9650
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	1.4	2.8	2	9	AVPKAEWTN	9651
1MT1	GH	LYASE	G	2.8	2.8	1	13	PLNAFDGALLNAG	9652
1MTP	AB	STRUCTURAL GENOMICS	A	2.8	2.8	1	18	DDHLEFALHLHRRLAEAV	9653
1MUJ	BC	IMMUNE SYSTEM	B	1.4	2.8	2	20	EILERTRAELDTVCRHNYEG	9654
1MWA	AB	IMMUNE SYSTEM	B	1.4	2.8	2	7	KAEIANK	9655
1N52	AB	RNA BINDING PROTEIN	A	2.8	2.8	1	11	FSHSFSALAKF	9656
1NGM	MN	TRANSCRIPTION/DNA	M	1.4	2.8	2	19	EDDSKLASRKYARIIQKIG	9657
1NIW	EF	SIGNALING PROTEIN/OXIDOREDUCTASE	E	2.8	2.8	1	13	SEEEIREAFRVFD	9658
1NTK	DG	OXIDOREDUCTASE	D	1.4	2.8	2	13	YAMKRHKWSVLKS	9659
1O94	BE	ELECTRON TRANSPORT	E	2.8	2.8	1	10	LRGIKQAATK	9660
1OAO	BD	OXIDOREDUCTASE	D	2.8	2.8	1	14	LGDLPPILNRKRAQ	9661

1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.4	2.8	2	25	PAMMWALGFIFLFTVGGLTGIVLAN	9662
1OCC	PW	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	W	1.4	2.8	2	10	VAEKQKLFQE	9663
1OL5	AB	TRANSFERASE/CELL CYCLE	A	2.8	2.8	1	13	EHQLRREVEIQSH	9664
1OW3	AB	GENE REGULATION/SIGNALING PROTEIN	A	2.8	2.8	1	7	AAITLKA	9665
1OW7	AD	TRANSFERASE	A	2.8	2.8	1	35	QQEYKKQMLTAAHALAVDAKNLLDVIDQARLKMLG	9666
1OXK	EF	SIGNALING PROTEIN	F	1.4	2.8	2	14	HVNQEVIKRMLNLE	9667
1P22	AB	SIGNALING PROTEIN	A	2.8	2.8	1	9	KEWYRVTSD	9668
1P4E	BC	DNA BINDING PROTEIN/RECOMBINATION/DNA	C	1.4	2.8	2	12	PKVLVRQFVERF	9669
1PIV	12	VIRUS	2	2.8	2.8	1	5	YANAN	9670
1PMA	JW	PROTEASE	W	1.4	2.8	2	22	VGDAQVLVRYMKAELELYRLQR	9671
1PQ1	AB	APOPTOSIS	A	2.8	2.8	1	21	WGRIVAFFSFGGALCVESVDK	9672
1PRC	MH	PHOTOSYNTHETIC REACTION CENTER	M	2.8	2.8	1	8	WYLWCVKH	9673
1PTO	GH	TOXIN	H	1.4	2.8	2	18	WSMYSRLRKMLYLIYVAG	9674
1PYT	AD	TERNARY COMPLEX (ZYMOGEN)	A	2.8	2.8	1	15	VQSLLDEEQEQMFAS	9675
1Q16	AB	OXIDOREDUCTASE	A	1.4	2.8	2	7	EADAKDL	9676
1Q90	AN	PHOTOSYNTHESIS	A	1.4	2.8	2	35	PARIQGLLVFFSFVLLTQVLLVLKKKQFEKVQLAE	9677
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	A	1.4	2.8	2	16	DTDSEEELKEAFRVFD	9678
1R4A	DH	PROTEIN TRANSPORT	H	2.8	2.8	1	15	TEFEYLRKVLFEYMM	9679
1R4M	HL	CELL CYCLE	H	1.4	2.8	2	15	IIARRWINGMLISLL	9680
1R5V	CD	SIGNALING PROTEIN	C	2.8	2.8	1	5	EEFAK	9681
1R5V	EB	SIGNALING PROTEIN	B	2.8	2.8	1	9	RPDAENWNS	9682
1RCO	RP	LYASE	R	1.4	2.8	2	6	WTDGLT	9683
1RD8	ED	VIRAL PROTEIN	D	1.4	2.8	2	23	QKSTQNAIDGITNKVNSVIEKMN	9684
1RKE	AB	CELL ADHESION, STRUCTURAL PROTEIN	B	1.4	2.8	2	28	KRALIQCAKDIAKASDEVTRLAKEVAKQ	9685
1RP3	CD	TRANSCRIPTION	C	1.4	2.8	2	15	PYSNQIEREELILKY	9686
1RYP	JZ	MULTICATALYTIC PROTEINASE	Z	1.4	2.8	2	13	VGELFWKVKEEEG	9687
1RYP	OP	MULTICATALYTIC PROTEINASE	O	1.4	2.8	2	18	CDVLAKRMANLSQIYTQR	9688
1RYP	YZ	MULTICATALYTIC PROTEINASE	Z	2.8	2.8	1	15	VAAASKILSNLVYQY	9689
1S4Z	AC	GENE REGULATION	A	2.8	2.8	1	11	PQVVISFYEER	9690
1SCT	AD	OXYGEN TRANSPORT	D	1.4	2.8	2	15	ADQKDLLRMSWGVLS	9691
1SR4	BC	TOXIN	B	1.4	2.8	2	14	NESKWNINVRQLLS	9692
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	B	2.8	2.8	1	16	ADEIKRLGKRFKKLDL	9693
1TFC	BD	TRANSCRIPTION	B	2.8	2.8	1	9	KLFLEMLEA	9694
1TN6	AB	TRANSFERASE	B	2.8	2.8	1	15	RPWLCYWILHSLELL	9695
1TU3	BG	PROTEIN TRANSPORT	G	2.8	2.8	1	33	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	9696

1TUE	DE	REPLICATION	D	1.4	2.8	2	13	FITFLGALKSFLK	9697
1TZN	Mm	TOXIN RECEPTOR/TOXIN	m	1.4	2.8	2	14	LVPSYAEKEAKISR	9698
1U35	AB	STRUCTURAL PROTEIN/DNA	A	1.4	2.8	2	12	PKDIQLARRIRG	9699
1U54	AB	TRANSFERASE	B	1.4	2.8	2	6	PESLKT	9700
1U6G	AC	LIGASE	C	1.4	2.8	2	19	DGLDIRKAAFECMYTLLDS	9701
1UM9	CD	OXIDOREDUCTASE	C	2.8	2.8	1	12	WHLLRQEALLKE	9702
1UZD	EF	LYASE	E	1.4	2.8	2	21	NAPGAAANRVALEACTQARNE	9703
1UZH	BC	LYASE	B	2.8	2.8	1	14	AKNYGRAVYECLRG	9704
1UZH	EF	LYASE	E	2.8	2.8	1	14	AKNYGRAVYECLRG	9705
1V54	AT	OXIDOREDUCTASE	T	2.8	2.8	1	24	ARTWRFLTFGLALPSVALCTLNSW	9706
1V54	BI	OXIDOREDUCTASE	I	2.8	2.8	1	17	FAVAEKRKKAYADFYRN	9707
1V54	NG	OXIDOREDUCTASE	G	2.8	2.8	1	24	ARTWRFLTFGLALPSVALCTLNSW	9708
1V54	NP	OXIDOREDUCTASE	N	1.4	2.8	2	33	LFVWSVMITAVLLLLSLPVLAAGITMLLTDRNL	9709
1VYJ	KL	DNA-BINDING PROTEIN	L	2.8	2.8	1	5	ITDYF	9710
1VYW	AB	TRANSFERASE	A	1.4	2.8	2	13	STAIREISLLKEL	9711
1VZJ	CI	HYDROLASE	C	2.8	2.8	1	10	HWKNQFDHYS	9712
1W1I	CG	HYDROLASE	G	2.8	2.8	1	18	RDAIKRIAYEFVEMKAKD	9713
1W5C	BD	PHOTOSYNTHESIS	B	1.4	2.8	2	10	FAHAVFALLF	9714
1W63	DN	ENDOCYTOSIS	D	1.4	2.8	2	12	LKKLVYLYLMNY	9715
1W63	JR	ENDOCYTOSIS	R	2.8	2.8	1	5	LQEFI	9716
1WDC	AB	MUSCLE PROTEIN	B	1.4	2.8	2	11	EETIRNAFAMF	9717
1WEJ	HF	COMPLEX (ANTIBODY/ELECTRON TRANSPORT)	F	2.8	2.8	1	10	EETLMEYLEN	9718
1WQ1	RG	COMPLEX (GTP-BINDING/GTPASE ACTIVATION)	G	1.4	2.8	2	14	LASTLMEQYMKATA	9719
1WYU	AB	OXIDOREDUCTASE	B	2.8	2.8	1	16	KETLEAFAEAMGALLK	9720
1WYU	EF	OXIDOREDUCTASE	E	1.4	2.8	2	15	QLTALMGAMYLAALG	9721
1WYU	GH	OXIDOREDUCTASE	H	2.8	2.8	1	16	KETLEAFAEAMGALLK	9722
1XFU	AO	LYASE/METAL BINDING PROTEIN	O	2.8	2.8	1	5	AFSLF	9723
1XFU	BP	LYASE/METAL BINDING PROTEIN	B	1.4	2.8	2	15	SLEKQKGVTNLLIKY	9724
1XFU	FT	LYASE/METAL BINDING PROTEIN	T	2.8	2.8	1	5	AFSLF	9725
1XFV	AO	LYASE/METAL BINDING PROTEIN	A	1.4	2.8	2	13	SAEFIKNLSSIRR	9726
1XFV	AO	LYASE/METAL BINDING PROTEIN	O	2.8	2.8	1	7	KEAFSLF	9727
1XFV	BP	LYASE/METAL BINDING PROTEIN	P	2.8	2.8	1	11	IAEFKEAFSLF	9728
1XFV	CQ	LYASE/METAL BINDING PROTEIN	Q	2.8	2.8	1	7	KEAFSLF	9729
1XFV	ES	LYASE/METAL BINDING PROTEIN	S	1.4	2.8	2	9	VDQMIREAD	9730
1XFV	FT	LYASE/METAL BINDING PROTEIN	T	2.8	2.8	1	7	KEAFSLF	9731
1XL3	AC	CELL INVASION	C	2.8	2.8	1	6	RFYQDL	9732
1XQ5	CD	OXYGEN STORAGE/TRANSPORT	C	2.8	2.8	1	16	AEEIGSDALSRMLAVY	9733
1XQS	AC	CHAPERONE	A	2.8	2.8	1	13	QEELEFCEKLLQT	9734

1Y8R	DE	LIGASE	D	1.4	2.8	2	14	GLGAEIAKNLILAG	9735
1YA7	AR	HYDROLASE/HYDROLASE ACTIVATOR	A	1.4	2.8	2	13	FQVEYAREAVKKG	9736
1YA7	BS	HYDROLASE/HYDROLASE ACTIVATOR	B	1.4	2.8	2	13	FQVEYAREAVKKG	9737
1YE9	BF	OXIDOREDUCTASE	F	1.4	2.8	2	13	PYIRERVVDQLAH	9738
1YE9	CF	OXIDOREDUCTASE	F	1.4	2.8	2	18	PLLQGRLFSYTDTQISRL	9739
1YE9	DH	OXIDOREDUCTASE	H	1.4	2.8	2	13	PYIRERVVDQLAH	9740
1YE9	IN	OXIDOREDUCTASE	I	1.4	2.8	2	9	DTFWDYVSL	9741
1YNJ	BD	TRANSFERASE	B	1.4	2.8	2	10	VVEIILNLKE	9742
1YOK	AB	TRANSCRIPTION	A	2.8	2.8	1	7	LLIEMLH	9743
1YOV	CD	SIGNALING PROTEIN	C	1.4	2.8	2	5	LVLPG	9744
1YQ3	AB	OXIDOREDUCTASE	A	2.8	2.8	1	26	TDLVETLELQNLMLCALQTIYGAEAR	9745
1Z0K	CD	PROTEIN TRANSPORT	D	1.4	2.8	2	23	MDEVRTLQENLRQLQDEYDQQQT	9746
1Z5S	AD	LIGASE	A	1.4	2.8	2	15	ALSRLAQERKAWRKD	9747
1Z6O	EM	METAL BINDING PROTEIN	E	1.4	2.8	2	16	LSLALYVFDEYLQKTV	9748
1Z7Q	AI	HYDROLASE/HYDROLASE ACTIVATOR	I	2.8	2.8	1	22	AADTEAVTQLIGSNIELHSLYT	9749
1Z7Q	FM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.4	2.8	2	22	AADGDALVKRFKNSVKWYHFDH	9750
1Z7Q	Vb	HYDROLASE/HYDROLASE ACTIVATOR	b	1.4	2.8	2	20	ISDMQHIERLLKDLVTENAY	9751
1ZAV	AZ	STRUCTURAL PROTEIN	A	1.4	2.8	2	41	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK	9752
1ZBB	gh	STRUCTURAL PROTEIN/DNA	g	1.4	2.8	2	10	PRHLQLAVRN	9753
1ZGL	HI	IMMUNE SYSTEM	H	1.4	2.8	2	8	RPDAEYWN	9754
2A1J	AB	DNA BINDING PROTEIN	B	1.4	2.8	2	20	DLLMEKLEQDFVSRVTECLT	9755
2A4J	AB	STRUCTURAL PROTEIN	A	1.4	2.8	2	10	EQEFLRIMKK	9756
2AA1	AD	OXYGEN STORAGE/TRANSPORT	A	1.4	2.8	2	19	PSNFKILNHCILVVISTMF	9757
2AGH	BC	TRANSCRIPTION	B	2.8	2.8	1	20	RRMENLVAYAKKVEGDMYES	9758
2AVU	BE	TRANSCRIPTION ACTIVATOR	B	2.8	2.8	1	9	KASAMFRLG	9759
2AXT	AC	ELECTRON TRANSPORT	C	2.8	2.8	1	26	GEAYLSYSLGALSMMGFIATCFVWFN	9760
2AXT	BU	ELECTRON TRANSPORT	U	2.8	2.8	1	6	VVDEKL	9761
2AXT	DL	ELECTRON TRANSPORT	L	1.4	2.8	2	21	RTSLYLGLLLILVLALLFSSY	9762
2B87	AB	PROTEIN BINDING	B	1.4	2.8	2	14	NKERVIAIGEIMRL	9763
2BA1	CH	RNA BINDING PROTEIN	H	1.4	2.8	2	19	PEDILVDIKRDYVLSKLRD	9764
2BE6	AD	MEMBRANE PROTEIN	A	2.8	2.8	1	12	EEEIREAFRVFD	9765
2BKR	AB	PROTEIN BINDING/HYDROLASE	A	1.4	2.8	2	9	PEVTQFIKC	9766
2BKY	BY	DNA BINDING PROTEIN	B	1.4	2.8	2	18	RAISKAVDTVEIVRNRFL	9767
2BOV	AB	TRANSFERASE	A	1.4	2.8	2	11	VEEAKNRAEQW	9768
2BSK	EB	PROTEIN TRANSPORT	E	1.4	2.8	2	27	PEETTCSEHCLQKYLKMTQRISMRFQE	9769
2BV8	ED	PHOTOSYNTHESIS	E	1.4	2.8	2	8	LSEINRSF	9770
2C7J	AB	ELECTRON TRANSPORT	A	2.8	2.8	1	12	PLTEAIAAADLR	9771
2CLY	BC	HYDROLASE	B	2.8	2.8	1	21	KAVANSLKSWNETLTSRLATL	9772
2D0V	AB	OXIDOREDUCTASE	B	1.4	2.8	2	5	PKELN	9773
2D2M	BC	OXYGEN STORAGE/TRANSPORT	B	1.4	2.8	2	14	VPVLNALLARLNSQ	9774

2DBU	AB	TRANSFERASE	A	1.4	2.8	2	13	EAEKYAYADRSEY	9775
2DXB	AB	HYDROLASE	B	2.8	2.8	1	9	AEERRRKQN	9776
2DXB	QR	HYDROLASE	R	2.8	2.8	1	6	RDCLIG	9777
2DYM	CD	PROTEIN TURNOVER/PROTEIN TURNOVER	C	1.4	2.8	2	11	HMNDIKQLLWN	9778
2E1M	AC	OXIDOREDUCTASE	A	1.4	2.8	2	13	IAGLVAGDLLTRA	9779
2E5L	GK	RIBOSOME	K	2.8	2.8	1	18	PYAAQLAALDAAKKAMAY	9780
2ES4	BE	HYDROLASE	E	2.8	2.8	1	18	GDEQRRQRHDLERIRIAN	9781
2FJ7	FH	STRUCTURAL PROTEIN/DNA	F	1.4	2.8	2	11	AMDVVYALKRQ	9782
2FK0	IJ	VIRAL PROTEIN	J	1.4	2.8	2	23	KESTQKAIDGVTNKVNSIIDKMN	9783
2FM8	BC	CHAPERONE/CELL INVASION	B	1.4	2.8	2	22	GEKFSTALNGFYNYLEVFSRSL	9784
2FUG	AB	OXIDOREDUCTASE	B	2.8	2.8	1	11	PTEVMGVASFY	9785
2FUG	ST	OXIDOREDUCTASE	T	2.8	2.8	1	11	PTEVMGVASFY	9786
2FYZ	EF	PROTEIN BINDING	E	1.4	2.8	2	53	LGSAVSLVQAQTNARAIAAMKNSIQATNRAVFEVKEGTQRLAIAVQAIQDHIN	9787
2GOO	AB	TRANSFERASE	A	1.4	2.8	2	13	NHAIVQTLVNSVN	9788
2GV5	DF	CELL CYCLE	D	1.4	2.8	2	8	ENEFIAIC	9789
2GWF	AB	HYDROLASE/LIGASE	A	1.4	2.8	2	9	DDSKDTWKK	9790
2H1O	CF	GENE REGULATION/DNA COMPLEX	F	2.8	2.8	1	13	EATHNAIKFRARA	9791
2H62	BC	HORMONE/GROWTH FACTOR	C	2.8	2.8	1	7	SDFQCKD	9792
2HLD	GH	HYDROLASE	G	2.8	2.8	1	53	LKEVEMRLKSIKNIEKITKTMKIVASTRLSKAEKAKISAKKMDEAEQLFYKNA	9793
2HP0	AB	ISOMERASE	B	1.4	2.8	2	14	HSVQVALKYVAATG	9794
2HY5	BC	TRANSFERASE	C	2.8	2.8	1	9	SLESCLKFA	9795
2I2R	BF	TRANSPORT PROTEIN	F	1.4	2.8	2	12	EDTFKQIYAQFF	9796
2I2X	AB	TRANSFERASE	A	2.8	2.8	1	12	DKVLRDLMMLSD	9797
2IAM	AB	IMMUNE SYSTEM	A	2.8	2.8	1	6	EEFGRF	9798
2IVF	AB	OXIDOREDUCTASE	B	2.8	2.8	1	5	WSDRF	9799
2J03	UV	RIBOSOME	U	1.4	2.8	2	24	FRKARETLFAAGNYAYAHRKRRKR	9800
2J28	L3	RIBOSOME	3	2.8	2.8	1	7	KGDLGLV	9801
2JBA	AB	TRANSCRIPTION	B	2.8	2.8	1	14	APIREMVCFVLEQN	9802
2JF9	CR	TRANSCRIPTION	R	1.4	2.8	2	8	REWFKDML	9803
2JIZ	HK	HYDROLASE	K	2.8	2.8	1	9	PAPATTFAH	9804
2JKI	CT	CHAPERONE	C	1.4	2.8	2	12	ERRIKDLVKRHS	9805
2JKR	AS	ENDOCYTOSIS	A	1.4	2.8	2	18	DSVKQSAALCLLRLYRTS	9806
2NV2	KL	LYASE/TRANSFERASE	K	1.4	2.8	2	10	ERVKRGMAEM	9807
2NXX	CG	HORMONE/GROWTH FACTOR	C	1.4	2.8	2	11	RLPALRSIGLK	9808
2NXX	DH	HORMONE/GROWTH FACTOR	D	1.4	2.8	2	11	RLPALRSIGLK	9809
2OGX	AB	METAL BINDING PROTEIN	B	1.4	2.8	2	12	TDAGCFLLAEQF	9810
2ONL	AC	TRANSFERASE	C	1.4	2.8	2	12	PLLLKRRKKARA	9811

2OS8	AC	CONTRACTILE PROTEIN	C	1.4	2.8	2	11	DEEVDEIINLT	9812
2OV2	CK	PROTEIN BINDING/TRANSFERASE	C	1.4	2.8	2	14	LKTVFDEAIRAVLG	9813
2OV2	FN	PROTEIN BINDING/TRANSFERASE	F	2.8	2.8	1	5	DRLRP	9814
2P2C	DQ	HYDROLASE	Q	2.8	2.8	1	8	PLHLAADN	9815
2P2C	IJ	HYDROLASE	I	1.4	2.8	2	15	GDVDHSTLVTLFKLL	9816
2PMZ	DL	TRANSLATION, TRANSFERASE	L	1.4	2.8	2	22	PKDALLKAIENIRGMTSHYIDE	9817
2PUK	EG	ELECTRON TRANSPORT	G	1.4	2.8	2	17	GPSKLIAPVIDELAKEY	9818
2PUQ	LH	BLOOD CLOTTING	H	1.4	2.8	2	9	RTFSERTLA	9819
2Q9Q	AD	REPLICATION	A	1.4	2.8	2	29	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	9820
2QJP	DE	ELECTRON TRANSPORT	D	1.4	2.8	2	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	9821
2QJP	GL	ELECTRON TRANSPORT	G	1.4	2.8	2	15	QMSFWGATVITGLFG	9822
2QJY	JK	OXIDOREDUCTASE	J	1.4	2.8	2	15	VDLAFASVEHIMRNV	9823
2QKL	AB	HYDROLASE	B	2.8	2.8	1	7	PLLWKWS	9824
2QQD	AE	LYASE	A	1.4	2.8	2	13	PLNAFDGALLNAG	9825
2QRV	EF	TRANSFERASE/TRANSFERASE REGULATOR	E	2.8	2.8	1	11	VSDKRDISRFL	9826
2RAO	AB	OXYGEN BINDING	B	1.4	2.8	2	20	PENFRLLGNVLVIVLSHHFG	9827
2UUN	OP	ELECTRON TRANSPORT	P	1.4	2.8	2	13	VAQIDALSQMVAE	9828
2UZ1	DC	LYASE	D	2.8	2.8	1	7	DGSVGYS	9829
2V36	AB	TRANSFERASE	A	1.4	2.8	2	7	QEKLSRT	9830
2V4I	AB	TRANSFERASE	B	2.8	2.8	1	22	AGEFEEALHTAALALVKDIASD	9831
2V4I	GH	TRANSFERASE	H	2.8	2.8	1	14	PAEQDRLFRRVMDR	9832
2V4J	DE	OXIDOREDUCTASE	D	2.8	2.8	1	12	SQAACYELTMEY	9833
2V7Q	AD	HYDROLASE	A	2.8	2.8	1	14	RSTVAQLVKRLTDA	9834
2VDW	EF	TRANSFERASE	E	2.8	2.8	1	14	FATIIERSKKFING	9835
2VLH	AB	LYASE	A	1.4	2.8	2	9	DKQWAGMMM	9836
2VOG	AB	APOPTOSIS	A	1.4	2.8	2	16	IDTARIIFNQVMEKEF	9837
2VOL	AB	IMMUNE SYSTEM	A	1.4	2.8	2	6	HQDWLN	9838
2VPG	CD	GENE REGULATION	C	1.4	2.8	2	10	ETAYGLLTAE	9839
2VXS	HL	CYTOKINE	L	1.4	2.8	2	6	SEELQA	9840
2W2M	PA	HYDROLASE/RECEPTOR	A	1.4	2.8	2	18	VSGTLIGLEFIRKSQLVQ	9841
2Z2S	CD	TRANSCRIPTION	C	2.8	2.8	1	5	TVWQK	9842
2Z2S	EF	TRANSCRIPTION	F	1.4	2.8	2	17	DECRARAGALDAVGGSL	9843
2Z2S	GH	TRANSCRIPTION	G	2.8	2.8	1	5	TVWQK	9844
2Z4Q	AB	IMMUNE SYSTEM	A	1.4	2.8	2	7	SEQLTSG	9845
2ZAE	CD	HYDROLASE	C	1.4	2.8	2	6	TWIFRG	9846
2ZT9	FG	PHOTOSYNTHESIS	F	1.4	2.8	2	28	SGELLNAALLSFGLIFVGWALGALLLKI	9847
2ZXX	DF	CELL CYCLE/REPLICATION	F	2.8	2.8	1	5	AYQRF	9848
3A0B	bh	ELECTRON TRANSPORT	h	2.8	2.8	1	5	PLNSE	9849
3A0B	CO	ELECTRON TRANSPORT	C	1.4	2.8	2	7	LNKIKND	9850

3B9J	IK	OXIDOREDUCTASE	I	2.8	2.8	1	9	LLAYLRRKL	9851
3BC1	AF	SIGNALING PROTEIN/TRANSPORT PROTEIN	F	1.4	2.8	2	29	PEFEEQEAIMKVLQRDAALKRAEEERVRH	9852
3BPS	PA	HYDROLASE/LIPID TRANSPORT	A	1.4	2.8	2	13	RVLNAACQRLARA	9853
3BQO	AB	DNA BINDING PROTEIN	A	2.8	2.8	1	17	SEDFRRTRNSAEAIIHG	9854
3BQU	CD	IMMUNE SYSTEM	C	1.4	2.8	2	6	SEQLTS	9855
3BTP	AB	DNA BINDING PROTEIN, CHAPERONE	A	2.8	2.8	1	8	SKYLESWE	9856
3BVH	AC	BLOOD CLOTTING	C	1.4	2.8	2	26	YLQEIYNSNNQKIVNLKEKVAQLEAQ	9857
3C5J	BC	MEMBRANE PROTEIN	B	2.8	2.8	1	9	RPVAESWNS	9858
3C6L	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	G	2.8	2.8	1	7	PEFGQLA	9859
3C7B	AB	OXIDOREDUCTASE	B	2.8	2.8	1	5	YFYSE	9860
3C7B	DE	OXIDOREDUCTASE	E	1.4	2.8	2	5	YEYFT	9861
3CW2	AK	TRANSLATION	A	2.8	2.8	1	13	ALSQYRQIKQFTK	9862
3CXH	AC	OXIDOREDUCTASE	A	1.4	2.8	2	18	IDDLIHFTLKQWNRLTIS	9863
3CXH	BR	OXIDOREDUCTASE	B	1.4	2.8	2	12	ALKLVRESELLG	9864
3CXH	DE	OXIDOREDUCTASE	D	1.4	2.8	2	36	EHDERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	9865
3D2E	AB	CHAPERONE	A	1.4	2.8	2	29	AQDKLVAETEDRKNTLEEYIYTLRGKLEE	9866
3D5B	FP	RIBOSOME	F	2.8	2.8	1	12	PHLLWEVVRWQL	9867
3D5B	I1	RIBOSOME	1	1.4	2.8	2	13	IPKVYELVERAKG	9868
3DBH	EF	CELL CYCLE	F	2.8	2.8	1	13	KAEVAAEFLNDRV	9869
3DBJ	EF	PHOTOSYNTHESIS	E	1.4	2.8	2	12	VVTKSIVNADAE	9870
3DBJ	GH	PHOTOSYNTHESIS	H	2.8	2.8	1	13	TAAMEKLKAYFAT	9871
3DUF	AD	OXIDOREDUCTASE/TRANSFERASE	A	1.4	2.8	2	7	VTDLISI	9872
3DW8	AB	HYDROLASE	A	1.4	2.8	2	12	LYPIAVLIDELR	9873
3DWL	FG	STRUCTURAL PROTEIN	G	1.4	2.8	2	9	VLLNWHEKV	9874
3EA5	CD	TRANSPORT PROTEIN	D	1.4	2.8	2	28	DKVASMTVEFWSTICEEEIDIAYELAQF	9875
3ETR	BC	OXIDOREDUCTASE	B	2.8	2.8	1	24	IEFRRTLTLSFFFKFYLTVLKKLG	9876
3EVS	BC	CYTOKINE/TRANSFERASE RECEPTOR	C	2.8	2.8	1	5	SDFQC	9877
3EX7	EG	HYDROLASE/RNA BINDING PROTEIN/RNA	E	2.8	2.8	1	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	9878
3EXG	IJ	OXIDOREDUCTASE	I	2.8	2.8	1	16	AQVPLGAGIALACKYN	9879
3EXG	ON	OXIDOREDUCTASE	N	1.4	2.8	2	6	KILEDN	9880
3EXG	WX	OXIDOREDUCTASE	X	1.4	2.8	2	14	EMGFAGIAVGAAMA	9881
3F1E	JN	RIBOSOME	N	1.4	2.8	2	11	RICLRELAHKG	9882
3F1F	QZ	RIBOSOME	Z	1.4	2.8	2	10	VEKLAEEAAA	9883
3F75	AP	HYDROLASE	A	1.4	2.8	2	5	MPFQF	9884
3F75	AP	HYDROLASE	P	1.4	2.8	2	23	EEEKQRRYAIFKNNLVYIHTHNQ	9885
3F9K	Ya	VIRAL PROTEIN, RECOMBINATION	a	1.4	2.8	2	10	TEMITTLKKI	9886
3FCU	AB	CELL ADHESION/BLOOD CLOTTING	B	1.4	2.8	2	11	VNLYQNYSELI	9887

3FGC	CD	OXIDOREDUCTASE	C	1.4	2.8	2	17	QTEVMKRLVNLGKASEG	9888
3FKS	GH	HYDROLASE	G	1.4	2.8	2	21	KAKISAKKMDEAEQLFYKNAE	9889
3FWC	JK	CELL CYCLE, TRANSCRIPTION	K	1.4	2.8	2	16	NYELISNELKARLLQE	9890
3FWC	MN	CELL CYCLE, TRANSCRIPTION	M	2.8	2.8	1	13	PLDEIKRAFQLFD	9891
3G33	AD	CELL CYCLE	D	1.4	2.8	2	15	DQRVLQSLLRLEERY	9892
3G3B	AB	HYDROLASE/IMMUNE SYSTEM	B	2.8	2.8	1	8	VAWRNRCK	9893
3G6D	LH	IMMUNE SYSTEM	L	1.4	2.8	2	6	SEELQA	9894
3GHG	AB	BLOOD CLOTTING	B	2.8	2.8	1	8	AQMEYCRT	9895
3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	1.4	2.8	2	16	FEGKKDVAQIFNNILR	9896
3GTM	AS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	S	2.8	2.8	1	10	AYKARYRIIY	9897
3H4P	Kk	HYDROLASE	k	2.8	2.8	1	6	LYKMRT	9898
3H87	AC	TOXIN/ANTITOXIN	A	1.4	2.8	2	13	IPDLLIAATAELS	9899
3HD7	AD	EXOCYTOSIS	A	1.4	2.8	2	41	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA	9900
3HH2	BC	SIGNALING PROTEIN/CYTOKINE	C	2.8	2.8	1	12	ACHLRKATCLLG	9901
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.4	2.8	2	11	EMERDCMIAHG	9902
3HOU	BI	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.4	2.8	2	10	PARLMETLRT	9903
3HOU	DG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	2.8	2.8	1	9	PFEVAQLGS	9904
1AJS	AB	AMINOTRANSFERASE	A	1.4	2.7	2	15	GTGALRIGAEFLARW	9905
1AJS	AB	AMINOTRANSFERASE	A	2.7	2.7	1	11	LVFKLIADFRE	9906
1ALL	AB	LIGHT HARVESTING PROTEIN	B	2.7	2.7	1	13	ASAIQKLKAYFAT	9907
1B33	JK	PHOTOSYNTHESIS	K	1.4	2.7	2	13	AITAVINSSDVQG	9908
1BCP	AD	TOXIN	A	2.7	2.7	1	6	YESIAY	9909
1BCP	EF	TOXIN	E	1.4	2.7	2	13	PMEVMLRAVFMQQ	9910
1BEV	14	VIRUS	1	2.7	2.7	1	6	VESFFG	9911
1BGY	AB	ELECTRON TRANSPORT	A	2.7	2.7	1	10	ALEKEVESMG	9912
1BGY	BR	ELECTRON TRANSPORT	B	2.7	2.7	1	11	SFKITRGIEAV	9913
1BGY	OQ	ELECTRON TRANSPORT	Q	1.4	2.7	2	35	EARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSA	9914
1BVY	AF	OXIDOREDUCTASE	F	1.4	2.7	2	20	FEGTYEEWREHMWSDVAAYF	9915
1BXN	CJ	LYASE	C	1.4	2.7	2	22	IQAGATANRVALEAMVLARNEG	9916
1BXR	AB	AMIDOTRANSFERASE	A	1.4	2.7	2	21	RWFLVQIEELVRLEEKVAEVG	9917
1D2Z	AB	APOPTOSIS	A	1.4	2.7	2	13	ASNEFLNIWGGQY	9918
1DAN	LH	COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	H	1.4	2.7	2	10	RTFSERTLAF	9919
1DCE	CD	TRANSFERASE	D	2.7	2.7	1	14	PFHTLFGIAGLSLL	9920
1DGH	AB	OXIDOREDUCTASE	A	1.4	2.7	2	19	KMLQGRLFAYPDTHRHRLG	9921

1DIO	AG	LYASE	G	1.4	2.7	2	14	PETLRLQASIAKDA	9922
1DIO	LM	LYASE	M	1.4	2.7	2	13	DRLAMNFERAAEL	9923
1EAH	23	VIRUS	3	1.4	2.7	2	5	MDMYR	9924
1EF1	AC	MEMBRANE PROTEIN	A	1.4	2.7	2	15	REDAVLEYLKIAQDL	9925
1EQZ	EF	STRUCTURAL PROTEIN/DNA	E	1.4	2.7	2	10	PRHLQLAIRN	9926
1EQZ	GH	STRUCTURAL PROTEIN/DNA	G	1.4	2.7	2	11	PKDIQLARRIR	9927
1F3J	DE	IMMUNE SYSTEM	E	1.4	2.7	2	36	ELGRHSAEYYNKQYLERTRAELDTACRHNYEETEVP	9928
1F3M	BD	TRANSFERASE	B	2.7	2.7	1	7	KSEQKKN	9929
1F99	AB	PHOTOSYNTHESIS	A	2.7	2.7	1	12	PLTEAIAAADSQ	9930
1F9E	GH	APOPTOSIS	H	1.4	2.7	2	16	WYIQSLCQSLRERCPR	9931
1F9E	KL	APOPTOSIS	L	1.4	2.7	2	16	WYIQSLCQSLRERCPR	9932
1FE8	HL	IMMUNE SYSTEM	L	1.4	2.7	2	6	SEQLTS	9933
1FFU	DE	HYDROLASE	D	2.7	2.7	1	8	EAEIRMGM	9934
1FHJ	AB	OXYGEN STORAGE/TRANSPORT	A	2.7	2.7	1	16	AGDYGGEALDRTFQSF	9935
1FHJ	CD	OXYGEN STORAGE/TRANSPORT	C	2.7	2.7	1	16	AGDYGGEALDRTFQSF	9936
1FNS	HA	IMMUNE SYSTEM	A	1.4	2.7	2	11	FVRYVQGLKKK	9937
1FNT	EL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.4	2.7	2	22	ADCQFWETWLGSQCRLHELREK	9938
1FNT	Ja	HYDROLASE/HYDROLASE ACTIVATOR	J	1.4	2.7	2	12	SDQLFGMCESLY	9939
1FNT	MN	HYDROLASE/HYDROLASE ACTIVATOR	N	2.7	2.7	1	17	PSYIFEYLATVMYQRRS	9940
1FSX	AB	OXYGEN STORAGE/TRANSPORT	A	2.7	2.7	1	16	AAEYGAEALERMFLSF	9941
1FSX	AD	OXYGEN STORAGE/TRANSPORT	D	2.7	2.7	1	7	PWTQRFF	9942
1FYZ	AC	OXIDOREDUCTASE	A	1.4	2.7	2	7	AQEVHRW	9943
1G0U	TU	HYDROLASE	U	2.7	2.7	1	22	IPDARNAALRAKAEAAEFRYKY	9944
1G20	AB	OXIDOREDUCTASE	B	2.7	2.7	1	8	KEYQELNF	9945
1G72	AB	OXIDOREDUCTASE	B	1.4	2.7	2	5	PVELN	9946
1G72	CD	OXIDOREDUCTASE	D	1.4	2.7	2	5	PVELN	9947
1G73	AD	APOPTOSIS/APOPTOSIS INHIBITOR	D	2.7	2.7	1	9	PWEQHAKWY	9948
1GCV	AD	OXYGEN STORAGE/TRANSPORT	A	1.4	2.7	2	19	PQNFPMLSECIIVTLATHL	9949
1GH0	IJ	PHOTOSYNTHESIS	J	1.4	2.7	2	13	TAQIDALSQMVAE	9950
1GH0	UV	PHOTOSYNTHESIS	V	1.4	2.7	2	13	TAQIDALSQMVAE	9951
1H0H	KL	DEHYDROGENASE	K	2.7	2.7	1	5	RTSTK	9952
1H0H	KL	DEHYDROGENASE	L	2.7	2.7	1	5	IDRIT	9953
1H2S	AB	MEMBRANE PROTEIN	B	1.4	2.7	2	27	VFIFVGALTVLFGAIAYGEVTAAAATG	9954
1HBH	AB	OXYGEN CARRIER	A	1.4	2.7	2	16	ADAIGNDALSRMIVVY	9955
1HBM	DE	METHANOGENESIS	E	1.4	2.7	2	12	KVEGTAVGFSFF	9956
1HBX	BG	GENE REGULATION	B	1.4	2.7	2	26	KLRRYTTFSKRKTGIMKKAYELSTLT	9957
1HV4	AD	OXYGEN STORAGE/TRANSPORT	D	2.7	2.7	1	6	PWTQRF	9958
1I3Q	BJ	TRANSCRIPTION	B	2.7	2.7	1	7	ESDLYKL	9959
1I3R	CD	IMMUNE SYSTEM	D	2.7	2.7	1	23	PEFLEQKRAEVDTVCRHNYEIFD	9960
1I3R	GH	IMMUNE SYSTEM	G	2.7	2.7	1	6	EEFAKF	9961

1IB1	CG	SIGNALING PROTEIN/TRANSFERASE	C	1.4	2.7	2	31	NEERNLLSVAYKNVVGARRSSWRVVSSIEQK	9962
1IBG	LH	IMMUNOGLOBULIN	L	1.4	2.7	2	6	SEQLTS	9963
1ICF	CD	HYDROLASE	C	2.7	2.7	1	5	ESFLF	9964
1IR2	EN	LYASE	E	1.4	2.7	2	14	AKNYGRAVYECLRG	9965
1IR2	GJ	LYASE	G	2.7	2.7	1	6	WTDGLT	9966
1IR2	HP	LYASE	H	2.7	2.7	1	15	AKNYGRAVYECLRGG	9967
1IRU	CJ	HYDROLASE	C	1.4	2.7	2	23	TSDANVLTNELRLIAQRYLLQYQ	9968
1IRU	CK	HYDROLASE	C	2.7	2.7	1	23	TSDANVLTNELRLIAQRYLLQYQ	9969
1IRU	KZ	HYDROLASE	K	1.4	2.7	2	8	TLSILDRY	9970
1IRU	QY	HYDROLASE	Q	2.7	2.7	1	23	TSDANVLTNELRLIAQRYLLQYQ	9971
1IRU	Z1	HYDROLASE	1	2.7	2.7	1	15	TGAIAAMLSTILYSR	9972
1IXR	BC	HYDROLASE	B	1.4	2.7	2	11	AQDLIKEALKR	9973
1IZL	JN	PHOTOSYNTHESIS	N	2.7	2.7	1	11	GGALLCAIHGA	9974
1JB0	AB	PHOTOSYNTHESIS	B	1.4	2.7	2	32	AWDAFYLAMFWMLNTIGWVTFYWHWKHLGVWE	9975
1JB0	AB	PHOTOSYNTHESIS	B	2.7	2.7	1	7	LMGWLRD	9976
1JD2	Z1	HYDROLASE	1	2.7	2.7	1	12	FQVEYAVKAVEN	9977
1JNR	CD	OXIDOREDUCTASE	D	1.4	2.7	2	6	ACEYIC	9978
1JOW	AB	CELL CYCLE/TRANSFERASE	A	2.7	2.7	1	10	VLNNLKLREL	9979
1JPW	AD	CELL ADHESION	D	1.4	2.7	2	6	ADVKSS	9980
1K3B	BC	HYDROLASE	B	2.7	2.7	1	5	DDFLH	9981
1K7L	CF	TRANSCRIPTION	F	1.4	2.7	2	10	KILHRLLQEG	9982
1KF6	MN	OXIDOREDUCTASE	M	2.7	2.7	1	9	MLHTLFQTS	9983
1KF9	DF	HORMONE/GROWTH FACTOR	D	1.4	2.7	2	28	LSRLADNAWLRADRLNQLAFDTYQEFEE	9984
1KFY	MN	OXIDOREDUCTASE	M	2.7	2.7	1	26	TDLLYTIELGHGLNVAECMAHSAMAR	9985
1KFY	OP	OXIDOREDUCTASE	P	1.4	2.7	2	27	EPVFWGLFGAGGMWSAIIAPVMILLVG	9986
1KN1	AB	ELECTRON TRANSPORT	B	2.7	2.7	1	13	SSAIEKLKGYFQT	9987
1KYO	OS	OXIDOREDUCTASE/ELECTRON TRANSPORT	O	2.7	2.7	1	34	DERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	9988
1L1O	DE	DNA BINDING PROTEIN	E	1.4	2.7	2	19	NEFTTHILEVINAHMVLSK	9989
1L9J	LM	PHOTOSYNTHESIS	L	1.4	2.7	2	28	GLWQIITICATGAFVSWALREVEICRKL	9990
1L9J	LM	PHOTOSYNTHESIS	M	1.4	2.7	2	28	GLWLIASFFMFVAVWSWWGRTYLRAQAL	9991
1LB1	AB	SIGNALING PROTEIN	A	2.7	2.7	1	33	EEESLAILRRHVMNELLDTERAYVEELLCVLEG	9992
1LB1	CD	SIGNALING PROTEIN	C	2.7	2.7	1	39	EEESLAILRRHVMNELLDTERAYVEELLCVLEGYAAEMD	9993
1LB1	GH	SIGNALING PROTEIN	H	1.4	2.7	2	7	LRPLSYP	9994
1LNU	GH	SUGAR BINDING PROTEIN	G	2.7	2.7	1	7	PEFGQLA	9995
1LOT	AB	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	A	1.4	2.7	2	11	NDEICEAFRKD	9996
1LP9	AE	IMMUNE SYSTEM	A	1.4	2.7	2	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	9997
1LP9	HL	IMMUNE SYSTEM	H	1.4	2.7	2	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	9998
1LWU	EF	BLOOD CLOTTING	E	1.4	2.7	2	15	VKIRIESTVAGSLRS	9999

1LWU	GH	BLOOD CLOTTING	H	2.7	2.7	1	9	VKIRIESTV	10000
1M1Y	AB	OXIDOREDUCTASE	B	2.7	2.7	1	14	QDYKDMLAKKRDGF	10001
1M1Y	IJ	OXIDOREDUCTASE	J	2.7	2.7	1	14	QDYKDMLAKKRDGF	10002
1M1Y	IL	OXIDOREDUCTASE	L	2.7	2.7	1	17	ASLTKERGRLVDMMTDS	10003
1M45	AB	CELL CYCLE PROTEIN	A	1.4	2.7	2	8	LGDYLRAI	10004
1MIO	AB	MOLYBDENUM-IRON PROTEIN	A	1.4	2.7	2	6	IGCSFY	10005
1MIO	AD	MOLYBDENUM-IRON PROTEIN	D	1.4	2.7	2	16	VSATDEFIMALSEATG	10006
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	G	2.7	2.7	1	20	VNYFLDGERQLGTRLMELRN	10007
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	E	2.7	2.7	1	6	ARRTRT	10008
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	H	2.7	2.7	1	5	FRQAY	10009
1MMO	EH	OXIDOREDUCTASE (MONOOXYGENASE)	E	2.7	2.7	1	33	PASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYG	10010
1MO1	AD	TRANSPORT PROTEIN	A	1.4	2.7	2	13	ARPAALFVQEANR	10011
1MTY	EH	MONOOXYGENASE	E	2.7	2.7	1	32	PASAKYLNTDLNNAFWTQQKYFTPVLGMLFEY	10012
1MVW	GI	CONTRACTILE PROTEIN	I	1.4	2.7	2	10	GAELRHVLAT	10013
1N0W	AB	GENE REGULATION/ANTITUMOR PROTEIN	A	1.4	2.7	2	13	TDHQTQLLYQASA	10014
1N5W	EF	OXIDOREDUCTASE	E	1.4	2.7	2	11	RYVAADAIELV	10015
1NC2	CD	IMMUNE SYSTEM	C	1.4	2.7	2	6	SEELET	10016
1NIW	CD	SIGNALING PROTEIN/OXIDOREDUCTASE	C	1.4	2.7	2	15	EEQIAEFKEAFSLFD	10017
1NPQ	AB	STRUCTURAL PROTEIN	B	1.4	2.7	2	8	DAMLRALL	10018
1NTK	AC	OXIDOREDUCTASE	A	1.4	2.7	2	18	IDDMMFVLQGQWMRLCTS	10019
1NVM	AB	LYASE/OXIDOREDUCTASE	A	1.4	2.7	2	11	KQHIEYARNLG	10020
1O94	CD	ELECTRON TRANSPORT	C	1.4	2.7	2	11	STGISVASYLN	10021
1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	2.7	2.7	1	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	10022
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	2.7	2.7	1	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	10023
1OVA	AB	SERPIN	B	1.4	2.7	2	16	ADQARELINSWVESQT	10024
1P27	AB	RNA BINDING PROTEIN	A	1.4	2.7	2	15	KSVMEELKRIIDDSE	10025
1PMA	ER	PROTEASE	R	1.4	2.7	2	22	VGDAQVLVRYMKAELELYRLQR	10026
1PMA	LY	PROTEASE	Y	1.4	2.7	2	22	VGDAQVLVRYMKAELELYRLQR	10027
1POV	1	VIRUS	0	2.7	2.7	1	5	YQNAN	10028
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	2.7	2.7	1	5	LEQIA	10029
1PTO	LH	TOXIN	H	1.4	2.7	2	18	WSMYSRLRKMLYLIYVAG	10030
1Q16	AB	OXIDOREDUCTASE	B	1.4	2.7	2	11	TCSVTCKNVWT	10031

1QHH	BC	HYDROLASE	C	1.4	2.7	2	9	LIAFLTDLA	10032
1QPW	CD	OXYGEN TRANSPORT	C	2.7	2.7	1	18	PVNFKLLSHCLLVTLAAH	10033
1R27	CD	OXIDOREDUCTASE	C	2.7	2.7	1	7	EADAKDL	10034
1R27	CD	OXIDOREDUCTASE	D	2.7	2.7	1	5	YEDRF	10035
1R4M	AB	CELL CYCLE	B	1.4	2.7	2	21	ASTNAVIAAVCATEVFKIATS	10036
1R4M	GH	CELL CYCLE	G	1.4	2.7	2	11	DDYVHEFCRYG	10037
1RCO	EC	LYASE	E	1.4	2.7	2	6	WTDGLT	10038
1RCO	KI	LYASE	K	1.4	2.7	2	6	WTDGLT	10039
1RJL	AB	IMMUNE SYSTEM	A	1.4	2.7	2	5	SEQLT	10040
1RSO	CD	NEUROPEPTIDE/MEMBRANE PROTEIN	C	1.4	2.7	2	15	RQLRSSIERVISIFQ	10041
1RYP	AB	MULTICATALYTIC PROTEINASE	B	2.7	2.7	1	18	GPDYRVLVDKSRKVAHTS	10042
1RYP	BC	MULTICATALYTIC PROTEINASE	B	2.7	2.7	1	15	TKLLVSEVAKIMQEA	10043
1RYP	FM	MULTICATALYTIC PROTEINASE	F	2.7	2.7	1	22	APDARVLSNYLRQQCNYSSLVF	10044
1RYP	VN	MULTICATALYTIC PROTEINASE	N	2.7	2.7	1	6	WDFAKD	10045
1S5L	ck	PHOTOSYNTHESIS	k	1.4	2.7	2	19	LPVIPVLFLALAFVWQAAV	10046
1S5L	de	PHOTOSYNTHESIS	e	1.4	2.7	2	13	AKQQVETFLEQLK	10047
1SCT	EF	OXYGEN TRANSPORT	E	2.7	2.7	1	19	SKLRGHAITLTYALNNFVD	10048
1SEB	EH	COMPLEX (MHC II/PEPTIDE/TOXIN)	E	1.4	2.7	2	22	AQGALANIAVDKANLEIMTKRS	10049
1SQB	EJ	OXIDOREDUCTASE	J	1.4	2.7	2	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	10050
1SQX	DF	OXIDOREDUCTASE	F	1.4	2.7	2	20	ENLYDDRVFRIKRALDLSMR	10051
1SUV	AE	METAL TRANSPORT	E	2.7	2.7	1	15	HHERLKCDEWSVTSG	10052
1T0F	AC	DNA BINDING PROTEIN	A	1.4	2.7	2	13	DLELAVFLSLEWE	10053
1T0Q	AB	OXIDOREDUCTASE	B	1.4	2.7	2	7	EYEVVST	10054
1TQY	EF	TRANSFERASE	E	2.7	2.7	1	12	SVMPAEVAWAVG	10055
1U35	GH	STRUCTURAL PROTEIN/DNA	G	1.4	2.7	2	11	PRHILLAVAND	10056
1UDI	EI	HYDROLASE/INHIBITOR	I	1.4	2.7	2	9	PEEVEEVIG	10057
1UPT	BA	HYDROLASE/PROTEIN-BINDING	A	2.7	2.7	1	7	RPYWRCY	10058
1V54	CH	OXIDOREDUCTASE	H	2.7	2.7	1	21	TRNCWQNYLDFHRCEKAMTAK	10059
1V54	DM	OXIDOREDUCTASE	M	1.4	2.7	2	25	PKEQAIGLSVTFLSFLLPAGWVLYH	10060
1V54	PU	OXIDOREDUCTASE	U	2.7	2.7	1	21	TRNCWQNYLDFHRCEKAMTAK	10061
1V54	QX	OXIDOREDUCTASE	X	2.7	2.7	1	5	FHDKY	10062
1W63	DN	ENDOCYTOSIS	D	1.4	2.7	2	18	VDFVRKAVRAIGRCAIKV	10063
1WPX	AB	HYDROLASE	A	1.4	2.7	2	8	DINRNFLF	10064
1WYU	AB	OXIDOREDUCTASE	A	1.4	2.7	2	25	PEGLREVALKSVEMAHKLHALLLEV	10065
1WYU	CD	OXIDOREDUCTASE	D	2.7	2.7	1	16	KETLEAFAEAMGALLK	10066
1WYU	EF	OXIDOREDUCTASE	F	1.4	2.7	2	15	FLALVRAWAYIRTLG	10067
1WYU	EF	OXIDOREDUCTASE	F	2.7	2.7	1	15	KETLEAFAEAMGALL	10068
1XCG	AB	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	A	1.4	2.7	2	19	SEMQRLTKYPLLLESIIKH	10069
1XFU	DR	LYASE/METAL BINDING PROTEIN	D	1.4	2.7	2	15	SLEKQKGVTNLLIKY	10070

1XFU	ES	LYASE/METAL BINDING PROTEIN	E	1.4	2.7	2	15	SLEKQKGVTNLLIKY	10071
1XFU	FT	LYASE/METAL BINDING PROTEIN	T	1.4	2.7	2	9	VDQMIREAD	10072
1XM4	AB	HYDROLASE	A	1.4	2.7	2	17	KKQRQTLRKMVIDMVLA	10073
1XM4	AB	HYDROLASE	B	1.4	2.7	2	15	VLENHHLAVGFKLLQ	10074
1XQS	BD	CHAPERONE	D	1.4	2.7	2	20	GEDFDNRLVNHFVEEFKRKH	10075
1XV9	CG	DNA BINDING PROTEIN	C	2.7	2.7	1	6	TFLMEM	10076
1Y3A	AE	SIGNALING PROTEIN	A	2.7	2.7	1	8	RKKWIHCF	10077
1Y74	AD	TRANSPORT PROTEIN	A	1.4	2.7	2	20	RFCSAIREVYEQLYDTLDIT	10078
1YA7	FM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.4	2.7	2	23	VGDAQVLVRYMKAELELYRLQRR	10079
1YAG	AG	CONTRACTILE PROTEIN	A	2.7	2.7	1	12	SVWIGGSILASL	10080
1YE9	AH	OXIDOREDUCTASE	H	1.4	2.7	2	10	PLLQGRLFSY	10081
1YE9	KO	OXIDOREDUCTASE	O	1.4	2.7	2	19	PLLQGRLFSYTDTQISRLG	10082
1YE9	LP	OXIDOREDUCTASE	P	1.4	2.7	2	13	PYIRERVVDQLAH	10083
1YEW	EG	OXIDOREDUCTASE, MEMBRANE PROTEIN	E	1.4	2.7	2	10	IFIPRLLMVD	10084
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	1.4	2.7	2	6	IADIQG	10085
1YL3	JL	RIBOSOME	J	2.7	2.7	1	13	KIQVIKVVREITG	10086
1YOK	AB	TRANSCRIPTION	A	1.4	2.7	2	22	TFGLMCKMADQTLFSIVEWARS	10087
1YQ3	BD	OXIDOREDUCTASE	D	2.7	2.7	1	26	AASLHWTSERAVSALLLGLLPAAYLY	10088
1Z5X	UE	HORMONE/GROWTH FACTOR RECEPTOR	U	1.4	2.7	2	7	RFAKLLL	10089
1Z6O	LQ	METAL BINDING PROTEIN	L	2.7	2.7	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	10090
1Z7M	BG	TRANSFERASE	G	2.7	2.7	1	10	PNDVITFLEH	10091
1Z7Q	EM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.4	2.7	2	15	INSAARNIQHLLYGK	10092
1Z7Q	OV	HYDROLASE/HYDROLASE ACTIVATOR	O	2.7	2.7	1	21	IPDARNAALRAKAEAAEFRYK	10093
1Z7S	23	VIRUS	3	1.4	2.7	2	5	MEMYQ	10094
1ZBB	AB	STRUCTURAL PROTEIN/DNA	A	1.4	2.7	2	12	PKDIQLARRIRG	10095
1ZBB	ag	STRUCTURAL PROTEIN/DNA	a	1.4	2.7	2	13	TVALREIRRYQKS	10096
1ZBB	AG	STRUCTURAL PROTEIN/DNA	A	1.4	2.7	2	13	TVALREIRRYQKS	10097
1ZBB	bd	STRUCTURAL PROTEIN/DNA	d	1.4	2.7	2	12	SREIQTAVRLLL	10098
1ZBB	GH	STRUCTURAL PROTEIN/DNA	G	1.4	2.7	2	10	PRHLQLAVRN	10099
1ZE3	CD	CHAPERONE/STRUCTURAL/MEMBRANE PROTEIN	C	1.4	2.7	2	5	KSKLT	10100
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	H	1.4	2.7	2	12	AIYVYKVLKQVH	10101
1ZNV	AB	HYDROLASE/PROTEIN BINDING	A	1.4	2.7	2	6	TDLIYY	10102
1ZUD	12	TRANSFERASE/BIOSYNTHETIC PROTEIN	1	2.7	2.7	1	14	MATRQEINAACVAL	10103
1ZV5	LA	HYDROLASE/IMMUNE SYSTEM	L	2.7	2.7	1	12	LGNWVCAAKFES	10104
1ZVV	AW	TRANSCRIPTION/DNA	W	1.4	2.7	2	8	IMGLMSLA	10105

2A1D	FH	HYDROLASE	H	1.4	2.7	2	35	KEYKDAKDKLMTRILGEDQYLLERKKVQYEEYKKL	10106
2A1T	RS	OXIDOREDUCTASE/ELECTRON TRANSPORT	S	1.4	2.7	2	6	EDLVAK	10107
2A5T	AB	METAL TRANSPORT,MEMBRANE PROTEIN	B	1.4	2.7	2	16	PWKRQIDLALLQFVGD	10108
2ACZ	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	2.7	2.7	1	8	PEQREKLD	10109
2AVU	BE	TRANSCRIPTION ACTIVATOR	E	1.4	2.7	2	16	GVDAVIKAYRLYLEQC	10110
2AXT	ad	ELECTRON TRANSPORT	d	2.7	2.7	1	26	KRWLHFFMLFVPVTGLWMSAIGVVGL	10111
2AXT	BD	ELECTRON TRANSPORT	B	1.4	2.7	2	16	PRGWFTFAHAVFALLF	10112
2AXT	BD	ELECTRON TRANSPORT	D	1.4	2.7	2	26	KRWLHFFMLFVPVTGLWMSAIGVVGL	10113
2AXT	BH	ELECTRON TRANSPORT	B	2.7	2.7	1	6	RYQWDS	10114
2AXT	DM	ELECTRON TRANSPORT	D	1.4	2.7	2	10	ISQEIRAAED	10115
2AXT	LM	ELECTRON TRANSPORT	L	1.4	2.7	2	21	RTSLYLGLLLILVLALLFSSY	10116
2AXT	lm	ELECTRON TRANSPORT	l	1.4	2.7	2	21	RTSLYLGLLLILVLALLFSSY	10117
2BA0	DG	RNA BINDING PROTEIN	G	1.4	2.7	2	22	EKLFDELLDVSINCARKLREKF	10118
2BA0	FI	RNA BINDING PROTEIN	F	2.7	2.7	1	16	RRSIEISKVSKEAFEA	10119
2BGN	BE	HYDROLASE	E	2.7	2.7	1	18	RDAIKRIAYEFVEMKAKD	10120
2CCI	DI	CELL CYCLE	D	1.4	2.7	2	18	NSMRAILVDWLVEVGEEY	10121
2CDE	EF	CELL RECEPTOR	F	2.7	2.7	1	8	EAEISHTQ	10122
2CG5	AB	TRANSFERASE/HYDROLASE	A	2.7	2.7	1	23	EWTQLDMFYRNWALKESFIKAIG	10123
2CJS	AC	EXOCYTOSIS	C	2.7	2.7	1	7	NLCRKQQ	10124
2D2M	AD	OXYGEN STORAGE/TRANSPORT	D	1.4	2.7	2	17	RATCDSLLSHLNAQHRA	10125
2DBU	AB	TRANSFERASE	B	2.7	2.7	1	6	VNSIDY	10126
2DF4	AC	LIGASE	A	1.4	2.7	2	14	GIPSYYVIASSEAS	10127
2DSR	GI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	G	1.4	2.7	2	16	SCQSELHRALERLAAS	10128
2DT7	AB	RNA BINDING PROTEIN	B	2.7	2.7	1	11	RQFLTQLMQKE	10129
2EC6	AC	CONTRACTILE PROTEIN	C	1.4	2.7	2	7	VKKVMAG	10130
2EHO	IJ	REPLICATION	J	1.4	2.7	2	35	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW	10131
2EHO	IK	REPLICATION	K	2.7	2.7	1	9	AAEVEFLAE	10132
2EQB	AC	ENDOCYTOSIS/EXOCYTOSIS	C	1.4	2.7	2	46	EEEADKLNKEVEDLTASLFDEANNMVADARKEKYAIEILNKRLTEQ	10133
2ES4	BE	HYDROLASE	E	1.4	2.7	2	26	PDERAQQAALHAQQDAVTKIADLQKA	10134
2F8N	EF	STRUCTURAL PROTEIN/DNA	E	1.4	2.7	2	12	PKDIQLARRIRG	10135
2FHH	ST	HYDROLASE	T	1.4	2.7	2	23	AAVAVEFARLYAVELEHYEKLEG	10136
2FJF	WX	IMMUNE SYSTEM	W	1.4	2.7	2	7	DEQLKSG	10137
2FJH	WA	HORMONE/GROWTH FACTOR/IMMUNE SYSTEM	W	1.4	2.7	2	8	FMDVYQRS	10138

2FK0	CD	VIRAL PROTEIN	D	1.4	2.7	2	23	KESTQKAIDGVTNKVNSIIDKMN	10139
2FUG	49	OXIDOREDUCTASE	4	1.4	2.7	2	14	RERETILDLFEWVT	10140
2FUG	VX	OXIDOREDUCTASE	X	2.7	2.7	1	8	CCAIEMMA	10141
2FYM	DE	LYASE	E	2.7	2.7	1	6	PELASG	10142
2G38	CD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	C	1.4	2.7	2	28	ALTVAATEVRRIRDRAIQSDAQVAPMTT	10143
2GEZ	AD	HYDROLASE	D	1.4	2.7	2	7	GEEIIRA	10144
2GEZ	EH	HYDROLASE	H	2.7	2.7	1	7	GEEIIRA	10145
2GHO	AC	TRANSFERASE	A	1.4	2.7	2	14	FGVTLGNPLRRILL	10146
2GID	AB	TRANSLATION	B	1.4	2.7	2	19	HFAVTLEHFLESALDESFG	10147
2GID	GD	TRANSLATION	D	1.4	2.7	2	16	HFAVTLEHFLESALDE	10148
2GID	GD	TRANSLATION	G	1.4	2.7	2	12	QRFLTQALHYNT	10149
2GTL	NO	OXYGEN STORAGE/TRANSPORT	N	1.4	2.7	2	17	PEHFVSEIDARVTKIEG	10150
2GUZ	OB	CHAPERONE, PROTEIN TRANSPORT	B	1.4	2.7	2	15	MDKINNRFNYLFEVN	10151
2H1L	AM	VIRAL PROTEIN	A	2.7	2.7	1	14	LSVYQKMKFNVAMG	10152
2H1O	BF	GENE REGULATION/DNA COMPLEX	B	1.4	2.7	2	18	KKKNVLHERMEQSILPLF	10153
2H4M	BD	PROTEIN TRANSPORT	B	2.7	2.7	1	18	ISVCNNATWAIGEISIQM	10154
2HHH	JN	RIBOSOME	N	1.4	2.7	2	9	ICLRELAHK	10155
2HLD	BF	HYDROLASE	B	1.4	2.7	2	12	VFYLHSRLLERA	10156
2HLD	JM	HYDROLASE	J	2.7	2.7	1	14	RSTVAQLVQTLEQH	10157
2HRP	LH	COMPLEX (IMMUNOGLOBULIN/PEPTIDE)	L	1.4	2.7	2	7	SEQLTSG	10158
2HVY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	2.7	2.7	1	12	SHEVVAWIKKIL	10159
2HWN	DF	TRANSFERASE	F	1.4	2.7	2	18	LAWKIAKMIVSDVMQQCK	10160
2HYB	DE	TRANSFERASE	D	1.4	2.7	2	11	LGQLVEAAIQA	10161
2HYB	NR	TRANSFERASE	N	2.7	2.7	1	6	DGVYQL	10162
2HYI	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.4	2.7	2	11	VGEDIRKLDYG	10163
2HYI	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.4	2.7	2	13	DDIRILRDIEQYY	10164
2HZS	CD	TRANSCRIPTION	C	1.4	2.7	2	6	PALVFN	10165
2IBZ	DH	OXIDOREDUCTASE	D	1.4	2.7	2	17	TSQMAKDVTTFLNWCAE	10166
2IX2	AB	REPLICATION	A	1.4	2.7	2	15	ESVLNVIAADVTLVG	10167
2J0Q	AT	HYDROLASE	A	2.7	2.7	1	12	DIRILRDIEQYY	10168
2J59	AM	HYDROLASE	A	2.7	2.7	1	10	KTTILYKLKL	10169
2JBL	HM	ELECTRON TRANSPORT	M	2.7	2.7	1	14	TAVERAALFWRWTI	10170
2JEA	AB	HYDROLASE	A	2.7	2.7	1	27	LQDIDQAENTARSTAVKLLEELKKHLG	10171
2JIY	LM	PHOTOSYNTHESIS	M	2.7	2.7	1	7	ELEQIAD	10172
2JIY	MH	PHOTOSYNTHESIS	H	2.7	2.7	1	17	LLEEDKICGYVAGGLMY	10173

2JTT	BD	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	D	1.4	2.7	2	13 DMKRTINKAWVES	10174
2NPP	AC	SIGNALING PROTEIN,HYDROLASE	A	2.7	2.7	1	17 YLHRMTTLFCINVLSEV	10175
2NPT	CB	TRANSFERASE	C	2.7	2.7	1	21 DEEMKAMLSYYYSTVMEQQVN	10176
2NTY	BD	SIGNALING PROTEIN	D	1.4	2.7	2	19 KASYENVAKKWIPELRHYA	10177
2NV2	CD	LYASE/TRANSFERASE	D	1.4	2.7	2	11 STTMRRLIDTY	10178
2NZD	BD	STRUCTURAL PROTEIN/DNA	D	1.4	2.7	2	29 SKAMSIMNSFVNDVFERIAGEASRLAHYN	10179
2OM0	12	HORMONE	2	1.4	2.7	2	18 NQHLCGSHLVEALYLVCG	10180
2P58	BC	TRANSPORT PROTEIN/CHAPERONE	B	2.7	2.7	1	8 ADLQHSIN	10181
2P58	BC	TRANSPORT PROTEIN/CHAPERONE	B	1.4	2.7	2	6 GILQKF	10182
2PKQ	QP	OXIDOREDUCTASE	P	2.7	2.7	1	10 VKQASHLLKY	10183
2PMZ	AC	TRANSLATION, TRANSFERASE	C	1.4	2.7	2	12 TVKHLLDAAARG	10184
2PQR	AC	APOPTOSIS	A	1.4	2.7	2	15 RRECLYYLTIGCYKL	10185
2QA4	FM	RIBOSOME	M	2.7	2.7	1	9 AYSYIRDAW	10186
2QAG	BC	CELL CYCLE, STRUCTURAL PROTEIN	C	1.4	2.7	2	12 MQDLKDVTNNVH	10187
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	B	2.7	2.7	1	8 RPRFERVL	10188
2QIE	AB	TRANSFERASE	A	2.7	2.7	1	19 IPMAEKKLAQIGDEINEKW	10189
2QJK	AB	ELECTRON TRANSPORT	A	2.7	2.7	1	7 IEEDFNA	10190
2QQN	HL	SIGNALING PROTEIN	L	2.7	2.7	1	7 DEQLKSG	10191
2QQP	CB	VIRUS	B	2.7	2.7	1	14 PSVIKGIAQQAVGA	10192
2QQP	CD	VIRUS	D	1.4	2.7	2	10 ASIGLGLLGK	10193
2QR1	DE	TRANSFERASE	E	2.7	2.7	1	5 SYDVL	10194
2R1H	AD	OXYGEN BINDING	D	2.7	2.7	1	6 PWTQRH	10195
2R5Y	AB	TRANSCRIPTION/DNA	B	2.7	2.7	1	18 VSQVSNWFGNKRIRYKKN	10196
2R6G	EG	HYDROLASE/TRANSPORT PROTEIN	E	1.4	2.7	2	11 PWAWSNIDTSK	10197
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	G	1.4	2.7	2	15 IALHVWTIKGYFETI	10198
2RAO	CD	OXYGEN BINDING	C	1.4	2.7	2	19 PVNFKLLSHCLLVTLANHH	10199
2RAO	CD	OXYGEN BINDING	D	1.4	2.7	2	20 PENFRLLGNVLVIVLSHHFG	10200
2RGN	BC	SIGNALING PROTEIN COMPLEX	C	2.7	2.7	1	7 DRLRPLS	10201
2UWJ	EF	CHAPERONE	F	1.4	2.7	2	17 STVTRALRDLMQGILQK	10202
2UZ1	DC	LYASE	C	2.7	2.7	1	7 QVAMAAP	10203
2UZ6	JT	RECEPTOR	T	1.4	2.7	2	7 PPCILNN	10204
2V4J	AB	OXIDOREDUCTASE	A	2.7	2.7	1	12 SQAACYELTMEY	10205
2V4J	AB	OXIDOREDUCTASE	A	1.4	2.7	2	15 FVSDIKQEAAYRAAN	10206
2V51	BF	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	B	2.7	2.7	1	9 QAVLSLYAS	10207
2V51	DE	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	E	2.7	2.7	1	10 NVLQLKLQQR	10208
2VGL	AB	PROTEIN TRANSPORT	A	2.7	2.7	1	14 EEVWYRVIQIVINR	10209

2VHO	CN	RIBOSOME	N	2.7	2.7	1	7	REAAMRG	10210
2VJH	CB	PHOTOSYNTHESIS	C	1.4	2.7	2	18	PQALTEFRSYLDYVINAL	10211
2VJT	AB	PHOTOSYNTHESIS	A	2.7	2.7	1	12	VLTKAIVNADAE	10212
2VML	IJ	PHOTOSYNTHESIS	J	1.4	2.7	2	12	AFTKAIVAADLR	10213
2VPG	AB	GENE REGULATION	A	1.4	2.7	2	10	ETAYGLLTAE	10214
2VRW	AB	SIGNALING PROTEIN	B	1.4	2.7	2	13	KYHLLLQELVKHT	10215
2WAQ	AB	TRANSCRIPTION	B	1.4	2.7	2	17	LGQIMEGIAGKYAALSG	10216
2WB1	AB	TRANSCRIPTION	B	2.7	2.7	1	5	LPSRM	10217
2WB1	WY	TRANSCRIPTION	Y	2.7	2.7	1	8	IGIVAAQS	10218
2WB1	YI	TRANSCRIPTION	I	2.7	2.7	1	17	RYEIARVISARALQLAM	10219
2WBJ	FH	IMMUNE SYSTEM	F	2.7	2.7	1	9	RPDAEYWNS	10220
2WG3	AC	SIGNALING PROTEIN	C	1.4	2.7	2	7	LDDMEEM	10221
2WIN	BQ	IMMUNE SYSTEM	Q	2.7	2.7	1	17	EYQNEKLANELKSLLDE	10222
2WIN	FP	IMMUNE SYSTEM	P	1.4	2.7	2	21	TYYKRTIKISGQKAMYALKSK	10223
2Z2T	AF	VIRAL PROTEIN/INHIBITOR	A	1.4	2.7	2	35	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	10224
2Z7X	AB	IMMUNE SYSTEM	A	2.7	2.7	1	8	EEYLKNSA	10225
2ZAE	CD	HYDROLASE	D	2.7	2.7	1	19	PDLAKRYVELALEIQKKAK	10226
2ZCY	FN	HYDROLASE	F	1.4	2.7	2	22	IPDGRHLVNRGREEAASFKKLY	10227
2ZCY	FN	HYDROLASE	N	1.4	2.7	2	15	TETAASVFKELCYEN	10228
2ZCY	JY	HYDROLASE	J	2.7	2.7	1	19	TEEGLDLLKLCVQELEKRM	10229
2ZCY	RY	HYDROLASE	R	2.7	2.7	1	22	TADARSMIEHARTAAVTHNLYY	10230
2ZCY	XK	HYDROLASE	X	2.7	2.7	1	19	TEEGLDLLKLCVQELEKRM	10231
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	A	2.7	2.7	1	5	QYLKD	10232
2ZJQ	BM	RIBOSOME	M	1.4	2.7	2	8	RGELLRGI	10233
2ZJQ	NO	RIBOSOME	N	1.4	2.7	2	9	LNAATYEYR	10234
3A0B	ac	ELECTRON TRANSPORT	c	1.4	2.7	2	28	PRSWLATSHFVLAFFFLVGHLWHAGRAR	10235
3A0B	AI	ELECTRON TRANSPORT	A	1.4	2.7	2	6	LWERFC	10236
3A1G	AB	TRANSFERASE	A	1.4	2.7	2	11	ICSTIEELRRQ	10237
3B4V	BC	HORMONE REGULATOR COMPLEX	C	2.7	2.7	1	12	SCHMRQATCFLG	10238
3B4V	FG	HORMONE REGULATOR COMPLEX	G	2.7	2.7	1	8	KINLLGFL	10239
3BBO	VZ	RIBOSOME	Z	1.4	2.7	2	12	ELFMLRLQKSAR	10240
3BLH	AB	TRANSCRIPTION	B	1.4	2.7	2	21	EAYLQQVQDLVILESIILQTL	10241
3BO0	AC	RIBOSOME	A	1.4	2.7	2	19	FKEKLKWTGIVLVLYFIMG	10242
3BPN	AC	CYTOKINE/CYTOKINE RECEPTOR	A	1.4	2.7	2	16	ITLQEIIKTLNSLTEQ	10243
3BVH	AC	BLOOD CLOTTING	A	1.4	2.7	2	22	NVRAQLVDMKRLEVDIDIKIRS	10244
3C01	CG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	G	1.4	2.7	2	10	IKLARSLFKT	10245
3C5W	AC	HYDROLASE	A	1.4	2.7	2	17	ANVRFNVAKSLQKIGPI	10246
3C5W	AC	HYDROLASE	A	1.4	2.7	2	14	VDVKYFAQEALTVL	10247
3C7B	DE	OXIDOREDUCTASE	E	2.7	2.7	1	5	YFYSE	10248

3C91	AH	HYDROLASE	A	1.4	2.7	2	23	VADARVLVDFARISAQQEKVTYG	10249
3C91	OV	HYDROLASE	O	1.4	2.7	2	23	VADARVLVDFARISAQQEKVTYG	10250
3CJB	AG	STRUCTURAL PROTEIN	A	2.7	2.7	1	12	SVWIGGSILASL	10251
3CJT	CD	TRANSFERASE/RIBOSOMAL PROTEIN	D	1.4	2.7	2	8	PVGPALGQ	10252
3CMA	AZ	RIBOSOME	Z	1.4	2.7	2	12	RRVAEIESEMNE	10253
3CQC	AB	PROTEIN TRANSPORT	B	1.4	2.7	2	8	SWLHEINS	10254
3CQX	AD	CHAPERONE	D	2.7	2.7	1	25	LEDQKKIKRRLETLLRNIDNSDKAI	10255
3CW2	EG	TRANSLATION	G	2.7	2.7	1	12	GVEKIKEVISKA	10256
3CXH	MG	OXIDOREDUCTASE	M	1.4	2.7	2	12	ALKLVRESELLG	10257
3CXH	PT	OXIDOREDUCTASE	T	2.7	2.7	1	8	SLYKTFFK	10258
3D3C	CL	TRANSCRIPTION	C	2.7	2.7	1	16	YKVAINEAIELAKSFG	10259
3D85	CD	IMMUNE SYSTEM/CYTOKINE	C	2.7	2.7	1	18	WTQCQQLSQKLCTLAWSA	10260
3D87	AB	CYTOKINE	A	2.7	2.7	1	7	PQGLRDN	10261
3DBH	AB	CELL CYCLE	B	2.7	2.7	1	13	KAEVAAEFLNDRV	10262
3DBJ	CD	PHOTOSYNTHESIS	D	2.7	2.7	1	13	TAAMEKLKAYFAT	10263
3DBJ	EF	PHOTOSYNTHESIS	F	2.7	2.7	1	13	TAAMEKLKAYFAT	10264
3DHR	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.4	2.7	2	19	PVNFKLLGHCFLVVVAVHF	10265
3DHR	EF	OXYGEN STORAGE, OXYGEN TRANSPORT	E	1.4	2.7	2	19	PVNFKLLGHCFLVVVAVHF	10266
3DKN	AC	PROTEIN TRANSPORT/RNA	A	1.4	2.7	2	27	PLLAFLVIIQIAFGSIILIYLDEIVSK	10267
3DL8	AG	PROTEIN TRANSPORT	A	2.7	2.7	1	39	KEQMREFEKVIVLRAVDSKWMDHIDAMDQLRQGIHLRAY	10268
3DUF	CD	OXIDOREDUCTASE/TRANSFERASE	C	1.4	2.7	2	14	FNLKEQYEIYKEKE	10269
3DUH	BD	IMMUNE SYSTEM/CYTOKINE	D	2.7	2.7	1	17	WTQCQQLSQKLCTLAWS	10270
3DZU	AD	TRANSCRIPTION/DNA	A	1.4	2.7	2	23	PAEVEALREKVYASLEAYCKHKY	10271
3E8C	BH	TRANSFERASE	B	2.7	2.7	1	18	KAVDWWALGVLIYEMAAG	10272
3EQS	AB	LIGASE	A	1.4	2.7	2	15	MKEVLFYLGQYIMTK	10273
3ET6	AB	LYASE	A	1.4	2.7	2	13	LLDELYQRFDAAI	10274
3EXG	34	OXIDOREDUCTASE	4	2.7	2.7	1	14	EMGFAGIAVGAAMA	10275
3EXG	AD	OXIDOREDUCTASE	D	2.7	2.7	1	6	KILEDN	10276
3EXG	CD	OXIDOREDUCTASE	D	2.7	2.7	1	5	TYYMS	10277
3EXG	ON	OXIDOREDUCTASE	N	1.4	2.7	2	7	FNFSMQA	10278
3F7P	AC	STRUCTURAL PROTEIN/CELL ADHESION	A	1.4	2.7	2	19	PKLTLGLIWTIILHFQISD	10279
3FDL	AB	APOPTOSIS	A	2.7	2.7	1	21	WGRIVAFFSFGGALCVESVDK	10280
3FGC	AB	OXIDOREDUCTASE	B	1.4	2.7	2	15	SDQVIEEMLDTAHYV	10281
3FHI	AB	TRANSFERASE	A	2.7	2.7	1	9	MFSHLRRIG	10282
3FIN	UV	RIBOSOME	U	1.4	2.7	2	24	FRKARETLFAAGNYAYAHRKRRKR	10283
3FKS	CD	HYDROLASE	C	2.7	2.7	1	12	VFYLHSRLLERA	10284
3FWB	AB	CELL CYCLE, TRANSCRIPTION	A	1.4	2.7	2	11	ENEFIAICTDS	10285

3FWC	BD	CELL CYCLE, TRANSCRIPTION	D	1.4	2.7	2	16	NYELISNELKARLLQE	10286
3FWC	JL	CELL CYCLE, TRANSCRIPTION	L	1.4	2.7	2	16	NYELISNELKARLLQE	10287
3G43	DF	METAL BINDING PROTEIN	D	1.4	2.7	2	8	AAELRHVM	10288
3GE8	AE	OXIDOREDUCTASE	A	1.4	2.7	2	16	FANMQFLGLAADAAEA	10289
3GE8	DH	OXIDOREDUCTASE	D	1.4	2.7	2	22	YPEYVSIQREKDAGAYSVKAAL	10290
3GHG	GI	BLOOD CLOTTING	I	1.4	2.7	2	13	VNLKEKVAQLEAQ	10291
3GHG	JL	BLOOD CLOTTING	L	1.4	2.7	2	25	TCGIADFLSTYQTKVDKDLQSLEDI	10292
3GLH	IJ	TRANSFERASE	J	1.4	2.7	2	20	APARLHWLATLLMDALKRHH	10293
3GLI	DO	TRANSFERASE/DNA	O	2.7	2.7	1	9	RRDWQLQQL	10294
3GLI	IP	TRANSFERASE/DNA	I	2.7	2.7	1	17	PTDIQLYYQTLLIGRKE	10295
3GM1	AF	TRANSFERASE	A	1.4	2.7	2	31	SSSRTEIEGTQKLLNKDLAELINKMRLAQQN	10296
3H0T	AB	IMMUNE SYSTEM/ANTIMICROBIAL PROTEIN	A	2.7	2.7	1	6	SEELQA	10297
3H2V	CG	CELL ADHESION	C	1.4	2.7	2	30	TKRALIQCAKDIAKASDEVTRLAKEVAKQC	10298
3H4P	Ga	HYDROLASE	a	1.4	2.7	2	9	LLSNILHSS	10299
3H87	AD	TOXIN/ANTITOXIN	A	2.7	2.7	1	10	MEIWSNRIER	10300
3HD7	EH	EXOCYTOSIS	H	1.4	2.7	2	54	DENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT	10301
3HH2	AD	SIGNALING PROTEIN/CYTOKINE	D	1.4	2.7	2	10	DNTLFKWMIF	10302
3HHL	AD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.4	2.7	2	10	KEVFAQFRAN	10303
3HOU	NU	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.4	2.7	2	10	PARLMETLRT	10304
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.7	2.7	1	18	AIEEAESLLQFHVATYMD	10305
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.4	2.7	2	16	VAHLIECLLSKVAALS	10306
3HOY	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	2.7	2.7	1	7	ESDLYKL	10307
3HRD	AD	OXIDOREDUCTASE	A	2.7	2.7	1	8	REESTTVS	10308
3HRD	EH	OXIDOREDUCTASE	E	2.7	2.7	1	8	REESTTVS	10309
3KIN	AB	MOTOR PROTEIN	B	2.7	2.7	1	16	KSLSALGNVISALAEG	10310
4RUB	CV	LYASE(CARBON-CARBON)	C	1.4	2.7	2	15	AKNYGRAVYECLRGG	10311
1A02	NJ	TRANSCRIPTION/DNA	J	2.6	2.6	1	50	KRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQ	10312
1AFV	AL	VIRAL PROTEIN/IMMUNE SYSTEM	A	1.3	2.6	2	21	QAAMQMLKETINEEAAEWDRL	10313
1AIP	AC	COMPLEX OF TWO ELONGATION FACTORS	C	2.6	2.6	1	13	VKELIQQAIAKIG	10314
1B33	CB	PHOTOSYNTHESIS	B	1.3	2.6	2	25	TRRYAACIRDLDYYLRYATYAMLAG	10315
1B33	CD	PHOTOSYNTHESIS	C	2.6	2.6	1	12	IVTKSIVNADAE	10316

1B33	JK	PHOTOSYNTHESIS	K	2.6	2.6	1	13	TAALEKLKSYFST	10317
1B8D	AB	PHOTOSYNTHESIS	A	1.3	2.6	2	27	SSDLESIQGNIQRAAARLEAAQKLSGN	10318
1BFO	EF	ANTIBODY	E	1.3	2.6	2	5	TEQLA	10319
1BGY	PQ	ELECTRON TRANSPORT	P	1.3	2.6	2	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	10320
1BXN	EJ	LYASE	E	1.3	2.6	2	14	GRNYGRVVYEGLKG	10321
1BXN	EK	LYASE	E	1.3	2.6	2	22	IQAGATANRVALEAMVLARNEG	10322
1CC0	AE	SIGNALING PROTEIN	A	1.3	2.6	2	19	PDSLENIPEKWTPEVKHFC	10323
1CM1	AB	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	A	2.6	2.6	1	10	EIREAFRVFD	10324
1CSE	EI	COMPLEX (SERINE PROTEINASE-INHIBITOR)	E	1.3	2.6	2	14	YSGIVSGIEWATTN	10325
1DCE	CD	TRANSFERASE	C	1.3	2.6	2	16	ATLWNCRREVLQHLET	10326
1DD4	AD	RIBOSOME	A	1.3	2.6	2	9	LKEAKDLVE	10327
1DFL	AY	CONTRACTILE PROTEIN	A	1.3	2.6	2	13	QDQRIGLSVIQRN	10328
1DGR	AV	PLANT PROTEIN	A	2.6	2.6	1	9	KNFLEASYD	10329
1DOW	AB	CELL ADHESION	B	2.6	2.6	1	10	NVQRLAEPSQ	10330
1E6E	AB	OXIDOREDUCTASE	A	2.6	2.6	1	9	IKELREMIQ	10331
1E7P	AB	OXIDOREDUCTASE	A	1.3	2.6	2	9	QEICEYFAG	10332
1EV1	34	VIRUS	3	2.6	2.6	1	6	LMEIAE	10333
1F3U	AB	TRANSCRIPTION	A	2.6	2.6	1	9	KYLSQQWAK	10334
1F51	DH	TRANSFERASE	H	1.3	2.6	2	11	SGIRILLNEVF	10335
1F5Q	CD	TRANSFERASE	C	1.3	2.6	2	13	STAIREISLLKEL	10336
1F9E	IJ	APOPTOSIS	J	1.3	2.6	2	16	WYIQSLCQSLRERCPR	10337
1FAV	AC	VIRAL PROTEIN	C	1.3	2.6	2	11	TSLIHSLIEES	10338
1FDH	BH	OXYGEN TRANSPORT	H	2.6	2.6	1	18	ENFKLLGNVLVTVLAIHF	10339
1FFU	EF	HYDROLASE	E	1.3	2.6	2	11	RYIAADAVEAV	10340
1FLC	EF	HYDROLASE	F	1.3	2.6	2	24	KGFEKIGNDIQILKSSINIAIEKL	10341
1FNT	DL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.3	2.6	2	22	ADCQFWETWLGSQCRLHELREK	10342
1FNT	EL	HYDROLASE/HYDROLASE ACTIVATOR	E	1.3	2.6	2	22	TADARSMIEHARTAAVTHNLYY	10343
1FNT	SZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.3	2.6	2	22	ADCQFWETWLGSQCRLHELREK	10344
1FNT	VN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.3	2.6	2	11	FGAHMANPLLR	10345
1FNT	Za	HYDROLASE/HYDROLASE ACTIVATOR	Z	2.6	2.6	1	22	ADCQFWETWLGSQCRLHELREK	10346
1FQJ	DE	SIGNALING PROTEIN	E	1.3	2.6	2	22	DAAQTHIYMLMKKDSYARYLKS	10347
1FQV	AB	LIGASE	B	1.3	2.6	2	10	EEEEAQVRKE	10348
1FQV	IJ	LIGASE	J	1.3	2.6	2	8	PEEIRKTF	10349
1FS2	AB	LIGASE	A	1.3	2.6	2	8	KRWYRLAS	10350
1FS2	AB	LIGASE	B	1.3	2.6	2	8	PEEIRKTF	10351
1FSX	CD	OXYGEN STORAGE/TRANSPORT	C	2.6	2.6	1	19	PAVHASLDKFLANVSTVLT	10352
1G0U	QX	HYDROLASE	X	1.3	2.6	2	22	AGDTVQFAEYIQANIQLYSIRE	10353
1G0U	XY	HYDROLASE	X	1.3	2.6	2	22	AGDTVQFAEYIQANIQLYSIRE	10354

1G20	CD	OXIDOREDUCTASE	C	1.3	2.6	2	16	KPEWEAVVAKYRPRLE	10355
1G3N	AB	CELL CYCLE, SIGNALING PROTEIN	B	2.6	2.6	1	8	VIHDAARA	10356
1G4B	LO	CHAPERONE/HYDROLASE	O	1.3	2.6	2	16	ADAFTLFELFERKLEM	10357
1GOT	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	B	1.3	2.6	2	5	LSQIT	10358
1H0H	AB	DEHYDROGENASE	B	2.6	2.6	1	5	IDRIT	10359
1H0T	AB	IMMUNE SYSTEM	A	2.6	2.6	1	15	KFNKEQQNAFYEILH	10360
1H1L	AB	OXIDOREDUCTASE	B	2.6	2.6	1	12	LWHFRSLMFTRQ	10361
1H5R	AB	TRANSFERASE	B	1.3	2.6	2	19	HQSLIEASNFIATIEERQG	10362
1HBM	BC	METHANOGENESIS	B	1.3	2.6	2	9	LVFDLVKAN	10363
1HV2	AB	SIGNALING PROTEIN	A	2.6	2.6	1	21	SHILEKAVEYLNYNLKYSGVS	10364
1HV4	AB	OXYGEN STORAGE/TRANSPORT	A	2.6	2.6	1	18	AEVHASLDKFLCAVGTVL	10365
1HV4	CD	OXYGEN STORAGE/TRANSPORT	C	2.6	2.6	1	18	AEVHASLDKFLCAVGTVL	10366
1I3Q	AB	TRANSCRIPTION	A	1.3	2.6	2	7	VSENVIL	10367
1I3Q	BI	TRANSCRIPTION	B	2.6	2.6	1	14	WQMLEMLKPCVEDG	10368
1I94	DE	RIBOSOME	E	2.6	2.6	1	10	AVPRAILELA	10369
1IBR	CD	CELL CYCLE, TRANSLATION	D	1.3	2.6	2	27	DEVALQGIEFWSNVCDEEMDLAIEASE	10370
1IM9	AD	IMMUNE SYSTEM	A	2.6	2.6	1	29	PEYWDRETQKYKRQAQADRVNLRKLRGYY	10371
1IR2	AI	LYASE	A	1.3	2.6	2	14	AKNYGRAVYECLRG	10372
1IRU	KZ	HYDROLASE	Z	1.3	2.6	2	10	SVYAYGVMDR	10373
1IRU	LM	HYDROLASE	M	2.6	2.6	1	15	TGAIAAMLSTILYSR	10374
1IWP	AG	LYASE	A	1.3	2.6	2	7	EAVFTDG	10375
1IZN	AB	PROTEIN BINDING	B	2.6	2.6	1	12	IEKNLSDLIDLV	10376
1IZN	CD	PROTEIN BINDING	C	2.6	2.6	1	13	FNEVFNDVRLLLN	10377
1JD2	AB	HYDROLASE	B	2.6	2.6	1	12	YQVEYALESISH	10378
1JD2	JR	HYDROLASE	R	1.3	2.6	2	12	QTFAYGVLDSNY	10379
1JEB	AB	OXYGEN STORAGE/TRANSPORT	A	1.3	2.6	2	19	PVNFKLLSHCLLVTLAARF	10380
1JY7	AB	OXYGEN STORAGE/TRANSPORT	A	2.6	2.6	1	18	AHAGEYGAEALERMFLSF	10381
1JY7	UV	OXYGEN STORAGE/TRANSPORT	V	2.6	2.6	1	23	PPVQAAYQKVVAGVANALAHKYH	10382
1KDX	AB	TRANSCRIPTION REGULATION COMPLEX	B	1.3	2.6	2	11	DSQKRREILSR	10383
1KF6	BC	OXIDOREDUCTASE	B	1.3	2.6	2	21	PAAAIQQGKVESSKDFLIATL	10384
1KF9	AC	HORMONE/GROWTH FACTOR	A	1.3	2.6	2	28	LSRLADNAWLRADRLNQLAFDTYQEFEE	10385
1KI1	CD	SIGNALING PROTEIN	D	2.6	2.6	1	12	RYPLIIKNILEN	10386
1KI6	AB	PHOSPHOTRANSFERASE	A	2.6	2.6	1	17	SIPTICDLARTFAREMG	10387
1KJY	CD	SIGNALING PROTEIN	C	1.3	2.6	2	14	RMHESMKLFDSICN	10388
1KMI	YZ	SIGNALING PROTEIN	Y	2.6	2.6	1	14	STMRRIVRNLLKEL	10389
1KQF	AB	OXIDOREDUCTASE	A	2.6	2.6	1	7	LLNAIAQ	10390
1KYO	BR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	2.6	2.6	1	20	YLLPYILEAEAAAKEKDELD	10391

1KYO	NS	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	1.3	2.6	2	35	PYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIG	10392
1LB1	EF	SIGNALING PROTEIN	E	2.6	2.6	1	13	LDSYLLKPVQRIT	10393
1LJ2	AD	VIRAL PROTEIN/ TRANSLATION	D	1.3	2.6	2	6	TEEIMS	10394
1LVC	AD	LYASE	A	1.3	2.6	2	33	PEYKNYFQYLKERITNQVQLLLTHQKFKLLYKQ	10395
1LWU	HI	BLOOD CLOTTING	H	1.3	2.6	2	16	RSMKSVLEHLRAKMQR	10396
1M1E	AB	STRUCTURAL PROTEIN	B	1.3	2.6	2	19	PEEMYIQQKVRVLLMLRKM	10397
1M1J	AC	BLOOD CLOTTING	A	1.3	2.6	2	27	GIIDDTDQNYSQRIDNIRQQLADSQNK	10398
1M1Y	KL	OXIDOREDUCTASE	K	2.6	2.6	1	6	FIFQKM	10399
1MIO	CD	MOLYBDENUM-IRON PROTEIN	C	2.6	2.6	1	12	HHDMEVVLEKLK	10400
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	C	2.6	2.6	1	15	SDYNRTVMRNWTGKW	10401
1MTY	CH	MONOOXYGENASE	H	1.3	2.6	2	20	VNYFLDGERQLGTRLMELRN	10402
1MU2	AB	TRANSFERASE	B	1.3	2.6	2	7	PLVRLAF	10403
1N4Q	AB	TRANSFERASE	A	1.3	2.6	2	13	NSVWNQRHFVISN	10404
1N4Q	GH	TRANSFERASE	G	1.3	2.6	2	13	NSVWNQRHFVISN	10405
1N86	AC	BLOOD CLOTTING	C	2.6	2.6	1	20	THDSSIRYLQEIYNSNNQKI	10406
1NEX	CD	LIGASE, CELL CYCLE	C	1.3	2.6	2	8	PEEIRRTF	10407
1NI4	CB	OXIDOREDUCTASE	B	2.6	2.6	1	6	KILEDN	10408
1OCC	AD	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.3	2.6	2	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	10409
1OCC	CG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	G	1.3	2.6	2	16	LALPSVALCTLNSWLH	10410
1OCC	DE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	E	2.6	2.6	1	16	FASAVRILEVVKDKAG	10411
1OZS	AB	STRUCTURAL PROTEIN	A	2.6	2.6	1	13	SEEELSDLFRMFD	10412
1PMA	KX	PROTEASE	X	1.3	2.6	2	22	VGDAQVLVRYMKAELELYRLQR	10413
1PTO	BF	TOXIN	B	1.3	2.6	2	18	WSMYSRLRKMLYLIYVAG	10414
1Q16	BC	OXIDOREDUCTASE	B	2.6	2.6	1	7	RAMLLGK	10415
1Q5R	FM	HYDROLASE	M	1.3	2.6	2	23	AGIAIELVRLFAVELEHYEKIEG	10416
1QGW	BD	PHOTOSYNTHESIS	D	1.3	2.6	2	10	ADLQALKKFI	10417
1R4M	AB	CELL CYCLE	A	1.3	2.6	2	11	DDYVHEFCRYG	10418
1R5V	AB	SIGNALING PROTEIN	A	2.6	2.6	1	5	EEFAK	10419
1R8U	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	B	1.3	2.6	2	16	PHCRTMKNVLNHMTHC	10420
1RCO	BF	LYASE	B	1.3	2.6	2	6	WTDGLT	10421
1RCO	HM	LYASE	H	1.3	2.6	2	6	WTDGLT	10422
1RGI	GA	CONTRACTILE PROTEIN	A	2.6	2.6	1	12	SVWIGGSILASL	10423
1RM6	EF	OXIDOREDUCTASE	E	1.3	2.6	2	7	PTHRAAA	10424
1RP3	EF	TRANSCRIPTION	E	2.6	2.6	1	32	TEELFKTLDKINFSYILSLEEVFRDFARDYSE	10425

1RYP	AI	MULTICATALYTIC PROTEINASE	I	2.6	2.6	1	22	AADTEAVTQLIGSNIELHSLYT	10426
1RYP	GN	MULTICATALYTIC PROTEINASE	G	1.3	2.6	2	22	IPDGRHLVNRGREEAASFKKLY	10427
1RYP	KZ	MULTICATALYTIC PROTEINASE	Z	2.6	2.6	1	11	QTFAYGVLDSN	10428
1RYP	YL	MULTICATALYTIC PROTEINASE	Y	2.6	2.6	1	19	TEEGLDLLKLCVQELEKRM	10429
1RZR	AS	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	S	2.6	2.6	1	5	IMGVM	10430
1S5L	DE	PHOTOSYNTHESIS	E	2.6	2.6	1	7	LAYDVFG	10431
1S5L	KZ	PHOTOSYNTHESIS	Z	2.6	2.6	1	26	WDRSKQLIFLGSGLWIALVLVVGVLN	10432
1SB0	AB	TRANSCRIPTION	A	1.3	2.6	2	16	QDLRSHLVHKLVQAIF	10433
1SCT	GH	OXYGEN TRANSPORT	G	1.3	2.6	2	17	PSRLKCVVEKFAVNHIN	10434
1SEQ	LH	IMMUNE SYSTEM	L	1.3	2.6	2	6	SEQLTS	10435
1SQX	CE	OXIDOREDUCTASE	C	2.6	2.6	1	24	NFGSLLGICLILQILTGLFLAMHY	10436
1SVX	AB	DE NOVO PROTEIN/SUGAR BINDING PROTEIN	A	2.6	2.6	1	8	PLHLAAYW	10437
1TBG	BF	COMPLEX (GTP-BINDING/TRANSDUCER)	B	1.3	2.6	2	5	LSQIT	10438
1TBG	DH	COMPLEX (GTP-BINDING/TRANSDUCER)	D	1.3	2.6	2	5	LSQIT	10439
1TIL	CD	TRANSCRIPTION	C	2.6	2.6	1	23	MDELTEIKTVVSEAVTNAIIHGY	10440
1TO9	AB	BIOSYNTHETIC PROTEIN	A	1.3	2.6	2	6	RSVLSG	10441
1TQY	AB	TRANSFERASE	A	2.6	2.6	1	10	PIVVACFDAI	10442
1TUE	FG	REPLICATION	F	2.6	2.6	1	5	WSRLD	10443
1TUE	KL	REPLICATION	L	2.6	2.6	1	23	IDSQIQYWQLIRWENAIFFAARE	10444
1U35	GH	STRUCTURAL PROTEIN/DNA	H	1.3	2.6	2	19	ELAKHAVSEGTKAVTKYTS	10445
1U6G	AB	LIGASE	A	2.6	2.6	1	16	LERSYQRFTAFYASRH	10446
1U6G	AC	LIGASE	A	2.6	2.6	1	24	SVLKFYTQQWEDYRFSSKVLNGIC	10447
1U6G	AC	LIGASE	C	1.3	2.6	2	15	KVRRAAAKCLDAVVS	10448
1UM9	CD	OXIDOREDUCTASE	D	2.6	2.6	1	12	YEAVMNSVAKTG	10449
1UPT	HG	HYDROLASE/PROTEIN-BINDING	H	2.6	2.6	1	13	TEFEYLRKVLFEY	10450
1UYW	NM	IMMUNE SYSTEM	N	1.3	2.6	2	6	SEQLTS	10451
1UZH	RM	LYASE	R	1.3	2.6	2	21	NAPGAAANRVALEACTQARNE	10452
1V54	AB	OXIDOREDUCTASE	A	2.6	2.6	1	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	10453
1V54	NG	OXIDOREDUCTASE	N	1.3	2.6	2	33	LFVWSVMITAVLLLLSLPVLAAGITMLLTDRNL	10454
1VF5	BC	PHOTOSYNTHESIS	B	1.3	2.6	2	20	VFPVVIMGTFACIVALSVLD	10455
1VF5	BC	PHOTOSYNTHESIS	C	1.3	2.6	2	25	PNRVKWMIAFICLVMLAQLMLILKK	10456
1VF5	FG	PHOTOSYNTHESIS	F	1.3	2.6	2	26	EMLYAALLSFGLIFVGWGLGVLLLKI	10457
1VF5	PQ	PHOTOSYNTHESIS	P	1.3	2.6	2	25	PNRVKWMIAFICLVMLAQLMLILKK	10458
1VSP	DJ	RIBOSOME	D	1.3	2.6	2	14	PHLLWEVVRWQLAK	10459
1VYW	AB	TRANSFERASE	B	1.3	2.6	2	15	KKQVLRMEHLVLKVL	10460
1W2W	EF	ISOMERASE	E	2.6	2.6	1	16	VNLSNSLVEIKNILKS	10461

1WCM	BC	TRANSCRIPTION	C	1.3	2.6	2	14	LAMANSLRRVMIAE	10462
1WMI	CD	HYDROLASE/HYDROLASE INHIBITOR	C	1.3	2.6	2	17	KAHYRRFLEFRDILEYE	10463
1WQ1	RG	COMPLEX (GTP-BINDING/GTPASE ACTIVATION)	R	1.3	2.6	2	18	TKSFEDIHQYREQIKRVK	10464
1WYU	AB	OXIDOREDUCTASE	A	2.6	2.6	1	11	EEEIREMLRRV	10465
1WYU	EF	OXIDOREDUCTASE	F	2.6	2.6	1	5	AEDLI	10466
1XD2	BC	SIGNALING PROTEIN	C	2.6	2.6	1	16	EKEFTDYLFNKSLEIE	10467
1XFU	AO	LYASE/METAL BINDING PROTEIN	A	1.3	2.6	2	15	SLEKQKGVTNLLIKY	10468
1XFU	CQ	LYASE/METAL BINDING PROTEIN	C	1.3	2.6	2	15	SLEKQKGVTNLLIKY	10469
1XFU	DR	LYASE/METAL BINDING PROTEIN	R	2.6	2.6	1	5	AFSLF	10470
1XFV	CQ	LYASE/METAL BINDING PROTEIN	C	1.3	2.6	2	13	SAEFIKNLSSIRR	10471
1XGP	AC	IMMUNE SYSTEM	C	1.3	2.6	2	12	TASVNCAKKIVS	10472
1XK4	FL	METAL BINDING PROTEIN	F	1.3	2.6	2	18	ELEKALNSIIDVYHKYSL	10473
1XLS	FN	TRANSCRIPTION	N	1.3	2.6	2	9	ALLRYLLDK	10474
1XQ5	CD	OXYGEN STORAGE/TRANSPORT	C	1.3	2.6	2	19	PANFKILSHCILVLLAVKF	10475
1Y14	AB	TRANSFERASE	A	1.3	2.6	2	8	ADEAKTLI	10476
1Y3A	DH	SIGNALING PROTEIN	D	2.6	2.6	1	8	RKKWIHCF	10477
1Y8R	AB	LIGASE	A	1.3	2.6	2	14	GLGAEIAKNLILAG	10478
1Y96	CD	RNA BINDING PROTEIN	D	2.6	2.6	1	24	LESQEQRARAALRERYLRSLLAMV	10479
1YA7	CJ	HYDROLASE/HYDROLASE ACTIVATOR	C	2.6	2.6	1	23	VADARVLVDFARISAQQEKVTYG	10480
1YA7	FL	HYDROLASE/HYDROLASE ACTIVATOR	F	1.3	2.6	2	23	VADARVLVDFARISAQQEKVTYG	10481
1YE9	LP	OXIDOREDUCTASE	P	1.3	2.6	2	8	FFAENEQA	10482
1Z2C	AB	SIGNALING PROTEIN	B	1.3	2.6	2	9	EEKQQPLRE	10483
1Z5S	AC	LIGASE	A	1.3	2.6	2	10	AEAYTIYCQN	10484
1Z6O	AM	METAL BINDING PROTEIN	M	2.6	2.6	1	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	10485
1Z6O	BP	METAL BINDING PROTEIN	B	2.6	2.6	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	10486
1Z6O	EQ	METAL BINDING PROTEIN	Q	2.6	2.6	1	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	10487
1Z6O	JV	METAL BINDING PROTEIN	V	2.6	2.6	1	28	RSCRNSMRQQIQMEVGASLQYLAMGAHF	10488
1Z7Q	EL	HYDROLASE/HYDROLASE ACTIVATOR	E	1.3	2.6	2	23	TADARSMIEHARTAAVTHNLYYD	10489
1Z7Q	Ib	HYDROLASE/HYDROLASE ACTIVATOR	b	1.3	2.6	2	7	FGAHMAN	10490
1Z7Q	IJ	HYDROLASE/HYDROLASE ACTIVATOR	I	2.6	2.6	1	22	AADTEAVTQLIGSNIELHSLYT	10491
1ZBB	fh	STRUCTURAL PROTEIN/DNA	f	2.6	2.6	1	11	AMDVVYALKRQ	10492
1ZL8	AB	PROTEIN BINDING	A	2.6	2.6	1	12	NAKLASLQQVLQ	10493
1ZLA	AB	PROTEIN BINDING/VIRUS/DNA	A	1.3	2.6	2	12	PKDIQLARRIRG	10494
1ZLA	AG	PROTEIN BINDING/VIRUS/DNA	A	1.3	2.6	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	10495
1ZNV	CD	HYDROLASE/PROTEIN BINDING	D	2.6	2.6	1	9	RNNNDRMKV	10496
2ABZ	AC	HYDROLASE/HYDROLASE INHIBITOR	C	1.3	2.6	2	7	PWAREGA	10497
2ACL	CH	TRANSCRIPTION	C	1.3	2.6	2	11	LDDQVILLRAG	10498
2ACL	GD	TRANSCRIPTION	G	1.3	2.6	2	23	PVTNICQAADKQLFTLVEWAKRI	10499
2AHM	BF	VIRAL PROTEIN, REPLICATION	B	1.3	2.6	2	19	KMSDVKCTSVVLLSVLQQL	10500

2APO	AB	ISOMERASE/RNA BINDING PROTEIN	B	2.6	2.6	1	5	GKYRR	10501
2APO	AB	ISOMERASE/RNA BINDING PROTEIN	B	2.6	2.6	1	6	KRALKN	10502
2AXT	dl	ELECTRON TRANSPORT	1	1.3	2.6	2	21	RTSLYLGLLLILVLALLFSSY	10503
2B8K	BC	TRANSFERASE	C	1.3	2.6	2	14	LAMANSLRRVMIAE	10504
2BE6	AD	MEMBRANE PROTEIN	A	1.3	2.6	2	12	DEEVDEMIREAD	10505
2BEC	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	A	2.6	2.6	1	13	RRNKLHYAFQLYD	10506
2BKY	AX	DNA BINDING PROTEIN	X	1.3	2.6	2	16	ISKAVDVYNSLKDRLG	10507
2BL0	AC	MUSCLE PROTEIN	C	1.3	2.6	2	11	EDILRQAFRTF	10508
2BS4	DE	OXIDOREDUCTASE	D	1.3	2.6	2	11	RDVQEICEYFA	10509
2BTO	AT	CYTOSKELETAL PROTEIN	A	2.6	2.6	1	6	ANWYLN	10510
2D2M	BD	OXYGEN STORAGE/TRANSPORT	B	1.3	2.6	2	15	SLNRLLVKRQWAEAY	10511
2DE5	BE	OXIDOREDUCTASE	B	2.6	2.6	1	7	EAILKRV	10512
2DSQ	CH	PROTEIN BINDING/HORMONE/GROWTH FACTOR	H	2.6	2.6	1	13	PCRIELYRVVESL	10513
2DSR	GI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	1.3	2.6	2	7	IVDECCF	10514
2DYM	AB	PROTEIN TURNOVER/PROTEIN TURNOVER	A	1.3	2.6	2	12	HMNDIKQLLWNG	10515
2E 74	BH	PHOTOSYNTHESIS	B	1.3	2.6	2	26	PNDLLYVFPVVIMGTFACIVALSVLD	10516
2E 74	CE	PHOTOSYNTHESIS	E	2.6	2.6	1	27	ILGAVFYIVFIALFFGIAVGIIFAIKS	10517
2E9X	BD	REPLICATION	B	1.3	2.6	2	10	LWLAINLKQR	10518
2E9X	EG	REPLICATION	E	2.6	2.6	1	13	EKAMELIRELHRA	10519
2EHO	AB	REPLICATION	A	1.3	2.6	2	13	NTESYLKNVALKH	10520
2EHO	CD	REPLICATION	C	2.6	2.6	1	11	SGTFLTQALNH	10521
2EQ9	BC	OXIDOREDUCTASE	C	1.3	2.6	2	10	PAARKLAREL	10522
2F43	AB	HYDROLASE	A	1.3	2.6	2	8	YRQMSLLL	10523
2F49	AC	TRANSFERASE	A	1.3	2.6	2	21	DDHIQYFIYQTLRAVKVLHGS	10524
2F4O	AB	HYDROLASE	B	1.3	2.6	2	12	PQFQQMRQIIQQ	10525
2F66	AB	TRANSPORT PROTEIN	B	1.3	2.6	2	29	SKDKEVIETLSEIYSIVITLDHVEKAYLK	10526
2F8N	HG	STRUCTURAL PROTEIN/DNA	H	1.3	2.6	2	11	AIYVYKVLKQV	10527
2F9D	AP	RNA BINDING PROTEIN	P	1.3	2.6	2	16	PEQLQAWRWEREIDER	10528
2F9I	AD	TRANSFERASE	A	1.3	2.6	2	17	PEGYRKALRLMKQAEKF	10529
2FEP	AS	TRANSCRIPTION	S	1.3	2.6	2	8	IMGVMSLG	10530
2FM8	AC	CHAPERONE/CELL INVASION	A	2.6	2.6	1	8	SMVVLQQR	10531
2FUG	23	OXIDOREDUCTASE	2	1.3	2.6	2	11	PTEVMGVASFY	10532
2FUG	34	OXIDOREDUCTASE	4	1.3	2.6	2	10	VIYHFKHYTE	10533
2FUG	97	OXIDOREDUCTASE	7	1.3	2.6	2	5	PDFIY	10534

2FUN	AB	APOPTOSIS/HYDROLASE	B	2.6	2.6	1	15	ILTILTEVNYEVSNK	10535
2FYN	AB	OXIDOREDUCTASE	A	2.6	2.6	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	10536
2GAG	BD	OXIDOREDUCTASE	B	1.3	2.6	2	7	LERFETG	10537
2GFB	AB	IMMUNOGLOBULIN	A	1.3	2.6	2	6	SEQLTS	10538
2GFB	KL	IMMUNOGLOBULIN	K	1.3	2.6	2	7	SEQLTSG	10539
2GTL	IC	OXYGEN STORAGE/TRANSPORT	C	1.3	2.6	2	15	EEDHRIVQKQWDILW	10540
2GTL	IJ	OXYGEN STORAGE/TRANSPORT	J	1.3	2.6	2	16	VLEGLKVKSEWGRAYG	10541
2GTL	MN	OXYGEN STORAGE/TRANSPORT	M	1.3	2.6	2	15	KKTIRQLKARISNLE	10542
2GTP	AD	SIGNALING PROTEIN	D	1.3	2.6	2	21	DEAQKVIYTLMEKDSYPRFLK	10543
2GTP	BC	SIGNALING PROTEIN	C	1.3	2.6	2	21	DEAQKVIYTLMEKDSYPRFLK	10544
2GUZ	OP	CHAPERONE, PROTEIN TRANSPORT	O	1.3	2.6	2	8	SKEALQIL	10545
2HLD	LO	HYDROLASE	L	1.3	2.6	2	15	LSKQAVAYRQLSLLL	10546
2HVY	CD	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	D	1.3	2.6	2	10	AHLPPLCEEK	10547
2HYE	AB	PROTEIN BINDING	B	2.6	2.6	1	12	YKGVKLAKFGKE	10548
2HYI	IJ	HYDROLASE/RNA BINDING PROTEIN/RNA	I	2.6	2.6	1	14	KRKVDWLTEKMREA	10549
2HZM	CD	TRANSCRIPTION	D	1.3	2.6	2	9	VSSLMNGLG	10550
2I2R	DH	TRANSPORT PROTEIN	H	1.3	2.6	2	12	EDTFKQIYAQFF	10551
2I2X	EF	TRANSFERASE	F	2.6	2.6	1	9	PEEAAEELY	10552
2I2X	KJ	TRANSFERASE	J	1.3	2.6	2	8	EASLKKVL	10553
2I3S	EF	CELL CYCLE	F	1.3	2.6	2	5	FNLIY	10554
2IAN	LM	IMMUNE SYSTEM	L	1.3	2.6	2	9	RPDAEYWNS	10555
2IPK	AC	IMMUNE SYSTEM	A	1.3	2.6	2	22	AQGALANIAVDKANLEIMTKRS	10556
2IZV	AC	TRANSCRIPTION	A	2.6	2.6	1	8	SSMKLYLK	10557
2J0Q	AC	HYDROLASE	A	1.3	2.6	2	12	DIRILRDIEQYY	10558
2J3R	AB	TRANSPORT	A	1.3	2.6	2	26	DEDVNKQLDRMGYNIGVRLIEDFLAR	10559
2J59	BN	HYDROLASE	B	2.6	2.6	1	11	KTTILYKLKLG	10560
2J59	CO	HYDROLASE	C	2.6	2.6	1	10	KTTILYKLKL	10561
2J5G	AD	HYDROLASE	A	1.3	2.6	2	11	TLNLRYTRVAL	10562
2J5G	AD	HYDROLASE	D	2.6	2.6	1	17	GKTHREFPDAFYDISRD	10563
2J88	AH	HYDROLASE	A	2.6	2.6	1	31	DQRVEQEAKRRFEKYGQLFMEETLKAAKRMR	10564
2JGD	AB	OXIDOREDUCTASE	B	1.3	2.6	2	7	GDFANGA	10565
2JJ0	LM	PHOTOSYNTHESIS	M	2.6	2.6	1	26	MEGIHRWAIWMAVLVTLTGGIGILLS	10566
2JJZ	AB	METAL BINDING PROTEIN	A	2.6	2.6	1	19	ILKARQERRLAEINREFLC	10567
2JQK	AB	PROTEIN TRANSPORT	B	1.3	2.6	2	11	EEIERQLKALG	10568
2K3S	AB	PROTEIN BINDING	A	1.3	2.6	2	18	SKCVYTYIQELYRSLVQK	10569
2KA4	AB	TRANSCRIPTION REGULATOR	B	2.6	2.6	1	6	HDLRHL	10570
2NPP	AB	SIGNALING PROTEIN,HYDROLASE	A	1.3	2.6	2	16	PMVRRAAASKLGEFAK	10571
2NPP	BC	SIGNALING PROTEIN,HYDROLASE	C	2.6	2.6	1	8	FYDECLRK	10572

2NV2	QR	LYASE/TRANSFERASE	R	1.3	2.6	2	11	STTMRRLIDTY	10573
2NVU	BC	PROTEIN TURNOVER, LIGASE	B	2.6	2.6	1	7	DTFYRQF	10574
2NYL	DE	HYDROLASE	D	2.6	2.6	1	5	WRVRY	10575
2NZD	CD	STRUCTURAL PROTEIN/DNA	C	1.3	2.6	2	10	PRHLQLAVRN	10576
2NZD	CD	STRUCTURAL PROTEIN/DNA	D	1.3	2.6	2	12	AIYVYKVLKQVH	10577
2NZD	GH	STRUCTURAL PROTEIN/DNA	H	1.3	2.6	2	19	ELAKHAVSEGTKAVTKYTS	10578
2OBH	BD	CELL CYCLE	B	1.3	2.6	2	11	FKNLKRVAKEL	10579
2ODB	AB	PROTEIN BINDING	A	1.3	2.6	2	14	LKNVFDEAILAALE	10580
2OI9	AB	IMMUNE SYSTEM	A	2.6	2.6	1	11	AAEYYRAYLEG	10581
2OOB	AB	LIGASE	A	2.6	2.6	1	11	FEEVKRALEIA	10582
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	B	1.3	2.6	2	10	KELALYVLSF	10583
2P1L	EF	APOPTOSIS	E	1.3	2.6	2	13	AYQSFEQVVNELF	10584
2P1N	DE	SIGNALING PROTEIN	D	1.3	2.6	2	16	KNLLDLTCQTVADMIK	10585
2P1N	DE	SIGNALING PROTEIN	E	1.3	2.6	2	7	KSWYEIE	10586
2P22	AD	TRANSPORT PROTEIN	A	1.3	2.6	2	30	DGLNQLYNLVAQDYALTDTIECLSRMLHRG	10587
2P22	CD	TRANSPORT PROTEIN	C	2.6	2.6	1	11	RHQLELYVTKF	10588
2P2C	EF	HYDROLASE	F	2.6	2.6	1	15	VADMLVKVNALIKDR	10589
2P5T	EF	TRANSCRIPTION REGULATOR	F	1.3	2.6	2	13	QVEKEMLQVGEKR	10590
2PMZ	QG	TRANSLATION, TRANSFERASE	G	1.3	2.6	2	12	TVKHLLDAAARG	10591
2PO6	GH	LIPID BINDING PROTEIN/IMMUNE SYSTEM	H	1.3	2.6	2	7	EAEISHT	10592
2PON	AB	APOPTOSIS INHIBITOR	B	1.3	2.6	2	13	AYQSFEQVVNELF	10593
2Q9Q	AB	REPLICATION	A	1.3	2.6	2	16	GTFLTQALNHMYKLRT	10594
2QE7	CD	HYDROLASE	D	1.3	2.6	2	11	TREGNDLYHEM	10595
2QIE	KJ	TRANSFERASE	K	2.6	2.6	1	19	IPMAEKKLAQIGDEINEKW	10596
2QJK	AB	ELECTRON TRANSPORT	A	1.3	2.6	2	11	FASVEHIMRNV	10597
2QJK	JK	ELECTRON TRANSPORT	J	2.6	2.6	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	10598
2QJP	DC	ELECTRON TRANSPORT	D	2.6	2.6	1	11	IGHSIQTWLLG	10599
2QJY	EF	OXIDOREDUCTASE	F	2.6	2.6	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	10600
2QL2	CB	TRANSCRIPTION/DNA	B	2.6	2.6	1	19	KIETLRLAKNYIWALSEIL	10601
2QLV	DF	TRANSFERASE/PROTEIN BINDING	D	1.3	2.6	2	12	PQIHRANMLAQG	10602
2QLV	DF	TRANSFERASE/PROTEIN BINDING	F	2.6	2.6	1	8	VGEALMRR	10603
2QOW	KG	RIBOSOME	K	1.3	2.6	2	13	PFAAQVAAERCAD	10604
2QQD	BC	LYASE	C	1.3	2.6	2	13	PLNAFDGALLNAG	10605
2R5C	AB	TRANSFERASE	B	2.6	2.6	1	11	YEALYATIQGH	10606
2R6G	BF	HYDROLASE/TRANSPORT PROTEIN	B	2.6	2.6	1	7	FGLKLAG	10607
2RGN	AB	SIGNALING PROTEIN COMPLEX	B	1.3	2.6	2	10	IQQIYEWHRD	10608
2RHK	AC	VIRAL PROTEIN/NUCLEAR PROTEIN	C	2.6	2.6	1	5	KHWLR	10609
2RI4	IJ	OXYGEN STORAGE, OXYGEN TRANSPORT	J	2.6	2.6	1	19	PENFKLLGNVLVVVLARHH	10610

2UUN	GH	ELECTRON TRANSPORT	H	1.3	2.6	2	13	VAQIDALSQMVAE	10611
2UUN	MN	ELECTRON TRANSPORT	N	2.6	2.6	1	12	AFTKVAAQADTR	10612
2UUN	WX	ELECTRON TRANSPORT	X	1.3	2.6	2	13	VAQIDALSQMVAE	10613
2UY1	AB	RNA BINDING PROTEIN	B	2.6	2.6	1	16	PHVFIYCAFIEYYATG	10614
2UZ1	AB	LYASE	A	2.6	2.6	1	7	DGSVGYS	10615
2UZ1	AC	LYASE	A	1.3	2.6	2	17	TEHIPRLVMQAIRAALS	10616
2V5H	FJ	TRANSCRIPTION	F	2.6	2.6	1	10	IPQSRELIAQ	10617
2V7Q	AE	HYDROLASE	A	1.3	2.6	2	10	VFYLHSRLLE	10618
2VDO	AB	CELL ADHESION/IMMUNE SYSTEM	B	2.6	2.6	1	5	DGRLA	10619
2VDW	GH	TRANSFERASE	H	2.6	2.6	1	21	FSNRVYEALYYVHSLLYSSMT	10620
2VZD	AC	CELL ADHESION	C	1.3	2.6	2	9	DLDALLADL	10621
2VZI	AB	CELL ADHESION	B	1.3	2.6	2	15	LKSTLRVLYNLFTKY	10622
2W19	BD	TRANSFERASE/ISOMERASE	B	1.3	2.6	2	20	HFDRIVDEVQGFFEVHRALG	10623
2W83	BD	PROTEIN TRANSPORT	B	1.3	2.6	2	7	RPLWRHY	10624
2WAQ	EF	TRANSCRIPTION	F	2.6	2.6	1	6	LLSDVI	10625
2WH2	FP	RIBOSOME	F	2.6	2.6	1	16	PHLLWEVVRWQLAKRR	10626
2WH2	UV	RIBOSOME	U	2.6	2.6	1	23	RKARETLFAAGNYAYAHRKRRKR	10627
2WII	AB	IMMUNE SYSTEM	B	2.6	2.6	1	21	LEKRQGALELIKKGYTQQLAF	10628
2Z2S	AB	TRANSCRIPTION	B	2.6	2.6	1	5	SLASV	10629
2Z2Y	AB	HYDROLASE	A	1.3	2.6	2	12	YLYDMIIQAYNA	10630
2ZCY	UV	HYDROLASE	V	2.6	2.6	1	22	AADTEAVTQLIGSNIELHSLYT	10631
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	A	1.3	2.6	2	11	KEEWRSLVLRH	10632
2ZIV	AB	HYDROLASE	B	1.3	2.6	2	10	PQLLVQAYQQ	10633
2ZNE	BC	APOPTOSIS	B	2.6	2.6	1	12	YEQYLSMVFSIV	10634
2ZNL	AB	TRANSCRIPTION	A	1.3	2.6	2	11	SWIQNEFNKAC	10635
2ZT9	CD	PHOTOSYNTHESIS	D	1.3	2.6	2	31	MGRRQFMNLLTFGTVTGVALGALYPVVNYFI	10636
3A0B	AD	ELECTRON TRANSPORT	A	2.6	2.6	1	12	IVAAHGYFGRLI	10637
3A0B	AI	ELECTRON TRANSPORT	A	1.3	2.6	2	6	WELSYR	10638
3A0B	LT	ELECTRON TRANSPORT	T	1.3	2.6	2	10	CIIALFFFAI	10639
3BBN	DE	RIBOSOME	D	2.6	2.6	1	8	LLVVEYYS	10640
3BP8	BD	TRANSCRIPTION	B	1.3	2.6	2	16	LLDRIISHIDQFFIRH	10641
3BPL	AC	CYTOKINE/CYTOKINE RECEPTOR	A	2.6	2.6	1	19	LENFLERLKTIMREKYSKC	10642
3BZ1	yZ	ELECTRON TRANSPORT	Z	1.3	2.6	2	28	TILFQLALAALVILSFVMVIGVPVAYAS	10643
3C1B	AG	STRUCTURAL PROTEIN/DNA	A	1.3	2.6	2	13	TVALREIRRYQKS	10644
3C1B	CD	STRUCTURAL PROTEIN/DNA	D	1.3	2.6	2	12	AIYVYKVLKQVH	10645
3C1B	FH	STRUCTURAL PROTEIN/DNA	H	1.3	2.6	2	12	SREIQTAVRLLL	10646
3C5J	AB	MEMBRANE PROTEIN	A	2.6	2.6	1	5	EEFGR	10647
3C8G	CD	TRANSCRIPTION REGULATOR	D	2.6	2.6	1	16	KTALTLAVTTTLKELT	10648
3CFV	AF	HISTONE/CHAPERONE	A	2.6	2.6	1	22	TVEERVINEEYKIWKKNTPFLY	10649
3CJH	AB	PROTEIN TRANSPORT	A	2.6	2.6	1	16	TELVNKISENCFEKCL	10650

3CJH	AD	PROTEIN TRANSPORT	A	1.3	2.6	2	16	TELVNKISENCFEKCL	10651
3CJT	CD	TRANSFERASE/RIBOSOMAL PROTEIN	C	2.6	2.6	1	10	DPILPGLFDG	10652
3CWB	CD	OXIDOREDUCTASE	C	2.6	2.6	1	29	GWLIRNLHANGASFFFICIFLHIGRGLYY	10653
3CXH	EI	OXIDOREDUCTASE	I	2.6	2.6	1	7	SLYKTFF	10654
3D54	KL	LIGASE	K	2.6	2.6	1	15	PRGETIERVLREEKG	10655
3DBH	CD	CELL CYCLE	D	2.6	2.6	1	13	KAEVAAEFLNDRV	10656
3DBH	CD	CELL CYCLE	D	1.3	2.6	2	21	ASTNAVIAAVCATEVFKIATS	10657
3DHR	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	2.6	2.6	1	17	QAGDLGGEALERLFITY	10658
3DNL	BC	VIRAL PROTEIN	C	1.3	2.6	2	9	MRDNWRSEL	10659
3DQV	BD	LIGASE	D	1.3	2.6	2	22	EEENEGIVQLRILRTQEAIIQI	10660
3DUF	AB	OXIDOREDUCTASE/TRANSFERASE	B	1.3	2.6	2	5	IRYRT	10661
3DWL	IK	STRUCTURAL PROTEIN	K	2.6	2.6	1	24	KHKLVDFIIEFMEEVDAEISEMKL	10662
3DWL	KL	STRUCTURAL PROTEIN	L	1.3	2.6	2	9	VLLNWHEKV	10663
3E0J	GH	TRANSFERASE	G	1.3	2.6	2	9	EGEQCSAAH	10664
3EA5	AB	TRANSPORT PROTEIN	B	1.3	2.6	2	25	LEDAQSLQELQSNILTVLAAVIRKS	10665
3EDQ	AB	HYDROLASE	A	1.3	2.6	2	15	TDVDAANLRETFRNL	10666
3ESW	AB	HYDROLASE	A	1.3	2.6	2	20	DDEIYQLACRDEQEQIELIR	10667
3ETR	LM	OXIDOREDUCTASE	M	2.6	2.6	1	7	KQVKSVA	10668
3EUB	AC	OXIDOREDUCTASE	A	1.3	2.6	2	9	RPILQGFRT	10669
3EUB	JL	OXIDOREDUCTASE	J	2.6	2.6	1	10	LLAYLRRKLG	10670
3EX7	HI	HYDROLASE/RNA BINDING PROTEIN/RNA	H	1.3	2.6	2	14	KRKVDWLTEKMREA	10671
3EYF	AB	IMMUNE SYSTEM	A	1.3	2.6	2	6	DEQLKS	10672
3F1E	CN	RIBOSOME	C	1.3	2.6	2	19	KQYRHLLLEDQRIRGLLEK	10673
3FCU	EF	CELL ADHESION/BLOOD CLOTTING	F	1.3	2.6	2	11	VNLYQNYSELI	10674
3FKS	JN	HYDROLASE	N	2.6	2.6	1	15	TREGNDLYREMKETG	10675
3FKU	GH	VIRAL PROTEIN/IMMUNE SYSTEM	H	1.3	2.6	2	22	GFLDVWTYNAELLVLMENERTL	10676
3FMP	CD	ONCOPROTEIN/HYDROLASE	D	2.6	2.6	1	11	HQDQSIRIQRM	10677
3FWC	IJ	CELL CYCLE, TRANSCRIPTION	I	2.6	2.6	1	9	ENEFIAICT	10678
3FWC	NP	CELL CYCLE, TRANSCRIPTION	P	1.3	2.6	2	16	NYELISNELKARLLQE	10679
3G3A	EF	HYDROLASE/IMMUNE SYSTEM	F	2.6	2.6	1	8	VAWRNRCK	10680
3GCG	AB	SIGNALING PROTEIN/TRANSCRIPTION	B	1.3	2.6	2	28	QQWFQQEQTTYISRTVNRTLDDYCRSNN	10681
3GE8	AB	OXIDOREDUCTASE	B	1.3	2.6	2	5	EYDIV	10682
3GHG	KL	BLOOD CLOTTING	K	1.3	2.6	2	20	MYLLKDLWQKRQKQVKDNEN	10683
3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	1.3	2.6	2	10	QAKLIEFLSK	10684
3GTM	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	1.3	2.6	2	9	HTLGNLIRA	10685
3H0L	MO	LIGASE	M	2.6	2.6	1	8	PIEMYLSD	10686

3H0L	PR	LIGASE	P	2.6	2.6	1	6	PIEMYL	10687
3H2V	AE	CELL ADHESION	A	1.3	2.6	2	20	DIIAAAKRMALLMAEMSRLV	10688
3H9R	AB	ISOMERASE/PROTEIN KINASE	A	1.3	2.6	2	9	FLVQRTVAR	10689
3HD7	EH	EXOCYTOSIS	E	1.3	2.6	2	41	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA	10690
3HHL	BC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.3	2.6	2	10	KEVFAQFRAN	10691
3HHR	AB	HORMONE/RECEPTOR	A	1.3	2.6	2	31	ALLKNYGLLYCFRKDMDKVETFLRIVQCRSV	10692
3HKZ	QR	TRANSFERASE	R	1.3	2.6	2	6	LLTDVI	10693
3HOU	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	2.6	2.6	1	7	SDLYKLK	10694
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	2.6	2.6	1	12	VGFIAKIKKVCE	10695
3HPG	DI	TRANSFERASE	D	1.3	2.6	2	11	ESTQLLMKYLG	10696
4RUB	DV	LYASE(CARBON-CARBON)	D	2.6	2.6	1	21	NAPGAVANRVALEACVKARNE	10697
7CEI	AB	IMMUNE SYSTEM	A	1.3	2.6	2	6	TDLIYY	10698
1AHJ	AB	LYASE	A	2.5	2.5	1	6	KDCLIG	10699
1AOI	AB	DNA BINDING PROTEIN/DNA	A	1.3	2.5	2	12	PKDIQLARRIRG	10700
1AR1	BD	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	B	2.5	2.5	1	34	PLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVR	10701
1B4U	CD	DIOXYGENASE	C	1.3	2.5	2	10	YNLNQFAMSL	10702
1B6C	CD	COMPLEX (ISOMERASE/PROTEIN KINASE)	D	1.3	2.5	2	10	LLVQRTIART	10703
1B8D	KL	PHOTOSYNTHESIS	L	1.3	2.5	2	12	SDLQSLKSFIND	10704
1BGY	CE	ELECTRON TRANSPORT	E	2.5	2.5	1	35	EARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSA	10705
1BGY	NU	ELECTRON TRANSPORT	N	2.5	2.5	1	14	PQAHVIENLHAAAY	10706
1BJO	AB	AMINOTRANSFERASE	B	2.5	2.5	1	13	YWAASAIKEAKKY	10707
1BXN	GL	LYASE	G	1.3	2.5	2	22	IQAGATANRVALEAMVLARNEG	10708
1BXR	CD	AMIDOTRANSFERASE	C	1.3	2.5	2	21	RWFLVQIEELVRLEEKVAEVG	10709
1CDL	AE	CALCIUM-BINDING PROTEIN	A	2.5	2.5	1	9	YEEFVQMMT	10710
1CP9	AB	HYDROLASE	A	1.3	2.5	2	11	LFQMEMAKRST	10711
1DFK	AY	CONTRACTILE PROTEIN	A	1.3	2.5	2	10	QWWKLYSKVK	10712
1DFL	BX	CONTRACTILE PROTEIN	X	2.5	2.5	1	11	DEDVDEIIKLT	10713
1DGR	AW	PLANT PROTEIN	A	2.5	2.5	1	9	KNFLEASYD	10714
1DKF	AB	HORMONE/GROWTH FACTOR RECEPTOR	B	1.3	2.5	2	9	PHMFPKMLM	10715
1E1C	AB	ISOMERASE	A	1.3	2.5	2	24	AYVEELTWDLARKAWGHIQEVEKV	10716
1E6E	CD	OXIDOREDUCTASE	C	2.5	2.5	1	9	IKELREMIQ	10717
1E6V	AC	OXIDOREDUCTASE	C	1.3	2.5	2	12	PYIRARMYMWRY	10718
1E6V	DF	OXIDOREDUCTASE	F	1.3	2.5	2	12	PYIRARMYMWRY	10719
1ED3	DF	IMMUNE SYSTEM	D	2.5	2.5	1	11	YAERLRAYLEG	10720

1EF1	BD	MEMBRANE PROTEIN	D	1.3	2.5	2	8	KYKTLRQI	10721
1EYS	CM	ELECTRON TRANSPORT	C	2.5	2.5	1	18	KRTTAWYAIRHVRDINQN	10722
1F3U	EF	TRANSCRIPTION	E	2.5	2.5	1	10	KYLSQQWAKA	10723
1F66	CD	STRUCTURAL PROTEIN/DNA	C	1.3	2.5	2	11	PRHLQLAIRGD	10724
1FFT	FG	OXIDOREDUCTASE	F	1.3	2.5	2	8	PGADFVLH	10725
1FFU	DE	HYDROLASE	E	2.5	2.5	1	8	RVENISTT	10726
1FHJ	CD	OXYGEN STORAGE/TRANSPORT	C	2.5	2.5	1	19	PAVHASLDKFFTAVSTVLT	10727
1FM6	XY	TRANSCRIPTION	X	2.5	2.5	1	23	LNDQVTLLKYGVHEIIYTMLASL	10728
1FNT	AG	HYDROLASE/HYDROLASE ACTIVATOR	A	2.5	2.5	1	14	YQVEYAFKATNQTN	10729
1FNT	OU	HYDROLASE/HYDROLASE ACTIVATOR	O	2.5	2.5	1	14	YQVEYAFKATNQTN	10730
1FS2	AB	LIGASE	B	1.3	2.5	2	16	KGLLDVTCKTVANMIK	10731
1FSX	AB	OXYGEN STORAGE/TRANSPORT	A	2.5	2.5	1	19	PAVHASLDKFLANVSTVLT	10732
1FYH	AB	IMMUNE SYSTEM	A	2.5	2.5	1	10	LNVQRKAIHE	10733
1G0U	DE	HYDROLASE	E	2.5	2.5	1	12	FQVEYALEAIKQ	10734
1G0U	LM	HYDROLASE	M	2.5	2.5	1	18	PSYIFEYLATVMYQRRSK	10735
1G0U	QR	HYDROLASE	R	2.5	2.5	1	12	FQVEYSLEAIKL	10736
1G20	AB	OXIDOREDUCTASE	B	2.5	2.5	1	8	LWHLRSLV	10737
1G3N	EG	CELL CYCLE, SIGNALING PROTEIN	G	1.3	2.5	2	17	FQKTGSACLLVASKLRS	10738
1GH0	KB	PHOTOSYNTHESIS	B	1.3	2.5	2	16	ASTIVSNAARSLFAEQ	10739
1GHF	LH	ANTIBODY FAB FRAGMENT	L	1.3	2.5	2	5	SEQLT	10740
1H1V	GA	ACTIN-BINDING	G	1.3	2.5	2	18	QDEVAASAILTAQLDEEL	10741
1H4J	EF	OXIDOREDUCTASE	F	1.3	2.5	2	5	PKELN	10742
1H59	AB	INSULIN	A	1.3	2.5	2	7	LRRLEMY	10743
1H6K	CZ	NUCLEAR PROTEIN	Z	2.5	2.5	1	11	EEQIYELFSKS	10744
1HR8	EF	HYDROLASE	E	1.3	2.5	2	19	EDEVSRAKNQLKSSLLMNL	10745
1HV4	EF	OXYGEN STORAGE/TRANSPORT	E	1.3	2.5	2	19	PVNFKFLGHCFLVVVAIHH	10746
1I84	VW	CONTRACTILE PROTEIN	W	2.5	2.5	1	11	YSQCGDVMRAL	10747
1IB1	DH	SIGNALING PROTEIN/TRANSFERASE	D	1.3	2.5	2	21	AESKVFYLKMKGDYYRYLAEV	10748
1ICF	AB	HYDROLASE	A	2.5	2.5	1	5	ESFLF	10749
1IR2	CK	LYASE	C	2.5	2.5	1	15	AKNYGRAVYECLRGG	10750
1IR2	T2	LYASE	T	2.5	2.5	1	14	AKNYGRAVYECLRG	10751
1IRE	AB	LYASE	A	2.5	2.5	1	5	NWFKE	10752
1IRU	DK	HYDROLASE	K	1.3	2.5	2	22	AGDTVQFAEYIQKNVQLYKMRN	10753
1IRU	YL	HYDROLASE	L	1.3	2.5	2	19	VEQAYDLARRAIYQATYRD	10754
1IW7	CD	TRANSFERASE	C	1.3	2.5	2	10	EMEVWALEAY	10755
1IWA	AN	LYASE	A	1.3	2.5	2	15	GKNYGRVVYEALKGG	10756
1J1D	DE	CONTRACTILE PROTEIN	D	1.3	2.5	2	12	EEELSDLFRMFD	10757
1J1D	DF	CONTRACTILE PROTEIN	F	1.3	2.5	2	6	ADAMMQ	10758
1JB0	AB	PHOTOSYNTHESIS	A	2.5	2.5	1	12	INGWLRDFLWAQ	10759
1JD2	CJ	HYDROLASE	C	1.3	2.5	2	21	NADSRILIEKARVEAQSHRLT	10760

1JD2	DK	HYDROLASE	K	1.3	2.5	2	15	ETWLGSQCRLHELRE	10761
1JD2	Z1	HYDROLASE	Z	1.3	2.5	2	15	VERAGHLLCDKAQKN	10762
1JFI	AB	TRANSCRIPTION/DNA	B	2.5	2.5	1	29	YISEVKEVLQECKTVALKRRKASSRLENL	10763
1JJ2	FL	RIBOSOME	L	1.3	2.5	2	15	QIAELMWHRMQEWRN	10764
1JRO	EF	OXIDOREDUCTASE	E	2.5	2.5	1	9	PVQQAMIDH	10765
1JRO	GH	OXIDOREDUCTASE	H	1.3	2.5	2	6	ARAHVT	10766
1KF6	AB	OXIDOREDUCTASE	A	2.5	2.5	1	11	PFICELAKAYV	10767
1KF6	BD	OXIDOREDUCTASE	B	2.5	2.5	1	10	KKERMAQLNS	10768
1KFU	LS	HYDROLASE	L	1.3	2.5	2	14	IAAKLAKDREAAEG	10769
1KFY	MN	OXIDOREDUCTASE	N	1.3	2.5	2	10	PAQMAKYHQF	10770
1KG0	BD	VIRAL PROTEIN/IMMUNE SYSTEM	B	2.5	2.5	1	11	ELGRPDAEYWN	10771
1KQF	BC	OXIDOREDUCTASE	C	1.3	2.5	2	8	RRWAKKHH	10772
1KTK	BF	IMMUNE SYSTEM	B	2.5	2.5	1	5	RSDIF	10773
1KX4	AB	STRUCTURAL PROTEIN/DNA	A	1.3	2.5	2	12	PKDIQLARRIRG	10774
1KYO	NE	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	2.5	2.5	1	10	GNDIVSWLWG	10775
1KYO	NP	OXIDOREDUCTASE/ELECTRON TRANSPORT	P	2.5	2.5	1	31	KGRSYAYFMVGAMGLLSSAGAKSTVETFISS	10776
1L2W	EK	CHAPERONE	K	1.3	2.5	2	10	HSVIGFIQRM	10777
1L9B	LM	PHOTOSYNTHESIS	M	2.5	2.5	1	15	IFSHLDWTNNFSLVH	10778
1L9B	LM	PHOTOSYNTHESIS	M	2.5	2.5	1	7	ELEQIAD	10779
1L9B	LM	PHOTOSYNTHESIS	M	2.5	2.5	1	7	PAVFLRD	10780
1L9B	MH	PHOTOSYNTHESIS	M	2.5	2.5	1	27	PFHGLSIAFLYGSALLFAMHGATILAV	10781
1L9J	LM	PHOTOSYNTHESIS	M	2.5	2.5	1	7	ELEQIAD	10782
1LB1	AB	SIGNALING PROTEIN	B	1.3	2.5	2	7	LRPLSYP	10783
1LB1	CD	SIGNALING PROTEIN	C	2.5	2.5	1	13	LDSYLLKPVQRIT	10784
1LK3	LH	IMMUNE SYSTEM	L	1.3	2.5	2	5	TEQLA	10785
1LOF	AB	LECTIN	B	1.3	2.5	2	5	LKEFV	10786
1LQM	CD	HYDROLASE/HYDROLASE INHIBITOR	C	2.5	2.5	1	6	PLSAHR	10787
1LWU	KL	BLOOD CLOTTING	L	1.3	2.5	2	31	AQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	10788
1M1J	DF	BLOOD CLOTTING	F	1.3	2.5	2	12	LLEIEGLLQQAT	10789
1M1Y	IJ	OXIDOREDUCTASE	J	1.3	2.5	2	16	QGCVAYFRSYFNRHFR	10790
1M93	AB	VIRAL PROTEIN	B	1.3	2.5	2	8	LVDALVKL	10791
1MCP	LH	IMMUNOGLOBULIN	L	2.5	2.5	1	5	SEQLT	10792
1MDU	AB	STRUCTURAL PROTEIN	B	2.5	2.5	1	12	SVWIGGSILASL	10793
1MDU	DE	STRUCTURAL PROTEIN	E	2.5	2.5	1	12	SVWIGGSILASL	10794
1MEE	AI	COMPLEX (SERINE PROTEINASE-INHIBITOR)	A	2.5	2.5	1	14	YSWIINGIEWAISN	10795
1MG2	IN	OXIDOREDUCTASE	I	1.3	2.5	2	21	QAQETQGQAAARAAAADLAAG	10796
1MHM	BA	LYASE	A	1.3	2.5	2	11	IPPILRLAETL	10797

1MT1	ED	LYASE	E	2.5	2.5	1	13	PLNAFDGALLNAG	10798
1MT1	GJ	LYASE	G	2.5	2.5	1	13	PLNAFDGALLNAG	10799
1MT1	IJ	LYASE	I	2.5	2.5	1	13	PLNAFDGALLNAG	10800
1MTY	DG	MONOOXYGENASE	D	2.5	2.5	1	33	PASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYG	10801
1MXE	AE	METAL BINDING PROTEIN	A	1.3	2.5	2	13	SEEEIREAFRVFD	10802
1N4Q	AB	TRANSFERASE	A	1.3	2.5	2	10	ESAWNYLKGI	10803
1N95	AB	TRANSFERASE	A	2.5	2.5	1	15	YQVWHHRRVLVEWLK	10804
1NEX	AB	LIGASE, CELL CYCLE	A	1.3	2.5	2	8	PEEIRRTF	10805
1NGM	EF	TRANSCRIPTION/DNA	F	1.3	2.5	2	5	EELNA	10806
1NHG	BC	OXIDOREDUCTASE	B	1.3	2.5	2	23	MSSAKAALESDTRVLAYHLGRNY	10807
1NIK	AB	TRANSCRIPTION	B	1.3	2.5	2	16	VAHLIECLLSKVAALS	10808
1NIK	AE	TRANSCRIPTION	A	1.3	2.5	2	25	LKLQVLLDEEYKQLVKDRKFLREVF	10809
1NIK	BC	TRANSCRIPTION	C	1.3	2.5	2	14	LAMANSLRRVMIAE	10810
1NIK	BJ	TRANSCRIPTION	B	2.5	2.5	1	7	ESDLYKL	10811
1NTK	EG	OXIDOREDUCTASE	E	2.5	2.5	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	10812
1NVM	CD	LYASE/OXIDOREDUCTASE	D	2.5	2.5	1	5	PGTRA	10813
1NVM	CD	LYASE/OXIDOREDUCTASE	D	2.5	2.5	1	17	IDEFTETTSKAIEVIGG	10814
1OCC	AB	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.3	2.5	2	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	10815
1OCC	BI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	I	2.5	2.5	1	11	SMKDFEEMRKA	10816
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.3	2.5	2	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	10817
1OCC	OV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	V	2.5	2.5	1	11	SMKDFEEMRKA	10818
1OCC	PT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	T	1.3	2.5	2	16	LALPSVALCTLNSWLH	10819
1OFU	XA	BACTERIAL CELL DIVISION INHIBITOR	X	1.3	2.5	2	7	HEWLRRA	10820
1OOP	CD	VIRUS	C	2.5	2.5	1	6	LMEIAE	10821
1OTR	AB	CELL CYCLE	A	2.5	2.5	1	12	HESKLSILMDMF	10822
1OXK	CD	SIGNALING PROTEIN	D	1.3	2.5	2	14	HVNQEVIKRMLNLE	10823
1P4B	HP	IMMUNE SYSTEM	P	2.5	2.5	1	10	HLENEVARLK	10824
1P4E	AD	DNA BINDING PROTEIN/RECOMBINATION/DNA	A	1.3	2.5	2	16	KSHIGRHLMTSFLSMK	10825
1P4E	BC	DNA BINDING PROTEIN/RECOMBINATION/DNA	B	1.3	2.5	2	15	SHIGRHLMTSFLSMK	10826
1PQ1	AB	APOPTOSIS	A	2.5	2.5	1	9	WDTFVDLYG	10827
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.3	2.5	2	26	IESVHRWGWFFSLMVMVSASVGILLT	10828
1PTO	EF	TOXIN	F	2.5	2.5	1	17	TWFDTMLGFAISAYALK	10829
1PTO	KL	TOXIN	L	2.5	2.5	1	17	TWFDTMLGFAISAYALK	10830

1Q16	BC	OXIDOREDUCTASE	C	2.5	2.5	1	6	PRVRAT	10831
1Q5R	GN	HYDROLASE	N	1.3	2.5	2	23	AGIAIELVRLFAVELEHYEKIEG	10832
1QO0	AE	BINDING PROTEIN	E	2.5	2.5	1	14	EVSDALVLQLIRIG	10833
1QPW	AB	OXYGEN TRANSPORT	A	2.5	2.5	1	16	AGAHGAEALERMFLGF	10834
1R0N	AB	TRANSCRIPTION/DNA	B	1.3	2.5	2	5	MYMRR	10835
1R4M	CD	CELL CYCLE	C	1.3	2.5	2	11	DDYVHEFCRYG	10836
1R4M	FK	CELL CYCLE	F	1.3	2.5	2	15	IIARRWINGMLISLL	10837
1R5V	AE	SIGNALING PROTEIN	A	1.3	2.5	2	23	AQGALANIAVDKANLDVMKERSN	10838
1RP3	GH	TRANSCRIPTION	H	2.5	2.5	1	12	RIELSRLIGLLL	10839
1RU7	GH	VIRAL PROTEIN	G	1.3	2.5	2	10	YEELREQLSS	10840
1RU7	IL	VIRAL PROTEIN	L	1.3	2.5	2	22	QKSTQNAINGITNKVNSVIEKM	10841
1RUZ	LK	VIRAL PROTEIN	K	2.5	2.5	1	46	RRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYE	10842
1RYP	H2	MULTICATALYTIC PROTEINASE	2	2.5	2.5	1	6	WDFAKD	10843
1RYP	HI	MULTICATALYTIC PROTEINASE	H	2.5	2.5	1	22	AADTQAIADIVQYHLELYTSQY	10844
1RYP	I2	MULTICATALYTIC PROTEINASE	2	1.3	2.5	2	19	VQVAEEAIVNAMRVLYYRD	10845
1RYP	U2	MULTICATALYTIC PROTEINASE	U	1.3	2.5	2	22	IPDGRHLVNRGREEAASFKKLY	10846
1RYP	WN	MULTICATALYTIC PROTEINASE	N	1.3	2.5	2	14	FGAHMANPLLRKVV	10847
1SCT	CD	OXYGEN TRANSPORT	C	2.5	2.5	1	18	PSRLKCVVEKFAVNHINR	10848
1SVX	AB	DE NOVO PROTEIN/SUGAR BINDING PROTEIN	B	2.5	2.5	1	16	AGAKAGLTFLVDLIKN	10849
1T0Q	AB	OXIDOREDUCTASE	A	1.3	2.5	2	5	RKWDW	10850
1T0Q	AB	OXIDOREDUCTASE	B	2.5	2.5	1	14	PAWQGFRELIEKAL	10851
1T3Q	BC	OXIDOREDUCTASE	B	2.5	2.5	1	10	PERIFRSIQE	10852
1T6O	AB	VIRAL PROTEIN	A	1.3	2.5	2	16	ANDLAKFHQMLMKIIM	10853
1TCE	AB	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)	A	2.5	2.5	1	11	VSHLISYHMDN	10854
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	B	2.5	2.5	1	13	KEQKLRFAFRIYD	10855
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	1.3	2.5	2	17	DSVLFYAITTLHNLLLH	10856
1TI2	CD	OXIDOREDUCTASE	C	1.3	2.5	2	14	ACEIRALARQWAKK	10857
1TOC	CD	COMPLEX (HYDROLASE/INHIBITOR)	C	1.3	2.5	2	7	EKELFES	10858
1TQY	EF	TRANSFERASE	E	2.5	2.5	1	10	PIVVACFDAI	10859
1TY4	BD	APOPTOSIS	B	2.5	2.5	1	13	AENFETFCEQLLA	10860
1U35	AB	STRUCTURAL PROTEIN/DNA	A	1.3	2.5	2	11	TVALREIRRYQ	10861
1U6G	AC	LIGASE	A	2.5	2.5	1	18	EAELEDTLNQVMVVFKYI	10862
1U9I	ED	CIRCADIAN CLOCK PROTEIN	D	2.5	2.5	1	11	RAQLLRNAYSW	10863
1UTB	AB	TRANSCRIPTION REGULATION	A	1.3	2.5	2	19	DIGEMYFMPPLMEALAQRA	10864
1UZD	AI	LYASE	A	2.5	2.5	1	15	AKNYGRAVYECLRGG	10865
1UZH	EF	LYASE	E	1.3	2.5	2	21	NAPGAAANRVALEACTQARNE	10866

1UZH	KP	LYASE	K	2.5	2.5	1	14	AKNYGRAVYECLRG	10867
1V02	BE	HYDROLASE	B	1.3	2.5	2	24	FLDQQAQERSMDKCLGWFLEPVVR	10868
1V54	NO	OXIDOREDUCTASE	N	1.3	2.5	2	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	10869
1VZJ	FJ	HYDROLASE	F	2.5	2.5	1	12	HWKNQFDHYSKQ	10870
1WCM	BC	TRANSCRIPTION	B	2.5	2.5	1	6	QSSIDR	10871
1WDD	EW	LYASE	E	2.5	2.5	1	14	AKNYGRACYECLRG	10872
1WDD	EW	LYASE	W	1.3	2.5	2	14	VEDLLKQIEYLLRS	10873
1WYU	AB	OXIDOREDUCTASE	B	1.3	2.5	2	19	QGALRLMWELGEYLKALTG	10874
1WYU	EF	OXIDOREDUCTASE	F	1.3	2.5	2	19	QGALRLMWELGEYLKALTG	10875
1WYU	EF	OXIDOREDUCTASE	F	2.5	2.5	1	19	GAHGELTGILIIRAYHEDR	10876
1WYU	GH	OXIDOREDUCTASE	H	2.5	2.5	1	5	AEDLI	10877
1XDK	AB	HORMONE/GROWTH FACTOR RECEPTOR	A	1.3	2.5	2	7	RFAKLLL	10878
1XFU	CQ	LYASE/METAL BINDING PROTEIN	Q	1.3	2.5	2	10	YEEFVQMMTA	10879
1XFV	BP	LYASE/METAL BINDING PROTEIN	B	1.3	2.5	2	13	SAEFIKNLSSIRR	10880
1XK4	FL	METAL BINDING PROTEIN	L	1.3	2.5	2	20	QLERNIETIINTFHQYSVKL	10881
1XK4	JH	METAL BINDING PROTEIN	J	2.5	2.5	1	18	ELEKALNSIIDVYHKYSL	10882
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	A	1.3	2.5	2	11	SLQYRTISGIS	10883
1XQS	AC	CHAPERONE	A	1.3	2.5	2	18	QKLKVKSAFLLQNLLVGH	10884
1XV9	AB	DNA BINDING PROTEIN	B	1.3	2.5	2	18	VEFLELLFHFHGTLRKLQ	10885
1XXI	FJ	TRANSFERASE	F	1.3	2.5	2	19	QTQLRQAVQLLTRTELTLK	10886
1Y8H	CD	OXYGEN STORAGE/TRANSPORT	D	1.3	2.5	2	19	PENFRLLGNVLVVVLARHF	10887
1YE9	DG	OXIDOREDUCTASE	D	1.3	2.5	2	9	DTFWDYVSL	10888
1YE9	IM	OXIDOREDUCTASE	M	1.3	2.5	2	13	PYIRERVVDQLAH	10889
1YE9	IO	OXIDOREDUCTASE	I	2.5	2.5	1	12	FILREKITHFDH	10890
1YE9	KN	OXIDOREDUCTASE	K	2.5	2.5	1	12	FILREKITHFDH	10891
1YE9	KP	OXIDOREDUCTASE	K	1.3	2.5	2	9	DTFWDYVSL	10892
1YEW	AB	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	1.3	2.5	2	26	YLFTAIVGAMGWGLIFYPGNWPIIAP	10893
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	1.3	2.5	2	7	YLWERYR	10894
1YHU	BC	OXYGEN STORAGE/TRANSPORT	B	1.3	2.5	2	15	PLQRLKVKRQWAEAY	10895
1YNJ	CD	TRANSFERASE	C	1.3	2.5	2	13	ESFRVLVKELQAL	10896
1YPZ	EF	IMMUNE SYSTEM	F	2.5	2.5	1	8	VAETNLHK	10897
1YTZ	TC	CONTRACTILE PROTEIN	T	2.5	2.5	1	46	EDKLRDKAKELWDWLYQLQTEKYDFAEQIKRKKYEIVTLRNRIDQA	10898
1YUC	BD	TRANSCRIPTION REGULATION	B	1.3	2.5	2	11	VDDQMKLLQNC	10899
1YY8	CD	IMMUNE SYSTEM	C	1.3	2.5	2	6	DEQLKS	10900
1Z00	AB	HYDROLASE	A	1.3	2.5	2	17	MEKLEQDFVSRVTECLT	10901
1Z6O	AX	METAL BINDING PROTEIN	A	2.5	2.5	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	10902

1Z6O	EM	METAL BINDING PROTEIN	E	2.5	2.5	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	10903
1Z6O	GR	METAL BINDING PROTEIN	G	2.5	2.5	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	10904
1Z6O	JS	METAL BINDING PROTEIN	J	1.3	2.5	2	16	LSLALYVFDEYLQKTV	10905
1Z7Q	OW	HYDROLASE/HYDROLASE ACTIVATOR	W	2.5	2.5	1	22	AADTEAVTQLIGSNIELHSLYT	10906
1Z7Q	Ta	HYDROLASE/HYDROLASE ACTIVATOR	a	1.3	2.5	2	22	AADGDALVKRFKNSVKWYHFDH	10907
1Z7Q	YL	HYDROLASE/HYDROLASE ACTIVATOR	L	2.5	2.5	1	19	VEDALYLGKRSILAAAHRD	10908
1Z7X	ZY	HYDROLASE/HYDROLASE INHIBITOR	Z	2.5	2.5	1	9	YCNQMMRRR	10909
1Z92	AB	IMMUNE SYSTEM	A	1.3	2.5	2	10	LKPLEEVLNL	10910
1ZAV	AX	STRUCTURAL PROTEIN	A	1.3	2.5	2	41	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK	10911
1ZBB	ab	STRUCTURAL PROTEIN/DNA	a	1.3	2.5	2	12	PKDIQLARRIRG	10912
1ZBB	ec	STRUCTURAL PROTEIN/DNA	e	1.3	2.5	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	10913
1ZBB	EC	STRUCTURAL PROTEIN/DNA	E	1.3	2.5	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	10914
1ZDT	AP	TRANSCRIPTION	A	1.3	2.5	2	11	VADQMTLLQNC	10915
1ZLA	FH	PROTEIN BINDING/VIRUS/DNA	H	1.3	2.5	2	11	REIQTAVRLLL	10916
1ZOQ	BD	TRANSCRIPTION/TRANSFERASE	B	1.3	2.5	2	13	LGPFIVDLITFTE	10917
1ZV8	KJ	VIRAL PROTEIN	J	1.3	2.5	2	16	QKEIDRLNEVAKNLNE	10918
2A1D	BD	HYDROLASE	D	1.3	2.5	2	35	KEYKDAKDKLMTRILGEDQYLLERKKVQYEEYKKL	10919
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	2.5	2.5	1	28	LALRLMLQLVIVVALVVYVIYGFVVVWG	10920
2AFH	CD	OXIDOREDUCTASE	D	1.3	2.5	2	15	QQNMKDGLQNCKATY	10921
2AFH	CD	OXIDOREDUCTASE	D	2.5	2.5	1	9	KEYQELNFQ	10922
2APO	AB	ISOMERASE/RNA BINDING PROTEIN	A	2.5	2.5	1	12	SHEVSTWVKKIL	10923
2AQ1	AB	IMMUNE SYSTEM	B	1.3	2.5	2	9	MGNMKYLYD	10924
2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	B	1.3	2.5	2	8	KRWYRLAS	10925
2AVU	DF	TRANSCRIPTION ACTIVATOR	D	2.5	2.5	1	9	KASAMFRLG	10926
2AXT	ad	ELECTRON TRANSPORT	a	1.3	2.5	2	15	ISGTFNFMIVFQAEH	10927
2AXT	BH	ELECTRON TRANSPORT	H	1.3	2.5	2	20	TPLMAVFMGLFLVFLLIILE	10928
2AXT	cz	ELECTRON TRANSPORT	z	2.5	2.5	1	28	TILFQLALAALVILSFVMVIGVPVAYAS	10929
2BC4	AB	IMMUNE SYSTEM	B	1.3	2.5	2	13	NSLANVLSQHLNQ	10930
2BC4	CD	IMMUNE SYSTEM	D	2.5	2.5	1	9	DTLMQRLRN	10931
2BYK	BC	DNA-BINDING PROTEIN	B	1.3	2.5	2	29	KEARAAIARAASVFAIFVTSSSTALAHKQ	10932
2CZV	BC	HYDROLASE	C	1.3	2.5	2	17	KDEVKELIWKSSLEVLG	10933
2CZY	AB	GENE REGULATION	A	1.3	2.5	2	15	VEDALTYLDQVKIRF	10934
2D1P	AH	TRANSLATION	A	2.5	2.5	1	7	ETEAGRL	10935
2DF4	AB	LIGASE	A	1.3	2.5	2	6	SNLSRF	10936
2DSQ	AC	PROTEIN BINDING/HORMONE/GROWTH FACTOR	C	2.5	2.5	1	12	AELVDALQFVCG	10937
2DXB	PQ	HYDROLASE	Q	2.5	2.5	1	9	AEERRRKQN	10938

2EHO	IJ	REPLICATION	J	1.3	2.5	2	12	WFNNYKRSLATY	10939
2EKE	AC	LIGASE/PROTEIN BINDING	A	2.5	2.5	1	16	LCLQRLQEERKKWRKD	10940
2EQ9	AC	OXIDOREDUCTASE	A	2.5	2.5	1	14	AGELIAEAALALEM	10941
2EY4	BF	ISOMERASE/BIOSYNTHETIC PROTEIN	F	1.3	2.5	2	13	GEYRRRWKREVLG	10942
2F2L	AX	MEMBRANE PROTEIN, IMMUNE SYSTEM, TOXIN	A	2.5	2.5	1	19	QAICVLRVRLLQTYDIESS	10943
2F66	DB	TRANSPORT PROTEIN	B	1.3	2.5	2	10	ASNAITRLER	10944
2FUG	JK	OXIDOREDUCTASE	J	2.5	2.5	1	5	YICGE	10945
2G4D	CD	HYDROLASE/PROTEIN BINDING	C	2.5	2.5	1	9	FFFTKLKTA	10946
2G77	AB	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	B	2.5	2.5	1	5	ERFRK	10947
2GBW	EF	OXIDOREDUCTASE	E	2.5	2.5	1	11	GENMSSATYIN	10948
2GHO	AC	TRANSFERASE	C	2.5	2.5	1	23	EPEIKELLAEAFNLYFGKRQGEG	10949
2GL7	DF	TRANSCRIPTION	F	1.3	2.5	2	14	LEHRERSLQTLRDI	10950
2GUZ	IJ	CHAPERONE, PROTEIN TRANSPORT	J	2.5	2.5	1	15	MDKINNRFNYLFEVN	10951
2GUZ	KD	CHAPERONE, PROTEIN TRANSPORT	K	2.5	2.5	1	15	KKKLKEVHRKIMLAN	10952
2H4C	AB	HYDROLASE	A	2.5	2.5	1	9	FFQFAEMIV	10953
2H62	AC	HORMONE/GROWTH FACTOR	C	2.5	2.5	1	7	SDFQCKD	10954
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	C	1.3	2.5	2	11	PKDIQLARRIR	10955
2HLD	CF	HYDROLASE	C	1.3	2.5	2	15	LSKQAVAYRQLSLLL	10956
2HP0	AB	ISOMERASE	A	2.5	2.5	1	15	TGSAARNGVLSAWLS	10957
2HYB	HL	TRANSFERASE	L	2.5	2.5	1	5	GIYAA	10958
2I2R	AE	TRANSPORT PROTEIN	E	2.5	2.5	1	14	FEDFVTALSILLRG	10959
2I2X	CD	TRANSFERASE	D	1.3	2.5	2	19	LPNVMMSADAMLEGIEYCK	10960
2I2X	GH	TRANSFERASE	G	1.3	2.5	2	12	CAQANTAMFIGG	10961
2I3T	EF	CELL CYCLE	F	1.3	2.5	2	5	FKLIY	10962
2IAE	DF	HYDROLASE	D	2.5	2.5	1	6	ANVRFN	10963
2IDO	CD	TRANSFERASE	C	2.5	2.5	1	8	PEAFGVHG	10964
2IFQ	CB	OXIDOREDUCTASE	B	1.3	2.5	2	17	GPCKMIKPFFHSLSEKY	10965
2INN	BL	OXIDOREDUCTASE	B	2.5	2.5	1	23	AYWKYQAEKEKKLYAIFDAFAQN	10966
2INP	BE	OXIDOREDUCTASE	B	2.5	2.5	1	7	PVHQIYQ	10967
2ISS	BE	LYASE, TRANSFERASE	E	1.3	2.5	2	11	STTMIRILKEM	10968
2IY1	AB	HYDROLASE/NUCLEAR PROTEIN	A	2.5	2.5	1	9	FFFTKLKTA	10969
2J3W	CF	TRANSPORT	F	1.3	2.5	2	11	ESVIARDKALD	10970
2J59	FR	HYDROLASE	F	2.5	2.5	1	10	KTTILYKLKL	10971
2J7A	EF	OXIDOREDUCTASE	F	1.3	2.5	2	5	RPFCT	10972
2JE6	AB	HYDROLASE	A	2.5	2.5	1	27	LQDIDQAENTARSTAVKLLEELKKHLG	10973
2JIZ	AG	HYDROLASE	G	1.3	2.5	2	38	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKP	10974
2JIZ	HK	HYDROLASE	K	1.3	2.5	2	12	LATDMGTMQERI	10975

2JJ0	MH	PHOTOSYNTHESIS	M	2.5	2.5	1	7	WYVWGQN	10976
2JKR	EU	ENDOCYTOSIS	E	1.3	2.5	2	18	PEVQYVALRNINLIVQKR	10977
2JTT	AD	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	D	1.3	2.5	2	13	DMKRTINKAWVES	10978
2JXC	AB	ENDOCYTOSIS/PROTEIN BINDING	A	1.3	2.5	2	12	VDILGRVWELSD	10979
2NGR	AB	HYDROLASE	A	2.5	2.5	1	6	DRLRPL	10980
2NNW	AB	TRANSFERASE	B	1.3	2.5	2	11	PRVLRELVPIV	10981
2NPP	AB	SIGNALING PROTEIN,HYDROLASE	A	2.5	2.5	1	10	WRVRYMVADK	10982
2NQB	AB	STRUCTURAL PROTEIN/DNA	A	1.3	2.5	2	12	PKDIQLARRIRG	10983
2NS8	BH	TRANSCRIPTION	B	1.3	2.5	2	31	LENALYALSAVGHFTLGSVLEDQEHQVAKEE	10984
2NS8	DF	TRANSCRIPTION	D	1.3	2.5	2	30	LENALYALSAVGHFTLGSVLEDQEHQVAKE	10985
2NTI	AB	DNA BINDING PROTEIN	A	1.3	2.5	2	15	ESVLNVIAADVTLVG	10986
2NTI	DE	DNA BINDING PROTEIN	D	1.3	2.5	2	15	ESVLNVIAADVTLVG	10987
2NU9	FG	LIGASE	F	1.3	2.5	2	14	GTLTYEAVKQTTDY	10988
2NUD	AC	TOXIN/PROTEIN BINDING	A	1.3	2.5	2	16	TEYLRDRVAHLRTELG	10989
2NV2	KL	LYASE/TRANSFERASE	L	1.3	2.5	2	11	STTMRRLIDTY	10990
2NV2	MN	LYASE/TRANSFERASE	M	1.3	2.5	2	12	ERVKRGMAEMQK	10991
2NV2	ST	LYASE/TRANSFERASE	T	1.3	2.5	2	11	STTMRRLIDTY	10992
2NZD	AB	STRUCTURAL PROTEIN/DNA	A	1.3	2.5	2	11	PKDIQLARRIR	10993
2NZD	GH	STRUCTURAL PROTEIN/DNA	G	1.3	2.5	2	10	PRHLQLAVRN	10994
2O97	AB	DNA BINDING PROTEIN	A	2.5	2.5	1	12	KTQLIDVIAEKA	10995
2O98	BQ	PROTEIN BINDING	B	1.3	2.5	2	19	PIRLGLALNFSVFYYEILN	10996
2OCY	AC	ENDOCYTOSIS/EXOCYTOSIS	C	2.5	2.5	1	5	FITTI	10997
2ODE	CB	SIGNALING PROTEIN	B	1.3	2.5	2	17	TAKLVSKAHRIFEEFVD	10998
2OM0	ST	HORMONE	T	1.3	2.5	2	18	NQHLCGSHLVEALYLVCG	10999
2OZN	AB	TOXIN	B	2.5	2.5	1	13	EYEISFINHRILN	11000
2P22	AC	TRANSPORT PROTEIN	C	1.3	2.5	2	10	KEIIDLIQTH	11001
2P5T	AB	TRANSCRIPTION REGULATOR	B	2.5	2.5	1	13	PELSYLSTLIRYE	11002
2PF4	BF	HYDROLASE REGULATOR/VIRAL PROTEIN	B	2.5	2.5	1	6	DSVRLL	11003
2PMZ	AK	TRANSLATION, TRANSFERASE	A	1.3	2.5	2	11	EEAIAEAKEIM	11004
2Q9Q	CD	REPLICATION	C	2.5	2.5	1	12	EKAMELIRELHR	11005
2QA4	FM	RIBOSOME	M	2.5	2.5	1	16	QLAELQWQRQQEWRNE	11006
2QAR	AB	HYDROLASE REGULATOR	B	2.5	2.5	1	8	KEDFRYRS	11007
2QHO	EF	PROTEIN BINDING/LIGASE	F	2.5	2.5	1	13	VNLAVNNLLSRDD	11008
2QI9	AF	MEMBRANE PROTEIN	F	1.3	2.5	2	11	ERQVDQLASLG	11009
2QIE	HG	TRANSFERASE	H	2.5	2.5	1	19	IPMAEKKLAQIGDEINEKW	11010
2QJK	GL	ELECTRON TRANSPORT	G	2.5	2.5	1	9	HSIQTWLLG	11011
2QJK	MN	ELECTRON TRANSPORT	M	2.5	2.5	1	7	IEEDFNA	11012
2QJK	MN	ELECTRON TRANSPORT	N	2.5	2.5	1	17	VHAMAEDVSAFLMWAAE	11013

2QJP	AB	ELECTRON TRANSPORT	A	1.3	2.5	2	15	VDLAFASVEHIMRNV	11014
2QJP	AF	ELECTRON TRANSPORT	A	2.5	2.5	1	11	IGHSIQTWLLG	11015
2QJP	JK	ELECTRON TRANSPORT	J	1.3	2.5	2	15	VDLAFASVEHIMRNV	11016
2QJY	AF	OXIDOREDUCTASE	A	2.5	2.5	1	11	IGHSIQTWLLG	11017
2QJY	GH	OXIDOREDUCTASE	G	1.3	2.5	2	15	VDLAFASVEHIMRNV	11018
2QJY	JI	OXIDOREDUCTASE	I	2.5	2.5	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	11019
2QM6	AB	TRANSFERASE	A	1.3	2.5	2	15	AIDAAVAIGFALAVV	11020
2QR1	BG	TRANSFERASE	G	2.5	2.5	1	5	SYDVL	11021
2QR1	CG	TRANSFERASE	C	2.5	2.5	1	14	FLDLCAMLVCKLFS	11022
2QSH	AX	DNA BINDING PROTEIN/DNA	A	2.5	2.5	1	14	DFGEKWFRKVITAL	11023
2QSH	AX	DNA BINDING PROTEIN/DNA	X	1.3	2.5	2	11	LAPLLENISAR	11024
2R00	AC	OXIDOREDUCTASE	A	2.5	2.5	1	14	GELSAKWAPIAAEA	11025
2R17	BD	PROTEIN TRANSPORT	D	2.5	2.5	1	17	SKAQLAAITLIIGTFER	11026
2R5C	AB	TRANSFERASE	B	1.3	2.5	2	12	VWVEYIQLAAQY	11027
2RAO	CD	OXYGEN BINDING	C	2.5	2.5	1	19	PAVHASLDKFLANVSTVLT	11028
2RGN	AB	SIGNALING PROTEIN COMPLEX	A	1.3	2.5	2	10	RSERRKWIHC	11029
2RMK	AB	MEMBRANE PROTEIN/TRANSFERASE	B	1.3	2.5	2	34	RKLLLTAQQMLQDSKTKIDIIRMQLRRALQADQL	11030
2UUN	CD	ELECTRON TRANSPORT	D	1.3	2.5	2	13	VAQIDALSQMVAE	11031
2UY1	AB	RNA BINDING PROTEIN	A	1.3	2.5	2	16	PHVFIYCAFIEYYATG	11032
2UZ1	DC	LYASE	C	2.5	2.5	1	7	DGSVGYS	11033
2UZ1	DC	LYASE	D	2.5	2.5	1	10	VTPIANAWLD	11034
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	B	1.3	2.5	2	15	TEEQLLAVQAIRKYG	11035
2V5H	AL	TRANSCRIPTION	A	2.5	2.5	1	10	IPQSRELIAQ	11036
2V8Q	AE	TRANSFERASE	A	1.3	2.5	2	15	HTIEFFEMCANLIKI	11037
2VAS	AB	MOTOR PROTEIN	B	1.3	2.5	2	11	EAELQDMINEV	11038
2VDU	DF	TRANSFERASE	F	2.5	2.5	1	11	NTLLSEYAYVL	11039
2VE7	BD	CELL CYCLE	B	2.5	2.5	1	16	FSAFLANVRKAFTATV	11040
2VGL	BM	PROTEIN TRANSPORT	B	1.3	2.5	2	14	PEVQYVALRNINLI	11041
2VML	ED	PHOTOSYNTHESIS	E	1.3	2.5	2	8	LREVNRTF	11042
2VOG	AB	APOPTOSIS	A	1.3	2.5	2	21	WGRIVTIFAFGGVLLKKLKQE	11043
2VRW	AB	SIGNALING PROTEIN	B	1.3	2.5	2	40	ATEKENLRLALDAMRDLAQCVNEVKRDNETLRQITNFQLS	11044
2VSO	BF	HYDROLASE/TRANSLATION	F	2.5	2.5	1	18	SRIKFKLIDIKELRHDKN	11045
2WB1	CK	TRANSCRIPTION	K	2.5	2.5	1	17	RYEIARVISARALQLAM	11046
2WB1	RS	TRANSCRIPTION	S	1.3	2.5	2	14	LEFVNAIRRAAMLY	11047
2WBJ	BC	IMMUNE SYSTEM	B	2.5	2.5	1	12	YCRHNYGVVESF	11048
2WEL	AD	TRANSFERASE	D	1.3	2.5	2	12	DEEVDEMIREAD	11049
2Z2S	AH	TRANSCRIPTION	A	1.3	2.5	2	18	LGTIKSRIRLALDRLRQH	11050
2Z2S	EF	TRANSCRIPTION	E	2.5	2.5	1	5	TVWQK	11051
2Z3R	EH	CYTOKINE/CYTOKINE RECEPTOR	E	1.3	2.5	2	20	KVTAMKCFLLELQVISLESG	11052
2ZCY	GH	HYDROLASE	H	2.5	2.5	1	23	AADTEAVTQLIGSNIELHSLYTS	11053

2ZCY	HZ	HYDROLASE	H	1.3	2.5	2	19	KEEAIKLASDAIQAGIWND	11054
2ZCY	T1	HYDROLASE	T	1.3	2.5	2	22	IPDGRHLVNRGREEAASFKKLY	11055
2ZIX	AB	HYDROLASE	A	1.3	2.5	2	5	QVIDG	11056
2ZME	AB	PROTEIN TRANSPORT	B	2.5	2.5	1	12	LTEVYCLVNRAR	11057
2ZNE	BD	APOPTOSIS	B	2.5	2.5	1	12	KNELKQALSGFG	11058
2ZT9	AB	PHOTOSYNTHESIS	B	2.5	2.5	1	23	PVATTVFLFGTLVTLWLGIGAAL	11059
2ZU0	AC	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	C	2.5	2.5	1	15	NQFFLQTALNAVRSY	11060
2ZYZ	AD	SPLICING	A	1.3	2.5	2	13	VLQEQVFKDLKSR	11061
3A0B	ad	ELECTRON TRANSPORT	d	2.5	2.5	1	5	RAWMA	11062
3A0B	AI	ELECTRON TRANSPORT	I	2.5	2.5	1	24	ETLKITVYIVVTFFVLLFVFGFLS	11063
3BDY	HL	HORMONE	L	1.3	2.5	2	7	DEQLKSG	11064
3BEJ	BF	TRANSCRIPTION REGULATOR	B	1.3	2.5	2	26	AEENFLILTEMATNHVQVLVEFTKKL	11065
3BLW	IJ	OXIDOREDUCTASE	I	2.5	2.5	1	14	KLGDGLFRNIITEI	11066
3BZ1	CK	ELECTRON TRANSPORT	C	1.3	2.5	2	26	LGAHVAHAGLIVFWAGAMTLFELAHF	11067
3C03	BC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	B	2.5	2.5	1	10	SGSLANNIKK	11068
3C1B	FH	STRUCTURAL PROTEIN/DNA	F	2.5	2.5	1	11	AMDVVYALKRQ	11069
3C91	OV	HYDROLASE	V	1.3	2.5	2	22	VGDAQVLVRYMKAELELYRLQR	11070
3CFI	GH	PROTEIN TRANSPORT/IMMUNE SYSTEM	H	1.3	2.5	2	25	LSQERTARLNELQRALVMMDSDFRQ	11071
3CHX	AB	MEMBRANE PROTEIN	B	1.3	2.5	2	7	LVVPALW	11072
3CHX	EF	MEMBRANE PROTEIN	F	1.3	2.5	2	7	LVVPALW	11073
3CHX	IJ	MEMBRANE PROTEIN	J	1.3	2.5	2	7	LVVPALW	11074
3CI0	JK	PROTEIN TRANSPORT	K	1.3	2.5	2	6	ISEMRV	11075
3CW2	AK	TRANSLATION	K	1.3	2.5	2	8	VEMLDRLY	11076
3CWZ	AB	TRANSPORT PROTEIN	B	1.3	2.5	2	32	VIAQTNWKFVEGLLKECRNKTKRMLVEKMGRE	11077
3CXH	CE	OXIDOREDUCTASE	E	2.5	2.5	1	33	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSMT	11078
3CXH	LM	OXIDOREDUCTASE	M	2.5	2.5	1	22	PHELTESVLPAARYDYAVAEQC	11079
3D3C	AJ	TRANSCRIPTION	A	2.5	2.5	1	16	YKVAINEAIELAKSFG	11080
3D5B	UV	RIBOSOME	U	2.5	2.5	1	42	FRKARETLFAAGNYAYAHRKRRKRDFRRLWIVRINAACRQHG	11081
3D5O	AF	IMMUNE SYSTEM	A	2.5	2.5	1	9	PENILSAYQ	11082
3DBH	EF	CELL CYCLE	E	1.3	2.5	2	21	HTIAAFLGGAAAQEVIKIITK	11083
3DGE	BD	TRANSFERASE/SIGNALING PROTEIN	D	2.5	2.5	1	13	PSQFIEEVKHLLN	11084
3DHH	AE	OXIDOREDUCTASE	A	1.3	2.5	2	22	YPEYVSIQREKDAGAYSVKAAL	11085
3DHR	GH	OXYGEN STORAGE, OXYGEN TRANSPORT	G	2.5	2.5	1	18	PEVHASLDKFVLAVGTVL	11086
3DIN	CE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.3	2.5	2	16	MLAGTMFLLWLGERIT	11087
3DWL	AH	STRUCTURAL PROTEIN	A	2.5	2.5	1	12	GRDVTYFVQSLL	11088

3E0J	AB	TRANSFERASE	A	1.3	2.5	2	16	GESLLGTQLLVDVVTG	11089
3E8C	BH	TRANSFERASE	H	2.5	2.5	1	8	TYADFIAS	11090
3E8C	DJ	TRANSFERASE	J	2.5	2.5	1	8	TYADFIAS	11091
3EO1	BF	IMMUNE SYSTEM/CYTOKINE	F	2.5	2.5	1	12	THSTVLGLYNTL	11092
3EOA	HI	IMMUNE SYSTEM/CELL ADHESION	I	2.5	2.5	1	18	PDEFQKILDFMKDVMKKL	11093
3ETR	BC	OXIDOREDUCTASE	B	2.5	2.5	1	9	EIGIEMKFK	11094
3ETR	MN	OXIDOREDUCTASE	M	1.3	2.5	2	9	EIGIEMKFK	11095
3EUB	AC	OXIDOREDUCTASE	A	2.5	2.5	1	10	LLAYLRRKLG	11096
3EXH	EH	OXIDOREDUCTASE	H	1.3	2.5	2	12	VKDIIFAIKKTL	11097
3F02	AC	HYDROLASE INHIBITOR	A	2.5	2.5	1	16	AIADLSVNMYNRLRAT	11098
3F6Q	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	2.5	2.5	1	8	PLHWACRE	11099
3F9K	Re	VIRAL PROTEIN, RECOMBINATION	R	2.5	2.5	1	15	LEKIEPAQEEHEKYH	11100
3FAL	AB	SIGNALING PROTEIN	A	2.5	2.5	1	23	PAEVEALREKVYASLEAYCKHKY	11101
3FAL	CB	SIGNALING PROTEIN	C	1.3	2.5	2	8	FLMEMLEA	11102
3FH6	IC	TRANSPORT PROTEIN	C	2.5	2.5	1	11	VAENMSFGLKL	11103
3FKS	AD	HYDROLASE	A	1.3	2.5	2	15	LSKQAVAYRQLSLLL	11104
3FKU	EB	VIRAL PROTEIN/IMMUNE SYSTEM	B	2.5	2.5	1	35	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLD	11105
3FMP	AB	ONCOPROTEIN/HYDROLASE	B	2.5	2.5	1	12	PGTVLDWCSKLK	11106
3G04	AB	IMMUNE SYSTEM	A	1.3	2.5	2	6	SEELQA	11107
3GE8	DF	OXIDOREDUCTASE	D	1.3	2.5	2	16	WAAIAAKHFFDDIITG	11108
3GE8	DG	OXIDOREDUCTASE	D	2.5	2.5	1	13	ELHHSYHMGVWYW	11109
3GHG	KL	BLOOD CLOTTING	L	1.3	2.5	2	25	TCGIADFLSTYQTKVDKDLQSLEDI	11110
3GLH	AE	TRANSFERASE	A	1.3	2.5	2	19	QTQLRQAVQLLTRTELTLK	11111
3H0L	EF	LIGASE	F	2.5	2.5	1	7	REKALMN	11112
3H0L	TU	LIGASE	U	2.5	2.5	1	7	REKALMN	11113
3H11	AB	APOPTOSIS	B	2.5	2.5	1	16	WYIQSLCQSLRERCPR	11114
3H42	AB	HYDROLASE/IMMUNE SYSTEM	B	1.3	2.5	2	13	RVLNAACQRLARA	11115
3HD7	EH	EXOCYTOSIS	E	1.3	2.5	2	41	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIII	11116
3HH2	AC	SIGNALING PROTEIN/CYTOKINE	C	2.5	2.5	1	10	DNTLFKWMIF	11117
3HKZ	IJ	TRANSFERASE	I	2.5	2.5	1	19	EYGKWLMDNLFRVFIRFVE	11118
3HOU	BI	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.3	2.5	2	14	WQMLEMLKPCVEDG	11119
3HOU	NV	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	2.5	2.5	1	7	SDLYKLK	11120
3HOU	OW	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	W	1.3	2.5	2	12	HTLGNLIRAELL	11121
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.3	2.5	2	11	EETRAELSQLC	11122
3HPG	CJ	TRANSFERASE	C	1.3	2.5	2	11	ESTQLLMKYLG	11123

4RUB	AT	LYASE(CARBON-CARBON)	A	1.3	2.5	2	15	AKNYGRAVYECLRGG	11124
1NOV	BE	VIRUS	B	1.2	2.4	2	13	EYALAAYRKIARD	11125
1ACY	LH	COMPLEX (ANTIBODY/HIV-1 FRAGMENT)	L	1.2	2.4	2	6	SEQLTS	11126
1AJ7	LH	IMMUNOGLOBULIN	L	1.2	2.4	2	6	DEQLKS	11127
1APY	AB	HYDROLASE	A	2.4	2.4	1	13	SASQALHSDWLAR	11128
1AXC	CD	COMPLEX (DNA-BINDING PROTEIN/DNA)	D	2.4	2.4	1	5	MTDFY	11129
1B33	DN	PHOTOSYNTHESIS	D	1.2	2.4	2	9	LKETYNSLG	11130
1B4U	CB	DIOXYGENASE	C	1.2	2.4	2	9	VHAYLAEFD	11131
1B6C	EF	COMPLEX (ISOMERASE/PROTEIN KINASE)	F	2.4	2.4	1	14	ERSWFREAEIYQTV	11132
1BCP	AE	TOXIN	A	1.2	2.4	2	21	RRYTEVYLEHRMQEAVEAERA	11133
1BCP	GK	TOXIN	G	1.2	2.4	2	21	RRYTEVYLEHRMQEAVEAERA	11134
1BD2	AD	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)	A	2.4	2.4	1	30	PEYWDGETRKVKAHSQTHRVDLGTLRGYYN	11135
1BGY	QV	ELECTRON TRANSPORT	Q	1.2	2.4	2	35	EARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSA	11136
1BXR	EF	AMIDOTRANSFERASE	F	2.4	2.4	1	19	DAAPLFDHFIELIEQYRKT	11137
1CDL	AE	CALCIUM-BINDING PROTEIN	A	2.4	2.4	1	11	AAELRHVMTNL	11138
1CG5	AB	OXYGEN TRANSPORT	A	2.4	2.4	1	19	PVTHCAVDKFLELVAYELS	11139
1CG5	AB	OXYGEN TRANSPORT	B	1.2	2.4	2	20	TQNFKLLGQTFMVELALHYK	11140
1CJF	AC	STRUCTURAL REGULATION PROTEIN	A	2.4	2.4	1	18	GGLINKKCYEMASHLRRS	11141
1D2Z	CD	APOPTOSIS	C	2.4	2.4	1	11	VQTLFALFKKL	11142
1D8D	AB	TRANSFERASE	B	2.4	2.4	1	15	RPWLCYWILHSLELL	11143
1D8D	AB	TRANSFERASE	B	1.2	2.4	2	12	LKSLLQWVTSRQ	11144
1D9K	DP	IMMUNE SYSTEM	D	1.2	2.4	2	9	RPDAEYWNK	11145
1DGH	AD	OXIDOREDUCTASE	A	1.2	2.4	2	11	PDMVWDFWSLR	11146
1DGH	CD	OXIDOREDUCTASE	C	2.4	2.4	1	7	YFAEVEQ	11147
1DGR	CY	PLANT PROTEIN	C	2.4	2.4	1	9	KNFLEASYD	11148
1E6Y	DB	OXIDOREDUCTASE	D	2.4	2.4	1	12	AAVADLSFAAKA	11149
1E7P	EF	OXIDOREDUCTASE	F	2.4	2.4	1	7	RMPAKLD	11150
1E7P	KL	OXIDOREDUCTASE	L	2.4	2.4	1	7	RMPAKLD	11151
1EFP	CD	ELECTRON TRANSPORT	C	1.2	2.4	2	11	LFSVVPELTGK	11152
1EQZ	AG	STRUCTURAL PROTEIN/DNA	G	1.2	2.4	2	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	11153
1EQZ	FH	STRUCTURAL PROTEIN/DNA	F	2.4	2.4	1	12	SREIQTAVRLLL	11154
1EYX	AB	PHOTOSYNTHESIS	A	2.4	2.4	1	12	VITTVISAADSA	11155
1F3M	BD	TRANSFERASE	B	2.4	2.4	1	12	PQAVLDVLEFYN	11156
1F66	BD	STRUCTURAL PROTEIN/DNA	D	2.4	2.4	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	11157
1F66	GH	STRUCTURAL PROTEIN/DNA	G	1.2	2.4	2	11	PRHLQLAIRGD	11158

1FCD	AC	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	C	2.4	2.4	1	5	CAGCH	11159
1FFU	DF	HYDROLASE	F	2.4	2.4	1	5	PQVRN	11160
1FNT	KZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	2.4	2.4	1	19	VEDALYLGKRSILAAAHRD	11161
1FNT	LM	HYDROLASE/HYDROLASE ACTIVATOR	L	1.2	2.4	2	22	ADCQFWETWLGSQCRLHELREK	11162
1FNT	RY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.2	2.4	2	23	AGDTVQFAEYIQANIQLYSIRED	11163
1FQJ	AB	SIGNALING PROTEIN	B	1.2	2.4	2	21	DAAQTHIYMLMKKDSYARYLK	11164
1G0U	DK	HYDROLASE	K	1.2	2.4	2	22	AADCQFWETWLGSQCRLHELRE	11165
1G0U	JY	HYDROLASE	J	2.4	2.4	1	19	TEEGLDLLKLCVQELEKRM	11166
1G0U	T1	HYDROLASE	T	1.2	2.4	2	22	IPDGRHLVNRGREEAASFKKLY	11167
1G2C	AD	VIRAL PROTEIN	A	2.4	2.4	1	45	EVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	11168
1G3I	DJ	CHAPERONE/HYDROLASE	J	1.2	2.4	2	11	LLKSAVELAKD	11169
1G3I	EL	CHAPERONE/HYDROLASE	L	2.4	2.4	1	18	TADAFTLFELFERKLEMH	11170
1G3N	AC	CELL CYCLE, SIGNALING PROTEIN	C	1.2	2.4	2	17	FQKTGSACLLVASKLRS	11171
1GH0	EB	PHOTOSYNTHESIS	B	1.2	2.4	2	25	SRRMAACLRDMEIILRYVTYAVFAG	11172
1GH0	OR	PHOTOSYNTHESIS	R	2.4	2.4	1	25	SRRMAACLRDMEIILRYVTYAVFAG	11173
1H0H	AB	DEHYDROGENASE	A	2.4	2.4	1	13	PISFKWVMRAKDK	11174
1H1L	CD	OXIDOREDUCTASE	D	1.2	2.4	2	11	AQRVQEVFAWT	11175
1H2S	AB	MEMBRANE PROTEIN	A	1.2	2.4	2	28	SGIKSLYVRLRNLTVILWAIYPFIWLLG	11176
1HH4	AD	SIGNALING PROTEIN/INHIBITOR	A	2.4	2.4	1	6	DRLRPL	11177
1HL6	AB	SIGNAL PROTEIN	A	2.4	2.4	1	12	EDGDQGIVRLKE	11178
1HQR	AB	IMMUNE SYSTEM	A	2.4	2.4	1	7	EEFGRFA	11179
1HV4	EF	OXYGEN STORAGE/TRANSPORT	E	2.4	2.4	1	18	AEVHASLDKFLCAVGTVL	11180
1I3R	AB	IMMUNE SYSTEM	B	2.4	2.4	1	23	PEFLEQKRAEVDTVCRHNYEIFD	11181
1I5K	AD	BLOOD CLOTTING	D	1.2	2.4	2	22	ADAELQRLKNERHEEAELERLK	11182
1I7W	CD	CELL ADHESION	D	1.2	2.4	2	10	IDENLKAADS	11183
1IBT	EF	LYASE	F	1.2	2.4	2	12	KPLQDALVEYFG	11184
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.2	2.4	2	15	EEQIAEFKEAFSLFD	11185
1IR2	DL	LYASE	D	2.4	2.4	1	14	AKNYGRAVYECLRG	11186
1IRU	QX	HYDROLASE	Q	1.2	2.4	2	23	TSDANVLTNELRLIAQRYLLQYQ	11187
1IRU	YL	HYDROLASE	Y	1.2	2.4	2	13	YGAFLTLSILDRY	11188
1IW7	AC	TRANSFERASE	C	1.2	2.4	2	23	EPEIKELLAQAFEVYFGKRKGEG	11189
1IW7	CF	TRANSFERASE	C	1.2	2.4	2	13	IEGRNAAYEAIIK	11190
1IWP	AB	LYASE	A	2.4	2.4	1	14	VVEDLSAVEEMMKR	11191
1IXS	AB	HYDROLASE	A	1.2	2.4	2	10	AQDLIKEALK	11192
1JD2	DE	HYDROLASE	E	2.4	2.4	1	12	FQVEYALEAIKQ	11193
1JD2	XQ	HYDROLASE	X	1.2	2.4	2	21	NADSRILIEKARVEAQSHRLT	11194
1JD2	YZ	HYDROLASE	Z	2.4	2.4	1	22	APDARVLSNYLRQQCNYSSLVF	11195
1JEB	CD	OXYGEN STORAGE/TRANSPORT	C	2.4	2.4	1	16	ADTIGTETLERLFLSH	11196

1JEB	CD	OXYGEN STORAGE/TRANSPORT	D	2.4	2.4	1	16	ADEVGGEALGRLLVVY	11197
1JGL	LH	IMMUNE SYSTEM	L	1.2	2.4	2	6	SEQLTS	11198
1JRO	CD	OXIDOREDUCTASE	D	2.4	2.4	1	10	HRAARIAARK	11199
1JRO	EF	OXIDOREDUCTASE	F	1.2	2.4	2	6	ARAHVT	11200
1JSU	AB	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	A	2.4	2.4	1	6	AKAALA	11201
1JY2	RS	BLOOD CLOTTING	R	1.2	2.4	2	27	GCKLQDTLVRQERPIRKSIEDLRNTVD	11202
1K74	AD	TRANSCRIPTION	A	1.2	2.4	2	17	RLPALRSIGLKCLEHLF	11203
1K7L	AB	TRANSCRIPTION	A	2.4	2.4	1	8	PLLQEIYR	11204
1KMC	AC	APOPTOSIS/HYDROLASE	C	2.4	2.4	1	8	HADYLLRT	11205
1KPS	CB	LIGASE/PROTEIN TRANSPORT	B	2.4	2.4	1	13	FARHNLLQTLYNI	11206
1KQS	FL	RIBOSOME	F	1.2	2.4	2	10	TNETTKSIER	11207
1KX4	GH	STRUCTURAL PROTEIN/DNA	G	1.2	2.4	2	10	PRHLQLAVRN	11208
1KYO	CE	OXIDOREDUCTASE/ELECTRON TRANSPORT	E	2.4	2.4	1	30	KGRSYAYFMVGAMGLLSSAGAKSTVETFIS	11209
1KYO	DG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	2.4	2.4	1	20	EDESYARAYRIIRAHQTELT	11210
1KYO	LP	OXIDOREDUCTASE/ELECTRON TRANSPORT	L	2.4	2.4	1	14	HPNRVLEHLHSTAF	11211
1L1O	BC	DNA BINDING PROTEIN	B	1.2	2.4	2	18	NEFTTHILEVINAHMVLS	11212
1L2W	FK	CHAPERONE	K	1.2	2.4	2	8	QYANNLAG	11213
1L9J	MH	PHOTOSYNTHESIS	M	2.4	2.4	1	14	MEGIHRWAIWMAVL	11214
1LDK	AD	LIGASE	D	2.4	2.4	1	14	QGTLFELILAANYL	11215
1LOC	CD	LECTIN	D	2.4	2.4	1	5	LKEFV	11216
1LVC	AD	LYASE	A	2.4	2.4	1	8	PITKAKIN	11217
1M1Y	AB	OXIDOREDUCTASE	B	1.2	2.4	2	15	QQNMKDGLQNCKATY	11218
1M2O	CD	PROTEIN TRANSPORT/SIGNALING PROTEIN	D	1.2	2.4	2	10	KTTLLHMLKN	11219
1M93	AB	VIRAL PROTEIN	A	1.2	2.4	2	10	DIFREIASSM	11220
1MF8	AB	HYDROLASE, LIGASE	B	2.4	2.4	1	13	KEQKLRFAFRIYD	11221
1MHY	BD	OXIDOREDUCTASE	D	1.2	2.4	2	8	ARRTRAIG	11222
1MMO	CE	OXIDOREDUCTASE (MONOOXYGENASE)	C	1.2	2.4	2	12	KSARLAVEGLWQ	11223
1MR1	AD	SIGNALING PROTEIN	A	2.4	2.4	1	8	YYLDREAG	11224
1MT1	KH	LYASE	K	2.4	2.4	1	13	PLNAFDGALLNAG	11225
1MTY	CH	MONOOXYGENASE	H	2.4	2.4	1	20	YLWIEAKLEEKVAVLKARAF	11226
1MVW	PQ	CONTRACTILE PROTEIN	P	2.4	2.4	1	39	TATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	11227
1N1J	AB	DNA BINDING PROTEIN	A	2.4	2.4	1	11	IANVARIMKNA	11228
1N4Q	EF	TRANSFERASE	E	1.2	2.4	2	13	NSVWNQRHFVISN	11229
1N4Q	EF	TRANSFERASE	E	1.2	2.4	2	17	PYLIAFLVDIYEDMLEN	11230

1N4Q	KL	TRANSFERASE	K	1.2	2.4	2	13	NSVWNQRHFVISN	11231
1NEX	CD	LIGASE, CELL CYCLE	C	1.2	2.4	2	13	KPLLDAGCKVVAE	11232
1NTK	EK	OXIDOREDUCTASE	K	2.4	2.4	1	19	VPTAQLWGAVGAVGLVWAT	11233
1OAO	AC	OXIDOREDUCTASE	C	2.4	2.4	1	30	VALFREVYHGAITATSYAEILLNQAIRTYG	11234
1OAO	BC	OXIDOREDUCTASE	C	1.2	2.4	2	30	VALFREVYHGAITATSYAEILLNQAIRTYG	11235
1OCC	BH	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	H	2.4	2.4	1	13	ISWVSTWDDRRAE	11236
1OCC	DE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	E	1.2	2.4	2	14	AWELRKGMNTLVGY	11237
1OCC	NG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	G	2.4	2.4	1	10	ARTWRFLTFG	11238
1OCC	OU	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	U	2.4	2.4	1	13	ISWVSTWDDRRAE	11239
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	R	1.2	2.4	2	14	AWELRKGMNTLVGY	11240
1OFU	XA	BACTERIAL CELL DIVISION INHIBITOR	A	2.4	2.4	1	15	LGEYSDVGNIIEQFA	11241
1P4E	BD	DNA BINDING PROTEIN/RECOMBINATION/DNA	D	2.4	2.4	1	12	SHSKKMLKALLS	11242
1P4Q	AB	TRANSCRIPTION/TRANSFERASE	B	1.2	2.4	2	14	CASSRQIISHWKNC	11243
1PMA	DQ	PROTEASE	Q	1.2	2.4	2	22	VGDAQVLVRYMKAELELYRLQR	11244
1PMA	MZ	PROTEASE	Z	1.2	2.4	2	22	VGDAQVLVRYMKAELELYRLQR	11245
1PQ1	AB	APOPTOSIS	A	1.2	2.4	2	13	AYQSFEQVVNELF	11246
1PSS	MH	PHOTOSYNTHETIC REACTION CENTER	M	2.4	2.4	1	25	PFHGLSIAFLYGSALLFAMHGATIL	11247
1PTO	BD	TOXIN	B	1.2	2.4	2	18	WSMYSRLRKMLYLIYVAG	11248
1Q5R	AH	HYDROLASE	H	1.2	2.4	2	23	AGIAIELVRLFAVELEHYEKIEG	11249
1R1R	BE	OXIDOREDUCTASE	B	1.2	2.4	2	14	MQQLLKDLLTAYKF	11250
1R8Q	BF	PROTEIN TRANSPORT/EXCHANGE FACTOR	B	2.4	2.4	1	9	RPLWRHYFQ	11251
1RCO	OT	LYASE	O	1.2	2.4	2	6	WTDGLT	11252
1RCO	VS	LYASE	V	1.2	2.4	2	6	WTDGLT	11253
1RH5	AB	PROTEIN TRANSPORT	A	1.2	2.4	2	34	EKAIEHRLKRYIPPLTVMSSAFVGFLATIANFIG	11254
1RIO	HB	TRANSCRIPTION/DNA	B	2.4	2.4	1	7	QESVADK	11255
1RP3	CD	TRANSCRIPTION	C	1.2	2.4	2	14	LPLVKAIATNIKKH	11256
1RP3	GH	TRANSCRIPTION	G	2.4	2.4	1	30	TEELFKTLDKINFSYILSLEEVFRDFARDY	11257
1RYP	FG	MULTICATALYTIC PROTEINASE	F	2.4	2.4	1	15	VERAGHLLCDKAQKN	11258
1RYP	MN	MULTICATALYTIC PROTEINASE	N	2.4	2.4	1	18	PSYIFEYLATVMYQRRSK	11259
1RYP	S1	MULTICATALYTIC PROTEINASE	S	2.4	2.4	1	13	VESLTQSVCDLAL	11260
1RYP	V2	MULTICATALYTIC PROTEINASE	V	2.4	2.4	1	15	TETAASVFKELCYEN	11261
1RYP	WX	MULTICATALYTIC PROTEINASE	X	1.2	2.4	2	12	SDQLFGMCESLY	11262
1S0Y	CF	LYASE	F	2.4	2.4	1	20	VARKQQLIRDVIDVTNKSIG	11263

1S0Y	IL	LYASE	I	1.2	2.4	2	14	ALSAGLLRVISEAT	11264
1S5L	AD	PHOTOSYNTHESIS	A	1.2	2.4	2	9	SRSLHFFLA	11265
1S5L	ck	PHOTOSYNTHESIS	c	1.2	2.4	2	18	AHAGLIVFWAGAMTLFEL	11266
1SQB	CE	OXIDOREDUCTASE	C	1.2	2.4	2	24	NFGSLLGICLILQILTGLFLAMHY	11267
1SQX	EG	OXIDOREDUCTASE	E	2.4	2.4	1	35	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMS	11268
1SVF	CD	VIRAL PROTEIN	D	2.4	2.4	1	26	SQNLAAVNKSLSDALQHLAQSDTYLS	11269
1T3M	AD	HYDROLASE	D	2.4	2.4	1	7	GEVFIRA	11270
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	2.4	2.4	1	16	INVVTCAAGILSNLTC	11271
1TI2	EF	OXIDOREDUCTASE	E	1.2	2.4	2	6	HTARLV	11272
1TI2	KL	OXIDOREDUCTASE	K	2.4	2.4	1	6	FKSMIY	11273
1TQY	AB	TRANSFERASE	B	2.4	2.4	1	16	AGGLDALGHARRTIRR	11274
1TU3	CG	PROTEIN TRANSPORT	G	1.2	2.4	2	33	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	11275
1TU3	CH	PROTEIN TRANSPORT	H	1.2	2.4	2	31	LQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	11276
1TUE	DE	REPLICATION	D	2.4	2.4	1	5	WSRLD	11277
1TZN	Oo	TOXIN RECEPTOR/TOXIN	o	1.2	2.4	2	14	LVPSYAEKEAKISR	11278
1U35	CD	STRUCTURAL PROTEIN/DNA	D	1.2	2.4	2	12	SIYVYKVLKQVH	11279
1U3H	CD	IMMUNE SYSTEM	D	1.2	2.4	2	34	DAEYYNKQYLERTRAELDTVCRYNYEETEVPTSL	11280
1U6H	AB	CELL ADHESION	A	1.2	2.4	2	24	TAPVSAVQAAVSNLVRVGKETVQT	11281
1USV	CD	CHAPERONE	C	1.2	2.4	2	24	KIMKVIRKNIVKKLIEAFNEIAED	11282
1UTB	AB	TRANSCRIPTION REGULATION	B	1.2	2.4	2	19	DIGEMYFMPPLMEALAQRA	11283
1UZD	BC	LYASE	C	2.4	2.4	1	14	DEQIAAQVDYIVAN	11284
1UZD	OT	LYASE	O	2.4	2.4	1	14	AKNYGRAVYECLRG	11285
1V4U	AB	OXYGEN STORAGE/TRANSPORT	A	1.2	2.4	2	19	PSNFKILSHCILVVVAKMF	11286
1V54	AB	OXIDOREDUCTASE	A	1.2	2.4	2	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	11287
1V54	AC	OXIDOREDUCTASE	A	1.2	2.4	2	33	LFVWSVMITAVLLLLSLPVLAAGITMLLTDRNL	11288
1V54	NO	OXIDOREDUCTASE	N	1.2	2.4	2	8	SSLDIVLH	11289
1V54	PW	OXIDOREDUCTASE	P	2.4	2.4	1	23	PWPLTGALSALLMTSGLTMWFHF	11290
1VF5	NQ	PHOTOSYNTHESIS	Q	2.4	2.4	1	22	LAFGTVTGVALGALYPLVKYFI	11291
1VF5	ST	PHOTOSYNTHESIS	T	1.2	2.4	2	10	YAAYQQYKRP	11292
1VZJ	GJ	HYDROLASE	G	2.4	2.4	1	8	HWKNQFDH	11293
1W1I	CG	HYDROLASE	G	1.2	2.4	2	19	PDEVVSLVNQGLQEGERDF	11294
1W5C	JK	PHOTOSYNTHESIS	J	1.2	2.4	2	8	FTRWCQLG	11295
1WCM	BJ	TRANSCRIPTION	B	2.4	2.4	1	6	ESDLYK	11296
1WDW	GH	LYASE	H	1.2	2.4	2	19	ETLIEPLKELEKAYKRFKD	11297
1WEJ	LH	COMPLEX (ANTIBODY/ELECTRON TRANSPORT)	L	1.2	2.4	2	7	SEQLTSG	11298
1WQL	AB	OXIDOREDUCTASE	A	2.4	2.4	1	16	YEQDDGENWVEVQRGL	11299
1WRD	AB	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	1.2	2.4	2	25	IGKLRSELEMVSGNVRVMSEMLTEL	11300

1WYU	AB	OXIDOREDUCTASE	A	2.4	2.4	1	5	GEFLT	11301
1WYU	GH	OXIDOREDUCTASE	H	1.2	2.4	2	10	KLHEEAARLF	11302
1XFV	FT	LYASE/METAL BINDING PROTEIN	F	1.2	2.4	2	15	SLEKQKGVTNLLIKY	11303
1XFV	FT	LYASE/METAL BINDING PROTEIN	F	1.2	2.4	2	13	SAEFIKNLSSIRR	11304
1XL3	AC	CELL INVASION	C	2.4	2.4	1	12	IHDIEHLANAFS	11305
1XLS	CK	TRANSCRIPTION	K	2.4	2.4	1	7	ALLRYLL	11306
1XXI	FG	TRANSFERASE	F	1.2	2.4	2	19	PLLLQESQDAVRQVAAAQG	11307
1Y14	CD	TRANSFERASE	C	2.4	2.4	1	8	PFEVAQLG	11308
1YA7	FL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.2	2.4	2	23	VGDAQVLVRYMKAELELYRLQRR	11309
1YA7	GM	HYDROLASE/HYDROLASE ACTIVATOR	G	1.2	2.4	2	23	VADARVLVDFARISAQQEKVTYG	11310
1YCP	KM	COMPLEX (SERINE PROTEASE/PEPTIDE)	M	1.2	2.4	2	7	KKWIQKV	11311
1YD8	UH	PROTEIN TRANSPORT, CHROMOSOMALPROTEIN	H	1.2	2.4	2	25	KVTKRLHTLEEVNNNVRLLSEMLLH	11312
1YE9	IO	OXIDOREDUCTASE	O	1.2	2.4	2	19	PLLQGRLFSYTDTQISRLG	11313
1YEW	BC	OXIDOREDUCTASE, MEMBRANE PROTEIN	B	2.4	2.4	1	25	GATVCVLGLLLGEWINRYFNFWGWT	11314
1YHU	MP	OXYGEN STORAGE/TRANSPORT	M	2.4	2.4	1	16	MLERAKVKDEWAKAYG	11315
1YMM	AB	IMMUNE SYSTEM	A	1.2	2.4	2	22	AQGALANIAVDKANLEIMTKRS	11316
1YSH	CD	STRUCTURAL PROTEIN/RNA	C	2.4	2.4	1	12	RKSEIEYYAMLA	11317
1Z6O	DW	METAL BINDING PROTEIN	D	2.4	2.4	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	11318
1Z6O	IT	METAL BINDING PROTEIN	I	2.4	2.4	1	16	LSLALYVFDEYLQKTV	11319
1Z7Q	OP	HYDROLASE/HYDROLASE ACTIVATOR	P	2.4	2.4	1	14	GPDYRVLVDKSRKV	11320
1Z7Z	34	VIRUS/RECEPTOR	3	2.4	2.4	1	5	MEMYQ	11321
1ZAV	AZ	STRUCTURAL PROTEIN	Z	1.2	2.4	2	13	VSELAELVKKLED	11322
1ZGL	HI	IMMUNE SYSTEM	H	1.2	2.4	2	13	AVDTYCRHNYGVG	11323
1ZHI	AB	TRANSCRIPTION/REPLICATION	A	1.2	2.4	2	12	LNYYNKLFSETA	11324
1ZY8	AK	OXIDOREDUCTASE	K	1.2	2.4	2	14	KEDALKLVQLKQTG	11325
1ZY8	CL	OXIDOREDUCTASE	C	1.2	2.4	2	6	CEDIAR	11326
2A1T	RS	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	2.4	2.4	1	15	EELTPLILATQKQFN	11327
2A3I	AB	TRANSFERASE	A	1.2	2.4	2	11	LEDQITLIQYS	11328
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	2.4	2.4	1	11	PEGFEQASAIM	11329
2AHM	CF	VIRAL PROTEIN, REPLICATION	F	1.2	2.4	2	21	KRAKVTSAMQTMLFTMLRKLD	11330
2AHM	DH	VIRAL PROTEIN, REPLICATION	D	1.2	2.4	2	20	SKMSDVKCTSVVLLSVLQQL	11331
2AKW	AB	LIGASE	B	2.4	2.4	1	17	APYRKEQRLREVLSGLG	11332
2AXT	ai	ELECTRON TRANSPORT	i	1.2	2.4	2	24	ETLKITVYIVVTFFVLLFVFGFLS	11333
2AXT	CK	ELECTRON TRANSPORT	C	1.2	2.4	2	18	GLIVFWAGAMTLFELAHF	11334
2AXT	DE	ELECTRON TRANSPORT	D	2.4	2.4	1	20	LLFPCAYLALGGWLTGTTFV	11335

2AXT	de	ELECTRON TRANSPORT	d	2.4	2.4	1	14	YLALGGWLTGTTFV	11336
2B8K	BJ	TRANSFERASE	B	2.4	2.4	1	6	ESDLYK	11337
2BA0	DG	RNA BINDING PROTEIN	D	1.2	2.4	2	30	RDEVKQAIELAKKGALQIYEMQREAILRRY	11338
2BA1	AI	RNA BINDING PROTEIN	I	1.2	2.4	2	19	PEDILVDIKRDYVLSKLRD	11339
2BEQ	CE	VIRAL PROTEIN	E	1.2	2.4	2	13	QKEIDRLNEVAKN	11340
2BV8	ED	PHOTOSYNTHESIS	D	1.2	2.4	2	25	NRRMAACLRDMEIVLRYVSYAEIAG	11341
2C0L	AB	TRANSPORT PROTEIN/RECEPTOR	A	2.4	2.4	1	9	SDAYGAADA	11342
2C35	AB	POLYMERASE	A	1.2	2.4	2	17	NSEVHMLLEHRKQQNES	11343
2CKF	AB	OXIDOREDUCTASE	A	2.4	2.4	1	8	GYHVGWTH	11344
2CLY	AC	HYDROLASE	C	2.4	2.4	1	19	PEYQQDLDRELFKLKQMYG	11345
2D1P	AH	TRANSLATION	H	1.2	2.4	2	11	ADALRRELANY	11346
2D1P	GH	TRANSLATION	G	2.4	2.4	1	7	VAAALRR	11347
2D26	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.2	2.4	2	5	PVSIA	11348
2DFK	CD	CELL CYCLE	C	1.2	2.4	2	29	SDYRYVAAALAVMRNVTQQINERKRRLEN	11349
2DFS	AE	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	E	1.2	2.4	2	10	YEEFVQMMTA	11350
2DXB	TU	HYDROLASE	U	2.4	2.4	1	6	RDCLIG	11351
2E5L	DE	RIBOSOME	E	2.4	2.4	1	10	AVPRAILELA	11352
2EHO	EG	REPLICATION	E	1.2	2.4	2	7	LKVSIHQ	11353
2EHO	FH	REPLICATION	F	2.4	2.4	1	8	LIRELHRA	11354
2EKE	BD	LIGASE/PROTEIN BINDING	B	2.4	2.4	1	16	LCLQRLQEERKKWRKD	11355
2EKV	AB	CONTRACTILE PROTEIN	B	2.4	2.4	1	7	GEKVSGT	11356
2EY4	AE	ISOMERASE/BIOSYNTHETIC PROTEIN	A	2.4	2.4	1	12	SHEVVAWIKKIL	11357
2EY4	BF	ISOMERASE/BIOSYNTHETIC PROTEIN	B	2.4	2.4	1	12	SHEVVAWIKKIL	11358
2F66	AB	TRANSPORT PROTEIN	A	1.2	2.4	2	29	DGLNQLYNLVAQDYALTDTIEALSRMLHR	11359
2F95	AB	MEMBRANE PROTEIN	A	1.2	2.4	2	28	SGIKSLYVRLRNLTVILWAIYPFIWLLG	11360
2F9D	BQ	RNA BINDING PROTEIN	Q	1.2	2.4	2	17	PEQLQAWRWEREIDERN	11361
2F9I	CD	TRANSFERASE	D	1.2	2.4	2	9	RRVIEQTIN	11362
2FBW	BD	OXIDOREDUCTASE	D	2.4	2.4	1	26	AASLHWTSERAVSALLLGLLPAAYLY	11363
2FBW	OQ	OXIDOREDUCTASE	Q	2.4	2.4	1	26	AASLHWTSERAVSALLLGLLPAAYLY	11364
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	A	2.4	2.4	1	11	AEFKEAFSLFD	11365
2FRV	AB	OXIDOREDUCTASE	B	1.2	2.4	2	29	AEVDLIATAHYLEALRVQVKAARAMAIFG	11366
2FRV	CD	OXIDOREDUCTASE	D	1.2	2.4	2	29	AEVDLIATAHYLEALRVQVKAARAMAIFG	11367
2FRV	EF	OXIDOREDUCTASE	E	1.2	2.4	2	9	GCSESVLRT	11368
2FRV	GH	OXIDOREDUCTASE	G	1.2	2.4	2	9	GCSESVLRT	11369
2FRV	GH	OXIDOREDUCTASE	H	1.2	2.4	2	29	AEVDLIATAHYLEALRVQVKAARAMAIFG	11370
2FRV	IJ	OXIDOREDUCTASE	J	1.2	2.4	2	29	AEVDLIATAHYLEALRVQVKAARAMAIFG	11371
2FRV	SL	OXIDOREDUCTASE	L	1.2	2.4	2	29	AEVDLIATAHYLEALRVQVKAARAMAIFG	11372

2FSE	CD	IMMUNE SYSTEM, STRUCTURAL PROTEIN	C	2.4	2.4	1	5	EEFGR	11373
2FTK	BF	TRANSFERASE	B	1.2	2.4	2	31	TALTNELIHLLGHSRHDWMNKLQLIKGNLSL	11374
2FUG	FG	OXIDOREDUCTASE	F	2.4	2.4	1	13	PEALIYAVMQLQK	11375
2FYN	NO	OXIDOREDUCTASE	N	1.2	2.4	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	11376
2FYN	QR	OXIDOREDUCTASE	Q	1.2	2.4	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	11377
2GBW	EF	OXIDOREDUCTASE	E	2.4	2.4	1	6	TLESDD	11378
2GGP	AB	CHAPERONE, METAL TRANSPORT	A	1.2	2.4	2	12	YDFILEKIKKTG	11379
2GL7	DE	TRANSCRIPTION	D	1.2	2.4	2	16	VKFLAITTDCLQILAY	11380
2GTL	MN	OXYGEN STORAGE/TRANSPORT	N	2.4	2.4	1	24	AFLIIRLDRIIEKLRTKLDEAEKI	11381
2GTP	BC	SIGNALING PROTEIN	B	1.2	2.4	2	10	RSERKKWIHC	11382
2GUZ	CD	CHAPERONE, PROTEIN TRANSPORT	D	1.2	2.4	2	15	MDKINNRFNYLFEVN	11383
2GV5	EF	CELL CYCLE	E	1.2	2.4	2	14	EEQKQEIYEAFSLF	11384
2H8P	AB	MEMBRANE PROTEIN	B	1.2	2.4	2	6	SEQLTS	11385
2H8P	CD	MEMBRANE PROTEIN	C	2.4	2.4	1	13	YPRALWWACETAT	11386
2HHF	AB	TRANSFERASE	A	2.4	2.4	1	5	SSLHY	11387
2HII	AB	REPLICATION	A	1.2	2.4	2	15	ESVLNVIAADVTLVG	11388
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	A	1.2	2.4	2	11	PRHLQLAIRND	11389
2HOD	AB	BLOOD CLOTTING	B	1.2	2.4	2	6	VLRSIL	11390
2HOD	EF	BLOOD CLOTTING	E	1.2	2.4	2	15	KIQKLESDVSAQMEY	11391
2HOD	GH	BLOOD CLOTTING	H	2.4	2.4	1	5	SILEN	11392
2HQW	AB	METAL BINDING PROTEIN	A	1.2	2.4	2	12	EAELQDMINEVD	11393
2HYB	BF	TRANSFERASE	B	2.4	2.4	1	5	GVYQL	11394
2HYB	QR	TRANSFERASE	R	2.4	2.4	1	9	SLESCLKFA	11395
2HYE	AC	PROTEIN BINDING	C	1.2	2.4	2	11	EELYQAVENLC	11396
2I2R	CG	TRANSPORT PROTEIN	G	1.2	2.4	2	12	EDTFKQIYAQFF	11397
2I2X	GH	TRANSFERASE	G	2.4	2.4	1	14	DKVLRDLMMLSDRY	11398
2IAN	FG	IMMUNE SYSTEM	F	2.4	2.4	1	5	EEFGR	11399
2IAN	LM	IMMUNE SYSTEM	L	2.4	2.4	1	9	KDLLEQRRA	11400
2ICW	AC	IMMUNE SYSTEM	A	1.2	2.4	2	17	AQGALANIAVDKANLEI	11401
2ICW	DH	IMMUNE SYSTEM	D	2.4	2.4	1	17	AQGALANIAVDKANLEI	11402
2INP	AC	OXIDOREDUCTASE	C	1.2	2.4	2	32	EETQKQLLRLLVPLRHVELGANMNNAKIAGDA	11403
2INP	AF	OXIDOREDUCTASE	A	2.4	2.4	1	7	PVHQIYQ	11404
2INP	BL	OXIDOREDUCTASE	B	1.2	2.4	2	25	MDAYWKYQAEKEKKLYAIFDAFAQN	11405
2IZX	BC	KINASE	C	1.2	2.4	2	17	IEYLAKQIVDNAIQQAK	11406
2J0T	CF	HYDROLASE	C	1.2	2.4	2	13	LHRVAAHELGHSL	11407
2J59	DP	HYDROLASE	D	2.4	2.4	1	10	KTTILYKLKL	11408
2J59	EQ	HYDROLASE	E	2.4	2.4	1	10	KTTILYKLKL	11409
2JBL	HM	ELECTRON TRANSPORT	M	2.4	2.4	1	8	WYLWCVKH	11410

2JFA	AP	TRANSCRIPTION	A	1.2	2.4	2	24	LHDQVHLLECAWLEILMIGLVWRS	11411
2JIY	MH	PHOTOSYNTHESIS	M	2.4	2.4	1	8	WYVWGQNH	11412
2JIZ	AD	HYDROLASE	A	1.2	2.4	2	15	LSKQAVAYRQMSLLL	11413
2JIZ	HK	HYDROLASE	H	1.2	2.4	2	15	LSKQAVAYRQMSLLL	11414
2JIZ	IM	HYDROLASE	I	1.2	2.4	2	12	VFYLHSRLLERA	11415
2JJ0	LM	PHOTOSYNTHESIS	L	1.2	2.4	2	28	GLWQIITICATGAFVSWALREVEICRKL	11416
2JJ0	MH	PHOTOSYNTHESIS	M	2.4	2.4	1	7	ELEQIAD	11417
2JKI	BS	CHAPERONE	B	1.2	2.4	2	12	ERRIKDLVKRHS	11418
2JKR	BM	ENDOCYTOSIS	B	1.2	2.4	2	18	PEVQYVALRNINLIVQKR	11419
2JKR	BM	ENDOCYTOSIS	M	2.4	2.4	1	9	FVLIYELLD	11420
2JKR	EU	ENDOCYTOSIS	E	2.4	2.4	1	14	IYVKLEKLDIMIRL	11421
2JKR	LE	ENDOCYTOSIS	E	2.4	2.4	1	18	TQVQLTLLTAIVKLFLKK	11422
2NNA	AC	IMMUNE SYSTEM	A	2.4	2.4	1	22	PQFALTNIAVLKHNLNIVIKRS	11423
2NPP	AC	SIGNALING PROTEIN,HYDROLASE	A	2.4	2.4	1	14	ANVRFNVAKSLQKI	11424
2NQB	AG	STRUCTURAL PROTEIN/DNA	A	1.2	2.4	2	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	11425
2NTI	BC	DNA BINDING PROTEIN	C	2.4	2.4	1	11	TQYLMKILKVA	11426
2NV2	EF	LYASE/TRANSFERASE	F	1.2	2.4	2	11	STTMRRLIDTY	11427
2NV2	UV	LYASE/TRANSFERASE	V	1.2	2.4	2	11	STTMRRLIDTY	11428
2O26	EU	CYTOKINE/SIGNALING PROTEIN	E	1.2	2.4	2	19	NYSIIDKLGKIVDDLVLCM	11429
2O60	AB	METAL BINDING PROTEIN	A	1.2	2.4	2	15	EEQIAEFKEAFSLFD	11430
2OS8	AC	CONTRACTILE PROTEIN	C	2.4	2.4	1	10	YADYMEAFKT	11431
2P22	AD	TRANSPORT PROTEIN	D	2.4	2.4	1	9	NVEELLRRI	11432
2PBI	CD	SIGNALING PROTEIN	C	1.2	2.4	2	14	AFLQKIEALVKDMQ	11433
2PKG	AC	HYDROLASE REGULATOR/VIRAL PROTEIN	C	2.4	2.4	1	8	FDCFRMWF	11434
2PMS	AC	METAL TRANSPORT, HYDROLASE	A	2.4	2.4	1	17	QPEATKCFQWQRNMRRV	11435
2PMZ	DL	TRANSLATION, TRANSFERASE	L	1.2	2.4	2	13	TLGNLIAGTLRRI	11436
2QJP	GL	ELECTRON TRANSPORT	G	2.4	2.4	1	11	IGHSIQTWLLG	11437
2QJP	JI	ELECTRON TRANSPORT	J	2.4	2.4	1	11	IGHSIQTWLLG	11438
2QJY	AB	OXIDOREDUCTASE	A	2.4	2.4	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	11439
2QL5	CD	HYDROLASE	D	1.2	2.4	2	13	WFVQALCSILEEH	11440
2QLV	AC	TRANSFERASE/PROTEIN BINDING	A	1.2	2.4	2	12	PQIHRANMLAQG	11441
2QQP	EF	VIRUS	E	2.4	2.4	1	10	QLANRLQMEL	11442
2QTV	AB	PROTEIN TRANSPORT	A	2.4	2.4	1	6	HHDIDS	11443
2QTV	AB	PROTEIN TRANSPORT	B	1.2	2.4	2	10	IQARRLWKDY	11444
2R17	AC	PROTEIN TRANSPORT	C	2.4	2.4	1	17	EETEQINKHFHNTLEHL	11445
2RAO	AD	OXYGEN BINDING	D	2.4	2.4	1	7	PWTQRFF	11446
2RF4	CB	TRANSFERASE	B	1.2	2.4	2	18	LSSSISQLKRIQRDFKGL	11447
2RGN	DE	SIGNALING PROTEIN COMPLEX	E	1.2	2.4	2	13	PIEYQRRESQTNS	11448
2ROD	AB	APOPTOSIS	A	1.2	2.4	2	11	ETAFQGMLRKL	11449

2SEB	AD	COMPLEX (MHC CLASS II/SUPERANTIGEN)	A	1.2	2.4	2	22	AQGALANIAVDKANLEIMTKRS	11450
2UUN	KL	ELECTRON TRANSPORT	L	1.2	2.4	2	13	VAQIDALSQMVAE	11451
2UUN	ST	ELECTRON TRANSPORT	T	1.2	2.4	2	13	VAQIDALSQMVAE	11452
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	B	1.2	2.4	2	8	QEDVEAVS	11453
2UYN	AB	UNKNOWN FUNCTION	A	1.2	2.4	2	15	FATINEVYKQFFDEH	11454
2V4J	DE	OXIDOREDUCTASE	D	2.4	2.4	1	9	IEAEVVNRC	11455
2V5H	DI	TRANSCRIPTION	D	2.4	2.4	1	10	IPQSRELIAQ	11456
2VBO	AB	HYDROLASE	B	2.4	2.4	1	12	RWFLDKLVDEIG	11457
2VDW	AB	TRANSFERASE	B	2.4	2.4	1	31	TEFINKFLEFSNRVYEALYYVHSLLYSSMTS	11458
2VDW	CD	TRANSFERASE	D	2.4	2.4	1	31	TEFINKFLEFSNRVYEALYYVHSLLYSSMTS	11459
2VGL	AM	PROTEIN TRANSPORT	A	1.2	2.4	2	19	YSIREEIVLKVAILAEKYA	11460
2VHM	QR	RIBOSOME	Q	1.2	2.4	2	6	QYAYRD	11461
2VML	AF	PHOTOSYNTHESIS	F	1.2	2.4	2	25	NRRMAACLRDMEIILRYVSYALLAG	11462
2VRC	BD	OXIDOREDUCTASE	D	2.4	2.4	1	17	EPFAEITAAIYDAISKG	11463
2W65	CD	IMMUNE SYSTEM	D	1.2	2.4	2	5	SEQLT	11464
2W84	AB	PROTEIN TRANSPORT	A	2.4	2.4	1	12	EPLIATAVKFLQ	11465
2WBJ	BC	IMMUNE SYSTEM	B	2.4	2.4	1	13	KDILEQARAAVDT	11466
2WME	BC	OXIDOREDUCTASE	C	1.2	2.4	2	11	LARAHRAIHRL	11467
2Z2S	CD	TRANSCRIPTION	C	1.2	2.4	2	12	QENARLGRAIAR	11468
2Z3R	EH	CYTOKINE/CYTOKINE RECEPTOR	E	2.4	2.4	1	20	ASIHDTVENLIILANNSLSS	11469
2ZCY	DL	HYDROLASE	L	1.2	2.4	2	15	INSAARNIQHLLYGK	11470
2ZCY	HI	HYDROLASE	I	1.2	2.4	2	12	SDQLFGMCESLY	11471
2ZCY	HI	HYDROLASE	I	2.4	2.4	1	15	PETFTQLVSSSLYER	11472
2ZCY	QR	HYDROLASE	R	2.4	2.4	1	13	FQVEYSLEAIKLG	11473
2ZCY	RZ	HYDROLASE	Z	1.2	2.4	2	15	INSAARNIQHLLYGK	11474
2ZCY	VW	HYDROLASE	V	2.4	2.4	1	22	AADTEAVTQLIGSNIELHSLYT	11475
3A0B	AT	ELECTRON TRANSPORT	T	1.2	2.4	2	9	TITYVFIFA	11476
3A0B	bh	ELECTRON TRANSPORT	b	2.4	2.4	1	5	LYKAL	11477
3A0B	lm	ELECTRON TRANSPORT	m	2.4	2.4	1	8	GFIATALF	11478
3B5N	JL	MEMBRANE PROTEIN	J	2.4	2.4	1	62	EVQARHQELLKLEKSMAELTQLFNDMEELVIEQQENVDVIDKNVEDAQ LDVEQGVGHTDKAV	11479
3B9J	AB	OXIDOREDUCTASE	B	2.4	2.4	1	7	KQVKSVA	11480
3B9J	AC	OXIDOREDUCTASE	A	2.4	2.4	1	10	LLAYLRRKLG	11481
3BMC	AC	OXIDOREDUCTASE	C	2.4	2.4	1	27	VETQVAELIGTNAIAPFLLTMSFAQRQ	11482
3BPQ	CB	TOXIN	C	2.4	2.4	1	22	RKEYEKIEEILDIGLAKAMEET	11483
3BXK	CD	MEMBRANE PROTEIN, SIGNALING PROTEIN	C	1.2	2.4	2	15	EEQIAEFKEAFSLFD	11484
3BZ1	CK	ELECTRON TRANSPORT	K	1.2	2.4	2	25	DPLVDVLPVIPVLFLALAFVWQAAV	11485

3C91	PW	HYDROLASE	W	2.4	2.4	1	22	VGDAQVLVRYMKAELELYRLQR	11486
3C91	QX	HYDROLASE	Q	1.2	2.4	2	23	VADARVLVDFARISAQQEKVTYG	11487
3C91	UV	HYDROLASE	U	2.4	2.4	1	23	VADARVLVDFARISAQQEKVTYG	11488
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.2	2.4	2	10	QLSMRMLSSC	11489
3CHW	PV	STRUCTURAL PROTEIN	P	1.2	2.4	2	18	GGLINKKCYEMASHLRRS	11490
3CHX	BC	MEMBRANE PROTEIN	C	2.4	2.4	1	5	GTWHM	11491
3CHX	FG	MEMBRANE PROTEIN	G	2.4	2.4	1	5	GTWHM	11492
3CJH	CD	PROTEIN TRANSPORT	C	1.2	2.4	2	15	ELVNKISENCFEKCL	11493
3CL3	BE	VIRAL PROTEIN/SIGNALING PROTEIN	E	2.4	2.4	1	52	VQVDQLRMQGQSVEAALRMERQAASEEKRKLAQLQVAYHQLFQEYD NHIKSS	11494
3CR3	BC	TRANSFERASE	B	2.4	2.4	1	5	RASYL	11495
3CUQ	AB	PROTEIN TRANSPORT	A	1.2	2.4	2	15	PEFRVQFQDMCATIG	11496
3D31	AC	TRANSPORT PROTEIN	A	2.4	2.4	1	12	VKKNLEFGMRMK	11497
3D5B	OT	RIBOSOME	O	1.2	2.4	2	5	RELRE	11498
3DAC	MP	CELL CYCLE	M	1.2	2.4	2	15	VKEVMHYLGQYIMMK	11499
3DBJ	AB	PHOTOSYNTHESIS	A	2.4	2.4	1	12	GERRLRIAQTLT	11500
3DBJ	AB	PHOTOSYNTHESIS	B	2.4	2.4	1	13	TAAMEKLKAYFAT	11501
3DBJ	AB	PHOTOSYNTHESIS	B	2.4	2.4	1	13	AITAVINASDVQG	11502
3DD7	CD	RIBOSOME INHIBITOR	C	1.2	2.4	2	16	NKRTALNSALLFLRRN	11503
3DGC	LS	CYTOKINE/SIGNALING PROTEIN	L	1.2	2.4	2	16	YMQEVVPFLARLSNRL	11504
3DHR	EF	OXYGEN STORAGE, OXYGEN TRANSPORT	E	2.4	2.4	1	19	PEVHASLDKFVLAVGTVLT	11505
3DHR	EF	OXYGEN STORAGE, OXYGEN TRANSPORT	F	2.4	2.4	1	20	PENFRLLGDILVIILAAHFG	11506
3DHT	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	2.4	2.4	1	19	PAMHASLDKFLASVSTVLT	11507
3DTP	AB	CONTRACTILE PROTEIN	A	2.4	2.4	1	6	EREKEM	11508
3DTP	AB	CONTRACTILE PROTEIN	B	2.4	2.4	1	10	VTDFTRSILT	11509
3DVE	AB	MEMBRANE PROTEIN	A	1.2	2.4	2	8	YEEFVQMM	11510
3DWL	BI	STRUCTURAL PROTEIN	B	2.4	2.4	1	16	DHMERFWQQSLFKYLR	11511
3DWL	DF	STRUCTURAL PROTEIN	F	1.2	2.4	2	8	KFMQFLMG	11512
3EG5	AB	SIGNALING PROTEIN	B	1.2	2.4	2	15	SRNQHEIIRCLKAFM	11513
3EG5	CD	SIGNALING PROTEIN	C	2.4	2.4	1	19	PSSFENVKEKWVPEITHHC	11514
3EIQ	AC	HYDROLASE/ANTITUMOR PROTEIN	C	1.2	2.4	2	10	TNEVAEMLRD	11515
3ETR	AB	OXIDOREDUCTASE	B	2.4	2.4	1	7	KQVKSVA	11516
3EUB	JL	OXIDOREDUCTASE	J	1.2	2.4	2	9	RPILQGFRT	11517
3EUB	ST	OXIDOREDUCTASE	T	2.4	2.4	1	7	KQVKSVA	11518
3EXG	34	OXIDOREDUCTASE	3	1.2	2.4	2	16	AQVPLGAGIALACKYN	11519
3EXG	QT	OXIDOREDUCTASE	T	2.4	2.4	1	6	KILEDN	11520
3EXG	SR	OXIDOREDUCTASE	R	2.4	2.4	1	6	KILEDN	11521

3EXH	BC	OXIDOREDUCTASE	B	1.2	2.4	2	12	VKDIIFAIKKTL	11522
3F9K	Ya	VIRAL PROTEIN, RECOMBINATION	a	1.2	2.4	2	15	MDSRLQRIHAEIKNS	11523
3FAL	CD	SIGNALING PROTEIN	C	1.2	2.4	2	13	RLPALRSIGLKCL	11524
3FGC	CD	OXIDOREDUCTASE	C	2.4	2.4	1	7	DKDFRVF	11525
3FH6	GA	TRANSPORT PROTEIN	A	2.4	2.4	1	11	VAENMSFGLKL	11526
3FKS	SV	HYDROLASE	S	1.2	2.4	2	15	LSKQAVAYRQLSLLL	11527
3FKS	TX	HYDROLASE	X	1.2	2.4	2	5	EVFTG	11528
3FKS	UX	HYDROLASE	U	2.4	2.4	1	6	AELFYK	11529
3FKU	DZ	VIRAL PROTEIN/IMMUNE SYSTEM	D	1.2	2.4	2	22	KESTQKAIDGVTNKVNSIIDKM	11530
3FLO	GH	TRANSFERASE	G	2.4	2.4	1	23	LQEASDVLDDQIESFTKIIQNHY	11531
3FXD	AB	UNKNOWN FUNCTION	B	1.2	2.4	2	19	IISPVKDCILTVAKAVSFN	11532
3GJF	LH	IMMUNE SYSTEM	L	1.2	2.4	2	6	SEELQA	11533
3GJX	FD	PROTEIN TRANSPORT	D	1.2	2.4	2	18	KVYIGKLNMILVQILKQE	11534
3GLH	IJ	TRANSFERASE	J	1.2	2.4	2	21	PSRLQAILGDVCHIREQLMSV	11535
3GLH	KO	TRANSFERASE	O	2.4	2.4	1	17	RELLITDLLLRIEHYLQ	11536
3GTM	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	F	1.2	2.4	2	7	RALQISM	11537
3GTM	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.2	2.4	2	13	LAMANSLRRVMIA	11538
3HAE	ST	IMMUNE SYSTEM	S	1.2	2.4	2	6	SEELQA	11539
3HGK	CG	TRANSFERASE	G	1.2	2.4	2	5	MPMHG	11540
3HKZ	IU	TRANSFERASE	I	2.4	2.4	1	11	EEAIAEAKEIM	11541
3HOU	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.2	2.4	2	11	EETRAELSQLC	11542
3HOU	NO	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	O	1.2	2.4	2	14	LAMANSLRRVMIAE	11543
1A0H	DE	COMPLEX (SERINE PROTEASE/INHIBITOR)	D	2.3	2.3	1	10	EKELFESYIE	11544
1AOI	FH	DNA BINDING PROTEIN/DNA	F	2.3	2.3	1	11	AMDVVYALKRQ	11545
1AOI	GH	DNA BINDING PROTEIN/DNA	G	1.2	2.3	2	9	PRHLQLAVR	11546
1APY	CB	HYDROLASE	B	1.2	2.3	2	7	GDILMRF	11547
1B33	LM	PHOTOSYNTHESIS	L	2.3	2.3	1	14	GEKRLRIAQILTDN	11548
1B6C	CD	COMPLEX (ISOMERASE/PROTEIN KINASE)	D	2.3	2.3	1	14	ERSWFREAEIYQTV	11549
1BGY	BR	ELECTRON TRANSPORT	R	1.2	2.3	2	20	YLEPYLKEVIRERKEREEWA	11550
1CGI	EI	SERINE PROTEASE/INHIBITOR COMPLEX	I	2.3	2.3	1	11	ECVLCFENRKR	11551
1CU4	LH	IMMUNE SYSTEM	L	2.3	2.3	1	5	SEQLT	11552
1DGH	AB	OXIDOREDUCTASE	B	2.3	2.3	1	7	YFAEVEQ	11553
1DKG	AD	COMPLEX (HSP24/HSP70)	D	1.2	2.3	2	18	PLAMQRLKEAAEKAKIEL	11554

1E3D	CD	HYDROGENASE	D	1.2	2.3	2	29	PEANLVCTAHYLQALRAQVEVAKGMAVFG	11555
1E7P	DE	OXIDOREDUCTASE	E	1.2	2.3	2	13	IFIVLNMIRETYD	11556
1EAH	13	VIRUS	3	1.2	2.3	2	7	MLGEILN	11557
1EAY	AC	SIGNAL TRANSDUCTION COMPLEX	C	1.2	2.3	2	13	EVDLLEEELGHLT	11558
1EM8	CD	GENE REGULATION	C	2.3	2.3	1	16	AVEQLVCEIAAERWRS	11559
1F3M	BD	TRANSFERASE	D	2.3	2.3	1	12	PLRALYLIATNG	11560
1F66	AG	STRUCTURAL PROTEIN/DNA	A	1.2	2.3	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	11561
1F80	BD	TRANSFERASE	B	1.2	2.3	2	11	LKRIASMAGRQ	11562
1F99	AB	PHOTOSYNTHESIS	B	1.2	2.3	2	13	NTQIDALLAIVSE	11563
1FNT	ab	HYDROLASE/HYDROLASE ACTIVATOR	b	2.3	2.3	1	18	PSYIFEYLATVMYQRRSK	11564
1FNT	FN	HYDROLASE/HYDROLASE ACTIVATOR	F	1.2	2.3	2	23	APDARVLSNYLRQQCNYSSLVFN	11565
1FNT	FN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.2	2.3	2	17	PSYIFEYLATVMYQRRS	11566
1FNT	PQ	HYDROLASE/HYDROLASE ACTIVATOR	Q	2.3	2.3	1	10	QVEYALESIS	11567
1FNT	Ta	HYDROLASE/HYDROLASE ACTIVATOR	a	1.2	2.3	2	21	AADGDALVKRFKNSVKWYHFD	11568
1FQ1	AB	HYDROLASE/TRANSFERASE	B	1.2	2.3	2	12	EIDQLFRIFRTL	11569
1FQV	EF	LIGASE	F	1.2	2.3	2	8	PEEIRKTF	11570
1FS1	CD	LIGASE	D	1.2	2.3	2	8	PEEIRKTF	11571
1FYH	DE	IMMUNE SYSTEM	D	1.2	2.3	2	7	LIQVMAE	11572
1FYZ	CE	OXIDOREDUCTASE	E	2.3	2.3	1	20	YLWIEAKLEEKVAVLKARAF	11573
1FYZ	DF	OXIDOREDUCTASE	D	2.3	2.3	1	28	SDYNRTVMRNWTGKWLEPTIAALRDFMG	11574
1G0U	DL	HYDROLASE	L	2.3	2.3	1	21	AADGDALVKRFKNSVKWYHFD	11575
1G0U	EF	HYDROLASE	F	1.2	2.3	2	22	IPDGRHLVNRGREEAASFKKLY	11576
1G0U	IJ	HYDROLASE	J	2.3	2.3	1	17	PQAVSSFVRQELAKSIR	11577
1G0U	IZ	HYDROLASE	I	1.2	2.3	2	18	PEDLFETISQALLNAADR	11578
1GH0	WN	PHOTOSYNTHESIS	W	2.3	2.3	1	17	DAAVEANSYLDYAINAL	11579
1GO3	MN	TRANSFERASE	M	2.3	2.3	1	14	LKETVKKILMEKYE	11580
1GO3	MN	TRANSFERASE	N	2.3	2.3	1	11	EKTAVKIADIL	11581
1GO4	EC	CELL CYCLE	C	2.3	2.3	1	20	LELIKYLNNVVEQLKDWLYK	11582
1HBH	CB	OXYGEN CARRIER	C	1.2	2.3	2	19	PANFKILNHCILVVISTMF	11583
1HBH	CD	OXYGEN CARRIER	C	2.3	2.3	1	19	PANFKILNHCILVVISTMF	11584
1HDM	AB	IMMUNE SYSTEM	B	1.2	2.3	2	13	NSLANVLSQHLNQ	11585
1HE1	AC	SIGNALING PROTEIN	C	2.3	2.3	1	9	DRLRPLSYP	11586
1HTL	HC	ENTEROTOXIN	H	1.2	2.3	2	20	DSQKKAIERMKDTLRITYLT	11587
1HV4	AB	OXYGEN STORAGE/TRANSPORT	A	1.2	2.3	2	19	PVNFKFLGHCFLVVVAIHH	11588
1HV4	EF	OXYGEN STORAGE/TRANSPORT	E	2.3	2.3	1	16	AEEYGAETLERMFTAY	11589
1HV4	GH	OXYGEN STORAGE/TRANSPORT	G	2.3	2.3	1	18	AEVHASLDKFLCAVGTVL	11590
1I3Q	AF	TRANSCRIPTION	A	2.3	2.3	1	11	EETRAELSQLC	11591
1IBR	AB	CELL CYCLE, TRANSLATION	A	1.2	2.3	2	10	VPNWHRDLVR	11592
1ID3	BD	STRUCTURAL PROTEIN/DNA	D	1.2	2.3	2	29	QKSMSILNSFVNDIFERIATEASKLAAYN	11593
1ID3	FH	STRUCTURAL PROTEIN/DNA	F	2.3	2.3	1	16	FLESVIRDSVTYTEHA	11594

1IR2	S1	LYASE	S	2.3	2.3	1	14	AKNYGRAVYECLRG	11595
1IR2	Z8	LYASE	Z	2.3	2.3	1	21	NAPGAAANRVALEACTQARNE	11596
1IRU	GH	HYDROLASE	H	2.3	2.3	1	23	AADTQAVADAVTYQLGFHSIELN	11597
1IRU	QX	HYDROLASE	X	1.2	2.3	2	22	ATDVQTVAQRLKFRLNLYELKE	11598
1IRU	UV	HYDROLASE	V	2.3	2.3	1	23	AADTQAVADAVTYQLGFHSIELN	11599
1IW7	AC	TRANSFERASE	A	1.2	2.3	2	17	FGVTLGNPLRRILLSSI	11600
1IW7	KM	TRANSFERASE	K	1.2	2.3	2	11	VVEIILNLKEL	11601
1IWA	MH	LYASE	M	1.2	2.3	2	5	WTDLL	11602
1IWP	AB	LYASE	A	2.3	2.3	1	19	ARYAPFNALALLVGSQCGR	11603
1IWP	AB	LYASE	B	2.3	2.3	1	16	LETYRQIGKNAARYAR	11604
1IZN	CD	PROTEIN BINDING	D	2.3	2.3	1	12	IEKNLSDLIDLV	11605
1J19	AB	CELL ADHESION	A	1.2	2.3	2	21	LRINKRILALCMGNHELYMRR	11606
1J1E	BC	CONTRACTILE PROTEIN	B	1.2	2.3	2	21	EREKKKKILAERRKVLAIDHL	11607
1J1E	DF	CONTRACTILE PROTEIN	D	1.2	2.3	2	12	EEELSDLFRMFD	11608
1JCH	AB	RIBOSOME INHIBITOR, HYDROLASE	A	2.3	2.3	1	7	FKDYGHD	11609
1JCH	CD	RIBOSOME INHIBITOR, HYDROLASE	C	2.3	2.3	1	7	FKDYGHD	11610
1JD2	EF	HYDROLASE	F	2.3	2.3	1	12	FQVEYAVKAVEN	11611
1JD2	FG	HYDROLASE	F	2.3	2.3	1	15	IPAFADRLGQYVQAH	11612
1JD2	VW	HYDROLASE	W	2.3	2.3	1	12	YQVEYALESISH	11613
1JD2	YZ	HYDROLASE	Z	2.3	2.3	1	12	FQVEYALEAIKQ	11614
1JJO	BC	SIGNALING PROTEIN	C	1.2	2.3	2	9	FLQMLKMYF	11615
1JMU	DH	VIRAL PROTEIN	H	2.3	2.3	1	9	VEKIRYALG	11616
1JMX	AG	OXIDOREDUCTASE	A	2.3	2.3	1	15	DDDRRTLVKYLADKQ	11617
1JNH	CD	IMMUNE SYSTEM	C	2.3	2.3	1	6	SEELET	11618
1JPW	CF	CELL ADHESION	C	2.3	2.3	1	14	DITEPAICALRHLT	11619
1JR3	BE	TRANSFERASE	E	2.3	2.3	1	20	APARLHWLATLLMDALKRHH	11620
1JRO	CD	OXIDOREDUCTASE	C	2.3	2.3	1	9	PVQQAMIDH	11621
1JW9	BD	LIGASE	B	2.3	2.3	1	6	YRCLSR	11622
1K6L	LM	PHOTOSYNTHESIS	L	2.3	2.3	1	26	TLGIHRLGLLLSLSAVFFSALCMIIT	11623
1K6L	MH	PHOTOSYNTHESIS	M	2.3	2.3	1	26	MEGIHRWAIWMAVLVTLTGGIGILLS	11624
1KFY	MN	OXIDOREDUCTASE	M	1.2	2.3	2	16	WAKIRDEMGLAMEEGC	11625
1KKQ	CG	TRANSCRIPTION	G	2.3	2.3	1	9	EAIIRKALM	11626
1KKQ	DH	TRANSCRIPTION	D	2.3	2.3	1	11	LNDQVTLLKYG	11627
1KYO	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	2.3	2.3	1	21	PHELTESVLPAARYDYAVAEQ	11628
1KYO	EI	OXIDOREDUCTASE/ELECTRON TRANSPORT	E	2.3	2.3	1	30	KGRSYAYFMVGAMGLLSSAGAKSTVETFIS	11629
1KYO	OQ	OXIDOREDUCTASE/ELECTRON TRANSPORT	O	2.3	2.3	1	17	TSQMAKDVTTFLNWCAE	11630
1KZ7	AB	SIGNALING PROTEIN	A	1.2	2.3	2	13	LDSYLLKPVQRIT	11631

1L4A	AE	ENDOCYTOSIS/EXOCYTOSIS	A	2.3	2.3	1	30	RLQQTQAQVEEVVDIMRVNVDKVLERDSKI	11632
1LDK	AB	LIGASE	B	1.2	2.3	2	15	KSPELLARYCDSLLK	11633
1LKY	AB	TRANSCRIPTION	A	2.3	2.3	1	7	GKALLLL	11634
1LO5	AC	IMMUNE SYSTEM/TOXIN	A	1.2	2.3	2	22	AQGALANIAVDKANLEIMTKRS	11635
1LQ8	AB	BLOOD CLOTTING	A	1.2	2.3	2	13	FTFDLYRALASAA	11636
1LQ8	GH	BLOOD CLOTTING	G	1.2	2.3	2	13	FTFDLYRALASAA	11637
1LWU	JL	BLOOD CLOTTING	L	1.2	2.3	2	31	AQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	11638
1M2O	AB	PROTEIN TRANSPORT/SIGNALING PROTEIN	B	1.2	2.3	2	6	RLWKDY	11639
1M8Q	GV	CONTRACTILE PROTEIN	V	1.2	2.3	2	9	QAVLSLYAS	11640
1MIO	CD	MOLYBDENUM-IRON PROTEIN	C	1.2	2.3	2	5	VIQKG	11641
1MIO	CD	MOLYBDENUM-IRON PROTEIN	D	2.3	2.3	1	14	GCCSYHRTVLSRHF	11642
1MJE	BA	GENE REGULATION/ANTITUMOR PROTEIN/DNA	A	2.3	2.3	1	14	ANHYRWIVWKLAAM	11643
1MJE	BA	GENE REGULATION/ANTITUMOR PROTEIN/DNA	A	2.3	2.3	1	19	PERVLLQLKYRYDVEIDNS	11644
1MT1	KL	LYASE	K	2.3	2.3	1	13	PLNAFDGALLNAG	11645
1MTY	BG	MONOOXYGENASE	B	2.3	2.3	1	33	SDYNRTVMRNWTGKWLEPTIAALRDFMGLFAKL	11646
1MTY	CH	MONOOXYGENASE	C	2.3	2.3	1	33	SDYNRTVMRNWTGKWLEPTIAALRDFMGLFAKL	11647
1MTY	EC	MONOOXYGENASE	C	2.3	2.3	1	11	PEMAAVILKAL	11648
1MTY	EC	MONOOXYGENASE	E	2.3	2.3	1	8	ARRTRTIG	11649
1MVW	GV	CONTRACTILE PROTEIN	V	1.2	2.3	2	9	QAVLSLYAS	11650
1N4Q	CD	TRANSFERASE	C	1.2	2.3	2	13	NSVWNQRHFVISN	11651
1N5W	DE	OXIDOREDUCTASE	D	1.2	2.3	2	8	EAEIRFGI	11652
1N86	DF	BLOOD CLOTTING	F	2.3	2.3	1	14	SSIRYLQEIYNSNN	11653
1N95	AB	TRANSFERASE	B	2.3	2.3	1	9	RPWLCYWIL	11654
1NBF	AD	HYDROLASE	A	2.3	2.3	1	17	VQELCRVLLDNVENKMK	11655
1NEX	AB	LIGASE, CELL CYCLE	B	2.3	2.3	1	8	QNWNKIIR	11656
1NF3	BD	SIGNALING PROTEIN	B	1.2	2.3	2	15	LKNVFDEAILAALEP	11657
1NGM	AB	TRANSCRIPTION/DNA	B	2.3	2.3	1	15	EEASKLKERIWIGLN	11658
1NGM	IJ	TRANSCRIPTION/DNA	J	2.3	2.3	1	5	EELNA	11659
1NLW	AB	TRANSCRIPTION/DNA	A	1.2	2.3	2	23	THNEMEKNRRAHLRLSLEKLKGL	11660
1NMU	CB	SUGAR BINDING PROTEIN/RIBOSOME	B	2.3	2.3	1	10	YKSTVKSLRQ	11661
1NU7	BD	HYDROLASE/PROTEIN BINDING	D	1.2	2.3	2	24	DWYLKGRLTSLESQFINALGILET	11662
1O18	JW	CONTRACTILE PROTEIN	W	1.2	2.3	2	9	QAVLSLYAS	11663
1O18	P1	CONTRACTILE PROTEIN	1	1.2	2.3	2	9	QAVLSLYAS	11664
1OQP	AB	PROTEIN BINDING	A	2.3	2.3	1	13	SREEILKAFRLFD	11665
1OUU	AB	OXYGEN TRANSPORT	A	2.3	2.3	1	16	ADVVGAEALGRMLTAY	11666
1OW7	CF	TRANSFERASE	F	1.2	2.3	2	10	RELDELMASL	11667
1P9D	SU	REPLICATION	S	2.3	2.3	1	11	EEEQIAYAMQM	11668

1P9M	AB	SIGNALING PROTEIN/CYTOKINE	B	1.2	2.3	2	18	KQIRYILDGISALRKETC	11669
1PH1	AB	DNA BINDING PROTEIN/DNA	B	2.3	2.3	1	6	ISKVAD	11670
1PMA	IV	PROTEASE	V	1.2	2.3	2	22	VGDAQVLVRYMKAELELYRLQR	11671
1Q16	AB	OXIDOREDUCTASE	A	2.3	2.3	1	5	EIAKL	11672
1Q5R	GN	HYDROLASE	N	2.3	2.3	1	7	FTDYLRG	11673
1QHH	BC	HYDROLASE	B	2.3	2.3	1	13	AQSRVMEEMLLKA	11674
1QLE	AB	OXIDOREDUCTASE/IMMUNE SYSTEM	A	1.2	2.3	2	6	APLDRV	11675
1QO3	AC	RECEPTOR/IMMUNE SYSTEM	A	2.3	2.3	1	24	AAERDRAYLEGECVEWLRRYLKNG	11676
1QPW	CD	OXYGEN TRANSPORT	D	1.2	2.3	2	14	EVGGEALGRLLVVY	11677
1QZ7	AB	CELL ADHESION	A	2.3	2.3	1	17	DSVLFYAITTLHNLLLH	11678
1R1R	CF	OXIDOREDUCTASE	C	1.2	2.3	2	9	KLMYTRLLK	11679
1R2B	BD	TRANSCRIPTION	B	2.3	2.3	1	14	EHVVDTCRKFIKAS	11680
1R4P	AE	TOXIN	A	2.3	2.3	1	7	QFLYTTG	11681
1R5V	CF	SIGNALING PROTEIN	C	1.2	2.3	2	23	AQGALANIAVDKANLDVMKERSN	11682
1RCO	BC	LYASE	B	2.3	2.3	1	14	AKNYGRAVYECLRG	11683
1RCO	EF	LYASE	E	2.3	2.3	1	14	AKNYGRAVYECLRG	11684
1RCO	HI	LYASE	H	2.3	2.3	1	14	AKNYGRAVYECLRG	11685
1RCO	KM	LYASE	K	2.3	2.3	1	14	AKNYGRAVYECLRG	11686
1RCO	LS	LYASE	L	2.3	2.3	1	14	AKNYGRAVYECLRG	11687
1RCO	OP	LYASE	O	2.3	2.3	1	14	AKNYGRAVYECLRG	11688
1RCO	RT	LYASE	R	2.3	2.3	1	14	AKNYGRAVYECLRG	11689
1RCO	VP	LYASE	V	1.2	2.3	2	14	AKNYGRAVYECLRG	11690
1RCO	VW	LYASE	V	2.3	2.3	1	14	AKNYGRAVYECLRG	11691
1RM6	AC	OXIDOREDUCTASE	C	1.2	2.3	2	9	KLQAAFHEK	11692
1RPQ	AW	MEMBRANE PROTEIN	W	2.3	2.3	1	6	HFCYEL	11693
1RYP	EL	MULTICATALYTIC PROTEINASE	E	1.2	2.3	2	22	TADARSMIEHARTAAVTHNLYY	11694
1RYP	PW	MULTICATALYTIC PROTEINASE	W	1.2	2.3	2	22	AADTEAVTQLIGSNIELHSLYT	11695
1RYP	XM	MULTICATALYTIC PROTEINASE	X	1.2	2.3	2	12	SDQLFGMCESLY	11696
1RZF	LH	IMMUNE SYSTEM	L	2.3	2.3	1	6	SEELQA	11697
1S1C	AY	SIGNALING PROTEIN	Y	1.2	2.3	2	21	NINTERTLKTQAVNKLAEIMN	11698
1S5E	AF	TRANSERASE,TOXIN	A	2.3	2.3	1	30	TCDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	11699
1S5E	BK	TRANSERASE,TOXIN	K	1.2	2.3	2	20	DSQKKAIERMKDTLRIAYLT	11700
1SB3	DE	OXIDOREDUCTASE	D	1.2	2.3	2	14	PDRITELLDAKEAA	11701
1SCT	AB	OXYGEN TRANSPORT	A	2.3	2.3	1	18	PSRLKCVVEKFAVNHINR	11702
1SQB	CE	OXIDOREDUCTASE	C	2.3	2.3	1	29	GWIIRYMHANGASMFFICLYMHVGRGLYY	11703
1SQB	DJ	OXIDOREDUCTASE	D	2.3	2.3	1	17	HTSIRRGFQVYKQVCSS	11704
1SQB	EG	OXIDOREDUCTASE	E	2.3	2.3	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	11705
1SQX	AB	OXIDOREDUCTASE	A	1.2	2.3	2	19	ESEVLRGKNLLRNALVSHL	11706
1SQX	AB	OXIDOREDUCTASE	A	2.3	2.3	1	8	YAQALQSV	11707
1SQX	CD	OXIDOREDUCTASE	C	2.3	2.3	1	15	TTTAFSSVTHICRDV	11708

1SVX	AB	DE NOVO PROTEIN/SUGAR BINDING PROTEIN	A	2.3	2.3	1	9	PLHLAAYSG	11709
1T3Q	AB	OXIDOREDUCTASE	A	2.3	2.3	1	8	RDEVREVM	11710
1T9G	RS	OXIDOREDUCTASE, ELECTRON TRANSPORT	S	1.2	2.3	2	10	QTGQMTAGFL	11711
1TI2	EF	OXIDOREDUCTASE	F	2.3	2.3	1	6	RCAHNC	11712
1TQY	GH	TRANSFERASE	G	2.3	2.3	1	10	PIVVACFDAI	11713
1TUE	AB	REPLICATION	B	2.3	2.3	1	24	IDSQIQYWQLIRWENAIFFAAREH	11714
1TYE	CD	CELL ADHESION	D	2.3	2.3	1	5	DGRLA	11715
1UB4	AC	DNA BINDING PROTEIN	C	2.3	2.3	1	7	LAELVND	11716
1UM9	AD	OXIDOREDUCTASE	A	2.3	2.3	1	5	PEWMF	11717
1UM9	CD	OXIDOREDUCTASE	C	2.3	2.3	1	13	GDWYAGINFAAVQ	11718
1URQ	BD	TRANSPORT PROTEIN	B	2.3	2.3	1	61	TRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY	11719
1UZD	HJ	LYASE	H	2.3	2.3	1	15	AKNYGRAVYECLRGG	11720
1UZD	KP	LYASE	K	2.3	2.3	1	15	AKNYGRAVYECLRGG	11721
1UZH	VW	LYASE	V	1.2	2.3	2	21	NAPGAAANRVALEACTQARNE	11722
1V4U	CD	OXYGEN STORAGE/TRANSPORT	C	1.2	2.3	2	19	PSNFKILSHCILVVVAKMF	11723
1V54	OV	OXIDOREDUCTASE	V	1.2	2.3	2	25	LLARRLRFHIVGAFMVSLGFATFYK	11724
1V54	QR	OXIDOREDUCTASE	Q	2.3	2.3	1	12	ASQKALKEKEKA	11725
1V54	QZ	OXIDOREDUCTASE	Q	1.2	2.3	2	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	11726
1V9U	23	VIRUS/RECEPTOR	3	2.3	2.3	1	7	LIGEISS	11727
1VQP	S2	RIBOSOME	2	1.2	2.3	2	14	KATKKRLAKLDNQN	11728
1WYU	CD	OXIDOREDUCTASE	D	1.2	2.3	2	19	QGALRLMWELGEYLKALTG	11729
1WYU	EF	OXIDOREDUCTASE	E	2.3	2.3	1	11	PEAVRRALAER	11730
1WYU	EF	OXIDOREDUCTASE	E	2.3	2.3	1	5	GEFLT	11731
1WYU	GH	OXIDOREDUCTASE	G	2.3	2.3	1	5	GEFLT	11732
1XDK	AF	HORMONE/GROWTH FACTOR RECEPTOR	A	2.3	2.3	1	21	RLPALRSIGLKCLEHLFFFKL	11733
1XFV	CQ	LYASE/METAL BINDING PROTEIN	Q	2.3	2.3	1	10	YEEFVQMMTA	11734
1XLS	BF	TRANSCRIPTION	F	2.3	2.3	1	21	REEIDQLQEEMALILNNHIME	11735
1XLS	DH	TRANSCRIPTION	D	1.2	2.3	2	23	PAEVEALREKVYASLEAYCKHKY	11736
1XLS	DL	TRANSCRIPTION	L	1.2	2.3	2	7	ALLRYLL	11737
1XQ5	CD	OXYGEN STORAGE/TRANSPORT	D	2.3	2.3	1	20	PDNFKLLSDCLTIVVAAQLG	11738
1XTC	CG	TOXIN	C	1.2	2.3	2	32	NTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQS	11739
1XV9	CG	DNA BINDING PROTEIN	C	1.2	2.3	2	10	LDDQVILLRA	11740
1Y74	AD	TRANSPORT PROTEIN	D	2.3	2.3	1	12	NDAKELKRILTQ	11741
1Y8H	AB	OXYGEN STORAGE/TRANSPORT	A	2.3	2.3	1	19	PAVHASLDKFLSSVSTVLT	11742
1YA7	DJ	HYDROLASE/HYDROLASE ACTIVATOR	D	1.2	2.3	2	23	VADARVLVDFARISAQQEKVTYG	11743
1YA7	DK	HYDROLASE/HYDROLASE ACTIVATOR	D	2.3	2.3	1	23	VADARVLVDFARISAQQEKVTYG	11744

1YE9	CG	OXIDOREDUCTASE	G	1.2	2.3	2	7	FFAENEQ	11745
1YE9	JN	OXIDOREDUCTASE	J	2.3	2.3	1	9	DTFWDYVSL	11746
1YE9	JP	OXIDOREDUCTASE	J	2.3	2.3	1	12	FILREKITHFDH	11747
1YE9	LM	OXIDOREDUCTASE	M	1.2	2.3	2	13	FHRRELWEAIEAG	11748
1YEW	EF	OXIDOREDUCTASE, MEMBRANE PROTEIN	F	2.3	2.3	1	34	HAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT	11749
1YHU	AD	OXYGEN STORAGE/TRANSPORT	A	2.3	2.3	1	16	MLERAKVKDEWAKAYG	11750
1YSL	AB	LYASE	A	1.2	2.3	2	9	AAVVLHRLM	11751
1Z6O	KN	METAL BINDING PROTEIN	K	1.2	2.3	2	16	LSLALYVFDEYLQKTV	11752
1Z7M	DF	TRANSFERASE	F	2.3	2.3	1	10	PNDVITFLEH	11753
1Z7Q	ab	HYDROLASE/HYDROLASE ACTIVATOR	b	2.3	2.3	1	17	PSYIFEYLATVMYQRRS	11754
1ZBB	ef	STRUCTURAL PROTEIN/DNA	e	1.2	2.3	2	12	PKDIQLARRIRG	11755
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	G	1.2	2.3	2	10	VGRVHRLLRK	11756
1ZOY	BC	OXIDOREDUCTASE	C	1.2	2.3	2	14	AKEEMERFWNKNLG	11757
1ZUD	34	TRANSFERASE/BIOSYNTHETIC PROTEIN	3	2.3	2.3	1	14	MATRQEINAACVAL	11758
2AA1	CB	OXYGEN STORAGE/TRANSPORT	C	1.2	2.3	2	19	PSNFKILNHCILVVISTMF	11759
2ADF	HL	BLOOD CLOTTING/IMMUNE SYSTEM	L	1.2	2.3	2	7	SEQLTSG	11760
2AXT	bu	ELECTRON TRANSPORT	u	2.3	2.3	1	6	VVDEKL	11761
2AXT	ck	ELECTRON TRANSPORT	c	1.2	2.3	2	18	GLIVFWAGAMTLFELAHF	11762
2B9I	AC	TRANSFERASE	A	2.3	2.3	1	21	DDHIQYFIYQTLRAVKVLHGS	11763
2BA1	EH	RNA BINDING PROTEIN	H	2.3	2.3	1	20	EKLFDELLDVSINCARKLRE	11764
2BH1	AX	TRANSPORT PROTEIN	X	2.3	2.3	1	7	FSFANRF	11765
2BH1	BY	TRANSPORT PROTEIN	Y	2.3	2.3	1	7	FSFANRF	11766
2BV8	OP	PHOTOSYNTHESIS	O	1.2	2.3	2	27	NGELQSINGRYQRATASLEAARSLTSN	11767
2CCI	AB	CELL CYCLE	A	1.2	2.3	2	13	STAIREISLLKEL	11768
2CDE	CD	CELL RECEPTOR	D	2.3	2.3	1	8	EAEISHTQ	11769
2CLY	AB	HYDROLASE	B	1.2	2.3	2	10	LVDDFEKKFN	11770
2CLY	BC	HYDROLASE	B	2.3	2.3	1	10	LVDDFEKKFN	11771
2CLY	DF	HYDROLASE	F	2.3	2.3	1	17	VQKLFVDKIREYRTKRQ	11772
2D1P	AB	TRANSLATION	A	2.3	2.3	1	7	VAAALRR	11773
2DBU	AB	TRANSFERASE	A	1.2	2.3	2	13	ATATQVGVDILKE	11774
2DXB	NO	HYDROLASE	N	1.2	2.3	2	9	AEERRRKQN	11775
2DXB	QR	HYDROLASE	Q	1.2	2.3	2	17	LTELHNKIVEMRERVAS	11776
2E1M	AC	OXIDOREDUCTASE	A	2.3	2.3	1	7	RAQYATD	11777
2E2D	AC	HYDROLASE/HYDROLASE INHIBITOR	C	2.3	2.3	1	5	DWVTE	11778
2E5L	LQ	RIBOSOME	L	1.2	2.3	2	8	INQLVRKG	11779
2ES4	BE	HYDROLASE	E	2.3	2.3	1	20	PAAMQLALDQRAALADRTLG	11780
2F5Z	HN	OXIDOREDUCTASE/PROTEIN BINDING	H	1.2	2.3	2	6	CEDIAR	11781
2F66	DF	TRANSPORT PROTEIN	F	2.3	2.3	1	26	GDIALKKKLEQNTKKLDEESSQLETT	11782

2F8N	DK	STRUCTURAL PROTEIN/DNA	D	1.2	2.3	2	12	SIYVYKVLKQVH	11783
2F9Y	AB	LIGASE	A	1.2	2.3	2	14	QSEAIARNLREMSR	11784
2FBW	CD	OXIDOREDUCTASE	C	2.3	2.3	1	11	FPHYVAVVKSL	11785
2FOI	AC	OXIDOREDUCTASE	C	2.3	2.3	1	12	STDIGSVASFLL	11786
2FRV	AB	OXIDOREDUCTASE	A	1.2	2.3	2	9	GCSESVLRT	11787
2FRV	CD	OXIDOREDUCTASE	C	1.2	2.3	2	9	GCSESVLRT	11788
2FRV	EF	OXIDOREDUCTASE	F	1.2	2.3	2	29	AEVDLIATAHYLEALRVQVKAARAMAIFG	11789
2FRV	SL	OXIDOREDUCTASE	S	1.2	2.3	2	9	GCSESVLRT	11790
2FX8	NJ	IMMUNE SYSTEM	N	1.2	2.3	2	6	DEQLKS	11791
2FYN	BC	OXIDOREDUCTASE	B	1.2	2.3	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	11792
2FYN	GL	OXIDOREDUCTASE	G	2.3	2.3	1	11	IGHSIQTWLLG	11793
2FYN	JI	OXIDOREDUCTASE	J	2.3	2.3	1	11	IGHSIQTWLLG	11794
2GFB	EF	IMMUNOGLOBULIN	E	2.3	2.3	1	6	SEQLTS	11795
2GGM	AC	CELL CYCLE	A	1.2	2.3	2	11	FKNLKRVAKEL	11796
2GID	HJ	TRANSLATION	J	2.3	2.3	1	19	HFAVTLEHFLESALDESFG	11797
2GID	PJ	TRANSLATION	J	1.2	2.3	2	19	HFAVTLEHFLESALDESFG	11798
2GRN	AB	LIGASE	A	2.3	2.3	1	10	AEAYTIYCQN	11799
2GRN	AB	LIGASE	B	2.3	2.3	1	13	KALAPLLLAFVTK	11800
2GTL	FN	OXYGEN STORAGE/TRANSPORT	F	2.3	2.3	1	19	DNYFDAFKTAILHVVAAQL	11801
2GV5	BC	CELL CYCLE	B	2.3	2.3	1	13	PLDEIKRAFQLFD	11802
2H8P	AC	MEMBRANE PROTEIN	C	2.3	2.3	1	29	LHWRAAGAATVLLVIVLLAGSYLAVLAER	11803
2HLD	GH	HYDROLASE	G	2.3	2.3	1	65	FEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYN RTRQAVITNELVDIITGA	11804
2HLD	KN	HYDROLASE	K	1.2	2.3	2	15	LSKQAVAYRQLSLLL	11805
2HP0	AB	ISOMERASE	B	2.3	2.3	1	15	TGSAARNGVLSAWLS	11806
2I2X	CD	TRANSFERASE	D	2.3	2.3	1	22	PIDLIDDALMVGMGVVIRLYDE	11807
2IAN	GI	IMMUNE SYSTEM	G	1.2	2.3	2	22	KDLLEQRRAAVDTYCRHNYGVG	11808
2IAN	KL	IMMUNE SYSTEM	K	1.2	2.3	2	21	QGALANIAVDKANLEIMTKRS	11809
2IAN	PQ	IMMUNE SYSTEM	P	2.3	2.3	1	7	EEFGRFA	11810
2IBZ	AE	OXIDOREDUCTASE	A	2.3	2.3	1	14	HPNRVLEHLHSTAF	11811
2IK8	CD	SIGNALING PROTEIN	D	1.2	2.3	2	13	HETRELTRMNLQT	11812
2INN	BD	OXIDOREDUCTASE	D	1.2	2.3	2	10	YGAYVGNRAK	11813
2INP	AC	OXIDOREDUCTASE	A	1.2	2.3	2	25	MDAYWKYQAEKEKKLYAIFDAFAQN	11814
2IVF	AB	OXIDOREDUCTASE	B	2.3	2.3	1	5	ACNRQ	11815
2IX7	CB	CONTRACTILE PROTEIN/METAL BINDING	B	2.3	2.3	1	8	LGTVMRSL	11816
2J5G	ED	HYDROLASE	D	2.3	2.3	1	11	TLNLRYTRVAL	11817
2J9D	FE	MEMBRANE TRANSPORT	F	1.2	2.3	2	13	VDNVIDIICENAR	11818
2JKR	MS	ENDOCYTOSIS	S	1.2	2.3	2	17	DDEKQKLIEEVHAVVTV	11819
2JQ9	AB	PROTEIN TRANSPORT	B	1.2	2.3	2	12	DQLSRRLAALRN	11820

2K42	AB	SIGNALING PROTEIN	A	2.3	2.3	1	11	PDLRSLFSRAG	11821
2NUD	AC	TOXIN/PROTEIN BINDING	A	2.3	2.3	1	11	AKALKQHLQRY	11822
2NV2	AB	LYASE/TRANSFERASE	B	1.2	2.3	2	11	STTMRRLIDTY	11823
2NV2	GH	LYASE/TRANSFERASE	H	2.3	2.3	1	11	VREHIHAIEAC	11824
2NXX	DH	HORMONE/GROWTH FACTOR	H	1.2	2.3	2	32	PGTIFAKLLSVLTELRTLGNQNSEMCFSLKLK	11825
2NYL	EF	HYDROLASE	E	2.3	2.3	1	5	SPKEV	11826
2NZD	AG	STRUCTURAL PROTEIN/DNA	A	1.2	2.3	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	11827
2O2V	AB	TRANSFERASE	A	1.2	2.3	2	21	DEEMKAMLSYYYSTVMEQQVN	11828
2OBH	AC	CELL CYCLE	A	1.2	2.3	2	11	FKNLKRVAKEL	11829
2ODE	CD	SIGNALING PROTEIN	D	2.3	2.3	1	15	EENLEFWLACEEFKK	11830
2ONK	CE	MEMBRANE PROTEIN	C	2.3	2.3	1	12	APTLIYERYLSE	11831
2OT8	BD	TRANSPORT PROTEIN	B	2.3	2.3	1	14	ALVRSITCWTLSRY	11832
2PF4	CE	HYDROLASE REGULATOR/VIRAL PROTEIN	C	2.3	2.3	1	19	YLHRMTTLFCINVLSEVCG	11833
2PMS	BD	METAL TRANSPORT, HYDROLASE	B	2.3	2.3	1	17	QPEATKCFQWQRNMRRV	11834
2PMS	BD	METAL TRANSPORT, HYDROLASE	D	1.2	2.3	2	38	LQSKLDAKKAKLSKLEELSDKIDELDAEIAKLEDQLKA	11835
2PMZ	AB	TRANSLATION, TRANSFERASE	A	2.3	2.3	1	17	IEDLWDLLQYHVATYFD	11836
2PUK	EG	ELECTRON TRANSPORT	E	1.2	2.3	2	19	LSVTAVVIEGLARHKEELG	11837
2Q86	AB	IMMUNE SYSTEM	B	1.2	2.3	2	8	KAEIANKQ	11838
2QJP	BC	ELECTRON TRANSPORT	B	1.2	2.3	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	11839
2QJY	BC	OXIDOREDUCTASE	B	1.2	2.3	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	11840
2QJY	BC	OXIDOREDUCTASE	C	2.3	2.3	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	11841
2QJY	EF	OXIDOREDUCTASE	E	1.2	2.3	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	11842
2QJY	GH	OXIDOREDUCTASE	G	2.3	2.3	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	11843
2QJY	GL	OXIDOREDUCTASE	G	2.3	2.3	1	11	IGHSIQTWLLG	11844
2QKM	AB	HYDROLASE	A	1.2	2.3	2	19	EDENILRNAVNLQVLKFHY	11845
2QQD	DC	LYASE	C	2.3	2.3	1	20	KKEAEKTVREMAKIGFEMRG	11846
2QTV	AB	PROTEIN TRANSPORT	A	2.3	2.3	1	8	ARFLLSKL	11847
2R17	AC	PROTEIN TRANSPORT	A	2.3	2.3	1	10	SLALLQRQFD	11848
2R1H	CB	OXYGEN BINDING	C	1.2	2.3	2	19	PTNFKILAHNLIVVIAAYF	11849
2R6C	CH	REPLICATION	H	2.3	2.3	1	10	FLTAARIAKE	11850
2RFK	AB	ISOMERASE/RNA	A	2.3	2.3	1	12	SHEVVAWIKKIL	11851
2RHS	AB	LIGASE	B	2.3	2.3	1	15	LLPHLIEATAYNVAR	11852
2RI4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	2.3	2.3	1	16	VDEVGAEALGRLLVVY	11853
2UUN	OR	ELECTRON TRANSPORT	R	1.2	2.3	2	25	SDRMAACLRDMEIILRYVTYAVFAG	11854
2UUN	QR	ELECTRON TRANSPORT	R	1.2	2.3	2	13	VAQIDALSQMVAE	11855
2UZ1	DC	LYASE	D	2.3	2.3	1	6	GGFTNA	11856
2V1S	EJ	OXIDOREDUCTASE	E	2.3	2.3	1	25	LKDAEAVQKFFLEEIQLGEELLAQG	11857
2V46	GI	RIBOSOME	I	2.3	2.3	1	9	VRAVAALEP	11858

2V55	CD	TRANSFERASE	D	2.3	2.3	1	10	HVATLACVNK	11859
2V5H	BH	TRANSCRIPTION	B	2.3	2.3	1	10	IPQSRELIAQ	11860
2V5H	FJ	TRANSCRIPTION	J	2.3	2.3	1	14	PFKLDEVKIALVNA	11861
2V7Q	CD	HYDROLASE	D	2.3	2.3	1	14	TREGNDLYHEMIES	11862
2V7Q	CG	HYDROLASE	G	2.3	2.3	1	11	DKIRSILHRTH	11863
2V8S	EV	PROTEIN TRANSPORT	E	2.3	2.3	1	16	YEQFPELMNMLWSRML	11864
2VDW	CD	TRANSFERASE	D	1.2	2.3	2	13	YFLQISRVNDLNR	11865
2VJM	AB	TRANSFERASE	B	2.3	2.3	1	6	MKELAH	11866
2VJT	AB	PHOTOSYNTHESIS	A	2.3	2.3	1	14	GERRLRIAQTLTEA	11867
2VLJ	DE	IMMUNE SYSTEM	E	2.3	2.3	1	8	EAEISHTQ	11868
2VN5	AB	CELL ADHESION	B	2.3	2.3	1	13	STDLAILKKYLLG	11869
2VPD	CD	GENE REGULATION	D	1.2	2.3	2	13	TEMANKAAEAVLK	11870
2W72	AB	OXYGEN TRANSPORT	B	2.3	2.3	1	20	PENFRLLGNVLVCVLAHHFG	11871
2WAQ	BC	TRANSCRIPTION	B	1.2	2.3	2	8	AMLLKDRL	11872
2WB1	AC	TRANSCRIPTION	A	1.2	2.3	2	16	RTSQSGYMQRRLINAL	11873
2WDI	W5	RIBOSOME	W	2.3	2.3	1	11	PRKVRLVVDLI	11874
2WIN	AN	IMMUNE SYSTEM	N	2.3	2.3	1	21	TYYKRTIKISGQKAMYALKSK	11875
2WIN	GQ	IMMUNE SYSTEM	Q	2.3	2.3	1	21	TYYKRTIKISGQKAMYALKSK	11876
2WME	BC	OXIDOREDUCTASE	B	2.3	2.3	1	22	LAETRSVDIVTGADVLEYYAGL	11877
2WME	BC	OXIDOREDUCTASE	C	2.3	2.3	1	18	AMQRSRILRRAVDILRER	11878
2WME	FE	OXIDOREDUCTASE	F	1.2	2.3	2	11	LARAHRAIHRL	11879
2ZCY	0N	HYDROLASE	N	1.2	2.3	2	6	PDEYEQ	11880
2ZCY	BC	HYDROLASE	C	1.2	2.3	2	13	FQVEYALEAVKRG	11881
2ZET	AC	SIGNALING PROTEIN	C	1.2	2.3	2	14	DPCHLARVVKIGSL	11882
2ZET	BD	SIGNALING PROTEIN	D	1.2	2.3	2	14	DPCHLARVVKIGSL	11883
2ZIV	AB	HYDROLASE	A	2.3	2.3	1	11	PALSRTIYQLY	11884
2ZME	AB	PROTEIN TRANSPORT	B	2.3	2.3	1	10	PEDLVNACKM	11885
2ZU0	AC	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	C	1.2	2.3	2	15	GGEKKRNDILQMAVL	11886
3A0B	ac	ELECTRON TRANSPORT	a	2.3	2.3	1	16	WRVVGVWFAALGISTM	11887
3B4V	AC	HORMONE REGULATOR COMPLEX	C	2.3	2.3	1	8	KINLLGFL	11888
3B4V	BC	HORMONE REGULATOR COMPLEX	B	2.3	2.3	1	11	FHSTVINHYRM	11889
3BG0	EF	PROTEIN TRANSPORT, HYDROLASE	F	2.3	2.3	1	17	SQLIFNAQALKDRYEGN	11890
3BIM	BJ	TRANSCRIPTION REPRESSOR	B	2.3	2.3	1	9	EHVVDTCRK	11891
3BIM	GO	TRANSCRIPTION REPRESSOR	G	2.3	2.3	1	11	EHVVDTCRKFI	11892
3BZ1	DE	ELECTRON TRANSPORT	D	2.3	2.3	1	24	WSGILLFPCAYLALGGWLTGTTFV	11893
3BZ1	DX	ELECTRON TRANSPORT	X	1.2	2.3	2	29	PSLKGFFIGLLSGAVVLGLTFAVLIAISQ	11894
3C0R	CD	CELL CYCLE, HYDROLASE	C	2.3	2.3	1	11	AIEIGIISDAL	11895
3C14	AB	LYASE/LYASE INHIBITOR	A	2.3	2.3	1	22	AQELVMTLNELFARFDKLAAEN	11896
3C1B	AG	STRUCTURAL PROTEIN/DNA	A	1.2	2.3	2	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	11897

3C3Q	AB	TRANSPORT PROTEIN	A	1.2	2.3	2	23	DEGLKIAAKHYQFASGAFLHIKE	11898
3CHX	AB	MEMBRANE PROTEIN	B	2.3	2.3	1	18	GATFAVSGLLIGEWINRY	11899
3CJT	OP	TRANSFERASE/RIBOSOMAL PROTEIN	O	2.3	2.3	1	8	LPGLFDGG	11900
3CR3	AD	TRANSFERASE	A	1.2	2.3	2	5	RASYL	11901
3CR3	AD	TRANSFERASE	D	2.3	2.3	1	14	LIEGAYTASALLEA	11902
3CUE	AF	PROTEIN TRANSPORT	A	1.2	2.3	2	21	SNEYLILASTLHGVFAIASQL	11903
3CUQ	AB	PROTEIN TRANSPORT	B	2.3	2.3	1	11	IRFKSYLLSMG	11904
3CXH	CE	OXIDOREDUCTASE	C	2.3	2.3	1	22	MGSLLGLCLVIQIVTGIFMAMH	11905
3CXH	NR	OXIDOREDUCTASE	R	1.2	2.3	2	20	EDESYARAYRIIRAHQTELT	11906
3D54	IL	LIGASE	I	2.3	2.3	1	17	PFAEKMLIEAFLEMVEE	11907
3DBH	CD	CELL CYCLE	C	1.2	2.3	2	11	DDYVHEFCRYG	11908
3DBH	CH	CELL CYCLE	C	2.3	2.3	1	22	NYQVEEDIGKLKSCLTGFLQEY	11909
3DBH	EF	CELL CYCLE	E	2.3	2.3	1	11	DDYVHEFCRYG	11910
3DBJ	CD	PHOTOSYNTHESIS	C	2.3	2.3	1	12	VVTKSIVNADAE	11911
3DHH	AB	OXIDOREDUCTASE	B	1.2	2.3	2	5	EYDIV	11912
3DIN	CD	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	2.3	2.3	1	16	IIFTFLALIVFRMGIY	11913
3DIN	FH	MEMBRANE PROTEIN, PROTEIN TRANSPORT	H	2.3	2.3	1	19	ITLVLSVLFFVSCVVTAFV	11914
3DOE	AB	SIGNALING PROTEIN/HYDROLASE	B	2.3	2.3	1	23	LIYTPIFNEYISLVEKYIEEQLL	11915
3DUF	CB	OXIDOREDUCTASE/TRANSFERASE	C	1.2	2.3	2	7	VTDLISI	11916
3DUF	EH	OXIDOREDUCTASE/TRANSFERASE	E	1.2	2.3	2	7	VTDLISI	11917
3DUF	GH	OXIDOREDUCTASE/TRANSFERASE	G	1.2	2.3	2	16	AQYIQAAGVALGLKMR	11918
3DUF	HJ	OXIDOREDUCTASE/TRANSFERASE	J	1.2	2.3	2	9	PSVRKYARE	11919
3DUH	AC	IMMUNE SYSTEM/CYTOKINE	C	1.2	2.3	2	31	RLLLRFKILRSLQAFVAVAARVFAHGAATLS	11920
3DVE	AB	MEMBRANE PROTEIN	A	1.2	2.3	2	12	DEEVDEMIREAD	11921
3E2K	AD	HYDROLASE/HYDROLASE INHIBITOR	A	1.2	2.3	2	6	PISEKY	11922
3E8C	BH	TRANSFERASE	B	2.3	2.3	1	9	MFSHLRRIG	11923
3EA5	CD	TRANSPORT PROTEIN	C	2.3	2.3	1	5	DGYYI	11924
3ECH	BC	TRANSCRIPTION, TRANSCRIPTION REGULATION	B	1.2	2.3	2	13	PPDVHVLKLIDEQ	11925
3EDQ	CD	HYDROLASE	D	2.3	2.3	1	15	WFIQSLCAMLKQYAD	11926
3EFF	DK	MEMBRANE PROTEIN	K	2.3	2.3	1	16	TTRALHERFDRLERML	11927
3EUB	24	OXIDOREDUCTASE	2	2.3	2.3	1	10	LLAYLRRKLG	11928
3EX7	AB	HYDROLASE/RNA BINDING PROTEIN/RNA	A	1.2	2.3	2	15	KSVMEELKRIIDDSE	11929
3EXG	UX	OXIDOREDUCTASE	X	1.2	2.3	2	6	KILEDN	11930
3F9K	EG	VIRAL PROTEIN, RECOMBINATION	E	1.2	2.3	2	12	IEPAQEEHEKYH	11931
3F9K	IK	VIRAL PROTEIN, RECOMBINATION	K	1.2	2.3	2	10	TEMITTLKKI	11932
3FAL	CB	SIGNALING PROTEIN	C	2.3	2.3	1	24	LDDQVILLRAGWNELLIASFSHRS	11933

3FBI	AB	TRANSCRIPTION	B	2.3	2.3	1	9	IQYVTYLLT	11934
3FDL	AB	APOPTOSIS	A	2.3	2.3	1	20	QMAAVKQALREAGDEFELRY	11935
3FKS	TX	HYDROLASE	X	2.3	2.3	1	15	TREGNDLYREMKETG	11936
3FN1	AB	LIGASE	A	2.3	2.3	1	7	TSIEERT	11937
3FS4	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	2.3	2.3	1	6	PWTQRF	11938
3FWB	AB	CELL CYCLE, TRANSCRIPTION	A	2.3	2.3	1	11	YHELKVAMKAL	11939
3FWC	BD	CELL CYCLE, TRANSCRIPTION	D	1.2	2.3	2	16	DSTRETVLKQIREFLE	11940
3FWC	FG	CELL CYCLE, TRANSCRIPTION	G	2.3	2.3	1	16	RETVLKQIREFLEEIV	11941
3FWC	MN	CELL CYCLE, TRANSCRIPTION	M	1.2	2.3	2	14	EEQKQEIYEAFSLF	11942
3GE8	AB	OXIDOREDUCTASE	B	1.2	2.3	2	8	ERELWEKE	11943
3GHG	DF	BLOOD CLOTTING	D	2.3	2.3	1	17	FSSANNRDNTYNRVSED	11944
3H87	BC	TOXIN/ANTITOXIN	C	2.3	2.3	1	14	RTEYIRRRLAQDAQ	11945
3HGK	AF	TRANSFERASE	A	2.3	2.3	1	7	PEYFIKG	11946
3HHL	AD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	1.2	2.3	2	10	KEVFAQFRAN	11947
3HHL	BC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	C	1.2	2.3	2	10	KEVFAQFRAN	11948
3HKZ	IJ	TRANSFERASE	J	2.3	2.3	1	6	MERDCL	11949
3HOU	DG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	1.2	2.3	2	8	ADEAKTLI	11950
3HPG	EL	TRANSFERASE	E	1.2	2.3	2	11	ESTQLLMKYLG	11951
3HRD	AB	OXIDOREDUCTASE	B	2.3	2.3	1	22	RSMVEGQIEGGVTMGQGFVLME	11952
3HRD	EF	OXIDOREDUCTASE	E	2.3	2.3	1	12	PHYDRGEVAGML	11953
3HRW	CD	OXYGEN TRANSPORT	D	2.3	2.3	1	15	DEVGGEALGRLLVVY	11954
3HRZ	AB	IMMUNE SYSTEM	A	1.2	2.3	2	11	QAKIWDTIEKS	11955
6RLX	AB	HORMONE (MUSCLE RELAXANT)	A	2.3	2.3	1	7	KRSLARF	11956
1A9W	CF	OXYGEN TRANSPORT	C	2.2	2.2	1	16	AGEYGAEALERMFLSF	11957
1ABR	AB	GLYCOSIDASE/CARBOHYDRATE	A	2.2	2.2	1	13	RYISNRVRVSIQT	11958
1AHW	AF	COMPLEX (IMMUNOGLOBULIN/TISSUE FACTOR)	F	2.2	2.2	1	7	TDEIVKD	11959
1B35	BC	VIRUS	B	1.1	2.2	2	7	LQGRSGC	11960
1B4U	CD	DIOXYGENASE	C	2.2	2.2	1	10	AENRERFKAD	11961
1BGY	CF	ELECTRON TRANSPORT	F	1.1	2.2	2	20	ENLYDDRVFRIKRALDLSMR	11962
1BGY	NF	ELECTRON TRANSPORT	F	1.1	2.2	2	20	YLEPYLKEVIRERKEREEWA	11963
1BGY	NF	ELECTRON TRANSPORT	N	2.2	2.2	1	11	SFKITRGIEAV	11964
1BX2	DE	IMMUNE SYSTEM	E	1.1	2.2	2	13	ELGRPDAEYWNSQ	11965
1BXN	CJ	LYASE	J	1.1	2.2	2	14	DEQITKQLEYCLNQ	11966
1CAX	EB	SEED STORAGE PROTEIN	E	1.1	2.2	2	9	KNFLEASYD	11967
1CDL	BF	CALCIUM-BINDING PROTEIN	B	2.2	2.2	1	12	DEEVDEMIREAD	11968

1CFF	AB	CALMODULIN	A	1.1	2.2	2	10	YEEFVQMMTA	11969
1DGH	CB	OXIDOREDUCTASE	C	1.1	2.2	2	11	PDMVWDFWSLR	11970
1DGH	CB	OXIDOREDUCTASE	C	1.1	2.2	2	19	KMLQGRLFAYPDTHRHRLG	11971
1DGR	BN	PLANT PROTEIN	B	2.2	2.2	1	8	KNFLEASY	11972
1DGR	CX	PLANT PROTEIN	C	2.2	2.2	1	9	KNFLEASYD	11973
1E1C	AB	ISOMERASE	A	2.2	2.2	1	19	DFSARIARNTQLFLQQESG	11974
1EER	AC	COMPLEX (CYTOKINE/RECEPTOR)	A	1.1	2.2	2	18	SRVLERYLLEAKEAEKIT	11975
1EF1	AC	MEMBRANE PROTEIN	A	2.2	2.2	1	17	PETAVLLASYAVQSKYG	11976
1EFP	AB	ELECTRON TRANSPORT	B	1.1	2.2	2	15	PLAVAKILAAVARAE	11977
1EJR	CA	HYDROLASE	A	1.1	2.2	2	19	YPESVALISAFIMEGARDG	11978
1F5Q	CD	TRANSFERASE	D	2.2	2.2	1	12	STDLICYILHIM	11979
1F66	EC	STRUCTURAL PROTEIN/DNA	E	1.1	2.2	2	12	TVALREIRRYQK	11980
1FFU	DE	HYDROLASE	D	2.2	2.2	1	15	QNIVKAVQYAARKLQ	11981
1FG9	AD	IMMUNE SYSTEM	A	2.2	2.2	1	10	LNVQRKAIHE	11982
1FHJ	AB	OXYGEN STORAGE/TRANSPORT	A	2.2	2.2	1	19	PAVHASLDKFFTAVSTVLT	11983
1FM6	UX	TRANSCRIPTION	U	1.1	2.2	2	23	RLPALRSIGLKCLEHLFFFKLIG	11984
1FNT	BC	HYDROLASE/HYDROLASE ACTIVATOR	C	2.2	2.2	1	10	QVEYALESIS	11985
1FNT	EF	HYDROLASE/HYDROLASE ACTIVATOR	F	2.2	2.2	1	13	FQVEYALEAIKQG	11986
1FNT	TU	HYDROLASE/HYDROLASE ACTIVATOR	U	2.2	2.2	1	13	FQVEYAVKAVENG	11987
1FQV	CD	LIGASE	D	1.1	2.2	2	16	KGLLDVTCKTVANMIK	11988
1FQV	OP	LIGASE	O	2.2	2.2	1	10	DELLLGIFSC	11989
1G0U	1N	HYDROLASE	1	2.2	2.2	1	19	VQVAEEAIVNAMRVLYYRD	11990
1G0U	DK	HYDROLASE	D	1.1	2.2	2	22	TADARSMIEHARTAAVTHNLYY	11991
1G0U	H1	HYDROLASE	1	2.2	2.2	1	19	VQVAEEAIVNAMRVLYYRD	11992
1G0U	JY	HYDROLASE	J	1.1	2.2	2	14	YSGFYTFSLLDHHY	11993
1G3I	CI	CHAPERONE/HYDROLASE	I	1.1	2.2	2	11	LLKSAVELAKD	11994
1G4U	SR	SIGNALING PROTEIN	S	1.1	2.2	2	14	PLRSLMTNLQNLNK	11995
1GH0	UP	PHOTOSYNTHESIS	U	2.2	2.2	1	17	DAAVEANSYLDYAINAL	11996
1GK0	AB	HYDROLASE	A	2.2	2.2	1	6	PGRTLG	11997
1GK0	CD	HYDROLASE	C	2.2	2.2	1	6	PGRTLG	11998
1GO4	FB	CELL CYCLE	B	2.2	2.2	1	20	LELIKYLNNVVEQLKDWLYK	11999
1GO4	GA	CELL CYCLE	A	2.2	2.2	1	20	LELIKYLNNVVEQLKDWLYK	12000
1GXS	CB	LYASE	B	2.2	2.2	1	12	VSSTRRSLAALE	12001
1GXS	CD	LYASE	D	2.2	2.2	1	10	LPVYRELIQA	12002
1HBH	AB	OXYGEN CARRIER	B	2.2	2.2	1	19	AETQGAFQKFLAVVVSALG	12003
1HBM	AC	METHANOGENESIS	C	2.2	2.2	1	11	KVAQNRRNFCN	12004
1HE1	BD	SIGNALING PROTEIN	D	2.2	2.2	1	9	DRLRPLSYP	12005
1HR8	GH	HYDROLASE	G	1.1	2.2	2	19	EDEVSRAKNQLKSSLLMNL	12006
1HV4	AB	OXYGEN STORAGE/TRANSPORT	B	2.2	2.2	1	19	PENFRLLGDILIIVLAAHF	12007
1HV4	EF	OXYGEN STORAGE/TRANSPORT	F	2.2	2.2	1	19	PENFRLLGDILIIVLAAHF	12008

1HV4	GH	OXYGEN STORAGE/TRANSPORT	H	2.2	2.2	1	19	PENFRLLGDILIIVLAAHF	12009
1HVU	DE	TRANSFERASE/RNA	E	2.2	2.2	1	12	KETWETWWTEYW	12010
1HXY	BC	IMMUNE SYSTEM/TOXIN	B	1.1	2.2	2	22	KDLLEQRRAAVDTYCRHNYGVG	12011
1I3Q	AB	TRANSCRIPTION	B	1.1	2.2	2	16	VAHLIECLLSKVAALS	12012
1I3Q	AE	TRANSCRIPTION	A	2.2	2.2	1	22	EIIQNAQRDAVTLFCCLLRSRL	12013
1I4O	AC	APOPTOSIS/HYDROLASE	C	2.2	2.2	1	8	HADYLLRT	12014
1I94	DE	RIBOSOME	D	2.2	2.2	1	6	LVIEFY	12015
1IAK	AB	HISTOCOMPATIBILITY ANTIGEN I-AK	B	1.1	2.2	2	22	LERTRAELDTVCRHNYEKTETP	12016
1IAO	AB	MHC II	B	1.1	2.2	2	13	ELGRPDAEYWNSQ	12017
1IR2	EM	LYASE	E	2.2	2.2	1	14	AKNYGRAVYECLRG	12018
1IR2	U3	LYASE	3	2.2	2.2	1	14	DEQIAAQVDYIVAN	12019
1IR2	W5	LYASE	W	2.2	2.2	1	14	AKNYGRAVYECLRG	12020
1IRU	CJ	HYDROLASE	J	1.1	2.2	2	22	ATDVQTVAQRLKFRLNLYELKE	12021
1IRU	J1	HYDROLASE	1	2.2	2.2	1	19	LDRAMRLVKDVFISAAERD	12022
1IRU	RS	HYDROLASE	R	2.2	2.2	1	15	VEYITRYIASLKQRY	12023
1IW7	DF	TRANSFERASE	F	1.1	2.2	2	16	STSDPVRQYLHEIGQV	12024
1IZL	AD	PHOTOSYNTHESIS	A	2.2	2.2	1	9	LHFFLAAWR	12025
1IZL	JN	PHOTOSYNTHESIS	N	2.2	2.2	1	7	PYNAIAF	12026
1J3I	AD	OXIDOREDUCTASE, TRANSFERASE	A	2.2	2.2	1	15	ESKYEKLKYKRCKYL	12027
1JB0	BI	PHOTOSYNTHESIS	B	2.2	2.2	1	10	TRRIWYAIAM	12028
1JD2	FN	HYDROLASE	N	2.2	2.2	1	22	AADTQAIADIVQYHLELYTSQY	12029
1JD2	MN	HYDROLASE	M	2.2	2.2	1	20	ISDMQHIERLLKDLVTENAY	12030
1JD2	YR	HYDROLASE	Y	1.1	2.2	2	22	TADARSMIEHARTAAVTHNLYY	12031
1JD2	ZS	HYDROLASE	Z	2.2	2.2	1	22	APDARVLSNYLRQQCNYSSLVF	12032
1JK0	AB	OXIDOREDUCTASE	A	2.2	2.2	1	12	PKESEFLFNAIH	12033
1JMU	EF	VIRAL PROTEIN	F	1.1	2.2	2	12	MQSVVKLLDDQL	12034
1JN5	AB	TRANSPORT PROTEIN	B	2.2	2.2	1	8	PTLRFRLL	12035
1JR3	BE	TRANSFERASE	E	1.1	2.2	2	21	PSRLQAILGDVCHIREQLMSV	12036
1JRO	AB	OXIDOREDUCTASE	A	2.2	2.2	1	8	LLELLRAE	12037
1JY7	PQ	OXYGEN STORAGE/TRANSPORT	P	2.2	2.2	1	18	AHAGEYGAEALERMFLSF	12038
1JY7	PQ	OXYGEN STORAGE/TRANSPORT	P	1.1	2.2	2	16	PVNFKLLSHCLLVTLA	12039
1K5D	JK	SIGNALING PROTEIN/SIGNALING ACTIVATOR	J	2.2	2.2	1	7	YEHDLEV	12040
1K6L	LM	PHOTOSYNTHESIS	M	2.2	2.2	1	7	PAVFLRD	12041
1K74	DE	TRANSCRIPTION	D	1.1	2.2	2	8	PLLQEIYK	12042
1KF6	NO	OXIDOREDUCTASE	N	2.2	2.2	1	6	YCSEVC	12043
1KF6	OP	OXIDOREDUCTASE	P	2.2	2.2	1	29	FIGRVFLFLMIVLPLWCGLHRMHHAMHDL	12044
1KF9	DE	HORMONE/GROWTH FACTOR	D	2.2	2.2	1	7	KEETQQK	12045
1KFY	MN	OXIDOREDUCTASE	M	1.1	2.2	2	11	PFICELAKAYV	12046
1KJY	AB	SIGNALING PROTEIN	A	2.2	2.2	1	15	SARADDARQLFVLAG	12047

1KJY	CD	SIGNALING PROTEIN	C	2.2	2.2	1	22	KAVVYSNTIQSIIAIIRAMGRL	12048
1KN1	AB	ELECTRON TRANSPORT	B	2.2	2.2	1	11	AITSVINSSDV	12049
1KPS	AB	LIGASE/PROTEIN TRANSPORT	B	2.2	2.2	1	10	LAPLLLAFVT	12050
1KYO	BR	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.1	2.2	2	21	PHELTESVLPAARYDYAVAEQ	12051
1KYO	LM	OXIDOREDUCTASE/ELECTRON TRANSPORT	M	1.1	2.2	2	12	ALKLVRESELLG	12052
1L2I	AC	TRANSCRIPTION RECEPTOR/COACTIVATOR	A	1.1	2.2	2	10	DLLLEMLDAH	12053
1L4A	BC	ENDOCYTOSIS/EXOCYTOSIS	C	2.2	2.2	1	6	DQINQD	12054
1L9B	MH	PHOTOSYNTHESIS	M	2.2	2.2	1	8	WYVWGQNH	12055
1L9J	LM	PHOTOSYNTHESIS	M	2.2	2.2	1	15	IFSHLDWTNNFSLVH	12056
1L9J	RS	PHOTOSYNTHESIS	S	2.2	2.2	1	7	ELEQIAD	12057
1LVC	BE	LYASE	E	1.1	2.2	2	11	EEIREAFRVFD	12058
1M4U	LA	HORMONE/GROWTH FACTOR	L	2.2	2.2	1	13	NHAIVQTLVHFIN	12059
1M8Q	A8	CONTRACTILE PROTEIN	8	1.1	2.2	2	9	QAVLSLYAS	12060
1MIO	AB	MOLYBDENUM-IRON PROTEIN	A	2.2	2.2	1	7	CPVGLIG	12061
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	H	1.1	2.2	2	20	VNYFLDGERQLGTRLMELRN	12062
1MT1	IL	LYASE	I	2.2	2.2	1	13	PLNAFDGALLNAG	12063
1MVW	A8	CONTRACTILE PROTEIN	8	1.1	2.2	2	9	QAVLSLYAS	12064
1MVW	D9	CONTRACTILE PROTEIN	9	1.1	2.2	2	9	QAVLSLYAS	12065
1MVW	GV	CONTRACTILE PROTEIN	V	2.2	2.2	1	12	SVWIGGSILASL	12066
1MWN	AX	STRUCTURAL PROTEIN	X	2.2	2.2	1	6	WNKILS	12067
1MXE	AE	METAL BINDING PROTEIN	A	2.2	2.2	1	15	FPEFLTMMARKMKDT	12068
1N2D	BC	CELL CYCLE	B	2.2	2.2	1	8	LGDYLRAI	12069
1N34	DE	RIBOSOME	E	2.2	2.2	1	11	AVPRAILELAG	12070
1N86	AC	BLOOD CLOTTING	A	2.2	2.2	1	18	DMKRLEVDIDIKIRSCRG	12071
1NEX	CD	LIGASE, CELL CYCLE	D	2.2	2.2	1	8	QNWNKIIR	12072
1NGM	AB	TRANSCRIPTION/DNA	B	2.2	2.2	1	14	ADFLLEQESKRLKQ	12073
1NHG	BD	OXIDOREDUCTASE	D	2.2	2.2	1	13	FIDYAIEYSEKYA	12074
1NVM	AB	LYASE/OXIDOREDUCTASE	B	2.2	2.2	1	17	IDEFTETTSKAIEVIGG	12075
1NWD	AC	BINDING PROTEIN/HYDROLASE	A	2.2	2.2	1	14	EQIAEFKEAFSLFD	12076
1NY7	12	VIRUS	2	1.1	2.2	2	7	AEMISRS	12077
1O18	D9	CONTRACTILE PROTEIN	9	1.1	2.2	2	9	QAVLSLYAS	12078
1O18	GV	CONTRACTILE PROTEIN	V	1.1	2.2	2	9	QAVLSLYAS	12079
1O5E	LH	SERINE PROTEASE, HYDROLASE	H	1.1	2.2	2	11	REWIFQAIKTH	12080
1OR0	AB	HYDROLASE	B	1.1	2.2	2	5	EQYFD	12081
1PNS	FR	RIBOSOME	R	1.1	2.2	2	18	GKEQRILAKTIKRARILG	12082
1PSB	BD	METAL BINDING PROTEIN	B	2.2	2.2	1	21	FQEFMAFVAMITTACHEFFEH	12083

1Q90	BD	PHOTOSYNTHESIS	B	2.2	2.2	1	12	AFASVQYIMTDV	12084
1QHH	BC	HYDROLASE	C	2.2	2.2	1	9	YREMLKAER	12085
1QLE	AC	OXIDOREDUCTASE/IMMUNE SYSTEM	A	2.2	2.2	1	24	PRLNNLSYWMYVCGVALGVASLLA	12086
1QLE	CD	OXIDOREDUCTASE/IMMUNE SYSTEM	D	2.2	2.2	1	31	RHQQATFAGFIKGATWVSILSIAVLVFLALA	12087
1QO0	BD	BINDING PROTEIN	D	2.2	2.2	1	14	EVSDALVLQLIRIG	12088
1QUQ	AB	DNA-BINDING PROTEIN	B	2.2	2.2	1	14	LGLYNEAVKIIHDF	12089
1QVF	FL	RIBOSOME	F	1.1	2.2	2	10	TNETTKSIER	12090
1R20	AD	HORMONE/GROWTH FACTOR RECEPTOR	A	2.2	2.2	1	19	RLPALRSISLKSFEHLFFF	12091
1R27	AB	OXIDOREDUCTASE	A	2.2	2.2	1	5	EIAKL	12092
1R4M	EF	CELL CYCLE	F	2.2	2.2	1	13	KAEVAAEFLNDRV	12093
1R4M	EF	CELL CYCLE	F	2.2	2.2	1	7	VKKFLER	12094
1R6O	AD	HYDROLASE	A	1.1	2.2	2	17	QELELSLNMAFARAREH	12095
1RP3	CD	TRANSCRIPTION	C	1.1	2.2	2	20	VEEEVIKRELTEKVKEAVSK	12096
1RP3	GH	TRANSCRIPTION	G	2.2	2.2	1	15	PYSNQIEREELILKY	12097
1RTD	AB	TRANSFERASE/DNA	A	2.2	2.2	1	15	DVKQLTEAVQKITTE	12098
1RYP	OW	MULTICATALYTIC PROTEINASE	O	2.2	2.2	1	18	CDVLAKRMANLSQIYTQR	12099
1RYP	VW	MULTICATALYTIC PROTEINASE	V	2.2	2.2	1	22	AADTQAIADIVQYHLELYTSQY	12100
1RYP	WX	MULTICATALYTIC PROTEINASE	X	2.2	2.2	1	15	PETFTQLVSSSLYER	12101
1S5L	DF	PHOTOSYNTHESIS	F	2.2	2.2	1	27	TVRWVAVHTLAVPTIFFLGAIAAMQFI	12102
1SB3	BC	OXIDOREDUCTASE	B	1.1	2.2	2	7	PTHRAAA	12103
1SCT	CD	OXYGEN TRANSPORT	D	2.2	2.2	1	16	MEGTGLMLMANLFKTS	12104
1SHZ	DC	SIGNALING PROTEIN	D	1.1	2.2	2	12	NKNQLHGDKLMA	12105
1SP4	AB	HYDROLASE	B	2.2	2.2	1	11	EKEIMAEIYKN	12106
1SQB	JK	OXIDOREDUCTASE	K	2.2	2.2	1	5	PYING	12107
1SVF	AB	VIRAL PROTEIN	B	2.2	2.2	1	27	SQNLAAVNKSLSDALQHLAQSDTYLSA	12108
1T3Q	BC	OXIDOREDUCTASE	C	2.2	2.2	1	25	RDLRLSLAKAITQRVILKAAQGAMY	12109
1T4K	AD	IMMUNE SYSTEM	A	2.2	2.2	1	5	KDEYE	12110
1TFC	BD	TRANSCRIPTION	D	2.2	2.2	1	9	KILHRLLQE	12111
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	2.2	2.2	1	15	INVVTCAAGILSNLT	12112
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	1.1	2.2	2	17	ENIQRVAAGVLCELAQD	12113
1UB4	AC	DNA BINDING PROTEIN	A	2.2	2.2	1	5	WRARG	12114
1UM9	AB	OXIDOREDUCTASE	A	2.2	2.2	1	13	GDWYAGINFAAVQ	12115
1UZD	BC	LYASE	B	2.2	2.2	1	14	AKNYGRAVYECLRG	12116
1UZD	KP	LYASE	P	2.2	2.2	1	14	DEQIAAQVDYIVAN	12117
1UZH	OT	LYASE	O	2.2	2.2	1	14	AKNYGRAVYECLRG	12118
1UZH	OT	LYASE	O	2.2	2.2	1	21	NAPGAAANRVALEACTQARNE	12119
1V02	FE	HYDROLASE	E	2.2	2.2	1	24	FLDQQAQERSMDKCLGWFLEPVVR	12120

1V54	EF	OXIDOREDUCTASE	E	2.2	2.2	1	12	AWELRKGMNTLV	12121
1VF5	NO	PHOTOSYNTHESIS	N	2.2	2.2	1	15	VTEAYASVQYIMNEV	12122
1VQP	FM	RIBOSOME	F	1.1	2.2	2	11	TNETTKSIERG	12123
1VQP	FM	RIBOSOME	F	2.2	2.2	1	9	MHIPELADE	12124
1VRQ	AB	OXIDOREDUCTASE	B	2.2	2.2	1	15	HDHVAWAFARKANEM	12125
1W5C	GJ	PHOTOSYNTHESIS	G	2.2	2.2	1	5	ICVAY	12126
1W5C	GJ	PHOTOSYNTHESIS	J	2.2	2.2	1	10	IHGATVENTL	12127
1WDD	AS	LYASE	A	2.2	2.2	1	14	AKNYGRACYECLRG	12128
1WDW	IJ	LYASE	I	1.1	2.2	2	8	YNPIYRAG	12129
1WQL	AB	OXIDOREDUCTASE	B	1.1	2.2	2	12	YESMRARIRARV	12130
1WYU	AB	OXIDOREDUCTASE	B	1.1	2.2	2	10	GSNPATASMA	12131
1WYU	CD	OXIDOREDUCTASE	C	2.2	2.2	1	11	PEAVRRALAER	12132
1WYU	CD	OXIDOREDUCTASE	D	2.2	2.2	1	18	GAHGELTGILIIRAYHED	12133
1X86	EF	SIGNALING PROTEIN/MEMBRANE PROTEIN	E	2.2	2.2	1	15	NQPFALEMIKSRQKK	12134
1XCQ	GH	IMMUNE SYSTEM	G	1.1	2.2	2	6	SEQLTS	12135
1XDK	EB	HORMONE/GROWTH FACTOR RECEPTOR	E	2.2	2.2	1	21	RLPALRSIGLKCLEHLFFFKL	12136
1XFU	DR	LYASE/METAL BINDING PROTEIN	D	2.2	2.2	1	23	EKKRKISIFRGIQAYNEIENVLK	12137
1XFU	ES	LYASE/METAL BINDING PROTEIN	E	2.2	2.2	1	23	EKKRKISIFRGIQAYNEIENVLK	12138
1XFU	FT	LYASE/METAL BINDING PROTEIN	F	2.2	2.2	1	23	EKKRKISIFRGIQAYNEIENVLK	12139
1Y75	AB	HYDROLASE	A	2.2	2.2	1	5	LKARC	12140
1YA7	BH	HYDROLASE/HYDROLASE ACTIVATOR	B	1.1	2.2	2	23	VADARVLVDFARISAQQEKVTYG	12141
1YA7	CJ	HYDROLASE/HYDROLASE ACTIVATOR	C	2.2	2.2	1	15	IENLVKRVADQMQQY	12142
1YHU	IL	OXYGEN STORAGE/TRANSPORT	I	2.2	2.2	1	16	MLERAKVKDEWAKAYG	12143
1YHU	UW	OXYGEN STORAGE/TRANSPORT	W	1.1	2.2	2	18	IPTLESMLDHLAGQHAVR	12144
1YKE	CD	GENE REGULATION	D	2.2	2.2	1	23	EKIEAIKKKEKLLRHVDSLIEDF	12145
1YOV	AB	SIGNALING PROTEIN	A	1.1	2.2	2	32	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS	12146
1YRT	AB	LAYSE, TOXIN	B	1.1	2.2	2	11	AAELRHVMTNL	12147
1YV0	TI	CONTRACTILE PROTEIN	T	1.1	2.2	2	16	EQIKRKKYEIVTLRNR	12148
1Z2C	AB	SIGNALING PROTEIN	B	2.2	2.2	1	16	MHLLSCLESLRVSLNN	12149
1Z6O	HO	METAL BINDING PROTEIN	H	2.2	2.2	1	16	LSLALYVFDEYLQKTV	12150
1Z7Q	HI	HYDROLASE/HYDROLASE ACTIVATOR	I	2.2	2.2	1	15	VVSALQMLKQHLFKY	12151
1Z7Q	MN	HYDROLASE/HYDROLASE ACTIVATOR	N	2.2	2.2	1	17	PSYIFEYLATVMYQRRS	12152
1Z7Q	SZ	HYDROLASE/HYDROLASE ACTIVATOR	S	1.1	2.2	2	23	TADARSMIEHARTAAVTHNLYYD	12153
1Z7Q	Ta	HYDROLASE/HYDROLASE ACTIVATOR	T	1.1	2.2	2	18	APDARVLSNYLRQQCNYS	12154
1Z7Q	VW	HYDROLASE/HYDROLASE ACTIVATOR	W	2.2	2.2	1	15	VVSALQMLKQHLFKY	12155
1Z7Q	WM	HYDROLASE/HYDROLASE ACTIVATOR	M	2.2	2.2	1	11	LIMPFLDNQVN	12156
1Z7S	12	VIRUS	2	2.2	2.2	1	5	YINAN	12157
1Z7X	XW	HYDROLASE/HYDROLASE INHIBITOR	X	2.2	2.2	1	9	YCNQMMRRR	12158

1Z7Z	12	VIRUS/RECEPTOR	2	2.2	2.2	1	5	YINAN	12159
1ZBB	bd	STRUCTURAL PROTEIN/DNA	d	1.1	2.2	2	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	12160
1ZC4	CB	SIGNALING PROTEIN	B	1.1	2.2	2	24	AKIKREWLEVLEETKRALSDKRRR	12161
1ZGL	KM	IMMUNE SYSTEM	K	2.2	2.2	1	8	RPDAEYWN	12162
1ZM2	AB	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	A	1.1	2.2	2	19	GGQIIPTMRRATYAGFLLA	12163
1ZT2	CD	REPLICATION, TRANSFERASE	D	2.2	2.2	1	8	FIDYLKYT	12164
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	A	2.2	2.2	1	12	EEEIREAFRVFD	12165
1ZVY	AB	HYDROLASE/IMMUNE SYSTEM	B	2.2	2.2	1	6	VAWRNR	12166
2A1T	DR	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	2.2	2.2	1	25	TRPVVAAGAVGLAQRALDEATKYAL	12167
2A5Y	AB	APOPTOSIS	B	2.2	2.2	1	11	RQMLDRKLLLG	12168
2AA1	CB	OXYGEN STORAGE/TRANSPORT	C	2.2	2.2	1	6	PQTKIY	12169
2ACL	EB	TRANSCRIPTION	E	1.1	2.2	2	23	LDDQVILLRAGWNELLIASFSHR	12170
2ACL	EF	TRANSCRIPTION	E	1.1	2.2	2	13	RLPALRSIGLKCL	12171
2ADV	AC	HYDROLASE	A	2.2	2.2	1	5	PGRTL	12172
2AHM	BF	VIRAL PROTEIN, REPLICATION	F	2.2	2.2	1	12	DALNNIINNARD	12173
2AQ1	GH	IMMUNE SYSTEM	H	1.1	2.2	2	9	MGNMKYLYD	12174
2AUS	CD	ISOMERASE/STRUCTURAL PROTEIN	D	1.1	2.2	2	13	GEYRRRLKRELLG	12175
2BA0	BG	RNA BINDING PROTEIN	B	2.2	2.2	1	16	LTDRVAEFIKRRKADV	12176
2BBM	AB	CALCIUM-BINDING PROTEIN	A	1.1	2.2	2	12	DEEVDEMIREAD	12177
2BC4	CD	IMMUNE SYSTEM	C	2.2	2.2	1	6	ADWAQE	12178
2BV8	AB	PHOTOSYNTHESIS	B	2.2	2.2	1	14	GNKRLDIVNRINSN	12179
2BV8	AF	PHOTOSYNTHESIS	A	1.1	2.2	2	10	TGPMDEYLIA	12180
2BV8	ON	PHOTOSYNTHESIS	O	1.1	2.2	2	10	TGPMDEYLIA	12181
2BZW	AB	TRANSCRIPTION	A	2.2	2.2	1	19	MAAVKQALREAGDEFELRY	12182
2C1M	AB	PROTEIN TRANSPORT/MEMBRANE PROTEIN	A	2.2	2.2	1	8	GLDKIEAL	12183
2C35	EF	POLYMERASE	E	1.1	2.2	2	17	NSEVHMLLEHRKQQNES	12184
2CLY	AB	HYDROLASE	B	1.1	2.2	2	23	AEFLTQSKTRIQEYEKELEKMRN	12185
2CZV	BC	HYDROLASE	B	2.2	2.2	1	10	HVLAKLMVKK	12186
2D0O	CD	CHAPERONE	C	2.2	2.2	1	7	GVLVSNR	12187
2D3G	AP	PROTEIN TRANSPORT	P	1.1	2.2	2	17	QEEEELQLALALSQSEA	12188
2DFK	AB	CELL CYCLE	A	2.2	2.2	1	37	RDQMRANVINEIMSTERHYIKHLKDICEGYLKQCRKR	12189
2DXB	WO	HYDROLASE	O	2.2	2.2	1	16	DFEILEMAVRELAIEK	12190
2E9X	BD	REPLICATION	B	1.1	2.2	2	22	LMEINTSGTFLTQALNHMYKLR	12191
2EH8	LH	IMMUNE SYSTEM	L	1.1	2.2	2	6	DEQLKS	12192
2EHO	AB	REPLICATION	A	2.2	2.2	1	10	PEELAFAREF	12193
2F5Z	GN	OXIDOREDUCTASE/PROTEIN BINDING	G	2.2	2.2	1	7	CEDIARV	12194

2FHH	ML	HYDROLASE	M	2.2	2.2	1	18	RQLANVYAQTLGTIFTEQ	12195
2FJ7	GH	STRUCTURAL PROTEIN/DNA	H	2.2	2.2	1	21	MNSFVNDVFERIAGEASRLAH	12196
2FJF	EF	IMMUNE SYSTEM	E	1.1	2.2	2	6	DEQLKS	12197
2FJU	AB	SIGNALING PROTEIN, APOPTOSIS/HYDROLASE	A	2.2	2.2	1	7	DRLRPLS	12198
2FK0	IL	VIRAL PROTEIN	I	1.1	2.2	2	10	YEELKHLLSR	12199
2FK0	KH	VIRAL PROTEIN	H	2.2	2.2	1	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	12200
2FUG	JK	OXIDOREDUCTASE	K	2.2	2.2	1	11	PTEVMGVASFY	12201
2FUG	SU	OXIDOREDUCTASE	S	1.1	2.2	2	19	TPCREGVAGFMVNLFAKIG	12202
2FYN	KL	OXIDOREDUCTASE	K	1.1	2.2	2	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	12203
2G2S	AB	LUMINESCENT PROTEIN	B	2.2	2.2	1	5	FFKSA	12204
2G2U	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	2.2	2	6	PVSEKH	12205
2G38	CD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	2.2	2.2	1	36	TAQIADLDQEYDDFWDEDGEVMRDYRLRVSDALSKL	12206
2GID	HJ	TRANSLATION	H	1.1	2.2	2	11	QRFLTQALHYN	12207
2GUZ	CD	CHAPERONE, PROTEIN TRANSPORT	D	1.1	2.2	2	8	LDESCKIL	12208
2GUZ	CJ	CHAPERONE, PROTEIN TRANSPORT	J	1.1	2.2	2	15	MDKINNRFNYLFEVN	12209
2GUZ	KL	CHAPERONE, PROTEIN TRANSPORT	L	2.2	2.2	1	15	MDKINNRFNYLFEVN	12210
2H4C	CD	HYDROLASE	C	2.2	2.2	1	11	FFQFAEMIVKM	12211
2H4Q	AB	HYDROLASE INHIBITOR	A	2.2	2.2	1	6	EQLERE	12212
2H9A	AB	OXIDOREDUCTASE	A	1.1	2.2	2	14	SLTYFCVAGDVEGA	12213
2HGP	MQ	RIBOSOME	Q	2.2	2.2	1	7	RELAHKG	12214
2HII	XY	REPLICATION	X	1.1	2.2	2	15	ESVLNVIAADVTLVG	12215
2HIO	BD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	D	2.2	2.2	1	27	GLIYEETRGVLKVFLENVIRDAVTYTE	12216
2HLD	KN	HYDROLASE	K	1.1	2.2	2	14	RSTVAQLVQTLEQH	12217
2HLD	LM	HYDROLASE	M	2.2	2.2	1	6	RGISEL	12218
2HLD	SW	HYDROLASE	S	2.2	2.2	1	12	VFYLHSRLLERA	12219
2HOD	JK	BLOOD CLOTTING	J	1.1	2.2	2	26	LLQKNVRAQLVDMKRLEVDIDIKIRS	12220
2HYI	GI	HYDROLASE/RNA BINDING PROTEIN/RNA	G	2.2	2.2	1	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	12221
2I2R	BF	TRANSPORT PROTEIN	F	2.2	2.2	1	15	KEEMMDIVKAIYDMM	12222
2I2R	KO	TRANSPORT PROTEIN	O	2.2	2.2	1	14	FEDFVTALSILLRG	12223
2ISS	CF	LYASE, TRANSFERASE	F	1.1	2.2	2	11	STTMIRILKEM	12224
2J0M	AB	TRANSFERASE	B	2.2	2.2	1	10	NNDVIGRIEN	12225
2J0S	AC	HYDROLASE	A	1.1	2.2	2	10	HEILEMTNKF	12226
2J7A	EF	OXIDOREDUCTASE	E	2.2	2.2	1	5	RNEMR	12227
2JIZ	BF	HYDROLASE	F	2.2	2.2	1	15	TREGNDLYHEMIESG	12228
2JIZ	EG	HYDROLASE	E	1.1	2.2	2	28	SEHYDVARGVQKILQDYKSLQDIIAILG	12229

2JIZ	JM	HYDROLASE	J	1.1	2.2	2	14	SKQAVAYRQMSLLL	12230
2K9F	AB	OXIDOREDUCTASE	A	1.1	2.2	2	15	PLCLSELGQTEKWAQ	12231
2KBR	AB	STRUCTURAL PROTEIN/CELL ADHESION	A	2.2	2.2	1	11	LPLFDAIRPLI	12232
2NOJ	CD	IMMUNE SYSTEM	C	1.1	2.2	2	15	MTPTVIAVHYLDETE	12233
2NU9	FB	LIGASE	B	2.2	2.2	1	11	PYQGRELAFKL	12234
2NV2	QR	LYASE/TRANSFERASE	Q	1.1	2.2	2	10	ERVKRGMAEM	12235
2NV2	UV	LYASE/TRANSFERASE	U	2.2	2.2	1	10	ERVKRGMAEM	12236
2NVU	AB	PROTEIN TURNOVER, LIGASE	B	2.2	2.2	1	9	NHVKKFLER	12237
2NXX	AE	HORMONE/GROWTH FACTOR	E	1.1	2.2	2	17	GETIEDLLHFCRTMYSM	12238
2NXX	BF	HORMONE/GROWTH FACTOR	F	1.1	2.2	2	32	PGTIFAKLLSVLTELRTLGNQNSEMCFSLKLK	12239
2O8A	BJ	HYDROLASE/INHIBITOR	B	2.2	2.2	1	12	IKLWKTFTDCFN	12240
2ODB	AB	PROTEIN BINDING	A	2.2	2.2	1	7	DRLRPLS	12241
2OJZ	MH	IMMUNE SYSTEM	M	2.2	2.2	1	7	KDEYERH	12242
2ONK	FH	MEMBRANE PROTEIN	H	1.1	2.2	2	13	PLRVFFTVSLPLS	12243
2OT3	AB	PROTEIN TRANSPORT	B	2.2	2.2	1	9	KTSLVLRYC	12244
2OV2	BJ	PROTEIN BINDING/TRANSFERASE	B	2.2	2.2	1	13	LKTVFDEAIRAVL	12245
2OV2	HP	PROTEIN BINDING/TRANSFERASE	H	2.2	2.2	1	5	DRLRP	12246
2OZB	AB	RNA BINDING PROTEIN/RNA	A	1.1	2.2	2	10	ANEATKTLNR	12247
2P1L	CD	APOPTOSIS	C	2.2	2.2	1	21	WGRIVAFFSFGGALCVESVDK	12248
2P1L	EF	APOPTOSIS	E	2.2	2.2	1	19	QMAAVKQALREAGDEFELR	12249
2P2C	AB	HYDROLASE	B	2.2	2.2	1	15	VADMLVKVNALIKDR	12250
2P5T	GH	TRANSCRIPTION REGULATOR	H	2.2	2.2	1	17	DSEFKHALARNLRSLTR	12251
2PKG	BD	HYDROLASE REGULATOR/VIRAL PROTEIN	D	2.2	2.2	1	8	FDCFRMWF	12252
2PVO	AB	ELECTRON TRANSPORT	A	2.2	2.2	1	6	VPMRER	12253
2Q26	CD	VIRUS/RNA	C	2.2	2.2	1	12	EVALQEYRTVAR	12254
2QIE	ED	TRANSFERASE	D	2.2	2.2	1	6	EIKDIL	12255
2QJK	JK	ELECTRON TRANSPORT	J	2.2	2.2	1	11	FASVEHIMRNV	12256
2QJY	DC	OXIDOREDUCTASE	D	2.2	2.2	1	11	IGHSIQTWLLG	12257
2QJY	KL	OXIDOREDUCTASE	K	1.1	2.2	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	12258
2QJY	KL	OXIDOREDUCTASE	L	2.2	2.2	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	12259
2QJY	PQ	OXIDOREDUCTASE	P	2.2	2.2	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	12260
2QM6	CD	TRANSFERASE	C	1.1	2.2	2	13	QVAELIEKDMKKN	12261
2QMU	AB	TRANSLATION	B	1.1	2.2	2	9	VEKIKEVIS	12262
2QRV	HG	TRANSFERASE/TRANSFERASE REGULATOR	G	2.2	2.2	1	11	KEDLDVASRFL	12263
2QVS	EB	TRANSFERASE/TRANSFERASE REGULATOR	E	2.2	2.2	1	16	KAVDWWALGVLIYEMA	12264
2QYF	CB	CELL CYCLE	B	2.2	2.2	1	13	TAACLRRLFRAIF	12265

2UUN	OP	ELECTRON TRANSPORT	P	2.2	2.2	1	13	ANKRLDAVNRITA	12266
2UZ1	AB	LYASE	B	2.2	2.2	1	7	DGSVGYS	12267
2V52	BM	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	M	2.2	2.2	1	7	RAELVRM	12268
2V5H	CG	TRANSCRIPTION	C	2.2	2.2	1	10	IPQSRELIAQ	12269
2VML	KH	PHOTOSYNTHESIS	H	1.1	2.2	2	25	NRRMAACLRDMEIILRYVSYALLAG	12270
2VML	KH	PHOTOSYNTHESIS	K	1.1	2.2	2	8	LREVNRTF	12271
2VOH	AB	APOPTOSIS	A	1.1	2.2	2	16	IDTARIIFNQVMEKEF	12272
2VOY	CD	HYDROLASE	D	2.2	2.2	1	22	LFFRYMAIGGYVGAATVGAAAW	12273
2VOY	GH	HYDROLASE	H	2.2	2.2	1	8	RGAIYYFK	12274
2W19	AC	TRANSFERASE/ISOMERASE	A	1.1	2.2	2	20	HFDRIVDEVQGFFEVHRALG	12275
2W72	DC	OXYGEN TRANSPORT	C	1.1	2.2	2	19	PVNFKLLSHCLLVTLAAHL	12276
2WB1	CH	TRANSCRIPTION	C	2.2	2.2	1	19	IEAAREIIIREISKVLAEQ	12277
2WBJ	AD	IMMUNE SYSTEM	A	1.1	2.2	2	22	AQGALANIAVDKANLEIMTKRS	12278
2WBJ	FG	IMMUNE SYSTEM	F	2.2	2.2	1	13	KDILEQARAAVDT	12279
2WC0	AD	HYDROLASE/HORMONE	A	2.2	2.2	1	10	LSHFLQHMLF	12280
2WME	BC	OXIDOREDUCTASE	C	2.2	2.2	1	22	LAETRSVDIVTGADVLEYYAGL	12281
2Z0E	AB	HYDROLASE/STRUCTURAL PROTEIN	A	2.2	2.2	1	14	PNTVAQVLKKLAVF	12282
2Z3R	ON	CYTOKINE/CYTOKINE RECEPTOR	O	2.2	2.2	1	21	ASIHDTVENLIILANNSLSSN	12283
2ZAE	AB	HYDROLASE	A	1.1	2.2	2	5	TWIFR	12284
2ZCY	FG	HYDROLASE	F	2.2	2.2	1	15	IPAFADRLGQYVQAH	12285
2ZCY	JY	HYDROLASE	J	1.1	2.2	2	13	YSGFYTFSLLDHH	12286
2ZFB	AB	METAL BINDING PROTEIN	A	2.2	2.2	1	12	PEAHASLDKFLC	12287
2ZHX	EF	HYDROLASE/HYDROLASE INHIBITOR	E	2.2	2.2	1	6	RDASTL	12288
2ZU6	AB	HYDROLASE	B	2.2	2.2	1	16	FEKTLTPIIQEYFEHG	12289
2ZVN	AD	SIGNALING PROTEIN/TRANSCRIPTION	D	2.2	2.2	1	46	VPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKL	12290
2ZVN	GD	SIGNALING PROTEIN/TRANSCRIPTION	D	1.1	2.2	2	46	VPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKL	12291
3A0B	AC	ELECTRON TRANSPORT	C	2.2	2.2	1	13	PWQERRAAEYMTH	12292
3A0B	ai	ELECTRON TRANSPORT	i	2.2	2.2	1	7	FVFGFLS	12293
3A1G	AB	TRANSFERASE	B	1.1	2.2	2	10	SRTREILTKT	12294
3B2U	KJ	IMMUNE SYSTEM/TRANSFERASE	K	1.1	2.2	2	5	DEQLK	12295
3BG0	EF	PROTEIN TRANSPORT, HYDROLASE	F	2.2	2.2	1	15	DKAAEDTIKRLVMRE	12296
3BJI	AD	SIGNALING PROTEIN	A	1.1	2.2	2	13	LRDLLMVPMQRVL	12297
3BL2	AC	VIRAL PROTEIN/APOPTOSIS	A	2.2	2.2	1	19	SGRIVGFFDVGRYVCEEVL	12298
3BSZ	AF	TRANSPORT PROTEIN/IMMUNE SYSTEM	A	2.2	2.2	1	9	TKSYWKALG	12299
3BUA	CG	DNA BINDING PROTEIN	C	1.1	2.2	2	15	SRLLRVMQCLSRIEE	12300

3BZL	AC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	A	2.2	2.2	1	8	SGSLANNI	12301
3C1B	GH	STRUCTURAL PROTEIN/DNA	H	2.2	2.2	1	12	SREIQTAVRLLL	12302
3C60	AB	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	B	2.2	2.2	1	7	EAEISHT	12303
3C7B	DB	OXIDOREDUCTASE	B	2.2	2.2	1	9	WERFFELTG	12304
3CJI	AB	VIRUS	B	2.2	2.2	1	7	LLQLARI	12305
3CJS	AB	TRANSFERASE/RIBOSOMAL PROTEIN	A	2.2	2.2	1	7	LPGLFDG	12306
3CR3	AC	TRANSFERASE	A	2.2	2.2	1	16	TSELIYAGLEAIQKRG	12307
3CR3	BC	TRANSFERASE	C	2.2	2.2	1	14	LIEGAYTASALLEA	12308
3CUQ	BD	PROTEIN TRANSPORT	D	2.2	2.2	1	19	VDTRQKQLAAWCSLVLSFC	12309
3CW2	EM	TRANSLATION	M	2.2	2.2	1	5	LDRLY	12310
3CXH	DH	OXIDOREDUCTASE	D	2.2	2.2	1	36	EHDERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKT	12311
3CXH	LP	OXIDOREDUCTASE	L	2.2	2.2	1	14	HPNRVLEHLHSTAF	12312
3CXH	PT	OXIDOREDUCTASE	T	1.1	2.2	2	27	VGTIFAGAFVFQTVFDTAITSWYENHN	12313
3D31	BD	TRANSPORT PROTEIN	D	2.2	2.2	1	13	LWKAFFFVTLPLS	12314
3D4X	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	2.2	2.2	1	19	PAVHASLDKFFSAVSTVLT	12315
3D5D	UV	RIBOSOME	U	2.2	2.2	1	42	FRKARETLFAAGNYAYAHRKRRKRDFRRLWIVRINAACRQHG	12316
3DBH	AB	CELL CYCLE	B	1.1	2.2	2	21	ASTNAVIAAVCATEVFKIATS	12317
3DBH	DJ	CELL CYCLE	D	1.1	2.2	2	15	IIARRWINGMLISLL	12318
3DBJ	CD	PHOTOSYNTHESIS	C	2.2	2.2	1	25	EEMTATCLRDLDYYLRLVTYGIVAG	12319
3DCG	BF	LIGASE/VIRAL PROTEIN	B	1.1	2.2	2	11	ALELLMAANFL	12320
3DD7	CD	RIBOSOME INHIBITOR	D	2.2	2.2	1	6	DSTNKE	12321
3DF0	AC	HYDROLASE	C	1.1	2.2	2	8	PEYRKLLE	12322
3DHR	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	2.2	2.2	1	19	PEVHASLDKFVLAVGTVLT	12323
3DHR	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	2.2	2.2	1	20	PENFRLLGDILVIILAAHFG	12324
3DIN	CD	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.1	2.2	2	18	LEWIFLIAVALITIFGII	12325
3DKN	AB	PROTEIN TRANSPORT/RNA	A	1.1	2.2	2	19	YIAPIIGTIIVFLMVVYAE	12326
3DWL	DF	STRUCTURAL PROTEIN	D	2.2	2.2	1	19	FRNTLHFHIKASKAYMHQR	12327
3DXC	CD	PROTEIN BINDING	D	1.1	2.2	2	6	PTYKFF	12328
3E3Q	YZ	IMMUNE SYSTEM	Y	2.2	2.2	1	24	AAEYYRAYLEGECVEWLHRYLKNG	12329
3E8C	EK	TRANSFERASE	E	2.2	2.2	1	9	MFSHLRRIG	12330
3ENO	AC	HYDROLASE/UNKNOWN FUNCTION	A	2.2	2.2	1	11	PLDAAVHHSEV	12331
3EPC	12	VIRAL PROTEIN	2	2.2	2.2	1	5	YQNAN	12332
3EUB	24	OXIDOREDUCTASE	2	1.1	2.2	2	7	RPILQGF	12333
3EXG	GF	OXIDOREDUCTASE	F	2.2	2.2	1	5	KILED	12334

3EYM	EF	VIRAL PROTEIN	E	2.2	2.2	1	12	YASLRSLVASSG	12335
3EYM	EF	VIRAL PROTEIN	F	1.1	2.2	2	19	LKSTQAAIDQINGKLNRVI	12336
3EZB	AB	TRANSFERASE	A	2.2	2.2	1	19	ADAAAHEVIEGQASALEEL	12337
3F1E	CN	RIBOSOME	N	2.2	2.2	1	11	RICLRELAHKG	12338
3F3P	EG	STRUCTURAL PROTEIN	G	1.1	2.2	2	14	PEIAKEIYTTLGNQ	12339
3F6Z	AB	HYDROLASE	A	1.1	2.2	2	8	VAWRNRCK	12340
3F9K	FG	VIRAL PROTEIN, RECOMBINATION	F	2.2	2.2	1	11	QEVKMVAWWIG	12341
3FCU	EF	CELL ADHESION/BLOOD CLOTTING	F	2.2	2.2	1	5	DGRLA	12342
3FKS	AD	HYDROLASE	A	2.2	2.2	1	7	AELFYKG	12343
3FKS	KP	HYDROLASE	P	2.2	2.2	1	29	MINRYSILYNRTRQAVITNELVDIITGAS	12344
3FLO	CD	TRANSFERASE	C	2.2	2.2	1	23	LQEASDVLDDQIESFTKIIQNHY	12345
3FWC	EF	CELL CYCLE, TRANSCRIPTION	E	2.2	2.2	1	12	IKNLRRVAKELG	12346
3FWC	FH	CELL CYCLE, TRANSCRIPTION	H	1.1	2.2	2	18	DSTRETVLKQIREFLEEI	12347
3G3A	CF	HYDROLASE/IMMUNE SYSTEM	F	2.2	2.2	1	5	VQAWI	12348
3G6J	AB	IMMUNE SYSTEM	B	2.2	2.2	1	5	KYELD	12349
3GE8	DH	OXIDOREDUCTASE	H	2.2	2.2	1	7	LADQALH	12350
3GHG	JL	BLOOD CLOTTING	L	1.1	2.2	2	29	IRYLQEIYNSNNQKIVNLKEKVAQLEAQC	12351
3GHG	KL	BLOOD CLOTTING	K	1.1	2.2	2	27	RVLRSILENLRSKIQKLESDVSAQMEY	12352
3GJX	CA	PROTEIN TRANSPORT	A	1.1	2.2	2	18	KVYIGKLNMILVQILKQE	12353
3GLI	DE	TRANSFERASE/DNA	D	1.1	2.2	2	14	RRMGVEMTLLRALA	12354
3H0L	MN	LIGASE	M	2.2	2.2	1	13	IFEMYARTRDEGF	12355
3H0L	QR	LIGASE	R	2.2	2.2	1	7	REKALMN	12356
3H2V	DH	CELL ADHESION	D	1.1	2.2	2	30	TKRALIQCAKDIAKASDEVTRLAKEVAKQC	12357
3H4P	Bb	HYDROLASE	b	2.2	2.2	1	6	LYKMRT	12358
3HAE	PS	IMMUNE SYSTEM	P	1.1	2.2	2	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	12359
3HEI	EF	TRANSFERASE/SIGNALING PROTEIN	E	2.2	2.2	1	6	SSDFEA	12360
3HH2	BD	SIGNALING PROTEIN/CYTOKINE	D	2.2	2.2	1	10	DNTLFKWMIF	12361
3HKZ	AB	TRANSFERASE	A	2.2	2.2	1	5	LEDVS	12362
3HKZ	AC	TRANSFERASE	C	1.1	2.2	2	6	IGIVAA	12363
3HO5	BH	SIGNALING PROTEIN	B	1.1	2.2	2	6	LDDMEE	12364
3HOU	NW	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	W	2.2	2.2	1	12	HTLGNLIRAELL	12365
3HRW	CD	OXYGEN TRANSPORT	C	1.1	2.2	2	16	PVNFKLLSHCLLVTLA	12366
6RLX	CB	HORMONE (MUSCLE RELAXANT)	B	1.1	2.2	2	14	RELVRAQIAICGMS	12367
1A4J	LH	IMMUNOGLOBULIN	L	2.1	2.1	1	6	DEQLKS	12368
1A9W	AF	OXYGEN TRANSPORT	F	2.1	2.1	1	7	PWTQRFF	12369
1AGR	DH	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	H	2.1	2.1	1	6	SYRRFL	12370
1AHJ	GH	LYASE	H	2.1	2.1	1	7	PRHYMMT	12371
1AJS	AB	AMINOTRANSFERASE	A	1.1	2.1	2	17	PDSILRVLSQMQKIVRV	12372

1ALL	AB	LIGHT HARVESTING PROTEIN	A	1.1	2.1	2	13	PGELDRIKSFVTS	12373
1AOI	BD	DNA BINDING PROTEIN/DNA	B	2.1	2.1	1	12	AMDVVYALKRQG	12374
1AWC	AB	TRANSCRIPTION/DNA	A	1.1	2.1	2	19	AAELNRLVIECEQKKLARM	12375
1AZZ	AC	COMPLEX (SERINE PROTEASE/INHIBITOR)	A	2.1	2.1	1	6	AHCMDG	12376
1B33	CD	PHOTOSYNTHESIS	C	2.1	2.1	1	14	GEKRLRIAQILTDN	12377
1B33	HI	PHOTOSYNTHESIS	H	2.1	2.1	1	14	GEKRLRIAQILTDN	12378
1B4U	AB	DIOXYGENASE	A	2.1	2.1	1	10	AENRERFKAD	12379
1BXN	AI	LYASE	I	1.1	2.1	2	14	DEQITKQLEYCLNQ	12380
1BXN	GL	LYASE	G	2.1	2.1	1	16	ILNEGPEILRDAARWC	12381
1BXN	GL	LYASE	L	1.1	2.1	2	14	DEQITKQLEYCLNQ	12382
1D3B	GH	RNA BINDING PROTEIN	G	2.1	2.1	1	9	PIKVLHEAE	12383
1D3B	KL	RNA BINDING PROTEIN	K	2.1	2.1	1	8	PIKVLHEA	12384
1DFL	AY	CONTRACTILE PROTEIN	Y	2.1	2.1	1	10	DKELTAMLKE	12385
1DFL	BW	CONTRACTILE PROTEIN	W	2.1	2.1	1	10	DKELTAMLKE	12386
1DS6	AB	SIGNALING PROTEIN	A	2.1	2.1	1	19	PASYENVRAKWFPEVRHHC	12387
1DX5	DP	SERINE PROTEINASE	P	1.1	2.1	2	11	KKWIQKVIDQF	12388
1DX5	PL	SERINE PROTEINASE	L	2.1	2.1	1	5	ECENG	12389
1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.1	2.1	1	15	AGKNRETIAAQFAQG	12390
1E3D	CD	HYDROGENASE	C	2.1	2.1	1	8	GCSEALLR	12391
1E6E	AB	OXIDOREDUCTASE	A	2.1	2.1	1	16	RPRKRLMELLLRTATE	12392
1E6V	EF	OXIDOREDUCTASE	F	1.1	2.1	2	20	EELLQVVQRIHELRTLAGYR	12393
1E6Y	AC	OXIDOREDUCTASE	C	1.1	2.1	2	12	PYFRSYFAAINF	12394
1E6Y	BF	OXIDOREDUCTASE	F	2.1	2.1	1	20	AEVVEWVHRIFDQRTKFGFQ	12395
1E6Y	DF	OXIDOREDUCTASE	F	2.1	2.1	1	11	SVAANRRKHMS	12396
1E7P	DE	OXIDOREDUCTASE	D	2.1	2.1	1	16	VFKIKNRMKDVMDDNV	12397
1E7P	GH	OXIDOREDUCTASE	G	2.1	2.1	1	16	VFKIKNRMKDVMDDNV	12398
1E7P	JK	OXIDOREDUCTASE	J	2.1	2.1	1	16	VFKIKNRMKDVMDDNV	12399
1E7P	JK	OXIDOREDUCTASE	K	1.1	2.1	2	13	IFIVLNMIRETYD	12400
1ED3	AC	IMMUNE SYSTEM	A	2.1	2.1	1	13	TCVEWLSRYLELG	12401
1ED3	DF	IMMUNE SYSTEM	D	2.1	2.1	1	13	FAAQITRNKWERA	12402
1EM8	CD	GENE REGULATION	D	1.1	2.1	2	10	PLVSDVLRAL	12403
1EQZ	AB	STRUCTURAL PROTEIN/DNA	A	2.1	2.1	1	7	EELNKLL	12404
1EQZ	EF	STRUCTURAL PROTEIN/DNA	F	2.1	2.1	1	12	SREIQTAVRLLL	12405
1EUC	AB	LIGASE	A	2.1	2.1	1	14	GTLTYEAVHQTTQV	12406
1EYX	AB	PHOTOSYNTHESIS	B	2.1	2.1	1	14	GNKRLDAVNYIVSN	12407
1F66	CD	STRUCTURAL PROTEIN/DNA	C	2.1	2.1	1	10	VGRIHRHLKS	12408
1F80	BD	TRANSFERASE	B	2.1	2.1	1	6	FAERIL	12409
1F93	AF	TRANSCRIPTION	F	1.1	2.1	2	13	QLQTELLAALLES	12410
1F93	BE	TRANSCRIPTION	E	1.1	2.1	2	13	QLQTELLAALLES	12411

1FM0	DE	TRANSFERASE	E	2.1	2.1	1	17	MTEKALAEIVDEARNRW	12412
1FNS	LA	IMMUNE SYSTEM	A	2.1	2.1	1	11	FVRYVQGLKKK	12413
1FNT	FG	HYDROLASE/HYDROLASE ACTIVATOR	G	2.1	2.1	1	13	FQVEYAVKAVENG	12414
1FQV	AB	LIGASE	A	2.1	2.1	1	9	LPELLKVSG	12415
1FQV	KL	LIGASE	L	1.1	2.1	2	8	PEEIRKTF	12416
1FQV	MN	LIGASE	M	2.1	2.1	1	10	DELLLGIFSC	12417
1FS0	EG	HYDROLASE	G	1.1	2.1	2	19	LNINLFKKLLAEMKTWTDK	12418
1FS1	CD	LIGASE	C	2.1	2.1	1	10	DELLLGIFSC	12419
1FYZ	CE	OXIDOREDUCTASE	C	2.1	2.1	1	10	WNESAFSVHA	12420
1G0U	12	HYDROLASE	1	2.1	2.1	1	20	ISDMQHIERLLKDLVTENAY	12421
1G0U	AH	HYDROLASE	H	1.1	2.1	2	22	AADTEAVTQLIGSNIELHSLYT	12422
1G0U	M2	HYDROLASE	2	2.1	2.1	1	19	KEETVDFIKHSLSQAIKWD	12423
1G20	AB	OXIDOREDUCTASE	A	2.1	2.1	1	7	EKDIVFG	12424
1G20	CH	OXIDOREDUCTASE	H	2.1	2.1	1	15	AGRGVITAINFLEEE	12425
1G2C	IJ	VIRAL PROTEIN	I	1.1	2.1	2	45	EVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	12426
1G3I	UN	CHAPERONE/HYDROLASE	N	2.1	2.1	1	16	ADAFTLFELFERKLEM	12427
1GCV	CD	OXYGEN STORAGE/TRANSPORT	D	2.1	2.1	1	19	PHIQGIWDKFFEVVIDAIS	12428
1GX7	AD	OXIDOREDUCTASE	A	2.1	2.1	1	7	TYGAERM	12429
1GXS	AB	LYASE	A	1.1	2.1	2	14	GHFIPQLSQVVYRN	12430
1GXS	AD	LYASE	A	2.1	2.1	1	14	DHEDMIGMFESWWH	12431
1GZS	DC	TOXIN/CELL CYCLE	D	2.1	2.1	1	16	IAPFLQEIGEAAKNAG	12432
1H0H	KL	DEHYDROGENASE	K	2.1	2.1	1	13	PISFKWVMRAKDK	12433
1H2R	SL	OXIDOREDUCTASE	L	2.1	2.1	1	6	LEIILK	12434
1H4J	CD	OXIDOREDUCTASE	D	2.1	2.1	1	5	PKELN	12435
1HDM	AB	IMMUNE SYSTEM	A	2.1	2.1	1	6	PEFADW	12436
1HR0	GK	RIBOSOME	K	2.1	2.1	1	18	PYAAQLAALDAAKKAMAY	12437
1HV4	EH	OXYGEN STORAGE/TRANSPORT	E	2.1	2.1	1	19	PVNFKFLGHCFLVVVAIHH	12438
1HV4	GH	OXYGEN STORAGE/TRANSPORT	G	1.1	2.1	2	19	PVNFKFLGHCFLVVVAIHH	12439
1HYR	BC	IMMUNE SYSTEM	C	1.1	2.1	2	21	KTHYHAMHADCLQELRRYLKS	12440
1I3O	AB	APOPTOSIS	B	2.1	2.1	1	13	WFIQSLCAMLKQY	12441
1I3Q	AE	TRANSCRIPTION	A	2.1	2.1	1	19	IEAGRAALYKEVYNVIASD	12442
1I3R	EF	IMMUNE SYSTEM	F	2.1	2.1	1	12	ELGRPDAENWNS	12443
1I7M	BA	LYASE	B	2.1	2.1	1	11	RSEWDILLKDV	12444
1I7W	AB	CELL ADHESION	A	2.1	2.1	1	16	INVVTCAAGILSNLTC	12445
1IAK	BP	HISTOCOMPATIBILITY ANTIGEN I-AK	B	2.1	2.1	1	14	ELGRPDAEYWNKQY	12446
1IBR	CD	CELL CYCLE, TRANSLATION	C	2.1	2.1	1	5	FHRKK	12447
1ICE	AB	CYTOKINE	A	2.1	2.1	1	11	LEEAQRIWKQK	12448
1IR2	HP	LYASE	H	2.1	2.1	1	21	NAPGAAANRVALEACTQARNE	12449
1IR2	V3	LYASE	V	1.1	2.1	2	14	AKNYGRAVYECLRG	12450
1IRU	KL	HYDROLASE	L	2.1	2.1	1	15	VAAASKLLANMVYQY	12451

1IRU	OU	HYDROLASE	U	1.1	2.1	2	15	LKHLADRVAMYVHAY	12452
1IRU	YZ	HYDROLASE	Z	2.1	2.1	1	15	VAAASKLLANMVYQY	12453
1IW7	MN	TRANSFERASE	M	2.1	2.1	1	13	IEGRNAAYEAIIK	12454
1IWA	MH	LYASE	H	2.1	2.1	1	15	PAAVLFEINACRKAR	12455
1IWP	AG	LYASE	A	2.1	2.1	1	11	GLDIVGALSRS	12456
1IWP	AG	LYASE	A	2.1	2.1	1	10	MIDRFIADYA	12457
1IZN	AB	PROTEIN BINDING	B	2.1	2.1	1	12	DQQLDCALDLMR	12458
1J19	AB	CELL ADHESION	B	2.1	2.1	1	5	VLAAW	12459
1J34	AC	PROTEIN BINDING/BLOOD CLOTTING	C	2.1	2.1	1	5	WKQYV	12460
1JB0	BL	PHOTOSYNTHESIS	L	2.1	2.1	1	27	ANLGGLISGIALILVATACLAAYGLVS	12461
1JB0	BX	PHOTOSYNTHESIS	X	1.1	2.1	2	21	FRTFWAVLLLAINFLVAAYYF	12462
1JB0	CD	PHOTOSYNTHESIS	D	1.1	2.1	2	15	KEQCLALAAQQLRPR	12463
1JD2	FG	HYDROLASE	G	2.1	2.1	1	11	YQVEYAFKATN	12464
1JD2	MU	HYDROLASE	U	2.1	2.1	1	19	KEETVDFIKHSLSQAIKWD	12465
1JFI	AB	TRANSCRIPTION/DNA	B	1.1	2.1	2	12	PEHVIQALESLG	12466
1JH4	AB	RNA BINDING PROTEIN	A	2.1	2.1	1	9	AGKITGMLL	12467
1JK0	AB	OXIDOREDUCTASE	B	1.1	2.1	2	13	HEIWAAYKKVEAS	12468
1JMU	FI	VIRAL PROTEIN	I	2.1	2.1	1	9	VEKIRYALG	12469
1JNR	CD	OXIDOREDUCTASE	C	2.1	2.1	1	12	LEDYVRYVTLDM	12470
1JPW	CF	CELL ADHESION	C	2.1	2.1	1	10	YKNKMMVCQV	12471
1JRO	EF	OXIDOREDUCTASE	E	2.1	2.1	1	20	AAYRMNAAQAMALRYVRELS	12472
1JSD	AB	VIRAL PROTEIN	A	2.1	2.1	1	11	LEELRSLFSSA	12473
1JY7	CD	OXYGEN STORAGE/TRANSPORT	C	2.1	2.1	1	19	PAVHASLDKFLASVSTVLT	12474
1K4C	AC	MEMBRANE PROTEIN	C	2.1	2.1	1	29	LHWRAAGAATVLLVIVLLAGSYLAVLAER	12475
1K8I	AB	IMMUNE SYSTEM	B	2.1	2.1	1	13	SRLAEIISNILNE	12476
1KCG	AC	IMMUNE SYSTEM	C	1.1	2.1	2	23	DAWGKQLEMLREVGQRLRLELAD	12477
1KF6	MN	OXIDOREDUCTASE	M	2.1	2.1	1	26	TDLLYTIELGHGLNVAECMAHSAMAR	12478
1KF9	AB	HORMONE/GROWTH FACTOR	A	2.1	2.1	1	7	KEETQQK	12479
1KFY	CD	OXIDOREDUCTASE	D	2.1	2.1	1	29	FIGRVFLFLMIVLPLWCGLHRMHHAMHDL	12480
1KQS	FL	RIBOSOME	F	2.1	2.1	1	13	EEIVMHIPELADE	12481
1KX4	BD	STRUCTURAL PROTEIN/DNA	D	2.1	2.1	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	12482
1KYO	BR	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.1	2.1	2	12	ALKLVRESELLG	12483
1L1O	DE	DNA BINDING PROTEIN	D	2.1	2.1	1	14	LGLYNEAVKIIHDF	12484
1LOC	GH	LECTIN	H	2.1	2.1	1	5	LKEFV	12485
1LTX	AB	TRANSFERASE/PROTEIN BINDING	A	2.1	2.1	1	11	QSAWFYHRWLL	12486
1LWU	GI	BLOOD CLOTTING	G	1.1	2.1	2	37	NMQLQQLTLLQHNIKTQVSQILRVEVDIDVALRACKG	12487
1M8Q	AB	CONTRACTILE PROTEIN	B	1.1	2.1	2	12	FTVFLTMFGEKL	12488
1MIO	AB	MOLYBDENUM-IRON PROTEIN	B	2.1	2.1	1	7	CLSETLG	12489
1MJG	AM	OXIDOREDUCTASE	M	2.1	2.1	1	13	MVKTAAAFGAIFT	12490

1MJG	AN	OXIDOREDUCTASE	N	2.1	2.1	1	30	VALFREVYHGAITATSYAEILLNQAIRTYG	12491
1MJG	BN	OXIDOREDUCTASE	N	2.1	2.1	1	13	MVKTAAAFGAIFT	12492
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	G	2.1	2.1	1	11	DTRDAWVNKIA	12493
1MPA	LH	COMPLEX (IMMUNOGLOBULIN/PEPTIDE)	L	1.1	2.1	2	7	SEQLTSG	12494
1MTY	EH	MONOOXYGENASE	E	2.1	2.1	1	8	LSEVIAEL	12495
1NGM	MN	TRANSCRIPTION/DNA	N	2.1	2.1	1	6	ADFLLE	12496
1NIW	GH	SIGNALING PROTEIN/OXIDOREDUCTASE	G	1.1	2.1	2	15	EEQIAEFKEAFSLFD	12497
1NMU	CB	SUGAR BINDING PROTEIN/RIBOSOME	C	2.1	2.1	1	7	PFTWDAV	12498
1NT2	AB	RNA BINDING PROTEIN	B	1.1	2.1	2	22	KDYYRILRKTALAVSEKMVEKE	12499
1NTK	AB	OXIDOREDUCTASE	A	2.1	2.1	1	8	YAQALQSV	12500
1NTK	FG	OXIDOREDUCTASE	F	1.1	2.1	2	20	ENLYDDRVFRIKRALDLSMR	12501
1O18	A8	CONTRACTILE PROTEIN	8	2.1	2.1	1	12	SVWIGGSILASL	12502
1O18	GH	CONTRACTILE PROTEIN	H	2.1	2.1	1	8	NICYVITH	12503
1OAO	AD	OXIDOREDUCTASE	D	2.1	2.1	1	13	MVKTAAAFGAIFT	12504
1OAO	BD	OXIDOREDUCTASE	D	2.1	2.1	1	30	VALFREVYHGAITATSYAEILLNQAIRTYG	12505
1OCC	PU	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	U	2.1	2.1	1	20	TRNCWQNYLDFHRCEKAMTA	12506
1OED	BC	ION CHANNEL/RECEPTOR	B	2.1	2.1	1	28	SLSISALLAVTVFLLLLADKVPETSLSV	12507
1OUU	AB	OXYGEN TRANSPORT	B	1.1	2.1	2	16	IDEIGPLALARVLIVY	12508
1OUU	CD	OXYGEN TRANSPORT	D	1.1	2.1	2	19	DNFRVLADVLTIVIAAKFG	12509
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	2.1	2.1	1	15	IWPHIDWLTAFSIRY	12510
1Q5Q	AI	HYDROLASE	I	2.1	2.1	1	23	AGIAIELVRLFAVELEHYEKIEG	12511
1Q5R	DK	HYDROLASE	K	2.1	2.1	1	7	FTDYLRG	12512
1Q86	HN	RIBOSOME	H	2.1	2.1	1	12	EIVMHIPELADE	12513
1QO0	AD	BINDING PROTEIN	A	1.1	2.1	2	16	IYPRESNHVMRHLYRQ	12514
1QVI	AY	CONTRACTILE PROTEIN	Y	2.1	2.1	1	8	DKELTAML	12515
1QVI	AZ	CONTRACTILE PROTEIN	A	2.1	2.1	1	26	YKKLQDQRIGLSVIQRNIRKWLVLRN	12516
1R4M	AB	CELL CYCLE	A	2.1	2.1	1	32	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS	12517
1R5V	FD	SIGNALING PROTEIN	D	2.1	2.1	1	9	RPDAENWNS	12518
1R5W	CD	SIGNALING PROTEIN	C	2.1	2.1	1	5	EEFAK	12519
1RCO	LF	LYASE	L	1.1	2.1	2	14	AKNYGRAVYECLRG	12520
1RDT	AD	HORMONE/GROWTH FACTOR	D	1.1	2.1	2	23	VKPIEDIQDNLLQALELQLKLNH	12521
1RYP	IJ	MULTICATALYTIC PROTEINASE	J	2.1	2.1	1	15	PETFTQLVSSSLYER	12522
1RYP	KZ	MULTICATALYTIC PROTEINASE	K	2.1	2.1	1	19	TEEGLDLLKLCVQELEKRM	12523
1RYP	T2	MULTICATALYTIC PROTEINASE	2	2.1	2.1	1	18	PSYIFEYLATVMYQRRSK	12524
1RZI	KF	IMMUNE SYSTEM	K	1.1	2.1	2	7	DEQLKSG	12525

1RZR	CT	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	T	2.1	2.1	1	5	IMGVM	12526
1S1H	CN	RIBOSOME	C	2.1	2.1	1	19	LVADGVFYAELNEFFTREL	12527
1S5L	AT	PHOTOSYNTHESIS	T	2.1	2.1	1	8	ETITYVFI	12528
1S5L	BD	PHOTOSYNTHESIS	D	1.1	2.1	2	20	LFVPVTGLWMSAIGVVGLAL	12529
1SB3	AC	OXIDOREDUCTASE	C	2.1	2.1	1	10	LLDYLRETVG	12530
1SB3	DF	OXIDOREDUCTASE	F	2.1	2.1	1	10	LLDYLRETVG	12531
1SQX	EK	OXIDOREDUCTASE	K	2.1	2.1	1	19	VPTASLWGAVGAVGLVWAT	12532
1SVX	AB	DE NOVO PROTEIN/SUGAR BINDING PROTEIN	B	1.1	2.1	2	14	WEEIPALDKELKAK	12533
1SXJ	CD	REPLICATION	C	1.1	2.1	2	19	EETRVHLLTKLADIEYSIS	12534
1SY9	AB	CALCIUM-BINDING PROTEIN	B	2.1	2.1	1	17	FRRIARLVGVLREWAYR	12535
1T0J	BC	SIGNALING PROTEIN	B	2.1	2.1	1	18	EVTDMMQKALFDFLKHRF	12536
1T3Q	AB	OXIDOREDUCTASE	B	1.1	2.1	2	22	PMIVEGQIRGGIAQAIGQTLLE	12537
1T3Q	EF	OXIDOREDUCTASE	F	2.1	2.1	1	25	RDLRLSLAKAITQRVILKAAQGAMY	12538
1TI2	EF	OXIDOREDUCTASE	E	2.1	2.1	1	13	ACEIRALARQWAK	12539
1TI2	GH	OXIDOREDUCTASE	H	2.1	2.1	1	6	RCAHNC	12540
1TIL	AB	TRANSCRIPTION	A	1.1	2.1	2	9	MGFTIMENF	12541
1TIL	AB	TRANSCRIPTION	A	2.1	2.1	1	23	MDELTEIKTVVSEAVTNAIIHGY	12542
1TQY	CD	TRANSFERASE	D	2.1	2.1	1	17	QAGGLDALGHARRTIRR	12543
1TU3	BF	PROTEIN TRANSPORT	F	1.1	2.1	2	33	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	12544
1TU3	DI	PROTEIN TRANSPORT	D	1.1	2.1	2	6	LAPMYY	12545
1U35	FH	STRUCTURAL PROTEIN/DNA	H	1.1	2.1	2	12	SREVQTAVRLLL	12546
1U6H	AB	CELL ADHESION	A	1.1	2.1	2	46	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTV	12547
1U9I	BC	CIRCADIAN CLOCK PROTEIN	C	2.1	2.1	1	17	NNAFRQFVIGVTGYAKQ	12548
1UKL	BF	PROTEIN TRANSPORT/DNA BINDING PROTEIN	B	2.1	2.1	1	12	TAWTVGRICELL	12549
1UZH	RM	LYASE	M	2.1	2.1	1	14	DEQIAAQVDYIVAN	12550
1V54	PT	OXIDOREDUCTASE	P	1.1	2.1	2	29	RKHMLQALFITITLGVYFTLLQASEYYEA	12551
1VF5	PT	PHOTOSYNTHESIS	P	1.1	2.1	2	25	PNRVKWMIAFICLVMLAQLMLILKK	12552
1VF5	PU	PHOTOSYNTHESIS	P	1.1	2.1	2	25	PNRVKWMIAFICLVMLAQLMLILKK	12553
1VSA	OP	RIBOSOME	O	2.1	2.1	1	12	TLFAAGNYAYAH	12554
1VZJ	EJ	HYDROLASE	E	2.1	2.1	1	6	HWKNQF	12555
1WYU	CD	OXIDOREDUCTASE	C	2.1	2.1	1	5	GEFLT	12556
1WYU	CD	OXIDOREDUCTASE	D	2.1	2.1	1	5	IFERS	12557
1WYU	GH	OXIDOREDUCTASE	G	2.1	2.1	1	8	PVVQALAA	12558
1WYU	GH	OXIDOREDUCTASE	H	1.1	2.1	2	19	QGALRLMWELGEYLKALTG	12559
1WYU	GH	OXIDOREDUCTASE	H	2.1	2.1	1	5	IFERS	12560
1XD2	BC	SIGNALING PROTEIN	C	2.1	2.1	1	23	PNLLKMIRHTTNLTLWFEKCIVE	12561
1XD2	BC	SIGNALING PROTEIN	C	1.1	2.1	2	13	FGIYLTNILKTEE	12562

1XL3	BC	CELL INVASION	B	2.1	2.1	1	9	IYAIWSDLQ	12563
1XLS	BF	TRANSCRIPTION	B	2.1	2.1	1	16	IFDRVLTELVSKMRDM	12564
1XMQ	CN	RIBOSOME	N	2.1	2.1	1	11	RICLRELAHKG	12565
1XTC	CE	TOXIN	E	2.1	2.1	1	16	DSQKKAIERMKDTLRI	12566
1XV9	BF	DNA BINDING PROTEIN	B	2.1	2.1	1	12	IEDQISLLKGAA	12567
1YA7	FM	HYDROLASE/HYDROLASE ACTIVATOR	F	2.1	2.1	1	23	VADARVLVDFARISAQQEKVTYG	12568
1YA7	GN	HYDROLASE/HYDROLASE ACTIVATOR	G	2.1	2.1	1	23	VADARVLVDFARISAQQEKVTYG	12569
1YD8	VG	PROTEIN TRANSPORT, CHROMOSOMALPROTEIN	G	2.1	2.1	1	26	DGDRELMKELFDQCENKRRTLFKLAS	12570
1YE9	DF	OXIDOREDUCTASE	F	1.1	2.1	2	18	PLLQGRLFSYTDTQISRL	12571
1YE9	DH	OXIDOREDUCTASE	H	2.1	2.1	1	7	FFAENEQ	12572
1YEW	BC	OXIDOREDUCTASE, MEMBRANE PROTEIN	C	2.1	2.1	1	8	PSHIIEFY	12573
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	2.1	2.1	1	34	HAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT	12574
1YHU	QT	OXYGEN STORAGE/TRANSPORT	Q	2.1	2.1	1	16	MLERAKVKDEWAKAYG	12575
1YHU	RS	OXYGEN STORAGE/TRANSPORT	R	1.1	2.1	2	15	PLQRLKVKRQWAEAY	12576
1YKE	AB	GENE REGULATION	B	2.1	2.1	1	28	EEFSNTIDELSTDIILKTRQINKLIDSL	12577
1YNJ	CD	TRANSFERASE	D	2.1	2.1	1	22	EKTARLLDALKYYGFTLSTTSG	12578
1YQ3	CD	OXIDOREDUCTASE	D	1.1	2.1	2	26	AASLHWTSERAVSALLLGLLPAAYLY	12579
1YU6	AC	HYDROLASE	A	2.1	2.1	1	14	YSGIVSGIEWATTN	12580
1Z6O	FV	METAL BINDING PROTEIN	F	2.1	2.1	1	16	LSLALYVFDEYLQKTV	12581
1Z6O	LQ	METAL BINDING PROTEIN	L	2.1	2.1	1	16	LSLALYVFDEYLQKTV	12582
1Z7Q	AH	HYDROLASE/HYDROLASE ACTIVATOR	A	2.1	2.1	1	21	IPDARNAALRAKAEAAEFRYK	12583
1Z7Q	MN	HYDROLASE/HYDROLASE ACTIVATOR	M	2.1	2.1	1	22	AADGDALVKRFKNSVKWYHFDH	12584
1Z7Q	RY	HYDROLASE/HYDROLASE ACTIVATOR	R	1.1	2.1	2	21	NADSRILIEKARVEAQSHRLT	12585
1Z7Q	Vb	HYDROLASE/HYDROLASE ACTIVATOR	V	2.1	2.1	1	15	TETAASVFKELCYEN	12586
1Z8U	CD	ELECTRON TRANSPORT	D	2.1	2.1	1	19	PVNFKLLSHCLLVTLAAHL	12587
1ZBB	cd	STRUCTURAL PROTEIN/DNA	d	2.1	2.1	1	12	SREIQTAVRLLL	12588
1ZBB	CD	STRUCTURAL PROTEIN/DNA	D	2.1	2.1	1	12	SREIQTAVRLLL	12589
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	D	2.1	2.1	1	12	SREIQTAVRLLL	12590
1ZLA	GK	PROTEIN BINDING/VIRUS/DNA	G	1.1	2.1	2	29	AGAPVYLAAVLEYLTAEILELAGNWERDN	12591
1ZOY	BD	OXIDOREDUCTASE	D	2.1	2.1	1	26	AASLHWTGERVVSVLLLGLLPAAYLN	12592
1ZRT	PE	OXIDOREDUCTASE/METAL TRANSPORT	P	2.1	2.1	1	11	IGPSIQAWLLG	12593
2A1J	AB	DNA BINDING PROTEIN	B	1.1	2.1	2	13	PQKARRLFDVLHE	12594
2A5Y	AB	APOPTOSIS	A	2.1	2.1	1	8	FSLYQDVV	12595
2ABZ	BE	HYDROLASE/HYDROLASE INHIBITOR	E	2.1	2.1	1	7	PWAREGA	12596
2ACZ	BD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	2.1	2.1	1	30	AFTKVFTLLALFSILIHAWIGMWQVLTDYV	12597

2AFH	CB	OXIDOREDUCTASE	B	2.1	2.1	1	5	HTWLH	12598
2AHM	DH	VIRAL PROTEIN, REPLICATION	H	2.1	2.1	1	12	DALNNIINNARD	12599
2AJQ	AB	TRANSFERASE,TRANSCRIPTION/DNA	B	2.1	2.1	1	6	GPCKMI	12600
2AJQ	FI	TRANSFERASE,TRANSCRIPTION/DNA	I	2.1	2.1	1	6	GPCKMI	12601
2AKW	AB	LIGASE	A	2.1	2.1	1	16	MAHLKGAIYELAQALF	12602
2AKW	AB	LIGASE	B	1.1	2.1	2	9	PEYANRLLG	12603
2AUH	AB	TRANSFERASE/SIGNALING PROTEIN	A	1.1	2.1	2	16	LRERIEFLNEASVMKG	12604
2AXT	CK	ELECTRON TRANSPORT	C	2.1	2.1	1	14	TFPFFVVGVVHLIS	12605
2B5I	AD	CYTOKINE/CYTOKINE RECEPTOR	A	2.1	2.1	1	10	LKPLEEVLNL	12606
2BO9	CD	HYDROLASE	D	2.1	2.1	1	18	YPASRAALVAQNYINYQQ	12607
2BS4	DE	OXIDOREDUCTASE	D	2.1	2.1	1	16	VFKIKNRMKDVMDDNV	12608
2BTW	AB	TRANSFERASE	B	2.1	2.1	1	7	EDFFPLS	12609
2CZV	BC	HYDROLASE	B	1.1	2.1	2	21	PYERANLLRFMMKAWKLVEKY	12610
2D1P	DE	TRANSLATION	D	2.1	2.1	1	7	VAAALRR	12611
2D1P	EI	TRANSLATION	E	2.1	2.1	1	7	DGVFQLL	12612
2D1P	GH	TRANSLATION	G	2.1	2.1	1	11	LGALAEASLTC	12613
2D1P	HI	TRANSLATION	H	1.1	2.1	2	11	ADALRRELANY	12614
2D2M	BC	OXYGEN STORAGE/TRANSPORT	B	2.1	2.1	1	23	SEFQAHSLRVLGGLDMCVASLDD	12615
2D74	AB	TRANSLATION	A	2.1	2.1	1	16	KEKALENYRQIKEFIK	12616
2DEN	AB	PROTEIN BINDING	A	2.1	2.1	1	12	DELSLRALQATG	12617
2DFK	CB	CELL CYCLE	B	2.1	2.1	1	10	PSTIEKLAKN	12618
2DSQ	BI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	2.1	2.1	1	12	AELVDALQFVCG	12619
2DXB	BC	HYDROLASE	C	2.1	2.1	1	10	PNYRRRLVRW	12620
2DXB	EI	HYDROLASE	I	2.1	2.1	1	16	DFEILEMAVRELAIEK	12621
2DXB	HF	HYDROLASE	F	2.1	2.1	1	16	DFEILEMAVRELAIEK	12622
2DXB	NO	HYDROLASE	O	2.1	2.1	1	6	RDCLIG	12623
2E5L	EH	RIBOSOME	E	2.1	2.1	1	8	KADVERLR	12624
2EFC	AD	TRANSPORT PROTEIN	A	2.1	2.1	1	19	EEELDSAGDGLEKYVMTKL	12625
2EHO	AB	REPLICATION	B	1.1	2.1	2	35	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW	12626
2EHO	AC	REPLICATION	C	2.1	2.1	1	10	LWLAINLKQR	12627
2EQ9	DF	OXIDOREDUCTASE	D	2.1	2.1	1	14	AGELIAEAALALEM	12628
2F9Y	AB	LIGASE	A	2.1	2.1	1	6	RPRLKE	12629
2FFD	DF	BLOOD CLOTTING	D	1.1	2.1	2	20	RAQLVDMKRLEVDIDIKIRS	12630
2FHH	OV	HYDROLASE	V	2.1	2.1	1	14	FAGKINRLAIMVRG	12631
2FHJ	CD	TRANSFERASE	C	2.1	2.1	1	17	QPAGLQAAEAAVDAIKG	12632
2FHJ	CD	TRANSFERASE	D	2.1	2.1	1	17	QPAGLQAAEAAVDAIKG	12633
2FHX	AB	HYDROLASE, METAL BINDING PROTEIN	B	2.1	2.1	1	11	EDLKRRILSSH	12634

2FK0	CF	VIRAL PROTEIN	F	2.1	2.1	1	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQL	12635
2FK0	GH	VIRAL PROTEIN	H	1.1	2.1	2	23	KESTQKAIDGVTNKVNSIIDKMN	12636
2FRV	AB	OXIDOREDUCTASE	B	2.1	2.1	1	6	LEMILK	12637
2FRV	CD	OXIDOREDUCTASE	D	2.1	2.1	1	6	LEMILK	12638
2FRV	EF	OXIDOREDUCTASE	F	2.1	2.1	1	6	LEMILK	12639
2FRV	GH	OXIDOREDUCTASE	H	2.1	2.1	1	6	LEMILK	12640
2FRV	IJ	OXIDOREDUCTASE	J	2.1	2.1	1	6	LEMILK	12641
2FRV	SL	OXIDOREDUCTASE	L	2.1	2.1	1	6	LEMILK	12642
2FUG	AC	OXIDOREDUCTASE	A	1.1	2.1	2	16	EKDVENLEALLPLIEG	12643
2FUN	CD	APOPTOSIS/HYDROLASE	D	2.1	2.1	1	15	ILTILTEVNYEVSNK	12644
2FYN	DC	OXIDOREDUCTASE	D	2.1	2.1	1	11	IGHSIQTWLLG	12645
2FYN	JK	OXIDOREDUCTASE	J	2.1	2.1	1	7	IEEDFNA	12646
2G5B	EF	APOPTOSIS	E	2.1	2.1	1	6	SEQLTS	12647
2G77	AB	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	B	2.1	2.1	1	5	SMVQH	12648
2GBW	EF	OXIDOREDUCTASE	E	2.1	2.1	1	8	GYHVGWTH	12649
2GL7	AB	TRANSCRIPTION	A	2.1	2.1	1	16	INVVTCAAGILSNLTC	12650
2GL7	AB	TRANSCRIPTION	A	2.1	2.1	1	10	YKNKMMVCQV	12651
2GL7	DE	TRANSCRIPTION	D	1.1	2.1	2	17	WPLIKATVGLIRNLALC	12652
2GTL	AD	OXYGEN STORAGE/TRANSPORT	D	1.1	2.1	2	19	PEFGAHSQRVLSGLDITIS	12653
2GTL	IL	OXYGEN STORAGE/TRANSPORT	L	2.1	2.1	1	14	PDMLAAQLAHLKVQ	12654
2H62	BC	HORMONE/GROWTH FACTOR	B	1.1	2.1	2	13	NHAIVQTLVNSVN	12655
2H9E	HC	HYDROLASE, BLOOD CLOTTING	H	2.1	2.1	1	8	LKWIDRSM	12656
2HLD	LO	HYDROLASE	L	2.1	2.1	1	7	AELFYKG	12657
2HOD	JL	BLOOD CLOTTING	J	1.1	2.1	2	26	LLQKNVRAQLVDMKRLEVDIDIKIRS	12658
2HT9	AX	OXIDOREDUCTASE	A	2.1	2.1	1	14	SYCTMAKKLFHDMN	12659
2HYB	EF	TRANSFERASE	E	2.1	2.1	1	11	SARVSELMNES	12660
2HYE	CD	PROTEIN BINDING	C	2.1	2.1	1	16	PEMIKLQEVFKAFYLG	12661
2HYE	CD	PROTEIN BINDING	C	2.1	2.1	1	17	DRQYQIDAAIVRIMKMR	12662
2HZS	CD	TRANSCRIPTION	C	2.1	2.1	1	9	IDTILSSKL	12663
2I2X	CB	TRANSFERASE	C	2.1	2.1	1	22	TVQCWSETLAYDCALMNTALET	12664
2I2X	KJ	TRANSFERASE	K	2.1	2.1	1	22	TVQCWSETLAYDCALMNTALET	12665
2IAE	EF	HYDROLASE	F	2.1	2.1	1	5	RQITQ	12666
2IAN	AB	IMMUNE SYSTEM	A	2.1	2.1	1	21	QGALANIAVDKANLEIMTKRS	12667
2IAN	KL	IMMUNE SYSTEM	K	2.1	2.1	1	7	EEFGRFA	12668
2IBZ	EI	OXIDOREDUCTASE	I	2.1	2.1	1	6	LYKTFF	12669
2INN	AC	OXIDOREDUCTASE	C	1.1	2.1	2	10	YGAYVGNRAK	12670
2INP	AC	OXIDOREDUCTASE	C	1.1	2.1	2	7	GHIARRF	12671
2IO5	BC	CHAPERONE/STRUCTURAL PROTEIN	C	1.1	2.1	2	11	KPAIRRLARRG	12672

2IZV	AC	TRANSCRIPTION	C	2.1	2.1	1	17	SHVLSKVCMYFTYKVRY	12673
2IZX	BC	KINASE	B	1.1	2.1	2	16	LTELLQGYTVEVLRQQ	12674
2J01	UV	RIBOSOME	U	1.1	2.1	2	24	FRKARETLFAAGNYAYAHRKRRKR	12675
2J7A	AC	OXIDOREDUCTASE	A	2.1	2.1	1	5	CADCH	12676
2J7Q	BC	HYDROLASE	B	2.1	2.1	1	12	IENVKAKIQDKE	12677
2JBL	HL	ELECTRON TRANSPORT	L	2.1	2.1	1	5	ERKYR	12678
2JIY	LM	PHOTOSYNTHESIS	L	2.1	2.1	1	10	WVDWWQWWVK	12679
2JIZ	CD	HYDROLASE	D	1.1	2.1	2	15	TREGNDLYHEMIESG	12680
2JJ0	LM	PHOTOSYNTHESIS	M	2.1	2.1	1	7	PAVFLRD	12681
2JKR	BM	ENDOCYTOSIS	B	2.1	2.1	1	17	PYVRKTAAVCVAKLHDI	12682
2JU0	AB	METAL BINDING PROTEIN/SIGNALING PROTEIN	B	2.1	2.1	1	12	FQVARRVLNNLQ	12683
2K2F	DB	METAL BINDING PROTEIN	D	2.1	2.1	1	11	KAVWHKLLSKQ	12684
2NQB	BD	STRUCTURAL PROTEIN/DNA	B	2.1	2.1	1	11	AMDVVYALKRQ	12685
2NQB	FH	STRUCTURAL PROTEIN/DNA	H	2.1	2.1	1	29	SKAMSIMNSFVNDIFERIAAEASRLAHYN	12686
2NQB	GH	STRUCTURAL PROTEIN/DNA	H	2.1	2.1	1	12	SREIQTAVRLLL	12687
2NU9	DE	LIGASE	D	1.1	2.1	2	14	GTLTYEAVKQTTDY	12688
2NV2	OP	LYASE/TRANSFERASE	P	1.1	2.1	2	11	STTMRRLIDTY	12689
2NYL	DE	HYDROLASE	D	2.1	2.1	1	10	FTSRTSACGL	12690
2NZD	CD	STRUCTURAL PROTEIN/DNA	D	2.1	2.1	1	12	SREIQTAVRLLL	12691
2NZD	GH	STRUCTURAL PROTEIN/DNA	G	1.1	2.1	2	10	VGRVHRLLRK	12692
2O9I	AC	TRANSCRIPTION	C	2.1	2.1	1	8	KILHRLLQ	12693
2OF5	EK	APOPTOSIS	K	2.1	2.1	1	11	YREVQRIRHEF	12694
2OM0	ij	HORMONE	i	2.1	2.1	1	5	IVEQC	12695
2ONK	AC	MEMBRANE PROTEIN	C	1.1	2.1	2	13	PLRVFFTVSLPLS	12696
2OS8	AB	CONTRACTILE PROTEIN	A	1.1	2.1	2	6	KLYAKV	12697
2P2C	DQ	HYDROLASE	D	2.1	2.1	1	15	VADMLVKVNALIKDR	12698
2P6A	AD	SIGNALING PROTEIN	D	1.1	2.1	2	12	ACHLRKATCLLG	12699
2PBD	PV	STRUCTURAL PROTEIN	P	2.1	2.1	1	18	GGLINKKCYEMASHLRRS	12700
2PL9	AD	SIGNALING PROTIEN	A	2.1	2.1	1	15	AATLEEKLNKIFEKL	12701
2PMZ	AB	TRANSLATION, TRANSFERASE	A	2.1	2.1	1	8	PDEIRKMS	12702
2PVG	AB	ELECTRON TRANSPORT	A	2.1	2.1	1	6	VPMRER	12703
2PXY	CD	IMMUNE SYSTEM	D	2.1	2.1	1	22	LERTRAELDTVCRYNYEETEVP	12704
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	A	2.1	2.1	1	9	MFSHLRRIG	12705
2QEX	FM	RIBOSOME	F	2.1	2.1	1	13	EEIVMHIPELADE	12706
2QJY	NO	OXIDOREDUCTASE	O	2.1	2.1	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	12707
2QJY	QR	OXIDOREDUCTASE	R	2.1	2.1	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	12708
2QME	AI	SIGNALING PROTEIN/TRANSFERASE	A	2.1	2.1	1	14	LKTVFDEAIRAVLG	12709
2QOU	GK	RIBOSOME	K	2.1	2.1	1	13	PFAAQVAAERCAD	12710

2QQP	GH	VIRUS	H	2.1	2.1	1	16	TVSALASIGLGLLGKS	12711
2QYF	AB	CELL CYCLE	B	1.1	2.1	2	13	TAACLRRLFRAIF	12712
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	2.1	2.1	1	17	TVFLTVAVGMVLACLVQ	12713
2REX	CD	SIGNALING PROTEIN/LIPOPROTEIN	D	1.1	2.1	2	9	DNVRPLCYS	12714
2RF9	BD	TRANSFERASE	B	2.1	2.1	1	10	DVYMIMVKCW	12715
2RI4	KL	OXYGEN STORAGE, OXYGEN TRANSPORT	K	2.1	2.1	1	21	PAVHASLDKFLANVSTVLTSK	12716
2RII	BY	OXIDOREDUCTASE COMPLEX	Y	1.1	2.1	2	9	LSDLRVYLG	12717
2RMS	AB	TRANSCRIPTION	A	1.1	2.1	2	16	QVYNDFLDIMKEFKSQ	12718
2ROC	AB	APOPTOSIS	A	1.1	2.1	2	15	EGDVKSFSRVMVHVF	12719
2SEB	AB	COMPLEX (MHC CLASS II/SUPERANTIGEN)	A	2.1	2.1	1	7	EEFGRFA	12720
2UUN	GH	ELECTRON TRANSPORT	H	2.1	2.1	1	13	ANKRLDAVNRITA	12721
2UVP	AB	UNKNOWN FUNCTION	A	2.1	2.1	1	12	HWFLNYILSNLN	12722
2UY1	AB	RNA BINDING PROTEIN	B	1.1	2.1	2	13	ILGRYHCFLDSFN	12723
2UZ6	IS	RECEPTOR	S	1.1	2.1	2	7	PPCILNN	12724
2V36	AB	TRANSFERASE	A	1.1	2.1	2	16	AIDAAVAIQFALNVTE	12725
2V5H	DI	TRANSCRIPTION	D	2.1	2.1	1	12	ADTVAGEIAAAL	12726
2VBL	AB	HYDROLASE	B	2.1	2.1	1	12	RWFLDKLVDEIG	12727
2VBN	AB	HYDROLASE	B	2.1	2.1	1	12	RWFLDKLVDEIG	12728
2VDU	BE	TRANSFERASE	E	2.1	2.1	1	11	NTLLSEYAYVL	12729
2VDW	EF	TRANSFERASE	E	1.1	2.1	2	17	PLGILSNYVKTLLISMY	12730
2VJM	AB	TRANSFERASE	A	2.1	2.1	1	6	MKELAH	12731
2VUS	FN	TRANSCRIPTION	N	1.1	2.1	2	11	NACGLFLKLHG	12732
2WB1	AC	TRANSCRIPTION	C	1.1	2.1	2	8	VVENIIIG	12733
2WB1	UT	TRANSCRIPTION	U	2.1	2.1	1	12	LQRTYDYLNSVE	12734
2WBJ	FG	IMMUNE SYSTEM	F	2.1	2.1	1	12	YCRHNYGVVESF	12735
2WG3	BD	SIGNALING PROTEIN	D	1.1	2.1	2	7	LDDMEEM	12736
2WG8	AB	HYDROLASE	A	1.1	2.1	2	15	ALDACCMVHDHCVDT	12737
2Z2S	EF	TRANSCRIPTION	E	2.1	2.1	1	13	VATWIFTIARNRR	12738
2Z2S	EF	TRANSCRIPTION	F	2.1	2.1	1	5	SLASV	12739
2Z2S	GH	TRANSCRIPTION	G	1.1	2.1	2	17	GTIKSRIRLALDRLRQH	12740
2Z5C	DF	CHAPERONE/HYDROLASE	F	1.1	2.1	2	20	ARSMIEHARTAAVTHNLYYD	12741
2ZBK	GH	ISOMERASE	G	2.1	2.1	1	10	ASIIYDALVS	12742
2ZCY	CD	HYDROLASE	D	2.1	2.1	1	12	FQVEYSLEAIKL	12743
2ZCY	TU	HYDROLASE	T	2.1	2.1	1	15	IPAFADRLGQYVQAH	12744
2ZCY	VM	HYDROLASE	V	1.1	2.1	2	11	SLAAMAVLESH	12745
2ZHX	CD	HYDROLASE/HYDROLASE INHIBITOR	C	2.1	2.1	1	6	RDASTL	12746
2ZHX	IJ	HYDROLASE/HYDROLASE INHIBITOR	I	2.1	2.1	1	10	RDASTLKPML	12747
2ZPK	LH	IMMUNE SYSTEM	L	2.1	2.1	1	6	SEELET	12748

2ZT9	AB	PHOTOSYNTHESIS	A	1.1	2.1	2	22	CLGGITLVCFLIQFATGFAMTF	12749
2ZU6	DE	HYDROLASE	D	2.1	2.1	1	10	PGRVFDMLNR	12750
2ZXX	AC	CELL CYCLE/REPLICATION	C	2.1	2.1	1	5	AYQRF	12751
3A1G	AB	TRANSFERASE	A	2.1	2.1	1	14	SRARIDARIDFESG	12752
3A1Q	DF	GENE REGULATION/SIGNALING PROTEIN	F	1.1	2.1	2	38	EEEQFALALKMSEQEAREVNNQEEKEEELLRKAIAESL	12753
3B4V	EG	HORMONE REGULATOR COMPLEX	G	2.1	2.1	1	8	KINLLGFL	12754
3BCQ	AB	TRANSPORT PROTEIN/OXYGEN BINDING	A	2.1	2.1	1	15	PANFKILSHNLLVVL	12755
3BIM	EM	TRANSCRIPTION REPRESSOR	E	2.1	2.1	1	9	GLFYSIFTD	12756
3BJI	AD	SIGNALING PROTEIN	D	2.1	2.1	1	5	DRLRP	12757
3BWN	DC	TRANSFERASE	C	2.1	2.1	1	16	STQLCQAAVHALSSLA	12758
3BZ1	AD	ELECTRON TRANSPORT	D	2.1	2.1	1	13	MVTANRFWSQIFG	12759
3BZ1	AI	ELECTRON TRANSPORT	I	2.1	2.1	1	20	ETLKITVYIVVTFFVLLFVF	12760
3BZ1	BD	ELECTRON TRANSPORT	B	2.1	2.1	1	24	TVLSSSIAAVFFAAFVVAGTMWYG	12761
3BZ1	CI	ELECTRON TRANSPORT	C	2.1	2.1	1	5	GWARR	12762
3C5W	CP	HYDROLASE	P	1.1	2.1	2	9	KDLTIGQMQ	12763
3C72	AB	TRANSFERASE	B	2.1	2.1	1	6	YEYCMS	12764
3C7B	AE	OXIDOREDUCTASE	A	2.1	2.1	1	10	AYTEELKKRG	12765
3C7N	AB	CHAPERONE/CHAPERONE	B	2.1	2.1	1	18	KRAVRRLRTACERAKRTL	12766
3C91	GN	HYDROLASE	G	1.1	2.1	2	23	VADARVLVDFARISAQQEKVTYG	12767
3CHW	AP	STRUCTURAL PROTEIN	A	2.1	2.1	1	8	PSIVHRKC	12768
3CJC	AG	STRUCTURAL PROTEIN/HYDROLASE	A	2.1	2.1	1	11	SVWIGGSILAS	12769
3CJT	OP	TRANSFERASE/RIBOSOMAL PROTEIN	P	2.1	2.1	1	9	PVGPALGQH	12770
3CWB	AB	OXIDOREDUCTASE	A	2.1	2.1	1	6	YAQTLQ	12771
3CXH	NO	OXIDOREDUCTASE	N	2.1	2.1	1	29	GYILRYLHANGASFFFMVMFMHMAKGLYY	12772
3CXH	OQ	OXIDOREDUCTASE	O	2.1	2.1	1	17	TSQMAKDVTTFLNWCAE	12773
3D4X	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	2.1	2.1	1	16	AGEYGAEALERTFCSF	12774
3D54	GH	LIGASE	G	2.1	2.1	1	15	PRGETIERVLREEKG	12775
3D7U	AB	TRANSFERASE	B	2.1	2.1	1	10	FEYLQAFLED	12776
3D7U	CD	TRANSFERASE	C	2.1	2.1	1	9	LVDYLRSRG	12777
3DBH	CD	CELL CYCLE	C	1.1	2.1	2	20	HTIAAFLGGAAAQEVIKIIT	12778
3DBJ	CD	PHOTOSYNTHESIS	C	2.1	2.1	1	12	GERRLRIAQTLT	12779
3DBJ	EF	PHOTOSYNTHESIS	E	2.1	2.1	1	12	GERRLRIAQTLT	12780
3DBJ	GH	PHOTOSYNTHESIS	G	2.1	2.1	1	12	GERRLRIAQTLT	12781
3DCG	DE	LIGASE/VIRAL PROTEIN	D	2.1	2.1	1	12	ALELLMAANFLD	12782
3DGC	LS	CYTOKINE/SIGNALING PROTEIN	L	2.1	2.1	1	18	PYITNRTFMLAKEASLAD	12783
3DIN	CE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	E	2.1	2.1	1	19	ITLVLSVLFFVSCVVTAFV	12784

3DVU	AC	VIRAL PROTEIN/APOPTOSIS	A	2.1	2.1	1	19	SGRIVGFFDVGRYVCEEVL	12785
3DWL	DF	STRUCTURAL PROTEIN	F	1.1	2.1	2	8	EIERILVR	12786
3DZU	AD	TRANSCRIPTION/DNA	D	2.1	2.1	1	9	KAKARAILT	12787
3E2Z	AB	TRANSFERASE, LYASE	B	1.1	2.1	2	16	TPLQAALAEAFWIDIK	12788
3ECH	BC	TRANSCRIPTION, TRANSCRIPTION REGULATION	C	2.1	2.1	1	12	YTEQLRRAARRN	12789
3EIQ	AC	HYDROLASE/ANTITUMOR PROTEIN	C	2.1	2.1	1	15	HHELVYEAIVMVLES	12790
3EUH	AC	CELL CYCLE	C	2.1	2.1	1	15	ELDMMVGKILCYLYL	12791
3EXG	EH	OXIDOREDUCTASE	H	2.1	2.1	1	6	KILEDN	12792
3EXG	EH	OXIDOREDUCTASE	H	2.1	2.1	1	12	VKDIIFAIKKTL	12793
3EXG	QT	OXIDOREDUCTASE	T	1.1	2.1	2	12	VKDIIFAIKKTL	12794
3EXG	WV	OXIDOREDUCTASE	V	2.1	2.1	1	6	KILEDN	12795
3EZQ	EF	APOPTOSIS	F	2.1	2.1	1	13	EEDLCAAFNVICD	12796
3F02	BD	HYDROLASE INHIBITOR	B	2.1	2.1	1	16	AIADLSVNMYNRLRAT	12797
3F1E	GK	RIBOSOME	K	2.1	2.1	1	18	PYAAQLAALDAAKKAMAY	12798
3F1S	AB	HYDROLASE INHIBITOR/HYDROLASE	A	2.1	2.1	1	7	HLALEDY	12799
3F8U	CD	IMMUNE SYSTEM/ISOMERASE	C	2.1	2.1	1	16	GHAKRLAPEYEAAATR	12800
3F9K	BK	VIRAL PROTEIN, RECOMBINATION	B	2.1	2.1	1	15	LEKIEPAQEEHEKYH	12801
3FDL	AB	APOPTOSIS	A	2.1	2.1	1	10	RRAFSDLTSQ	12802
3FIH	DE	RIBOSOME	D	1.1	2.1	2	9	EHLIVELYS	12803
3FKS	AE	HYDROLASE	A	2.1	2.1	1	10	VFYLHSRLLE	12804
3FKS	KO	HYDROLASE	K	2.1	2.1	1	5	LLERA	12805
3FKU	GJ	VIRAL PROTEIN/IMMUNE SYSTEM	G	2.1	2.1	1	11	YEELKHLLSRI	12806
3FUB	CD	HORMONE	C	1.1	2.1	2	11	NCLDAAKACNL	12807
3FWC	EF	CELL CYCLE, TRANSCRIPTION	E	1.1	2.1	2	11	DEELRAMIEEF	12808
3G3A	ED	HYDROLASE/IMMUNE SYSTEM	D	2.1	2.1	1	5	VQAWI	12809
3G43	DE	METAL BINDING PROTEIN	D	2.1	2.1	1	15	EEQIAEFKEAFSLFD	12810
3H0L	JK	LIGASE	J	2.1	2.1	1	15	PEVKRRIMLGTFALS	12811
3H0L	KL	LIGASE	L	2.1	2.1	1	7	REKALMN	12812
3H2U	AB	CELL ADHESION	A	2.1	2.1	1	29	TKRALIQCAKDIAKASDEVTRLAKEVAKQ	12813
3HEI	AB	TRANSFERASE/SIGNALING PROTEIN	A	2.1	2.1	1	6	SSDFEA	12814
3HEI	GH	TRANSFERASE/SIGNALING PROTEIN	G	2.1	2.1	1	7	SSDFEAR	12815
3HHR	AB	HORMONE/RECEPTOR	A	2.1	2.1	1	28	LSRLFDNAMLRAHRLHQLAFDTYQEFEE	12816
3HKZ	AB	TRANSFERASE	A	1.1	2.1	2	11	PTELFFHAAGG	12817
3HKZ	AC	TRANSFERASE	C	2.1	2.1	1	9	IRHILLIAD	12818
3HOU	BK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	2.1	2.1	1	12	HTLGNLIRAELL	12819
3HOU	NU	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.1	2.1	2	14	WQMLEMLKPCVEDG	12820
3I3T	AB	HYDROLASE	A	2.1	2.1	1	16	AQEFLKLLMERLHLEI	12821

3KIN	CD	MOTOR PROTEIN	D	2.1	2.1	1	6	KMTRIL	12822
1A0O	CD	CHEMOTAXIS	C	1.0	2.0	2	11	KENIIAAAQAG	12823
1A9W	CE	OXYGEN TRANSPORT	E	2.0	2.0	1	7	PWTQRFF	12824
1ALL	AB	LIGHT HARVESTING PROTEIN	B	2.0	2.0	1	9	SILDERVLN	12825
1APY	CD	HYDROLASE	C	2.0	2.0	1	15	ALDAVESGCAMCERE	12826
1B33	AB	PHOTOSYNTHESIS	A	2.0	2.0	1	14	GEKRLRIAQILTDN	12827
1B33	CD	PHOTOSYNTHESIS	D	2.0	2.0	1	14	GELRVRAATTIAAN	12828
1B33	EN	PHOTOSYNTHESIS	E	1.0	2.0	2	7	TPIEEIG	12829
1B33	JK	PHOTOSYNTHESIS	J	1.0	2.0	2	13	PGELDRIKSFVSS	12830
1B33	KO	PHOTOSYNTHESIS	O	1.0	2.0	2	12	WFREQQRIQKMG	12831
1B35	AC	VIRUS	C	2.0	2.0	1	7	HMGKVAN	12832
1B8D	AL	PHOTOSYNTHESIS	A	2.0	2.0	1	18	SQAGVEFTSALDYVINSL	12833
1B8D	KB	PHOTOSYNTHESIS	K	2.0	2.0	1	18	SQAGVEFTSALDYVINSL	12834
1B9X	AC	SIGNALING PROTEIN	C	2.0	2.0	1	21	DEGCLRKYRRQCMQDMHQKLS	12835
1BCC	EJ	OXIDOREDUCTASE	J	2.0	2.0	1	10	LTARLYSLLF	12836
1BGY	OR	ELECTRON TRANSPORT	R	2.0	2.0	1	6	GFNKLG	12837
1BIQ	AB	OXIDOREDUCTASE	B	2.0	2.0	1	10	PSVVFDDIVT	12838
1BR1	AB	MUSCLE PROTEIN	B	2.0	2.0	1	9	FEDYVEGLR	12839
1BXN	CJ	LYASE	C	2.0	2.0	1	16	ILNEGPEILRDAARWC	12840
1BXN	EK	LYASE	E	2.0	2.0	1	16	ILNEGPEILRDAARWC	12841
1BXR	AB	AMIDOTRANSFERASE	A	2.0	2.0	1	19	DKEYQIMRNASMAVLREIG	12842
1BZ7	AB	IMMUNE SYSTEM	A	2.0	2.0	1	5	EQLKS	12843
1CLV	AI	HYDROLASE	A	2.0	2.0	1	11	FQFGVSLGNAF	12844
1CUL	BC	LYASE/LYASE/SIGNALING PROTEIN	B	2.0	2.0	1	24	MHIGTMVEFAYALVGKLDAINKHS	12845
1D3B	EF	RNA BINDING PROTEIN	E	2.0	2.0	1	9	PIKVLHEAE	12846
1D4M	23	VIRUS	3	2.0	2.0	1	5	QMEMF	12847
1DEV	AB	SIGNALING PROTEIN	B	1.0	2.0	2	6	PLQQAQ	12848
1DGH	AB	OXIDOREDUCTASE	A	2.0	2.0	1	7	YFAEVEQ	12849
1DGH	CB	OXIDOREDUCTASE	B	1.0	2.0	2	11	PDMVWDFWSLR	12850
1DGR	AW	PLANT PROTEIN	A	2.0	2.0	1	8	YDEIEQTL	12851
1DKF	AB	HORMONE/GROWTH FACTOR RECEPTOR	B	1.0	2.0	2	23	PDRVDMLQEPLLEALKVYVRKRR	12852
1E0A	AB	SIGNALLING PROTEIN	A	2.0	2.0	1	14	LKNVFDEAILAALE	12853
1E3A	AB	ANTIBIOTIC RESISTANCE	A	2.0	2.0	1	6	QTAALL	12854
1E6V	AB	OXIDOREDUCTASE	B	2.0	2.0	1	12	RAEGTAVGFSFF	12855
1E6V	DE	OXIDOREDUCTASE	E	2.0	2.0	1	12	RAEGTAVGFSFF	12856
1E6Y	EC	OXIDOREDUCTASE	C	2.0	2.0	1	20	AEVVEWVHRIFDQRTKFGFQ	12857
1E7P	BC	OXIDOREDUCTASE	C	2.0	2.0	1	7	RMPAKLD	12858
1E7P	DE	OXIDOREDUCTASE	D	1.0	2.0	2	17	TGHTMLFAVANECLKLG	12859
1E7P	GH	OXIDOREDUCTASE	G	1.0	2.0	2	17	TGHTMLFAVANECLKLG	12860

1E7P	GH	OXIDOREDUCTASE	H	1.0	2.0	2	13	IFIVLNMIRETYD	12861
1E7P	HI	OXIDOREDUCTASE	I	2.0	2.0	1	7	RMPAKLD	12862
1E7P	JK	OXIDOREDUCTASE	J	1.0	2.0	2	17	TGHTMLFAVANECLKLG	12863
1E8O	CD	ALU RIBONUCLEOPROTEIN PARTICLE	D	1.0	2.0	2	16	VNKFQMAYSNLLRANM	12864
1EAH	34	VIRUS	4	2.0	2.0	1	5	SKFTE	12865
1EM8	AB	GENE REGULATION	A	2.0	2.0	1	16	AVEQLVCEIAAERWRS	12866
1EQZ	AB	STRUCTURAL PROTEIN/DNA	B	2.0	2.0	1	12	SREIQTAVRLLL	12867
1EYS	LM	ELECTRON TRANSPORT	M	2.0	2.0	1	6	FQFLKH	12868
1F5Q	CD	TRANSFERASE	D	2.0	2.0	1	17	YQSTAAVALHIAGKVRA	12869
1F99	AB	PHOTOSYNTHESIS	B	2.0	2.0	1	13	GNKRLDVVNKITN	12870
1F99	MN	PHOTOSYNTHESIS	N	2.0	2.0	1	12	AFAKVVAQADAR	12871
1FCD	BD	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	B	2.0	2.0	1	18	GYSANSQGKVAAAAVVVL	12872
1FG9	BC	IMMUNE SYSTEM	B	2.0	2.0	1	10	LNVQRKAIHE	12873
1FG9	BD	IMMUNE SYSTEM	B	2.0	2.0	1	14	PYVKEAENLKKYFN	12874
1FNT	QX	HYDROLASE/HYDROLASE ACTIVATOR	X	1.0	2.0	2	22	ATDVTTLNEMFRYKTNLYKLKE	12875
1FNT	ST	HYDROLASE/HYDROLASE ACTIVATOR	T	2.0	2.0	1	13	FQVEYALEAIKQG	12876
1FOE	EF	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	E	1.0	2.0	2	12	KYPLLLRELFAL	12877
1FQJ	AC	SIGNALING PROTEIN	A	1.0	2.0	2	14	RMHESMKLFDSICN	12878
1FQV	OP	LIGASE	O	2.0	2.0	1	8	KRWYRLAS	12879
1FQV	OP	LIGASE	P	2.0	2.0	1	14	QGTLFELILAANYL	12880
1FS2	CD	LIGASE	C	2.0	2.0	1	8	KRWYRLAS	12881
1FSX	CB	OXYGEN STORAGE/TRANSPORT	C	2.0	2.0	1	19	PVNFKLLSHSLLVTLASHL	12882
1FWA	BC	HYDROLASE	C	2.0	2.0	1	8	RQAYADMF	12883
1G0U	U2	HYDROLASE	2	2.0	2.0	1	22	AADTQAIADIVQYHLELYTSQY	12884
1G0U	VW	HYDROLASE	W	2.0	2.0	1	15	PETFTQLVSSSLYER	12885
1G20	CD	OXIDOREDUCTASE	C	2.0	2.0	1	16	FDGFAIFARDMDMTLN	12886
1G20	CD	OXIDOREDUCTASE	D	2.0	2.0	1	8	KEYQELNF	12887
1G3N	EF	CELL CYCLE, SIGNALING PROTEIN	E	2.0	2.0	1	6	LTTYLD	12888
1GH0	MN	PHOTOSYNTHESIS	M	2.0	2.0	1	10	TGPMDEYLIA	12889
1GX7	AD	OXIDOREDUCTASE	A	2.0	2.0	1	10	PIGMNGALAK	12890
1H1L	AB	OXIDOREDUCTASE	B	2.0	2.0	1	8	AEYEALNF	12891
1H2M	AS	TRANSCRIPTION ACTIVATOR/INHIBITOR	A	2.0	2.0	1	11	WNWINKQQGKR	12892
1H5R	AB	TRANSFERASE	B	2.0	2.0	1	12	NYGQYLYKQTKD	12893
1HR8	GH	HYDROLASE	G	1.0	2.0	2	11	GRAMAETLELL	12894
1HV4	AD	OXYGEN STORAGE/TRANSPORT	A	2.0	2.0	1	19	PVNFKFLGHCFLVVVAIHH	12895
1HXY	BD	IMMUNE SYSTEM/TOXIN	B	2.0	2.0	1	22	KDLLEQRRAAVDTYCRHNYGVG	12896
1I3O	CD	APOPTOSIS	D	2.0	2.0	1	13	WFIQSLCAMLKQY	12897

1I7Y	AB	PHOTOSYNTHESIS	B	2.0	2.0	1	13	AFAKVVAQADARG	12898
1IBC	AB	COMPLEX (HYDROLASE/PEPTIDE)	A	2.0	2.0	1	11	LEEAQRIWKQK	12899
1ICE	AB	CYTOKINE	A	2.0	2.0	1	6	AIFNML	12900
1ID3	EF	STRUCTURAL PROTEIN/DNA	E	2.0	2.0	1	12	KKEIKLARRLRG	12901
1IRU	DE	HYDROLASE	D	2.0	2.0	1	15	VEYITRYIASLKQRY	12902
1IW7	NP	TRANSFERASE	P	2.0	2.0	1	7	ARVRHIP	12903
1IWP	LM	LYASE	M	2.0	2.0	1	17	TVNAAFVRESAEVYQQR	12904
1IYJ	CD	GENE REGULATION/ANTITUMOR PROTEIN	D	1.0	2.0	2	22	SVWVSNHYRWIVWKLAAMEFAF	12905
1J1E	DF	CONTRACTILE PROTEIN	F	2.0	2.0	1	7	AMMQALL	12906
1JD2	FN	HYDROLASE	N	2.0	2.0	1	15	TETAASVFKELCYEN	12907
1JD2	JK	HYDROLASE	K	2.0	2.0	1	15	VAAASKILSNLVYQY	12908
1JD2	OU	HYDROLASE	O	2.0	2.0	1	15	VVSALQMLKQHLFKY	12909
1JEB	AB	OXYGEN STORAGE/TRANSPORT	A	2.0	2.0	1	19	AEAHAAWDKFLSVVSSVLT	12910
1JEB	AB	OXYGEN STORAGE/TRANSPORT	A	2.0	2.0	1	16	ADTIGTETLERLFLSH	12911
1JJ2	FL	RIBOSOME	F	1.0	2.0	2	10	TNETTKSIER	12912
1JJ2	RU	RIBOSOME	U	1.0	2.0	2	24	PAEREAELDDLKTELLNARAVQAA	12913
1JNH	GH	IMMUNE SYSTEM	G	2.0	2.0	1	6	SEELET	12914
1JY7	RS	OXYGEN STORAGE/TRANSPORT	R	2.0	2.0	1	19	PAVHASLDKFLASVSTVLT	12915
1JYO	BF	CHAPERONE	F	2.0	2.0	1	8	FINLIKSK	12916
1K3B	AC	HYDROLASE	A	2.0	2.0	1	5	YLDLL	12917
1K4C	AC	MEMBRANE PROTEIN	C	2.0	2.0	1	13	YPRALWWSVETAT	12918
1KFY	BC	OXIDOREDUCTASE	B	2.0	2.0	1	6	YCSEVC	12919
1KI6	AB	PHOSPHOTRANSFERASE	B	2.0	2.0	1	14	MPYAVTDAVLAPHI	12920
1KJ2	ID	IMMUNE SYSTEM	I	2.0	2.0	1	29	PEYWERETQKAKGNEQSFRVDLRTLLGYY	12921
1KJY	CD	SIGNALING PROTEIN	C	2.0	2.0	1	16	SARADDARQLFVLAGA	12922
1KX4	GH	STRUCTURAL PROTEIN/DNA	H	2.0	2.0	1	12	SREIQTAVRLLL	12923
1KYO	AE	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	2.0	2.0	1	14	HPNRVLEHLHSTAF	12924
1KYO	DH	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	2.0	2.0	1	32	PEHDERKRLGLKTVIILSSLYLLSIWVKKFKW	12925
1KYO	NE	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	2.0	2.0	1	33	NPTIQRFFALHYLVPFIIAAMVIMHLMALHIHG	12926
1KZ7	CD	SIGNALING PROTEIN	C	1.0	2.0	2	13	LDSYLLKPVQRIT	12927
1LB1	AB	SIGNALING PROTEIN	A	2.0	2.0	1	25	AEDLQEALSSILGILKAVNDSMHLI	12928
1LB1	GH	SIGNALING PROTEIN	G	2.0	2.0	1	13	LDSYLLKPVQRIT	12929
1LIA	AB	LIGHT HARVESTING PROTEIN	A	2.0	2.0	1	27	TSDLQSVQGNIQRAAARLEAAEKLGSN	12930
1LJ2	AD	VIRAL PROTEIN/ TRANSLATION	A	1.0	2.0	2	33	PLHAFDDLESVIRNLISDYDKLFLMFKGLIQRS	12931
1LO0	LH	IMMUNE SYSTEM	L	2.0	2.0	1	6	SEQLTS	12932
1LQM	EF	HYDROLASE/HYDROLASE INHIBITOR	E	1.0	2.0	2	12	PSLLNMYKELEN	12933

1M1J	EF	BLOOD CLOTTING	E	2.0	2.0	1	6	KDNLDN	12934
1M56	AB	OXIDOREDUCTASE	A	2.0	2.0	1	8	ASVDRYYH	12935
1MJG	CO	OXIDOREDUCTASE	O	2.0	2.0	1	13	MVKTAAAFGAIFT	12936
1MJG	DP	OXIDOREDUCTASE	P	2.0	2.0	1	13	MVKTAAAFGAIFT	12937
1MR1	AD	SIGNALING PROTEIN	D	2.0	2.0	1	5	WRAYI	12938
1N5W	DE	OXIDOREDUCTASE	D	2.0	2.0	1	9	ALQEGFRMM	12939
1NEX	CD	LIGASE, CELL CYCLE	C	1.0	2.0	2	10	YEIILAANYL	12940
1NTK	AE	OXIDOREDUCTASE	A	2.0	2.0	1	14	MRDVVFNYLHATAF	12941
1NTK	CE	OXIDOREDUCTASE	E	2.0	2.0	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	12942
1NZY	AB	LYASE	A	2.0	2.0	1	25	VAGVRDHFRIAALWWHQMIHKIIRV	12943
1O2F	AB	TRANSFERASE	A	2.0	2.0	1	5	VVFAE	12944
1O96	AB	ELECTRON TRANSFER	B	2.0	2.0	1	12	IFDIEEELKAQL	12945
1OAO	BC	OXIDOREDUCTASE	C	2.0	2.0	1	14	MVKTAAAFGAIFTG	12946
1OCC	DE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	2.0	2.0	1	5	FAEMN	12947
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	2.0	2.0	1	5	FAEMN	12948
1OSV	AC	DNA BINDING PROTEIN	A	1.0	2.0	2	25	AEENFLILTEMATSHVQILVEFTKR	12949
1OW7	AD	TRANSFERASE	D	2.0	2.0	1	10	RELDELMASL	12950
1PIV	13	VIRUS	3	2.0	2.0	1	7	MLGEVLN	12951
1POV	13	VIRUS	3	2.0	2.0	1	5	PRLSH	12952
1PRC	CM	PHOTOSYNTHETIC REACTION CENTER	C	2.0	2.0	1	9	YVVRLAKYT	12953
1PYU	AB	LYASE	B	2.0	2.0	1	6	DEEART	12954
1Q5R	CJ	HYDROLASE	J	2.0	2.0	1	7	FTDYLRG	12955
1Q5R	CK	HYDROLASE	K	2.0	2.0	1	23	AGIAIELVRLFAVELEHYEKIEG	12956
1Q5R	EM	HYDROLASE	M	2.0	2.0	1	23	AGIAIELVRLFAVELEHYEKIEG	12957
1Q5R	FN	HYDROLASE	N	2.0	2.0	1	23	AGIAIELVRLFAVELEHYEKIEG	12958
1QLE	AC	OXIDOREDUCTASE/IMMUNE SYSTEM	A	2.0	2.0	1	30	LFAWSVFITAWLILLSLPVLAGAITMLLMD	12959
1QLE	BL	OXIDOREDUCTASE/IMMUNE SYSTEM	B	2.0	2.0	1	33	PLAHDQQWLDHFVLYIITAVTIFVCLLLLICIV	12960
1QPW	AB	OXYGEN TRANSPORT	B	1.0	2.0	2	20	PENFRLLGNVIVVVLARRLG	12961
1R27	AB	OXIDOREDUCTASE	A	2.0	2.0	1	6	SADWYN	12962
1R5W	AB	SIGNALING PROTEIN	A	2.0	2.0	1	5	EEFAK	12963
1RU7	KL	VIRAL PROTEIN	L	1.0	2.0	2	22	QKSTQNAINGITNKVNSVIEKM	12964
1RYP	12	MULTICATALYTIC PROTEINASE	2	2.0	2.0	1	18	PSYIFEYLATVMYQRRSK	12965
1RYP	HI	MULTICATALYTIC PROTEINASE	I	2.0	2.0	1	15	VVSALQMLKQHLFKY	12966
1RYP	JZ	MULTICATALYTIC PROTEINASE	Z	2.0	2.0	1	19	VEDALYLGKRSILAAAHRD	12967
1RYP	VW	MULTICATALYTIC PROTEINASE	W	2.0	2.0	1	15	VVSALQMLKQHLFKY	12968
1S70	AB	HYDROLASE	B	2.0	2.0	1	8	QLKRWIGS	12969
1SEB	AD	COMPLEX (MHC II/PEPTIDE/TOXIN)	A	1.0	2.0	2	22	AQGALANIAVDKANLEIMTKRS	12970
1T3L	AB	TRANSPORT PROTEIN	A	2.0	2.0	1	11	PKVLQRLIKSR	12971

1T3Q	AB	OXIDOREDUCTASE	B	2.0	2.0	1	9	RAIAEDAAQ	12972
1T3Q	DE	OXIDOREDUCTASE	E	2.0	2.0	1	9	RAIAEDAAQ	12973
1T9G	RS	OXIDOREDUCTASE, ELECTRON TRANSPORT	R	2.0	2.0	1	16	PEELTPLILATQKQFN	12974
1TA3	AB	HYDROLASE INHIBITOR/HYDROLASE	A	1.0	2.0	2	9	YSSLIKYYA	12975
1TFC	AC	TRANSCRIPTION	A	2.0	2.0	1	11	LADQMSLLQSA	12976
1TFC	BD	TRANSCRIPTION	B	2.0	2.0	1	11	LADQMSLLQSA	12977
1TII	DC	ENTEROTOXIN	D	2.0	2.0	1	20	PDNVMTAEMRKIAMAAVLSG	12978
1TOC	AB	COMPLEX (HYDROLASE/INHIBITOR)	A	2.0	2.0	1	5	FEKKQ	12979
1TOC	CD	COMPLEX (HYDROLASE/INHIBITOR)	C	2.0	2.0	1	5	FEKKQ	12980
1TQY	AB	TRANSFERASE	A	1.0	2.0	2	15	SGLDSVGNAVRAIEE	12981
1TU3	CG	PROTEIN TRANSPORT	C	2.0	2.0	1	18	EESFARAKNWVKELQRQA	12982
1TUE	AB	REPLICATION	A	2.0	2.0	1	14	FITFLGALKSFLKG	12983
1U35	EC	STRUCTURAL PROTEIN/DNA	E	2.0	2.0	1	13	TVALREIRRYQKS	12984
1UKV	GY	PROTEIN TRANSPORT	G	2.0	2.0	1	18	ARPSFERILLYCQSVARY	12985
1UUZ	AD	HYDROLASE/INHIBITOR	A	2.0	2.0	1	5	EVMQT	12986
1UZH	EF	LYASE	F	2.0	2.0	1	14	DEQIAAQVDYIVAN	12987
1V54	AC	OXIDOREDUCTASE	A	2.0	2.0	1	15	LLPPSFLLLLASSMV	12988
1V54	QR	OXIDOREDUCTASE	R	2.0	2.0	1	12	AWELRKGMNTLV	12989
1V7N	IX	IMMUNE SYSTEM/CYTOKINE	X	2.0	2.0	1	6	LQSLLG	12990
1VF5	NR	PHOTOSYNTHESIS	R	2.0	2.0	1	25	ILGAVFYIVFIALFFGIAVGIIFAI	12991
1VRQ	BD	OXIDOREDUCTASE	B	2.0	2.0	1	15	FHVIEEQMAAAVELF	12992
1W5C	AD	PHOTOSYNTHESIS	D	2.0	2.0	1	10	IHGATVENTL	12993
1W63	DN	ENDOCYTOSIS	D	2.0	2.0	1	17	YVVQEAIVVIKDIFRKY	12994
1W63	JR	ENDOCYTOSIS	J	2.0	2.0	1	13	PLIRALAVRTMGC	12995
1W7P	AD	PROTEIN TRANSPORT	D	2.0	2.0	1	13	LVDLYAMYNKSMR	12996
1WDD	AS	LYASE	A	2.0	2.0	1	20	WRDRFVFCAEAIYKSQAETG	12997
1WR6	DH	PROTEIN TRANSPORT/SIGNALING PROTEIN	D	2.0	2.0	1	13	LEEVNNNVRLLSE	12998
1WR6	DH	PROTEIN TRANSPORT/SIGNALING PROTEIN	D	2.0	2.0	1	20	ELFDQCENKRRTLFKLASET	12999
1WYU	CD	OXIDOREDUCTASE	D	1.0	2.0	2	10	GSNPATASMA	13000
1X3Z	AB	HYDROLASE	B	2.0	2.0	1	11	PEVFVSMLLEA	13001
1X79	AB	PROTEIN TRANSPORT	A	2.0	2.0	1	24	EALAEILQANDNLTQVINLYKQLV	13002
1XFU	CQ	LYASE/METAL BINDING PROTEIN	C	2.0	2.0	1	5	PITKA	13003
1XKM	AB	ANTIBIOTIC	A	2.0	2.0	1	15	PGFTALIKTLRKCKI	13004
1XKM	CB	ANTIBIOTIC	C	2.0	2.0	1	14	PGFTALIKTLRKCK	13005
1XLS	BF	TRANSCRIPTION	F	1.0	2.0	2	25	LYAKLMGLLADLRSINNAYSYELQR	13006
1XQ5	AB	OXYGEN STORAGE/TRANSPORT	B	2.0	2.0	1	20	PDNFKLLSDCLTIVVAAQLG	13007
1XQ5	CD	OXYGEN STORAGE/TRANSPORT	C	2.0	2.0	1	21	PEVHISYDKFFSALARALAEK	13008

1XQS	BD	CHAPERONE	B	2.0	2.0	1	17	QKLKVKSAFLLQNLLVG	13009
1XWJ	AB	CELL ADHESION/PROTEIN BINDING	A	2.0	2.0	1	23	TAPVSAVQAAVSNLVRVGKETVQ	13010
1XXH	AB	TRANSFERASE	A	2.0	2.0	1	17	PLLLQESQDAVRQVAAA	13011
1XXI	DE	TRANSFERASE	E	2.0	2.0	1	20	APARLHWLATLLMDALKRHH	13012
1XXI	FG	TRANSFERASE	G	1.0	2.0	2	21	WEALLVEMLGLLHRIAMVQLS	13013
1YA7	BI	HYDROLASE/HYDROLASE ACTIVATOR	B	2.0	2.0	1	23	VADARVLVDFARISAQQEKVTYG	13014
1YA7	DK	HYDROLASE/HYDROLASE ACTIVATOR	D	2.0	2.0	1	15	IENLVKRVADQMQQY	13015
1YCP	KM	COMPLEX (SERINE PROTEASE/PEPTIDE)	K	2.0	2.0	1	8	KQTAAKLL	13016
1YE9	IM	OXIDOREDUCTASE	M	2.0	2.0	1	18	PLLQGRLFSYTDTQISRL	13017
1YHU	BD	OXYGEN STORAGE/TRANSPORT	B	2.0	2.0	1	20	PAFRAHATRVLGGLDMCIAL	13018
1YHU	EH	OXYGEN STORAGE/TRANSPORT	E	2.0	2.0	1	16	MLERAKVKDEWAKAYG	13019
1YKE	CD	GENE REGULATION	D	1.0	2.0	2	10	LQKKLVEVED	13020
1YNJ	DK	TRANSFERASE	D	2.0	2.0	1	22	EKTARLLDALKYYGFTLSTTSG	13021
1YV0	TC	CONTRACTILE PROTEIN	T	2.0	2.0	1	16	EQIKRKKYEIVTLRNR	13022
1Z6O	CU	METAL BINDING PROTEIN	C	2.0	2.0	1	16	LSLALYVFDEYLQKTV	13023
1Z6O	DW	METAL BINDING PROTEIN	D	2.0	2.0	1	16	LSLALYVFDEYLQKTV	13024
1Z7Q	RZ	HYDROLASE/HYDROLASE ACTIVATOR	R	1.0	2.0	2	15	VEYLTRYVAGVQQRY	13025
1Z7Q	WM	HYDROLASE/HYDROLASE ACTIVATOR	M	2.0	2.0	1	18	VEEVIKLVRDSFTSATER	13026
1ZBB	EF	STRUCTURAL PROTEIN/DNA	E	2.0	2.0	1	13	TVALREIRRYQKS	13027
1ZBB	gh	STRUCTURAL PROTEIN/DNA	h	2.0	2.0	1	12	SREIQTAVRLLL	13028
1ZBB	GH	STRUCTURAL PROTEIN/DNA	H	2.0	2.0	1	12	SREIQTAVRLLL	13029
1ZC4	CB	SIGNALING PROTEIN	C	2.0	2.0	1	10	AAIRDNYFRS	13030
1ZGL	JK	IMMUNE SYSTEM	J	2.0	2.0	1	20	ALANIAVDKANLEIMTKRSN	13031
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	H	2.0	2.0	1	11	REIQTAVRLLL	13032
1ZM2	EF	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	E	2.0	2.0	1	14	KDSVVAAFQWATKE	13033
1ZNV	CB	HYDROLASE/PROTEIN BINDING	B	2.0	2.0	1	9	RNNNDRMKV	13034
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	A	2.0	2.0	1	12	AAELRHVMTNLG	13035
1ZY8	IO	OXIDOREDUCTASE	I	1.0	2.0	2	7	CEDIARV	13036
2A0L	AD	MEMBRANE PROTEIN	A	2.0	2.0	1	23	FRLVRLLRFLRILLIISRGSKFL	13037
2A1D	FH	HYDROLASE	H	2.0	2.0	1	16	KTEALELKAKVDLVLG	13038
2A1D	FH	HYDROLASE	H	2.0	2.0	1	20	LKGRLTSLESQFINALDILE	13039
2AA1	CD	OXYGEN STORAGE/TRANSPORT	C	2.0	2.0	1	19	PSNFKILNHCILVVISTMF	13040
2ACM	AB	STRUCTURAL PROTEIN	B	2.0	2.0	1	11	VHDVETQFNQY	13041
2ACZ	BC	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	2.0	2.0	1	6	PSFWWN	13042
2AFH	CD	OXIDOREDUCTASE	D	2.0	2.0	1	6	CMAEVI	13043
2AKW	AB	LIGASE	B	2.0	2.0	1	11	PVSIRKTARRH	13044

2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	B	2.0	2.0	1	10	DELLLGIFSC	13045
2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	B	1.0	2.0	2	10	PDVTGRLLSQ	13046
2AXT	AC	ELECTRON TRANSPORT	C	2.0	2.0	1	28	PRSWLATSHFVLAFFFLVGHLWHAGRAR	13047
2AXT	ck	ELECTRON TRANSPORT	c	2.0	2.0	1	14	TFPFFVVGVVHLIS	13048
2AXT	ck	ELECTRON TRANSPORT	k	2.0	2.0	1	25	DPLVDVLPVIPVLFLALAFVWQAAV	13049
2AXT	DF	ELECTRON TRANSPORT	F	1.0	2.0	2	24	VRWVAVHTLAVPTIFFLGAIAAMQ	13050
2AXT	df	ELECTRON TRANSPORT	f	1.0	2.0	2	24	VRWVAVHTLAVPTIFFLGAIAAMQ	13051
2B8K	BC	TRANSFERASE	C	1.0	2.0	2	11	DEFIAHRLGLI	13052
2BCX	AB	CALCIUM BINDING PROTEIN	A	2.0	2.0	1	13	FPEFLTMMARKMK	13053
2BR2	OP	HYDROLASE	P	2.0	2.0	1	28	PDEFRQAFDLAVKGINIIYNLEREALKS	13054
2BS4	DE	OXIDOREDUCTASE	D	2.0	2.0	1	16	TGHTMLFAVANECLKL	13055
2BTW	AB	TRANSFERASE	A	2.0	2.0	1	7	EDFFPLS	13056
2BYP	AG	RECEPTOR	G	2.0	2.0	1	6	PRCAWR	13057
2C7J	AB	ELECTRON TRANSPORT	A	2.0	2.0	1	12	NTELQAVFGRFN	13058
2CLY	EF	HYDROLASE	E	2.0	2.0	1	12	LVDDFEKKFNAL	13059
2D0O	AB	CHAPERONE	B	2.0	2.0	1	16	SQAHRNTGNNAARLVK	13060
2D2M	AD	OXYGEN STORAGE/TRANSPORT	A	1.0	2.0	2	16	AAFTAHCLRVTGALNR	13061
2DD4	BL	HYDROLASE	L	2.0	2.0	1	16	DFEILEMAVRELAIEK	13062
2DD4	EI	HYDROLASE	I	2.0	2.0	1	16	DFEILEMAVRELAIEK	13063
2DD4	HF	HYDROLASE	F	2.0	2.0	1	16	DFEILEMAVRELAIEK	13064
2DD4	KC	HYDROLASE	C	2.0	2.0	1	16	DFEILEMAVRELAIEK	13065
2DOQ	BD	CELL CYCLE	B	2.0	2.0	1	8	ENEFIAIC	13066
2DXB	BL	HYDROLASE	L	2.0	2.0	1	16	DFEILEMAVRELAIEK	13067
2DXB	HF	HYDROLASE	H	2.0	2.0	1	8	HTLFRAYT	13068
2DXB	NX	HYDROLASE	X	2.0	2.0	1	16	DFEILEMAVRELAIEK	13069
2DXB	TR	HYDROLASE	R	2.0	2.0	1	16	DFEILEMAVRELAIEK	13070
2DXB	WO	HYDROLASE	W	2.0	2.0	1	8	HTLFRAYT	13071
2E 74	CH	PHOTOSYNTHESIS	H	1.0	2.0	2	24	IDVLGWVALLVVFTWSIAMVVWGR	13072
2E7L	AE	IMMUNE SYSTEM	E	2.0	2.0	1	24	AAEYYRAYLEGECVEWLHRYLKNG	13073
2E7L	BF	IMMUNE SYSTEM	F	2.0	2.0	1	21	AAEYYRAYLEGECVEWLHRYL	13074
2E9X	AF	REPLICATION	F	1.0	2.0	2	29	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	13075
2F54	KL	IMMUNE SYSTEM	L	2.0	2.0	1	8	EAEISHTQ	13076
2F5Z	EM	OXIDOREDUCTASE/PROTEIN BINDING	E	2.0	2.0	1	14	AGEMVNEAALALEY	13077
2F9I	CD	TRANSFERASE	C	2.0	2.0	1	6	GGALGI	13078
2FBW	OP	OXIDOREDUCTASE	P	2.0	2.0	1	24	LSQVEQSGVVVLILTLLSSAGIAA	13079
2FCW	AB	LIPID TRANSPORT/ENDOCYTOSIS/CHAPERONE	A	1.0	2.0	2	41	GERVSRSREKHALLEGRTKELGYTVKKHLQDLSGRISRARH	13080

2FDB	MP	HORMONE/GROWTH FACTOR/TRANSFERASE	M	2.0	2.0	1	8	TQHVREQS	13081
2FHH	YX	HYDROLASE	X	2.0	2.0	1	23	AAVAVEFARLYAVELEHYEKLEG	13082
2FJ7	BD	STRUCTURAL PROTEIN/DNA	B	2.0	2.0	1	11	AMDVVYALKRQ	13083
2FM8	AC	CHAPERONE/CELL INVASION	C	2.0	2.0	1	5	NLAAN	13084
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	A	2.0	2.0	1	8	FPEFLTMM	13085
2FRV	AB	OXIDOREDUCTASE	A	2.0	2.0	1	5	PEAKK	13086
2FRV	CD	OXIDOREDUCTASE	C	2.0	2.0	1	5	PEAKK	13087
2FRV	IJ	OXIDOREDUCTASE	I	2.0	2.0	1	5	PEAKK	13088
2FRV	SL	OXIDOREDUCTASE	S	2.0	2.0	1	5	PEAKK	13089
2FUG	DG	OXIDOREDUCTASE	G	2.0	2.0	1	5	CEEAC	13090
2FUG	ST	OXIDOREDUCTASE	S	2.0	2.0	1	17	RRAADRLEQAIKEARAR	13091
2FYM	CB	LYASE	B	2.0	2.0	1	6	PELASG	13092
2FYN	AB	OXIDOREDUCTASE	A	2.0	2.0	1	15	VDLAFASVEHIMRNV	13093
2FYN	AF	OXIDOREDUCTASE	A	2.0	2.0	1	11	IGHSIQTWLLG	13094
2GEZ	CB	HYDROLASE	B	2.0	2.0	1	7	GEEIIRA	13095
2GGM	BD	CELL CYCLE	B	1.0	2.0	2	11	FKNLKRVAKEL	13096
2GJX	HG	HYDROLASE	G	2.0	2.0	1	18	MDDAYDRLTRHRCRMVER	13097
2GL7	AB	TRANSCRIPTION	A	2.0	2.0	1	16	QRLVQNCLWTLRNLSD	13098
2GO5	12	TRANSLATION/RNA	1	1.0	2.0	2	10	VNALIRSVLL	13099
2GUZ	EF	CHAPERONE, PROTEIN TRANSPORT	F	2.0	2.0	1	15	MDKINNRFNYLFEVN	13100
2GYK	AB	ANTIBIOTIC/ANTIBIOTIC INHIBITOR	A	2.0	2.0	1	16	EEELVKLVTHFEEMTE	13101
2HHF	AB	TRANSFERASE	A	2.0	2.0	1	15	PWLNMDRMLRSAMRL	13102
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	B	2.0	2.0	1	12	SREIQTAVRLLL	13103
2HIO	BD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	B	1.0	2.0	2	29	SKAMGIMNSFVNDIFERIAGEASRLAHYN	13104
2HYB	DE	TRANSFERASE	E	1.0	2.0	2	16	IYAWEALEVVLIGAAF	13105
2HYB	KI	TRANSFERASE	K	2.0	2.0	1	5	GVYQL	13106
2HYI	GH	HYDROLASE/RNA BINDING PROTEIN/RNA	G	1.0	2.0	2	15	KSVMEELKRIIDDSE	13107
2HZS	EF	TRANSCRIPTION	E	2.0	2.0	1	9	IDTILSSKL	13108
2IBX	EF	VIRAL PROTEIN	F	1.0	2.0	2	22	KESTQKAIDGVTNKVNSIIDKM	13109
2IBZ	EG	OXIDOREDUCTASE	E	2.0	2.0	1	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	13110
2ICW	DE	IMMUNE SYSTEM	D	2.0	2.0	1	17	AQGALANIAVDKANLEI	13111
2IX2	AC	REPLICATION	C	2.0	2.0	1	15	SDGFKSAISEVSTVT	13112
2IZX	AC	KINASE	A	2.0	2.0	1	16	LTELLQGYTVEVLRQQ	13113
2J0Q	BD	HYDROLASE	B	2.0	2.0	1	9	LLRGIYAYG	13114
2J0S	AT	HYDROLASE	A	2.0	2.0	1	13	DDIRILRDIEQYY	13115

2J7Q	DA	HYDROLASE	D	2.0	2.0	1	13	IENVKAKIQDKEG	13116
2J9U	CD	PROTEIN TRANSPORT	D	2.0	2.0	1	7	YELTKSS	13117
2JEA	AB	HYDROLASE	B	2.0	2.0	1	29	PDEFRQAFDLAVKGINIIYNLEREALKSK	13118
2JIZ	HK	HYDROLASE	K	1.0	2.0	2	27	SEHYDVARGVQKILQDYKSLQDIIAIL	13119
2JKR	AE	ENDOCYTOSIS	E	2.0	2.0	1	16	PDLRDRGYIYWRLLST	13120
2NPP	AB	SIGNALING PROTEIN,HYDROLASE	A	2.0	2.0	1	9	FTSRTSACG	13121
2NPP	BC	SIGNALING PROTEIN,HYDROLASE	B	2.0	2.0	1	17	SPKEVMFLNELEEILDV	13122
2NQB	CD	STRUCTURAL PROTEIN/DNA	D	2.0	2.0	1	12	SREIQTAVRLLL	13123
2NVU	BC	PROTEIN TURNOVER, LIGASE	B	2.0	2.0	1	6	TSIEER	13124
2O02	AP	PROTEIN BINDING/TOXIN	A	2.0	2.0	1	18	PIRLGLALNFSVFYYEIL	13125
2OM0	CD	HORMONE	C	2.0	2.0	1	7	LYQLENY	13126
2OM0	gh	HORMONE	g	2.0	2.0	1	5	IVEQC	13127
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	A	2.0	2.0	1	16	KGLLDVTCKTVANMIK	13128
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	A	2.0	2.0	1	11	EEEEAQVRKEN	13129
2P1L	EF	APOPTOSIS	E	2.0	2.0	1	21	WGRIVAFFSFGGALCVESVDK	13130
2P24	AB	IMMUNE SYSTEM	B	2.0	2.0	1	22	LERTRAELDTVCRYNYEETEVP	13131
2P2C	IJ	HYDROLASE	J	2.0	2.0	1	15	VADMLVKVNALIKDR	13132
2P5T	CD	TRANSCRIPTION REGULATOR	D	1.0	2.0	2	17	DSEFKHALARNLRSLTR	13133
2PBI	CD	SIGNALING PROTEIN	C	1.0	2.0	2	13	GGDVLQWITQRLW	13134
2PE6	AB	PROTEIN BINDING, LIGASE	A	2.0	2.0	1	17	GIALSRLAQERKAWRKD	13135
2PF4	BF	HYDROLASE REGULATOR/VIRAL PROTEIN	B	2.0	2.0	1	9	FTSRTSACG	13136
2PI2	BF	REPLICATION, DNA BINDING PROTEIN	B	1.0	2.0	2	6	ISQLLS	13137
2PMZ	AB	TRANSLATION, TRANSFERASE	B	2.0	2.0	1	5	RLLDN	13138
2PMZ	AB	TRANSLATION, TRANSFERASE	B	2.0	2.0	1	10	QIMEGIAGKY	13139
2PMZ	GR	TRANSLATION, TRANSFERASE	R	2.0	2.0	1	13	YAFKLLIQELMSM	13140
2QAR	DE	HYDROLASE REGULATOR	D	2.0	2.0	1	7	GKALLLL	13141
2QJK	DE	ELECTRON TRANSPORT	D	2.0	2.0	1	11	FASVEHIMRNV	13142
2QJK	EF	ELECTRON TRANSPORT	E	1.0	2.0	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	13143
2QJK	NO	ELECTRON TRANSPORT	N	1.0	2.0	2	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	13144
2QJK	PQ	ELECTRON TRANSPORT	P	2.0	2.0	1	11	FASVEHIMRNV	13145
2QJY	HI	OXIDOREDUCTASE	I	2.0	2.0	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	13146
2QJY	JI	OXIDOREDUCTASE	J	2.0	2.0	1	11	IGHSIQTWLLG	13147
2QJY	MR	OXIDOREDUCTASE	M	2.0	2.0	1	11	IGHSIQTWLLG	13148
2QJY	PO	OXIDOREDUCTASE	P	2.0	2.0	1	11	IGHSIQTWLLG	13149
2QOY	JN	RIBOSOME	N	2.0	2.0	1	10	RIKVREAAMR	13150
2QQD	DC	LYASE	D	2.0	2.0	1	13	PLNAFDGALLNAG	13151
2QQP	AB	VIRUS	B	2.0	2.0	1	15	TVSALASIGLGLLGK	13152
2QR0	QR	IMMUNE SYSTEM	Q	1.0	2.0	2	7	DEQLKSG	13153
2R17	BD	PROTEIN TRANSPORT	D	2.0	2.0	1	17	EETEQINKHFHNTLEHL	13154

2R1T	AB	PROTEIN BINDING	B	2.0	2.0	1	13	SFEFALAIVEALN	13155
2R4R	LH	SIGNALING PROTEIN	L	2.0	2.0	1	7	SEQLTSG	13156
2SIV	ED	ENVELOPE GLYCOPROTEIN	D	2.0	2.0	1	32	QEWERKVDFLEENITALLEEAQIQQEKNMYEL	13157
2UUN	WX	ELECTRON TRANSPORT	X	2.0	2.0	1	13	ANKRLDAVNRITA	13158
2UZ6	IR	RECEPTOR	R	2.0	2.0	1	7	PPCILNN	13159
2V1S	CL	OXIDOREDUCTASE	L	2.0	2.0	1	9	LSRLLSYAG	13160
2V36	AB	TRANSFERASE	A	2.0	2.0	1	7	AAKDVFL	13161
2V36	AB	TRANSFERASE	A	2.0	2.0	1	16	SGGIFLLQMPKILDHF	13162
2V36	CD	TRANSFERASE	C	1.0	2.0	2	16	AIDAAVAIQFALNVTE	13163
2V4J	AB	OXIDOREDUCTASE	A	2.0	2.0	1	9	IEAEVVNRC	13164
2V7Q	CF	HYDROLASE	F	2.0	2.0	1	9	PAPATTFAH	13165
2V7Q	CJ	HYDROLASE	C	2.0	2.0	1	24	RAMKQVAGTMKLELAQYREVAAFA	13166
2VDB	AB	PROTEIN BINDING	A	2.0	2.0	1	8	VCKNYAEA	13167
2VE7	AC	CELL CYCLE	A	2.0	2.0	1	31	AFKLESLEAKNRALNEQIARLEQERSTANKA	13168
2VGL	AS	PROTEIN TRANSPORT	A	2.0	2.0	1	12	PWLSVKLLRLLQ	13169
2VGL	AS	PROTEIN TRANSPORT	S	2.0	2.0	1	7	ELDLVFN	13170
2VRC	AD	OXIDOREDUCTASE	A	1.0	2.0	2	18	NTLLIVQHANVVKAARDA	13171
2W73	AK	METAL BINDING PROTEIN	A	2.0	2.0	1	9	YEEFVQMMT	13172
2W80	GH	IMMUNE SYSTEM	G	2.0	2.0	1	6	ENMRRP	13173
2WAQ	CE	TRANSCRIPTION	E	2.0	2.0	1	8	LNEIALNE	13174
2WB1	BN	TRANSCRIPTION	N	2.0	2.0	1	5	SEVIH	13175
2WC0	AD	HYDROLASE/HORMONE	D	2.0	2.0	1	11	SHLVEALYLVC	13176
2WD7	AD	OXIDOREDUCTASE	D	2.0	2.0	1	11	EEEKDKWRRKV	13177
2WHP	AB	HYDROLASE	A	2.0	2.0	1	11	DLAAEAVVLHY	13178
2WIN	CM	IMMUNE SYSTEM	M	2.0	2.0	1	21	TYYKRTIKISGQKAMYALKSK	13179
2WIN	DP	IMMUNE SYSTEM	P	2.0	2.0	1	17	EYQNEKLANELKSLLDE	13180
2WIN	EP	IMMUNE SYSTEM	P	2.0	2.0	1	21	TYYKRTIKISGQKAMYALKSK	13181
2WIN	LN	IMMUNE SYSTEM	L	2.0	2.0	1	5	VKDME	13182
2Z2S	GH	TRANSCRIPTION	G	2.0	2.0	1	12	VATWIFTIARNR	13183
2ZET	BD	SIGNALING PROTEIN	B	2.0	2.0	1	5	RSLTT	13184
2ZFD	AB	SIGNALING PROTEIN/TRANSFERASE	A	2.0	2.0	1	13	IDDKIHFSFQLYD	13185
2ZME	AB	PROTEIN TRANSPORT	A	2.0	2.0	1	15	PEFRVQFQDMCATIG	13186
2ZYZ	CD	SPLICING	D	2.0	2.0	1	11	ATDITRGGRLS	13187
3A0B	ad	ELECTRON TRANSPORT	d	2.0	2.0	1	14	VAAIFRFLLFFQGF	13188
3A0B	de	ELECTRON TRANSPORT	e	2.0	2.0	1	7	LAYDVFG	13189
3A0B	de	ELECTRON TRANSPORT	e	2.0	2.0	1	13	AKQQVETFLEQLK	13190
3A1G	CD	TRANSFERASE	D	2.0	2.0	1	10	SRTREILTKT	13191
3B4V	AD	HORMONE REGULATOR COMPLEX	A	2.0	2.0	1	12	FHSTVINHYRMR	13192
3B4V	EH	HORMONE REGULATOR COMPLEX	H	2.0	2.0	1	12	SCHMRQATCFLG	13193
3B71	AD	PROTEIN BINDING	A	2.0	2.0	1	37	SLQQEYKKQMLTAAHALAVDAKNLLDVIDQARLKMLG	13194

3BBN	NS	RIBOSOME	N	2.0	2.0	1	6	EIHGKL	13195
3BC1	AB	SIGNALING PROTEIN/TRANSPORT PROTEIN	A	1.0	2.0	2	19	ISHAIEMLLDLIMKRMERS	13196
3BC1	EB	SIGNALING PROTEIN/TRANSPORT PROTEIN	E	2.0	2.0	1	7	RSLTTAF	13197
3BG0	AB	PROTEIN TRANSPORT, HYDROLASE	B	2.0	2.0	1	8	KLIMKERR	13198
3BIM	EM	TRANSCRIPTION REPRESSOR	E	2.0	2.0	1	9	EHVVDTCRK	13199
3BIM	HP	TRANSCRIPTION REPRESSOR	H	2.0	2.0	1	11	EHVVDTCRKFI	13200
3BLW	AB	OXIDOREDUCTASE	A	2.0	2.0	1	11	VDNASMQAVAK	13201
3BP8	AC	TRANSCRIPTION	A	2.0	2.0	1	16	LLDRIISHIDQFFIRH	13202
3BUA	BF	DNA BINDING PROTEIN	F	2.0	2.0	1	6	GLALKY	13203
3BZ1	AD	ELECTRON TRANSPORT	A	2.0	2.0	1	5	ICVAY	13204
3BZ1	BD	ELECTRON TRANSPORT	B	2.0	2.0	1	6	RYQWDS	13205
3BZ1	CZ	ELECTRON TRANSPORT	Z	2.0	2.0	1	28	TILFQLALAALVILSFVMVIGVPVAYAS	13206
3C0R	CD	CELL CYCLE, HYDROLASE	C	2.0	2.0	1	5	DAILD	13207
3C14	BC	LYASE/LYASE INHIBITOR	C	1.0	2.0	2	10	RDERRKWIQC	13208
3C72	AB	TRANSFERASE	A	2.0	2.0	1	15	KWCLLTIILLMRALD	13209
3CDK	AB	TRANSFERASE	B	2.0	2.0	1	10	SAESFAMIRG	13210
3CI0	IK	PROTEIN TRANSPORT	I	2.0	2.0	1	22	HVLEEKTVAGWVAENQTALLYL	13211
3CIP	AG	STRUCTURAL PROTEIN	A	2.0	2.0	1	8	KEEYDESG	13212
3CUQ	BC	PROTEIN TRANSPORT	C	1.0	2.0	2	22	VDTRQKQLAAWCSLVLSFCRLH	13213
3CWB	AD	OXIDOREDUCTASE	A	2.0	2.0	1	7	YNRIRSG	13214
3CXH	AE	OXIDOREDUCTASE	A	2.0	2.0	1	14	HPNRVLEHLHSTAF	13215
3CXH	DE	OXIDOREDUCTASE	E	2.0	2.0	1	33	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSMT	13216
3CXH	DF	OXIDOREDUCTASE	D	2.0	2.0	1	17	TSQMAKDVTTFLNWCAE	13217
3D5B	QZ	RIBOSOME	Q	2.0	2.0	1	15	AQQIEAARVAMVRHF	13218
3D5B	X2	RIBOSOME	2	2.0	2.0	1	25	PVELEKLVREKKRELMELRFQASIG	13219
3DBH	GH	CELL CYCLE	G	2.0	2.0	1	22	NYQVEEDIGKLKSCLTGFLQEY	13220
3DBJ	GH	PHOTOSYNTHESIS	G	2.0	2.0	1	25	EEMTATCLRDLDYYLRLVTYGIVAG	13221
3DCG	CD	LIGASE/VIRAL PROTEIN	C	2.0	2.0	1	12	VFELKRIVEGIL	13222
3DHR	GH	OXYGEN STORAGE, OXYGEN TRANSPORT	H	2.0	2.0	1	20	PENFRLLGDILVIILAAHFG	13223
3DOM	CD	TRANSCRIPTION	D	2.0	2.0	1	15	VEFVKHELNRLLSKN	13224
3DUF	AD	OXIDOREDUCTASE/TRANSFERASE	D	2.0	2.0	1	14	ESGIGGLAIGLALQ	13225
3DUF	EF	OXIDOREDUCTASE/TRANSFERASE	E	2.0	2.0	1	14	GDFYEGINFAGAFK	13226
3DXC	AB	PROTEIN BINDING	A	2.0	2.0	1	23	ASLSEAVQAACMLRYQKCLDARS	13227
3DZU	AD	TRANSCRIPTION/DNA	D	2.0	2.0	1	23	VKPIEDIQDNLLQALELQLKLNH	13228
3EXG	36	OXIDOREDUCTASE	6	2.0	2.0	1	6	KILEDN	13229
3EXG	AB	OXIDOREDUCTASE	B	2.0	2.0	1	15	EMGFAGIAVGAAMAG	13230
3EXG	AP	OXIDOREDUCTASE	A	2.0	2.0	1	28	REDGLKYYRMMQTVRRMELKADQLYKQK	13231

3EXH	AD	OXIDOREDUCTASE	D	1.0	2.0	2	12	VKDIIFAIKKTL	13232
3EXH	AG	OXIDOREDUCTASE	A	2.0	2.0	1	17	AQVPLGAGIALACKYNG	13233
3EZB	AB	TRANSFERASE	A	1.0	2.0	2	15	EEKEAIFEGHIMLLE	13234
3EZQ	MN	APOPTOSIS	M	2.0	2.0	1	15	SDVDLSKYITTIAGV	13235
3F1E	DE	RIBOSOME	E	2.0	2.0	1	9	AVPRAILEL	13236
3F8U	CB	IMMUNE SYSTEM/ISOMERASE	C	2.0	2.0	1	13	EAHSEFLKAASNL	13237
3FIE	AC	HYDROLASE, TOXIN/PROTEIN TRANSPORT	A	2.0	2.0	1	12	INEYKDYFQWKY	13238
3FIN	FP	RIBOSOME	F	2.0	2.0	1	12	PHLLWEVVRWQL	13239
3FKS	CF	HYDROLASE	C	2.0	2.0	1	12	RSTVAQLVQTLE	13240
3FKU	KJ	VIRAL PROTEIN/IMMUNE SYSTEM	J	2.0	2.0	1	40	GFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	13241
3FWC	IJ	CELL CYCLE, TRANSCRIPTION	I	2.0	2.0	1	11	DEELRAMIEEF	13242
3G3B	CD	HYDROLASE/IMMUNE SYSTEM	D	2.0	2.0	1	8	VAWRNRCK	13243
3G9K	DF	HYDROLASE	D	2.0	2.0	1	9	LDLAKPRIY	13244
3G9K	DF	HYDROLASE	D	2.0	2.0	1	6	GVTLLQ	13245
3GE8	DF	OXIDOREDUCTASE	D	2.0	2.0	1	5	ERMSG	13246
3GHG	BC	BLOOD CLOTTING	C	2.0	2.0	1	6	QSLEDI	13247
3GHG	DE	BLOOD CLOTTING	E	1.0	2.0	2	9	GCQLQEALL	13248
3GHG	GH	BLOOD CLOTTING	H	2.0	2.0	1	11	GCQLQEALLQQ	13249
3GLH	FG	TRANSFERASE	F	1.0	2.0	2	15	LLALAQALERLSLLW	13250
3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	2.0	2.0	1	18	FDIASDAFATFKDLLTRH	13251
3H0L	AC	LIGASE	C	2.0	2.0	1	11	REWVLKIAKLA	13252
3H0L	JK	LIGASE	J	2.0	2.0	1	13	IFEMYARTRDEGF	13253
3H4P	Lm	HYDROLASE	m	2.0	2.0	1	6	LYKMRT	13254
3HEI	MN	TRANSFERASE/SIGNALING PROTEIN	M	2.0	2.0	1	6	SSDFEA	13255
3HGK	BE	TRANSFERASE	B	2.0	2.0	1	7	PEYFIKG	13256
3HKZ	DL	TRANSFERASE	L	2.0	2.0	1	13	HTLGNLIAGTLRR	13257
3HKZ	EF	TRANSFERASE	F	2.0	2.0	1	6	TYDYLN	13258
3HKZ	MJ	TRANSFERASE	J	2.0	2.0	1	13	YAFKLLIQELMSM	13259
3HOU	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	2.0	2.0	1	11	EIIQNAQRDAV	13260
3HOU	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	2.0	2.0	1	10	YCCRRMILTH	13261
3HOU	NV	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	V	2.0	2.0	1	10	YCCRRMILTH	13262
3HOU	OV	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	V	2.0	2.0	1	7	LIEKFLR	13263
3HRZ	CD	IMMUNE SYSTEM	C	2.0	2.0	1	9	VPLQIEKAC	13264
3I3T	EF	HYDROLASE	E	2.0	2.0	1	16	AQEFLKLLMERLHLEI	13265

3I3T	GH	HYDROLASE	G	2.0	2.0	1	16	AQEFLKLLMERLHLEI	13266
3PRO	AC	PRO REGION	C	2.0	2.0	1	17	LKQLQSAMEQLDAGANA	13267
12 E8	MP	IMMUNOGLOBULIN	M	1.9	1.9	1	5	SEQLT	13268
1A3R	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.9	1.9	1	6	SEQLTS	13269
1A4Y	DE	COMPLEX (INHIBITOR/NUCLEASE)	D	1.9	1.9	1	14	EEMEDRLQALEKDK	13270
1AGR	AE	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	E	1.9	1.9	1	14	DEAQKKIFNLMEKD	13271
1AO7	AD	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)	A	1.9	1.9	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	13272
1AOI	AB	DNA BINDING PROTEIN/DNA	B	1.9	1.9	1	12	AMDVVYALKRQG	13273
1AOI	GH	DNA BINDING PROTEIN/DNA	H	1.9	1.9	1	19	ELAKHAVSEGTKAVTKYTS	13274
1B33	EF	PHOTOSYNTHESIS	E	1.9	1.9	1	14	GEKRLRIAQILTDN	13275
1B8D	KL	PHOTOSYNTHESIS	K	1.9	1.9	1	9	GPVDEWGIA	13276
1B8D	KL	PHOTOSYNTHESIS	L	1.9	1.9	1	14	GNKRLDAVNYIVSN	13277
1B9X	AB	SIGNALING PROTEIN	B	1.9	1.9	1	17	EKDKLKMEVDQLKKEVT	13278
1BFO	CD	ANTIBODY	C	1.9	1.9	1	5	TEQLA	13279
1BGY	JK	ELECTRON TRANSPORT	K	1.9	1.9	1	21	NWVPTAQLWGAVGAVGLVSAT	13280
1BGY	VW	ELECTRON TRANSPORT	W	1.9	1.9	1	21	NWVPTAQLWGAVGAVGLVSAT	13281
1BI4	AB	DNA INTEGRATION	A	1.9	1.9	1	13	GQETAYFLLKLAG	13282
1BJO	AB	AMINOTRANSFERASE	A	1.9	1.9	1	10	AEVLKQAQQE	13283
1BR1	CD	MUSCLE PROTEIN	C	1.9	1.9	1	5	FQEFR	13284
1BXN	AI	LYASE	A	1.9	1.9	1	16	ILNEGPEILRDAARWC	13285
1BXR	EF	AMIDOTRANSFERASE	E	1.9	1.9	1	21	RWFLVQIEELVRLEEKVAEVG	13286
1CC1	SL	OXIDOREDUCTASE	L	1.9	1.9	1	10	PRDSSQIVQR	13287
1CDL	BF	CALCIUM-BINDING PROTEIN	B	1.9	1.9	1	16	DTDSEEEIREAFRVFD	13288
1CPC	AB	LIGHT HARVESTING PROTEIN	A	1.9	1.9	1	12	PLTEAVAAADSQ	13289
1D2Z	CB	APOPTOSIS	B	1.9	1.9	1	13	DNDIYRLAKILDE	13290
1D3B	IJ	RNA BINDING PROTEIN	I	1.9	1.9	1	9	PIKVLHEAE	13291
1DE4	DF	METAL TRANSPORT INHIBITOR/RECEPTOR	F	1.9	1.9	1	23	QWLYSARGDFFRATSRLTTDFGN	13292
1DEE	DG	IMMUNE SYSTEM	G	1.9	1.9	1	14	EAQRNGFIQSLKDD	13293
1DFK	AY	CONTRACTILE PROTEIN	Y	1.9	1.9	1	10	DKELTAMLKE	13294
1DFL	AZ	CONTRACTILE PROTEIN	Z	1.9	1.9	1	18	QDEIDDLKDVFELFDFWD	13295
1E3A	AB	ANTIBIOTIC RESISTANCE	A	1.9	1.9	1	10	PDAIRAQIAA	13296
1E3D	AB	HYDROGENASE	A	1.9	1.9	1	5	EEARK	13297
1E3D	AB	HYDROGENASE	B	1.9	1.9	1	6	IETILK	13298
1E6Y	AC	OXIDOREDUCTASE	C	1.9	1.9	1	11	SVAANRRKHMS	13299
1E6Y	BC	OXIDOREDUCTASE	C	1.9	1.9	1	6	STRENV	13300
1E6Y	DC	OXIDOREDUCTASE	D	1.9	1.9	1	13	LDMAHETLEKRLG	13301
1E7P	EF	OXIDOREDUCTASE	F	1.9	1.9	1	15	DKTRANLKKLKTLMS	13302

1EBD	AC	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)	A	1.9	1.9	1	7	AEDIALT	13303
1EP3	AB	OXIDOREDUCTASE	A	1.9	1.9	1	6	TANFAD	13304
1EUV	AB	HYDROLASE	A	1.9	1.9	1	7	VRDFKTL	13305
1EYS	CM	ELECTRON TRANSPORT	M	1.9	1.9	1	8	WYLWAVKH	13306
1EYS	LM	ELECTRON TRANSPORT	L	1.9	1.9	1	26	ALAIHRLGLFLALSAAFWSAVCILIS	13307
1F80	AE	TRANSFERASE	A	1.9	1.9	1	6	LKRIAS	13308
1F93	DH	TRANSCRIPTION	D	1.9	1.9	1	10	RVALQAEKLD	13309
1F99	AB	PHOTOSYNTHESIS	A	1.9	1.9	1	9	GPMDDYLVA	13310
1FCD	AC	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	A	1.9	1.9	1	20	GYSANSQGKVAAAAVVVLLK	13311
1FCD	BD	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	D	1.9	1.9	1	7	AEMLTNN	13312
1FNT	EM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.9	1.9	1	7	VKWYHFD	13313
1FNT	JK	HYDROLASE/HYDROLASE ACTIVATOR	K	1.9	1.9	1	14	YSGFYTFSLLDHHY	13314
1FS1	AB	LIGASE	B	1.9	1.9	1	16	KGLLDVTCKTVANMIK	13315
1FS2	AB	LIGASE	A	1.9	1.9	1	11	DELLLGIFSCL	13316
1FS2	AD	LIGASE	A	1.9	1.9	1	11	EFALQTLLSSC	13317
1FYZ	BD	OXIDOREDUCTASE	B	1.9	1.9	1	6	SDGFIS	13318
1FYZ	CE	OXIDOREDUCTASE	E	1.9	1.9	1	12	DTRDAWVNKIAQ	13319
1G0U	1N	HYDROLASE	N	1.9	1.9	1	19	KEETVDFIKHSLSQAIKWD	13320
1G0U	GN	HYDROLASE	N	1.9	1.9	1	22	AADTQAIADIVQYHLELYTSQY	13321
1G0U	HN	HYDROLASE	H	1.9	1.9	1	15	VVSALQMLKQHLFKY	13322
1G0U	MN	HYDROLASE	M	1.9	1.9	1	20	ISDMQHIERLLKDLVTENAY	13323
1G0U	SZ	HYDROLASE	S	1.9	1.9	1	22	APDARVLSNYLRQQCNYSSLVF	13324
1G20	CD	OXIDOREDUCTASE	D	1.9	1.9	1	11	LWHLRSLVFTD	13325
1G2C	CD	VIRAL PROTEIN	C	1.9	1.9	1	47	EGEVNKIKSALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIV	13326
1G4B	FM	CHAPERONE/HYDROLASE	M	1.9	1.9	1	16	ADAFTLFELFERKLEM	13327
1G8K	GH	OXIDOREDUCTASE	G	1.9	1.9	1	7	SLMQERY	13328
1GH0	OV	PHOTOSYNTHESIS	O	1.9	1.9	1	17	DAAVEANSYLDYAINAL	13329
1GH0	UV	PHOTOSYNTHESIS	V	1.9	1.9	1	14	SNKRLDVVNRITSN	13330
1GPQ	BC	HYDROLASE/INHIBITOR	B	1.9	1.9	1	5	SLENH	13331
1H2A	SL	OXIDOREDUCTASE	L	1.9	1.9	1	29	KNATYIRNLVLGAQYLHDHIVHFYHLHAL	13332
1HBM	AE	METHANOGENESIS	A	1.9	1.9	1	12	EDQAETLKAEVG	13333
1HLE	AB	HYDROLASE INHIBITOR (SERINE PROTEINASE)	A	1.9	1.9	1	6	EKIEKQ	13334
1HQR	AB	IMMUNE SYSTEM	A	1.9	1.9	1	22	AQGALANIAVDKANLEIMTKRS	13335
1HQR	BD	IMMUNE SYSTEM	B	1.9	1.9	1	10	YCRHNYGVGE	13336
1HR0	FR	RIBOSOME	R	1.9	1.9	1	17	GKEQRILAKTIKRARIL	13337

1HV4	GF	OXYGEN STORAGE/TRANSPORT	G	1.9	1.9	1	19	PVNFKFLGHCFLVVVAIHH	13338
1I5K	BD	BLOOD CLOTTING	D	1.9	1.9	1	22	ADAELQRLKNERHEEAELERLK	13339
1I7W	AB	CELL ADHESION	A	1.9	1.9	1	14	EGVATYAAAVLFRM	13340
1I7Z	CD	IMMUNE SYSTEM	C	1.9	1.9	1	7	DEQLKSG	13341
1I84	VW	CONTRACTILE PROTEIN	W	1.9	1.9	1	7	NAEVMKV	13342
1IBT	CD	LYASE	D	1.9	1.9	1	9	PDKDMEIME	13343
1IBT	EF	LYASE	F	1.9	1.9	1	9	PDKDMEIME	13344
1IR2	U3	LYASE	U	1.9	1.9	1	14	AKNYGRAVYECLRG	13345
1IR2	Y7	LYASE	Y	1.9	1.9	1	21	NAPGAAANRVALEACTQARNE	13346
1IRU	I2	HYDROLASE	2	1.9	1.9	1	15	YGAYLAQPLLREVLE	13347
1IW7	MN	TRANSFERASE	N	1.9	1.9	1	8	SFAQAEAR	13348
1IW7	MP	TRANSFERASE	M	1.9	1.9	1	11	PEERLLRSIFG	13349
1J3I	AD	OXIDOREDUCTASE, TRANSFERASE	A	1.9	1.9	1	13	SLDMKYFCAVTTY	13350
1JB0	AB	PHOTOSYNTHESIS	A	1.9	1.9	1	30	GWDHVFLGLFWMYNCISVVIFHFSWKMQSD	13351
1JD2	HI	HYDROLASE	H	1.9	1.9	1	22	AADTEAVTQLIGSNIELHSLYT	13352
1JD2	IR	HYDROLASE	R	1.9	1.9	1	13	VGELFWKVKEEEG	13353
1JD2	ST	HYDROLASE	T	1.9	1.9	1	14	FGAHMANPLLRKVV	13354
1JD2	TN	HYDROLASE	N	1.9	1.9	1	19	KEETVDFIKHSLSQAIKWD	13355
1JD2	WQ	HYDROLASE	Q	1.9	1.9	1	22	AGDTVQFAEYIQANIQLYSIRE	13356
1JNH	AB	IMMUNE SYSTEM	A	1.9	1.9	1	6	SEELET	13357
1JTD	AB	HYDROLASE/INHIBITOR	A	1.9	1.9	1	6	PVTEKH	13358
1K5D	DE	SIGNALING PROTEIN/SIGNALING ACTIVATOR	D	1.9	1.9	1	12	KPFLWLARKLIG	13359
1K5D	JK	SIGNALING PROTEIN/SIGNALING ACTIVATOR	J	1.9	1.9	1	12	KPFLWLARKLIG	13360
1KCG	AC	IMMUNE SYSTEM	C	1.9	1.9	1	31	SGLTTFFKMVSMRDCKSWLRDFLMHRKKRLE	13361
1KF6	AB	OXIDOREDUCTASE	B	1.9	1.9	1	13	LLDALGYIKDNLA	13362
1KFY	AB	OXIDOREDUCTASE	B	1.9	1.9	1	13	LLDALGYIKDNLA	13363
1KG0	AB	VIRAL PROTEIN/IMMUNE SYSTEM	A	1.9	1.9	1	22	AQGALANIAVDKANLEIMTKRS	13364
1KIL	AE	MEMBRANE PROTEIN	E	1.9	1.9	1	37	EEERQEALRQAEEERKAKYAKMEAEREVMRQGIRDKY	13365
1KPS	AB	LIGASE/PROTEIN TRANSPORT	A	1.9	1.9	1	10	AEAYTIYCQN	13366
1KYO	BR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.9	1.9	1	10	PIMQTALRRL	13367
1KZ7	AB	SIGNALING PROTEIN	A	1.9	1.9	1	23	ELLDTERAYVEELLCVLEGYAAE	13368
1KZ7	AB	SIGNALING PROTEIN	A	1.9	1.9	1	22	EFQIYEKYCQNKPRSESLWRQC	13369
1L4A	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.9	1.9	1	7	AGKLKRK	13370
1L9J	LM	PHOTOSYNTHESIS	L	1.9	1.9	1	17	HIPFAFAFAILAYLTLV	13371
1L9J	RS	PHOTOSYNTHESIS	R	1.9	1.9	1	28	GLWQIITICATGAFVSWALREVEICRKL	13372
1LB1	GH	SIGNALING PROTEIN	G	1.9	1.9	1	39	EEESLAILRRHVMNELLDTERAYVEELLCVLEGYAAEMD	13373
1LEN	AB	LECTIN	B	1.9	1.9	1	5	LKDVV	13374

1LGH	AB	LIGHT HARVESTING COMPLEX	A	1.9	1.9	1	5	DYKIW	13375
1LGH	DE	LIGHT HARVESTING COMPLEX	D	1.9	1.9	1	5	DYKIW	13376
1LGH	GH	LIGHT HARVESTING COMPLEX	G	1.9	1.9	1	5	DYKIW	13377
1LGH	JK	LIGHT HARVESTING COMPLEX	J	1.9	1.9	1	5	DYKIW	13378
1LOC	AB	LECTIN	B	1.9	1.9	1	5	LKEFV	13379
1LQB	AB	GENE REGULATION	A	1.9	1.9	1	12	VFELKRIVEGIL	13380
1LQS	RL	IMMUNE SYSTEM	L	1.9	1.9	1	5	KPTLQ	13381
1LTX	AR	TRANSFERASE/PROTEIN BINDING	A	1.9	1.9	1	20	EKSTVLQSELESCKELQELE	13382
1LUJ	AB	STRUCTURAL PROTEIN	A	1.9	1.9	1	15	ENIQRVAAGVLCELA	13383
1LUJ	AB	STRUCTURAL PROTEIN	B	1.9	1.9	1	19	PEEMYIQQKVRVLLMLRKM	13384
1M1Y	AB	OXIDOREDUCTASE	A	1.9	1.9	1	15	DKKLAKLIDEVETLF	13385
1M1Y	AB	OXIDOREDUCTASE	A	1.9	1.9	1	6	FIFQKM	13386
1M1Y	IJ	OXIDOREDUCTASE	I	1.9	1.9	1	28	ESIQKKCEEVIAKYKPEWEAVVAKYRPR	13387
1M1Y	KJ	OXIDOREDUCTASE	J	1.9	1.9	1	17	ASLTKERGRLVDMMTDS	13388
1M1Y	KL	OXIDOREDUCTASE	K	1.9	1.9	1	28	ESIQKKCEEVIAKYKPEWEAVVAKYRPR	13389
1M2Z	AB	HORMONE/HORMONE ACTIVATOR	A	1.9	1.9	1	26	TWRIMTTLNMLGGRQVIAAVKWAKAI	13390
1M46	AB	CELL CYCLE PROTEIN	A	1.9	1.9	1	11	TEDFVKAFQVF	13391
1M56	AB	OXIDOREDUCTASE	B	1.9	1.9	1	17	PVATQIHWLDGFILVII	13392
1MHY	DG	OXIDOREDUCTASE	D	1.9	1.9	1	33	PASAKFLNTDLNNAFWTQQKYFTPVLGYLFEYG	13393
1MIO	AB	MOLYBDENUM-IRON PROTEIN	B	1.9	1.9	1	16	QGCCSYHRTVLSRHFK	13394
1MMO	DG	OXIDOREDUCTASE (MONOOXYGENASE)	D	1.9	1.9	1	33	PASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYG	13395
1MTP	AB	STRUCTURAL GENOMICS	A	1.9	1.9	1	14	PYSVACALGVLAAG	13396
1MTY	BG	MONOOXYGENASE	G	1.9	1.9	1	23	DNDYLWIEAKLEEKVAVLKARAF	13397
1MTY	EC	MONOOXYGENASE	C	1.9	1.9	1	13	KSARLAVEGLWQE	13398
1MVW	MO	CONTRACTILE PROTEIN	M	1.9	1.9	1	39	TATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	13399
1MWA	BH	IMMUNE SYSTEM	H	1.9	1.9	1	29	PEYWERETQKAKGNEQSFRVSLRTLLGYY	13400
1N4Q	GH	TRANSFERASE	G	1.9	1.9	1	17	PYLIAFLVDIYEDMLEN	13401
1N4Q	KL	TRANSFERASE	K	1.9	1.9	1	16	EKFRDVYDYFRAVLQR	13402
1N5W	AB	OXIDOREDUCTASE	A	1.9	1.9	1	8	EAEIRFGI	13403
1N73	BC	BLOOD CLOTTING	B	1.9	1.9	1	35	STVAGSLRSMKSVLEHLRAKMQRMEEAIKTQKELC	13404
1NAK	MI	IMMUNE SYSTEM	M	1.9	1.9	1	5	SEQLT	13405
1NBU	AC	LYASE	A	1.9	1.9	1	13	YVRLASRAAEIVA	13406
1NBW	CD	HYDROLASE	C	1.9	1.9	1	7	GVLVNNR	13407
1NIK	AB	TRANSCRIPTION	A	1.9	1.9	1	21	PQVCAKLFGNIQKVVNFWLLH	13408
1NIK	AF	TRANSCRIPTION	A	1.9	1.9	1	11	EETRAELSQLC	13409
1NIW	AB	SIGNALING PROTEIN/OXIDOREDUCTASE	A	1.9	1.9	1	13	SEEEIREAFRVFD	13410
1NIW	EF	SIGNALING PROTEIN/OXIDOREDUCTASE	E	1.9	1.9	1	7	AAELRHV	13411

1NT2	AB	RNA BINDING PROTEIN	B	1.9	1.9	1	7	FEESFLK	13412
1NTK	AB	OXIDOREDUCTASE	A	1.9	1.9	1	15	TTPVCEDIGRSLLTY	13413
1O18	PR	CONTRACTILE PROTEIN	P	1.9	1.9	1	22	AEIITATQARCRGFLMRVEYRA	13414
1O94	CD	ELECTRON TRANSPORT	D	1.9	1.9	1	15	PDVFEASVSALIAAH	13415
1ONV	AB	TRANSCRIPTION	B	1.9	1.9	1	18	SEADEMAKALEAELNDLM	13416
1OR0	CD	HYDROLASE	C	1.9	1.9	1	11	GADVVAHAHRL	13417
1OR7	AC	TRANSCRIPTION	A	1.9	1.9	1	12	QHKVASLVSRYV	13418
1OWS	AB	HYDROLASE	A	1.9	1.9	1	5	LKARC	13419
1P8D	AC	MEMBRANE PROTEIN/PROTEIN BINDING	A	1.9	1.9	1	8	PLLSEIWD	13420
1PHN	AB	ELECTRON TRANSPORT	B	1.9	1.9	1	14	GNKRLDVVNRITSN	13421
1PID	CD	HORMONE	C	1.9	1.9	1	7	LYQLENY	13422
1PIV	14	VIRUS	1	1.9	1.9	1	5	PSDTV	13423
1PLG	LH	IMMUNOGLOBULIN	L	1.9	1.9	1	7	SEQLTSG	13424
1PMX	AB	HORMONE/GROWTH FACTOR	A	1.9	1.9	1	12	AELVDALQFVCG	13425
1POV	13	VIRUS	1	1.9	1.9	1	8	VQLRRKLE	13426
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.9	1.9	1	14	MEGIHRWAIWMAVL	13427
1Q5R	GH	HYDROLASE	H	1.9	1.9	1	23	AGIAIELVRLFAVELEHYEKIEG	13428
1QGW	AC	PHOTOSYNTHESIS	C	1.9	1.9	1	6	AFSRVV	13429
1QVI	AY	CONTRACTILE PROTEIN	Y	1.9	1.9	1	11	EETIRNAFAMF	13430
1QVI	AZ	CONTRACTILE PROTEIN	Z	1.9	1.9	1	11	DEDVDEIIKLT	13431
1R1A	13	VIRUS	3	1.9	1.9	1	7	LIGEIAS	13432
1R27	CD	OXIDOREDUCTASE	C	1.9	1.9	1	6	SADWYN	13433
1R2B	BC	TRANSCRIPTION	B	1.9	1.9	1	15	HASDVLLNLNRLRSR	13434
1RH5	AB	PROTEIN TRANSPORT	A	1.9	1.9	1	19	FKEKLKWTGIVLVLYFIMG	13435
1RHI	13	VIRUS	1	1.9	1.9	1	8	VQLRKKLE	13436
1RM6	AC	OXIDOREDUCTASE	C	1.9	1.9	1	10	LLDYLRETVG	13437
1RU7	IH	VIRAL PROTEIN	I	1.9	1.9	1	10	YEELREQLSS	13438
1SHZ	DC	SIGNALING PROTEIN	D	1.9	1.9	1	29	QRAREEFRPTIYSNVIKGMRVLVDAREKL	13439
1SM3	LH	COMPLEX (ANTIBODY/PEPTIDE EPITOPE)	L	1.9	1.9	1	6	SEELET	13440
1SP4	AB	HYDROLASE	A	1.9	1.9	1	5	AREQW	13441
1T4K	CD	IMMUNE SYSTEM	C	1.9	1.9	1	6	SEQLTS	13442
1TFC	AC	TRANSCRIPTION	A	1.9	1.9	1	9	KLFLEMLEA	13443
1TI2	AB	OXIDOREDUCTASE	B	1.9	1.9	1	6	RCAHNC	13444
1TII	GC	ENTEROTOXIN	G	1.9	1.9	1	19	DNVMTAEMRKIAMAAVLSG	13445
1TOC	EF	COMPLEX (HYDROLASE/INHIBITOR)	E	1.9	1.9	1	5	FEKKQ	13446
1TQY	GH	TRANSFERASE	H	1.9	1.9	1	10	VNTGQISIRH	13447
1TU3	CI	PROTEIN TRANSPORT	I	1.9	1.9	1	32	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIR	13448
1TY4	BD	APOPTOSIS	B	1.9	1.9	1	17	YGRLIGLISFGGFVAAK	13449

1UEX	BC	TOXIN/BLOOD CLOTTING	C	1.9	1.9	1	7	KQIRLIE	13450
1UZD	EF	LYASE	E	1.9	1.9	1	14	AKNYGRAVYECLRG	13451
1UZD	VW	LYASE	V	1.9	1.9	1	14	AKNYGRAVYECLRG	13452
1UZH	OT	LYASE	T	1.9	1.9	1	14	DEQIAAQVDYIVAN	13453
1V54	BH	OXIDOREDUCTASE	H	1.9	1.9	1	14	ISWVSTWDDRRAEG	13454
1V54	DE	OXIDOREDUCTASE	E	1.9	1.9	1	12	AWELRKGMNTLV	13455
1VF5	AC	PHOTOSYNTHESIS	A	1.9	1.9	1	29	GWLIRSIHRWSASMMVLMMILHVFRVYLT	13456
1VF5	SU	PHOTOSYNTHESIS	S	1.9	1.9	1	26	EMLYAALLSFGLIFVGWGLGVLLLKI	13457
1VYW	CD	TRANSFERASE	C	1.9	1.9	1	11	STAIREISLLK	13458
1WCM	AF	TRANSCRIPTION	A	1.9	1.9	1	12	EETRAELSQLCA	13459
1WDD	EW	LYASE	E	1.9	1.9	1	20	WRDRFVFCAEAIYKSQAETG	13460
1WMI	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.9	1.9	1	20	DVLKELERLKVEIQRLEAML	13461
1WYU	AB	OXIDOREDUCTASE	A	1.9	1.9	1	5	QYIRR	13462
1WYU	EF	OXIDOREDUCTASE	F	1.9	1.9	1	5	IFERS	13463
1WYU	GH	OXIDOREDUCTASE	G	1.9	1.9	1	11	EEEIREMLRRV	13464
1X86	CD	SIGNALING PROTEIN/MEMBRANE PROTEIN	C	1.9	1.9	1	31	PCEIKRQEVINELFYTERAHVRTLKVLDQVF	13465
1X86	CD	SIGNALING PROTEIN/MEMBRANE PROTEIN	C	1.9	1.9	1	22	IIPTQMQRLTKYPLLLDNIAKY	13466
1XFU	FT	LYASE/METAL BINDING PROTEIN	F	1.9	1.9	1	5	PITKA	13467
1XLS	AI	TRANSCRIPTION	A	1.9	1.9	1	22	PVTNICQAADKQLFTLVEWAKR	13468
1Y14	CD	TRANSFERASE	C	1.9	1.9	1	8	ADEAKTLI	13469
1Y74	AD	TRANSPORT PROTEIN	A	1.9	1.9	1	12	QKLQALQRVLQS	13470
1Y8H	CD	OXYGEN STORAGE/TRANSPORT	C	1.9	1.9	1	16	AGEYGAEALERMFLGF	13471
1Y96	AB	RNA BINDING PROTEIN	A	1.9	1.9	1	8	PLEWQDYI	13472
1YE9	KN	OXIDOREDUCTASE	N	1.9	1.9	1	7	FFAENEQ	13473
1Z2C	AB	SIGNALING PROTEIN	B	1.9	1.9	1	14	IVIKREMVSQYLHT	13474
1Z2C	CD	SIGNALING PROTEIN	D	1.9	1.9	1	10	LFEQMLVDMN	13475
1Z6O	BP	METAL BINDING PROTEIN	B	1.9	1.9	1	16	LSLALYVFDEYLQKTV	13476
1Z6O	GR	METAL BINDING PROTEIN	G	1.9	1.9	1	16	LSLALYVFDEYLQKTV	13477
1Z7Q	ab	HYDROLASE/HYDROLASE ACTIVATOR	a	1.9	1.9	1	22	AADGDALVKRFKNSVKWYHFDH	13478
1Z7Q	Ib	HYDROLASE/HYDROLASE ACTIVATOR	b	1.9	1.9	1	18	VQVAEEAIVNAMRVLYYR	13479
1Z7Q	Sa	HYDROLASE/HYDROLASE ACTIVATOR	S	1.9	1.9	1	23	TADARSMIEHARTAAVTHNLYYD	13480
1ZBB	ef	STRUCTURAL PROTEIN/DNA	e	1.9	1.9	1	13	TVALREIRRYQKS	13481
1ZVV	BP	TRANSCRIPTION/DNA	B	1.9	1.9	1	17	MYDIGAVAMRLLTKYMN	13482
1ZVV	GJ	TRANSCRIPTION/DNA	J	1.9	1.9	1	5	IMGLM	13483
2AA1	AB	OXYGEN STORAGE/TRANSPORT	A	1.9	1.9	1	19	PSNFKILNHCILVVISTMF	13484
2ACZ	BC	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.9	1.9	1	27	FEAGKRSAKISFVITVVLSLLAGVLVW	13485
2AFH	AB	OXIDOREDUCTASE	A	1.9	1.9	1	6	CPIGLI	13486

2AFH	CD	OXIDOREDUCTASE	C	1.9	1.9	1	6	CPIGLI	13487
2AUS	AB	ISOMERASE/STRUCTURAL PROTEIN	A	1.9	1.9	1	12	SHEVVAWIKRIL	13488
2AXT	ac	ELECTRON TRANSPORT	c	1.9	1.9	1	28	PRSWLATSHFVLAFFFLVGHLWHAGRAR	13489
2AXT	ad	ELECTRON TRANSPORT	d	1.9	1.9	1	9	AIHGATVEN	13490
2B5I	AD	CYTOKINE/CYTOKINE RECEPTOR	A	1.9	1.9	1	8	KLTRMLTF	13491
2BE6	AD	MEMBRANE PROTEIN	A	1.9	1.9	1	9	YEEFVQMMT	13492
2BEC	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	A	1.9	1.9	1	15	QASLLRLHHRFRALD	13493
2BL0	AC	MUSCLE PROTEIN	C	1.9	1.9	1	11	KAALQDALLNL	13494
2BR2	ST	HYDROLASE	S	1.9	1.9	1	17	NAIELARVVDRSLRDSK	13495
2BS4	DE	OXIDOREDUCTASE	D	1.9	1.9	1	21	QKVARMFVNTAPKAIRELAAW	13496
2BV8	ML	PHOTOSYNTHESIS	M	1.9	1.9	1	8	LSEINRSF	13497
2CCI	CD	CELL CYCLE	C	1.9	1.9	1	5	AKAAL	13498
2CKF	AB	OXIDOREDUCTASE	B	1.9	1.9	1	12	FEELKQRVERLY	13499
2CLY	AB	HYDROLASE	B	1.9	1.9	1	8	QVDAEEKE	13500
2CZV	AD	HYDROLASE	A	1.9	1.9	1	10	HVLAKLMVKK	13501
2D1P	HF	TRANSLATION	H	1.9	1.9	1	6	GVFQLL	13502
2D1P	HI	TRANSLATION	I	1.9	1.9	1	7	FAALLRL	13503
2DD4	BL	HYDROLASE	B	1.9	1.9	1	8	HTLFRAYT	13504
2DFS	MO	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	O	1.9	1.9	1	9	LGTVMRSLG	13505
2DFS	MQ	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	Q	1.9	1.9	1	9	LGTVMRSLG	13506
2DPP	AB	LYASE	A	1.9	1.9	1	8	PRQVLKEF	13507
2DQF	BC	IMMUNE SYSTEM/HYDROLASE	C	1.9	1.9	1	11	TASVNCAKKIV	13508
2EHO	KH	REPLICATION	H	1.9	1.9	1	19	NADISQSLLQTFIGRFRRI	13509
2EQ9	KL	OXIDOREDUCTASE	K	1.9	1.9	1	6	LTDLAL	13510
2F8N	EK	STRUCTURAL PROTEIN/DNA	E	1.9	1.9	1	13	TVALREIRRYQKS	13511
2FBW	PQ	OXIDOREDUCTASE	P	1.9	1.9	1	11	FPHYVAVVKSL	13512
2FHX	AB	HYDROLASE, METAL BINDING PROTEIN	B	1.9	1.9	1	16	NLGTQTLMDWVAKTMK	13513
2FO1	AD	GENE REGULATION/SIGNALLING PROTEIN/DNA	D	1.9	1.9	1	6	AFHSGE	13514
2FRV	EF	OXIDOREDUCTASE	E	1.9	1.9	1	5	PEAKK	13515
2FRV	GH	OXIDOREDUCTASE	G	1.9	1.9	1	5	PEAKK	13516
2FSE	AB	IMMUNE SYSTEM, STRUCTURAL PROTEIN	A	1.9	1.9	1	7	EEFGRFA	13517
2FUG	AB	OXIDOREDUCTASE	B	1.9	1.9	1	12	IMPLLRRVQQEE	13518
2FUG	JK	OXIDOREDUCTASE	J	1.9	1.9	1	17	RRAADRLEQAIKEARAR	13519
2FUG	MP	OXIDOREDUCTASE	P	1.9	1.9	1	5	CEEAC	13520

2FUG	VY	OXIDOREDUCTASE	Y	1.9	1.9	1	5	CEEAC	13521
2FYN	EF	OXIDOREDUCTASE	F	1.9	1.9	1	5	RDFLY	13522
2FYN	PO	OXIDOREDUCTASE	P	1.9	1.9	1	11	IGHSIQTWLLG	13523
2FYN	QR	OXIDOREDUCTASE	R	1.9	1.9	1	5	RDFLY	13524
2FYZ	CD	PROTEIN BINDING	C	1.9	1.9	1	49	AVSLVQAQTNARAIAAMKNSIQATNRAVFEVKEGTQRLAIAVQAIQDHI	13525
2G5B	GH	APOPTOSIS	G	1.9	1.9	1	6	SEQLTS	13526
2GAG	AB	OXIDOREDUCTASE	B	1.9	1.9	1	15	HDHVAWAFARKANEM	13527
2GAG	BD	OXIDOREDUCTASE	B	1.9	1.9	1	15	FHVIQEQMAAAVELF	13528
2GWW	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.9	1.9	1	48	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVAE	13529
2H4M	AC	PROTEIN TRANSPORT	A	1.9	1.9	1	13	ALVRSITCWTLSR	13530
2H4P	AB	HYDROLASE INHIBITOR	A	1.9	1.9	1	15	ENIHSGFKELLTAFN	13531
2HDI	AB	PROTEIN TRANSPORT, ANTIMICROBIAL PROTEIN	B	1.9	1.9	1	26	VEGDKKIYNAEVAEWDKLRQRLLDAR	13532
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	A	1.9	1.9	1	7	EELNKLL	13533
2HIO	CD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	D	1.9	1.9	1	11	AMDVVYALKRQ	13534
2HLD	GI	HYDROLASE	I	1.9	1.9	1	12	YAAYLNVAAQAI	13535
2HNT	EF	SERINE PROTEASE	E	1.9	1.9	1	8	RETAASLL	13536
2HSN	AB	LIGASE/RNA BINDING PROTEIN	A	1.9	1.9	1	9	ANAILRYVM	13537
2I26	OM	IMMUNE SYSTEM	M	1.9	1.9	1	8	VAWRNRCK	13538
2I2R	AE	TRANSPORT PROTEIN	E	1.9	1.9	1	16	KEEMMDIVKAIYDMMG	13539
2IAE	DE	HYDROLASE	E	1.9	1.9	1	17	EEHKIFLLKVLLPLHKV	13540
2IBF	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.9	1.9	1	7	RTIESIL	13541
2IBX	AD	VIRAL PROTEIN	D	1.9	1.9	1	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	13542
2IBZ	AC	OXIDOREDUCTASE	A	1.9	1.9	1	7	YMRIRSD	13543
2IBZ	CE	OXIDOREDUCTASE	E	1.9	1.9	1	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	13544
2IBZ	FG	OXIDOREDUCTASE	F	1.9	1.9	1	20	EDESYARAYRIIRAHQTELT	13545
2ICW	DE	IMMUNE SYSTEM	E	1.9	1.9	1	9	RPDAEYWNS	13546
2ICW	HL	IMMUNE SYSTEM	H	1.9	1.9	1	18	WWFRSLLVKGVYLIKRYY	13547
2IJ0	BC	PROTEIN BINDING	B	1.9	1.9	1	16	ISTLDFEIRHQLTQIH	13548
2INP	AC	OXIDOREDUCTASE	A	1.9	1.9	1	5	TRDMA	13549
2IPU	KG	IMMUNE SYSTEM	K	1.9	1.9	1	6	SEQLTS	13550
2IVF	AB	OXIDOREDUCTASE	B	1.9	1.9	1	8	ELMDLLIS	13551
2IX7	CB	CONTRACTILE PROTEIN/METAL BINDING	B	1.9	1.9	1	11	EAELQDMINEV	13552

2IZO	AC	HYDROLASE	A	1.9	1.9	1	24	EERVKNGIERLTKAIKEAKGASRQ	13553
2J5G	FD	HYDROLASE	F	1.9	1.9	1	11	TLNLRYTRVAL	13554
2J7A	GI	OXIDOREDUCTASE	G	1.9	1.9	1	6	CADCHM	13555
2J7A	NO	OXIDOREDUCTASE	O	1.9	1.9	1	10	NPVGVTHKLS	13556
2J7A	PR	OXIDOREDUCTASE	R	1.9	1.9	1	5	SMEAK	13557
2JBL	LM	ELECTRON TRANSPORT	M	1.9	1.9	1	7	EIEQITD	13558
2JE6	AB	HYDROLASE	B	1.9	1.9	1	30	PDEFRQAFDLAVKGINIIYNLEREALKSKY	13559
2JIY	MH	PHOTOSYNTHESIS	M	1.9	1.9	1	7	ELEQIAD	13560
2JIZ	AE	HYDROLASE	E	1.9	1.9	1	15	TREGNDLYHEMIESG	13561
2JIZ	HK	HYDROLASE	H	1.9	1.9	1	7	TELFYKG	13562
2JIZ	MN	HYDROLASE	M	1.9	1.9	1	8	QDIIAILG	13563
2JJ0	LM	PHOTOSYNTHESIS	M	1.9	1.9	1	17	HTAWAFLSAIWLWMVLG	13564
2JKR	BM	ENDOCYTOSIS	B	1.9	1.9	1	14	PLIRALAVRTMGCI	13565
2JTT	BD	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	B	1.9	1.9	1	20	ASPLDQAIGLLIGIFHKYSG	13566
2NLA	AB	APOPTOSIS	A	1.9	1.9	1	11	ETAFQGMLRKL	13567
2NN6	EF	HYDROLASE/TRANSFERASE	F	1.9	1.9	1	19	GCEERELALALQEALEPAV	13568
2NOJ	AB	IMMUNE SYSTEM	A	1.9	1.9	1	11	SQVLCGAVKWL	13569
2NOJ	CD	IMMUNE SYSTEM	C	1.9	1.9	1	18	KRQGALELIKKGYTQQLA	13570
2NPP	DE	SIGNALING PROTEIN,HYDROLASE	D	1.9	1.9	1	10	FTSRTSACGL	13571
2NQB	EF	STRUCTURAL PROTEIN/DNA	F	1.9	1.9	1	11	AMDVVYALKRQ	13572
2NQD	AB	HYDROLASE INHIBITOR/HYDROLASE	B	1.9	1.9	1	5	ESFLF	13573
2NV2	GH	LYASE/TRANSFERASE	G	1.9	1.9	1	11	AEQAKIAEEAG	13574
2NVU	AB	PROTEIN TURNOVER, LIGASE	B	1.9	1.9	1	13	KAEVAAEFLNDRV	13575
2NXX	CG	HORMONE/GROWTH FACTOR	C	1.9	1.9	1	9	PGRFAKLLL	13576
2NY7	GH	VIRAL PROTEIN/IMMUNE SYSTEM	G	1.9	1.9	1	5	PEIVT	13577
2NZD	CD	STRUCTURAL PROTEIN/DNA	C	1.9	1.9	1	7	EELNKLL	13578
2OCF	AD	HORMONE/GROWTH FACTOR	A	1.9	1.9	1	9	LHDQVHLLE	13579
2ODY	AB	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	A	1.9	1.9	1	5	EKTFG	13580
2OF5	BH	APOPTOSIS	H	1.9	1.9	1	11	YREVQRIRHEF	13581
2OF5	DJ	APOPTOSIS	J	1.9	1.9	1	11	YREVQRIRHEF	13582
2OJZ	LI	IMMUNE SYSTEM	L	1.9	1.9	1	7	KDEYERH	13583
2OM0	34	HORMONE	3	1.9	1.9	1	5	IVEQC	13584
2OM0	QR	HORMONE	Q	1.9	1.9	1	5	IVEQC	13585
2P1N	DE	SIGNALING PROTEIN	E	1.9	1.9	1	7	EVLEHVF	13586
2P2C	FR	HYDROLASE	F	1.9	1.9	1	13	WYIEALAQVFSER	13587
2PA8	DL	TRANSFERASE	L	1.9	1.9	1	12	TLGNLIAGTLRR	13588
2PF4	AE	HYDROLASE REGULATOR/VIRAL PROTEIN	E	1.9	1.9	1	8	FDCFRMWF	13589

2PMZ	BD	TRANSLATION, TRANSFERASE	D	1.9	1.9	1	10	DEILAHRLAL	13590
2PMZ	DN	TRANSLATION, TRANSFERASE	N	1.9	1.9	1	6	INEVIH	13591
2PMZ	GR	TRANSLATION, TRANSFERASE	G	1.9	1.9	1	6	VLARAA	13592
2PMZ	QR	TRANSLATION, TRANSFERASE	Q	1.9	1.9	1	17	IEDLWDLLQYHVATYFD	13593
2PRG	BC	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	B	1.9	1.9	1	23	LNDQVTLLKYGVHEIIYTMLASL	13594
2Q9Q	EF	REPLICATION	F	1.9	1.9	1	18	PAELIERLEQAWMNEKFA	13595
2QA4	S2	RIBOSOME	2	1.9	1.9	1	14	KATKKRLAKLDNQN	13596
2QBY	AB	REPLICATION/DNA	B	1.9	1.9	1	10	GDIVLYQLLR	13597
2QFA	AC	CELL CYCLE/CELL CYCLE/CELL CYCLE	A	1.9	1.9	1	5	PAWQP	13598
2QJK	AF	ELECTRON TRANSPORT	A	1.9	1.9	1	9	HSIQTWLLG	13599
2QJK	NO	ELECTRON TRANSPORT	O	1.9	1.9	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	13600
2QKI	AC	IMMUNE SYSTEM	C	1.9	1.9	1	5	KYELD	13601
2QQP	ED	VIRUS	D	1.9	1.9	1	12	PSVIKGIAQQAV	13602
2QQP	GH	VIRUS	G	1.9	1.9	1	12	EGAVGWFYKYMD	13603
2QRV	EF	TRANSFERASE/TRANSFERASE REGULATOR	F	1.9	1.9	1	11	KEDLDVASRFL	13604
2R17	BD	PROTEIN TRANSPORT	B	1.9	1.9	1	10	SLALLQRQFD	13605
2R1T	AB	PROTEIN BINDING	A	1.9	1.9	1	13	SFEFALAIVEALN	13606
2RD7	AC	IMMUNE SYSTEM	A	1.9	1.9	1	7	YRSWGRS	13607
2RHS	CD	LIGASE	D	1.9	1.9	1	16	DRQHKTRTLKETLEGA	13608
2ROC	AB	APOPTOSIS	A	1.9	1.9	1	11	ETAFQGMLRKL	13609
2UUN	CD	ELECTRON TRANSPORT	D	1.9	1.9	1	13	ANKRLDVVNRITA	13610
2UUN	IJ	ELECTRON TRANSPORT	J	1.9	1.9	1	13	ANKRLDAVNRITA	13611
2UUN	MN	ELECTRON TRANSPORT	N	1.9	1.9	1	13	ANKRLDAVNRITA	13612
2UUN	QR	ELECTRON TRANSPORT	R	1.9	1.9	1	13	ANKRLDAVNRITA	13613
2UUN	ST	ELECTRON TRANSPORT	T	1.9	1.9	1	13	ANKRLDAVNRITA	13614
2V1S	CJ	OXIDOREDUCTASE	C	1.9	1.9	1	24	LKDAEAVQKFFLEEIQLGEELLAQ	13615
2V36	AB	TRANSFERASE	A	1.9	1.9	1	13	PLASEIGADVLKK	13616
2V36	CD	TRANSFERASE	C	1.9	1.9	1	16	SGGIFLLQMPKILDHF	13617
2V4J	DE	OXIDOREDUCTASE	D	1.9	1.9	1	16	CPEDLLGVLELSYDEG	13618
2VGL	BM	PROTEIN TRANSPORT	B	1.9	1.9	1	14	LELKKLVYLYLMNY	13619
2VHM	EL	RIBOSOME	E	1.9	1.9	1	12	EALVHQVVVAYA	13620
2VJE	CB	LIGASE	C	1.9	1.9	1	10	FTCAKKLKKR	13621
2VLH	AB	LYASE	A	1.9	1.9	1	15	GRDMEAMAIGLREAM	13622
2VLH	AB	LYASE	B	1.9	1.9	1	12	GRGAENLLSQLA	13623
2W83	AD	PROTEIN TRANSPORT	D	1.9	1.9	1	61	MGREVENLILENTQLLETKNALNIVKNDLIAKVDELTCEKDVLQGELEA VKQAKLKLEEKN	13624
2W83	BD	PROTEIN TRANSPORT	D	1.9	1.9	1	61	MGREVENLILENTQLLETKNALNIVKNDLIAKVDELTCEKDVLQGELEA VKQAKLKLEEKN	13625

2W96	BA	CELL CYCLE	B	1.9	1.9	1	17	ISTVREVALLRRLEAFE	13626
2WAQ	AC	TRANSCRIPTION	A	1.9	1.9	1	10	VKHVYEFLKA	13627
2WAQ	BD	TRANSCRIPTION	D	1.9	1.9	1	11	DEILAHRLALI	13628
2WAQ	DL	TRANSCRIPTION	L	1.9	1.9	1	10	HTLGNLIAGT	13629
2WB1	YR	TRANSCRIPTION	R	1.9	1.9	1	13	YAFKLLIQELMSM	13630
2WC0	BF	HYDROLASE/HORMONE	F	1.9	1.9	1	11	HLVEALYLVCG	13631
2WIN	EF	IMMUNE SYSTEM	E	1.9	1.9	1	7	KGVFVLN	13632
2WIN	HN	IMMUNE SYSTEM	N	1.9	1.9	1	17	EYQNEKLANELKSLLDE	13633
2Z2S	CD	TRANSCRIPTION	C	1.9	1.9	1	11	ASQAEECAQDV	13634
2Z3R	AD	CYTOKINE/CYTOKINE RECEPTOR	A	1.9	1.9	1	20	ASIHDTVENLIILANNSLSS	13635
2ZC5	AB	BIOSYNTHETIC PROTEIN	B	1.9	1.9	1	12	DNYLKEVINQVE	13636
2ZCY	HN	HYDROLASE	H	1.9	1.9	1	15	VVSALQMLKQHLFKY	13637
2ZCY	U1	HYDROLASE	U	1.9	1.9	1	22	IPDARNAALRAKAEAAEFRYKY	13638
2ZCY	V1	HYDROLASE	V	1.9	1.9	1	15	VVSALQMLKQHLFKY	13639
2ZU0	BD	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	B	1.9	1.9	1	9	DEQIFYLRS	13640
2ZU0	BD	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	D	1.9	1.9	1	12	NQFFLQTALNAV	13641
3A0B	dx	ELECTRON TRANSPORT	d	1.9	1.9	1	9	WFDILDDWL	13642
3A1Q	AC	GENE REGULATION/SIGNALING PROTEIN	C	1.9	1.9	1	40	EEEQFALALKMSEQEAREVNNQEEKEEELLRKAIAESLNS	13643
3B4V	FD	HORMONE REGULATOR COMPLEX	F	1.9	1.9	1	5	FKDIG	13644
3BG0	AB	PROTEIN TRANSPORT, HYDROLASE	B	1.9	1.9	1	15	DKAAEDTIKRLVMRE	13645
3BH6	AB	SIGNALING PROTEIN	A	1.9	1.9	1	14	FEETGQELTELLEE	13646
3BIM	AI	TRANSCRIPTION REPRESSOR	A	1.9	1.9	1	11	EHVVDTCRKFI	13647
3BLW	GH	OXIDOREDUCTASE	G	1.9	1.9	1	11	VDNASMQAVAK	13648
3BMC	AD	OXIDOREDUCTASE	D	1.9	1.9	1	11	EEEKDKWRRKV	13649
3BT2	LH	IMMUNE SYSTEM	L	1.9	1.9	1	6	SEQLTS	13650
3BXK	CD	MEMBRANE PROTEIN, SIGNALING PROTEIN	C	1.9	1.9	1	12	EEEIREAFRVFD	13651
3BZ1	AC	ELECTRON TRANSPORT	C	1.9	1.9	1	26	GEAYLSYSLGALSMMGFIATCFVWFN	13652
3BZ1	DV	ELECTRON TRANSPORT	D	1.9	1.9	1	19	FYTKNLLLNEGIRAWMAPQ	13653
3C1B	EF	STRUCTURAL PROTEIN/DNA	F	1.9	1.9	1	11	AMDVVYALKRQ	13654
3C60	CD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	D	1.9	1.9	1	10	RPDAEYWNSQ	13655
3C60	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	H	1.9	1.9	1	10	RPDAEYWNSQ	13656
3CF4	AG	OXIDOREDUCTASE	A	1.9	1.9	1	5	ACLLA	13657
3CFI	DE	PROTEIN TRANSPORT/IMMUNE SYSTEM	E	1.9	1.9	1	24	SQERTARLNELQRALVMMDSDFRQ	13658

3CI0	JK	PROTEIN TRANSPORT	K	1.9	1.9	1	6	DSEYLA	13659
3CJS	AB	TRANSFERASE/RIBOSOMAL PROTEIN	B	1.9	1.9	1	9	PVGPALGQH	13660
3CWB	DH	OXIDOREDUCTASE	D	1.9	1.9	1	12	SSVRRGFQVYKQ	13661
3CXH	AB	OXIDOREDUCTASE	A	1.9	1.9	1	11	LGEAFKKIDAI	13662
3CXH	AB	OXIDOREDUCTASE	B	1.9	1.9	1	21	PHELTESVLPAARYDYAVAEQ	13663
3CXH	NP	OXIDOREDUCTASE	N	1.9	1.9	1	22	MGSLLGLCLVIQIVTGIFMAMH	13664
3CXH	OR	OXIDOREDUCTASE	R	1.9	1.9	1	20	EDESYARAYRIIRAHQTELT	13665
3CZU	AB	TRANSFERASE/SIGNALING PROTEIN	A	1.9	1.9	1	6	SSDFEA	13666
3D2E	CD	CHAPERONE	D	1.9	1.9	1	6	DAAKNQ	13667
3D5A	CN	RIBOSOME	C	1.9	1.9	1	5	LGITR	13668
3DHH	AB	OXIDOREDUCTASE	A	1.9	1.9	1	5	ERMSG	13669
3DHH	AB	OXIDOREDUCTASE	A	1.9	1.9	1	7	LEKWESY	13670
3DHR	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.9	1.9	1	20	PENFRLLGDILVIILAAHFG	13671
3DHW	BD	MEMBRANE PROTEIN/HYDROLASE	B	1.9	1.9	1	36	MQIVRKVLLPEALPGLVNAATITLITLVGYSAMGGA	13672
3DHW	FH	MEMBRANE PROTEIN/HYDROLASE	F	1.9	1.9	1	19	LLPEALPGLVNAATITLIT	13673
3DL8	HF	PROTEIN TRANSPORT	H	1.9	1.9	1	33	DYGRYKINEYTKYLTLFVATVQSLGIAFWIRGQ	13674
3DNL	DE	VIRAL PROTEIN	D	1.9	1.9	1	10	VEQMHEDIIS	13675
3DOM	AB	TRANSCRIPTION	A	1.9	1.9	1	10	QIRLWQLELD	13676
3DS3	AC	VIRAL PROTEIN	A	1.9	1.9	1	8	LEEMMTAC	13677
3DTU	AB	OXIDOREDUCTASE	A	1.9	1.9	1	31	ATWNFVSSLGAFLSFASFLFFLGVIFYTLTR	13678
3DUF	EF	OXIDOREDUCTASE/TRANSFERASE	E	1.9	1.9	1	14	YIQAAGVALGLKMR	13679
3DWL	BI	STRUCTURAL PROTEIN	B	1.9	1.9	1	13	PENRENTAEIMFE	13680
3DXC	CD	PROTEIN BINDING	C	1.9	1.9	1	21	ASLSEAVQAACMLRYQKCLDA	13681
3DXC	CD	PROTEIN BINDING	D	1.9	1.9	1	13	PEERHLSKMQQNG	13682
3E0J	AB	TRANSFERASE	B	1.9	1.9	1	14	GPLFNTDYDILKSN	13683
3E2Z	AB	TRANSFERASE, LYASE	B	1.9	1.9	1	13	AHLIKHLQTVQQN	13684
3E7S	AB	OXIDOREDUCTASE	B	1.9	1.9	1	5	WAWIV	13685
3EDL	AB	STRUCTURAL PROTEIN	A	1.9	1.9	1	8	IYDICRRN	13686
3EXG	54	OXIDOREDUCTASE	4	1.9	1.9	1	5	KILED	13687
3EXG	WV	OXIDOREDUCTASE	V	1.9	1.9	1	12	VKDIIFAIKKTL	13688
3EXG	Y2	OXIDOREDUCTASE	2	1.9	1.9	1	6	KILEDN	13689
3EXG	YZ	OXIDOREDUCTASE	Z	1.9	1.9	1	14	EMGFAGIAVGAAMA	13690
3EZJ	GH	PROTEIN TRANSPORT	G	1.9	1.9	1	12	APILRQMIDSAG	13691
3F1S	AB	HYDROLASE INHIBITOR/HYDROLASE	B	1.9	1.9	1	9	SLWFKQIMN	13692
3F2O	AC	APOPTOSIS/HYDROLASE	C	1.9	1.9	1	6	VERKRE	13693
3F9K	Za	VIRAL PROTEIN, RECOMBINATION	Z	1.9	1.9	1	11	QEVKMVAWWIG	13694
3FCS	CD	CELL ADHESION/BLOOD CLOTTING	D	1.9	1.9	1	11	LGLMTEKLSQK	13695
3FIC	KG	RIBOSOME	K	1.9	1.9	1	18	PYAAQLAALDAAKKAMAY	13696
3FKS	SW	HYDROLASE	W	1.9	1.9	1	15	TREGNDLYREMKETG	13697

3FKS	UV	HYDROLASE	V	1.9	1.9	1	12	TREGNDLYREMK	13698
3FWC	IJ	CELL CYCLE, TRANSCRIPTION	I	1.9	1.9	1	11	YHELKVAMKAL	13699
3G3A	AH	HYDROLASE/IMMUNE SYSTEM	H	1.9	1.9	1	5	VQAWI	13700
3G4S	FM	RIBOSOME	F	1.9	1.9	1	8	HIPELADE	13701
3G9K	LS	HYDROLASE	L	1.9	1.9	1	6	GVTLLQ	13702
3GE8	AB	OXIDOREDUCTASE	A	1.9	1.9	1	5	ERMSG	13703
3GJF	AL	IMMUNE SYSTEM	A	1.9	1.9	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	13704
3H0L	DE	LIGASE	D	1.9	1.9	1	15	PEVKRRIMLGTFALS	13705
3H0L	NO	LIGASE	O	1.9	1.9	1	7	REKALMN	13706
3H0L	PQ	LIGASE	P	1.9	1.9	1	15	PEVKRRIMLGTFALS	13707
3H0L	ST	LIGASE	S	1.9	1.9	1	15	PEVKRRIMLGTFALS	13708
3HD7	AD	EXOCYTOSIS	A	1.9	1.9	1	44	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIIIIVY	13709
3HFM	HY	COMPLEX (ANTIBODY-ANTIGEN)	Y	1.9	1.9	1	11	TASVNCAKKIV	13710
3HHR	AB	HORMONE/RECEPTOR	A	1.9	1.9	1	10	KEQKYSFLQN	13711
3HKI	AB	HYDROLASE	A	1.9	1.9	1	8	EKELLDSY	13712
3HKZ	CB	TRANSFERASE	B	1.9	1.9	1	13	YAFKLLIQELMSM	13713
3HOU	BC	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.9	1.9	1	6	QSSIDR	13714
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.9	1.9	1	7	IRGNLMG	13715
3HRD	AD	OXIDOREDUCTASE	D	1.9	1.9	1	9	LLDLLREDF	13716
3HRD	BD	OXIDOREDUCTASE	D	1.9	1.9	1	17	IKIHAAVRYAVERCANA	13717
1A2X	AB	COMPLEX (SKELETAL MUSCLE/MUSCLE PROTEIN)	A	1.8	1.8	1	12	EEELAECFRIFD	13718
1AHJ	CD	LYASE	C	1.8	1.8	1	5	WPILG	13719
1AL0	FB	VIRUS	F	1.8	1.8	1	15	KHLFQGYLNIYNNYF	13720
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	A	1.8	1.8	1	31	AYWNNISSIGAYISFASFLFFIGIVFYTLFA	13721
1B33	HM	PHOTOSYNTHESIS	M	1.8	1.8	1	25	TRRYAACIRDLDYYLRYATYAMLAG	13722
1B33	JK	PHOTOSYNTHESIS	J	1.8	1.8	1	14	GEKRLRIAQILTDN	13723
1B35	AB	VIRUS	A	1.8	1.8	1	5	RNEAQ	13724
1B8D	AB	PHOTOSYNTHESIS	A	1.8	1.8	1	9	GPVDEWGIA	13725
1BB1	AB	DE NOVO PROTEIN DESIGN	B	1.8	1.8	1	33	KIAAIKEEQAAIEEEIQAIKEEIAAIKYLIAQI	13726
1BEV	13	VIRUS	3	1.8	1.8	1	6	LLEIAQ	13727
1BGY	DE	ELECTRON TRANSPORT	E	1.8	1.8	1	35	EARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSA	13728
1BJO	AB	AMINOTRANSFERASE	B	1.8	1.8	1	10	AEVLKQAQQE	13729
1BR1	AH	MUSCLE PROTEIN	H	1.8	1.8	1	9	FEDYVEGLR	13730
1BVK	AC	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)	C	1.8	1.8	1	6	VQAWIR	13731
1C8O	AB	VIRAL PROTEIN	A	1.8	1.8	1	10	DIFREIASSM	13732

1DD4	AC	RIBOSOME	A	1.8	1.8	1	15 VSELAELVKKLEDKF	13733
1DEE	DG	IMMUNE SYSTEM	G	1.8	1.8	1	15 STNVLGEAKKLNESQ	13734
1DFL	BX	CONTRACTILE PROTEIN	B	1.8	1.8	1	13 QDQRIGLSVIQRN	13735
1DGH	CD	OXIDOREDUCTASE	C	1.8	1.8	1	12 VVFTDEMAHFDR	13736
1DGR	BM	PLANT PROTEIN	M	1.8	1.8	1	8 GEEVEELL	13737
1E7P	BC	OXIDOREDUCTASE	C	1.8	1.8	1	15 DKTRANLKKLKTLMS	13738
1E7P	HI	OXIDOREDUCTASE	I	1.8	1.8	1	15 DKTRANLKKLKTLMS	13739
1E7P	KL	OXIDOREDUCTASE	L	1.8	1.8	1	15 DKTRANLKKLKTLMS	13740
1EAH	34	VIRUS	3	1.8	1.8	1	6 MMELAE	13741
1EFU	CD	COMPLEX (TWO ELONGATION FACTORS)	D	1.8	1.8	1	11 MMDCKKALTEA	13742
1EQZ	AB	STRUCTURAL PROTEIN/DNA	A	1.8	1.8	1	11 VGRVHRLLRKG	13743
1EQZ	CD	STRUCTURAL PROTEIN/DNA	D	1.8	1.8	1	11 AMDVVYALKRQ	13744
1EYS	MH	ELECTRON TRANSPORT	M	1.8	1.8	1	7 EIDQITH	13745
1F3J	DE	IMMUNE SYSTEM	D	1.8	1.8	1	22 PQGGLQNIAAEKHNLGILTKRS	13746
1F66	CD	STRUCTURAL PROTEIN/DNA	D	1.8	1.8	1	12 AIYVYKVLKQVH	13747
1FNS	LH	IMMUNE SYSTEM	L	1.8	1.8	1	6 SEQLTS	13748
1FNT	JZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.8	1.8	1	13 VGELFWKVKEEEG	13749
1FNT	KZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.8	1.8	1	12 QTFAYGVLDSNY	13750
1FNT	MN	HYDROLASE/HYDROLASE ACTIVATOR	M	1.8	1.8	1	14 AADGDALVKRFKNS	13751
1FNT	Qp	HYDROLASE/HYDROLASE ACTIVATOR	Q	1.8	1.8	1	10 QVEYALESIS	13752
1FNT	XY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.8	1.8	1	14 YSGFYTFSLLDHHY	13753
1FPP	BA	PRENYLTRANSFERASE	A	1.8	1.8	1	14 YTVWHFRRVLLRSL	13754
1FQV	GH	LIGASE	G	1.8	1.8	1	10 DELLLGIFSC	13755
1FWA	AC	HYDROLASE	A	1.8	1.8	1	23 PREKDKLLLFTAALVAERRLARG	13756
1G0U	AB	HYDROLASE	A	1.8	1.8	1	16 TKLLVSEVAKIMQEAT	13757
1G0U	EL	HYDROLASE	E	1.8	1.8	1	22 APDARVLSNYLRQQCNYSSLVF	13758
1G0U	HI	HYDROLASE	I	1.8	1.8	1	15 PETFTQLVSSSLYER	13759
1G0U	WL	HYDROLASE	W	1.8	1.8	1	12 SDQLFGMCESLY	13760
1G0U	XY	HYDROLASE	Y	1.8	1.8	1	15 VAAASKILSNLVYQY	13761
1G20	AB	OXIDOREDUCTASE	B	1.8	1.8	1	6 CMAEVI	13762
1G20	CG	OXIDOREDUCTASE	G	1.8	1.8	1	16 AGRGVITAINFLEEEG	13763
1G20	DH	OXIDOREDUCTASE	D	1.8	1.8	1	6 CMAEVI	13764
1G20	DH	OXIDOREDUCTASE	H	1.8	1.8	1	15 AGRGVITAINFLEEE	13765
1G3I	DK	CHAPERONE/HYDROLASE	K	1.8	1.8	1	18 TADAFTLFELFERKLEMH	13766
1GH0	EF	PHOTOSYNTHESIS	F	1.8	1.8	1	14 SNKRLDVVNRITSN	13767
1GH0	GF	PHOTOSYNTHESIS	G	1.8	1.8	1	18 DAAVEANSYLDYAINALS	13768
1GH0	KL	PHOTOSYNTHESIS	L	1.8	1.8	1	14 SNKRLDVVNRITSN	13769
1GH0	UV	PHOTOSYNTHESIS	U	1.8	1.8	1	12 PLTEAVSVADSQ	13770
1GH6	AB	ANTITUMOR PROTEIN	A	1.8	1.8	1	12 WEQWWNAFNEEN	13771

1GH6	AB	ANTITUMOR PROTEIN	B	1.8	1.8	1	6	KTNILQ	13772
1GO3	EF	TRANSFERASE	F	1.8	1.8	1	11	EKTAVKIADIL	13773
1GPW	CD	LYASE/TRANSFERASE	D	1.8	1.8	1	13	MNLYRGVKRASEN	13774
1H1L	AD	OXIDOREDUCTASE	D	1.8	1.8	1	5	HTWLH	13775
1H1L	CD	OXIDOREDUCTASE	D	1.8	1.8	1	7	CMAEVIG	13776
1H2R	SL	OXIDOREDUCTASE	L	1.8	1.8	1	5	YDALT	13777
1H3O	CD	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	D	1.8	1.8	1	13	VKDVQLHLERQWN	13778
1H6K	BZ	NUCLEAR PROTEIN	B	1.8	1.8	1	9	MVTLENLLF	13779
1H6K	CX	NUCLEAR PROTEIN	C	1.8	1.8	1	9	MVTLENLLF	13780
1H8B	AB	STRUCTURAL PROTEIN	B	1.8	1.8	1	19	KKAEAVATVVAAVDQARVR	13781
1HBH	CD	OXYGEN CARRIER	D	1.8	1.8	1	19	PDNFKLLSDCITIVLAAKM	13782
1HBM	AE	METHANOGENESIS	E	1.8	1.8	1	19	SAAPLVTATAFVQAIINEF	13783
1I1A	AC	IMMUNE SYSTEM	C	1.8	1.8	1	6	HRDWLN	13784
1I3R	AB	IMMUNE SYSTEM	A	1.8	1.8	1	5	EEFAK	13785
1I3R	CD	IMMUNE SYSTEM	D	1.8	1.8	1	9	RPDAENWNS	13786
1IBR	CD	CELL CYCLE, TRANSLATION	D	1.8	1.8	1	13	QVARVAAGLQIKN	13787
1IBT	AB	LYASE	B	1.8	1.8	1	9	PDKDMEIME	13788
1ID3	GH	STRUCTURAL PROTEIN/DNA	H	1.8	1.8	1	16	ELAKHAVSEGTRAVTK	13789
1IR2	T2	LYASE	2	1.8	1.8	1	14	DEQIAAQVDYIVAN	13790
1IR2	V4	LYASE	V	1.8	1.8	1	14	AKNYGRAVYECLRG	13791
1IR2	Y7	LYASE	Y	1.8	1.8	1	14	AKNYGRAVYECLRG	13792
1IRU	GN	HYDROLASE	N	1.8	1.8	1	22	YADFQYLKQVLGQMVIDEELLG	13793
1IRU	HI	HYDROLASE	I	1.8	1.8	1	15	VVTANRMLKQMLFRY	13794
1IRU	J1	HYDROLASE	J	1.8	1.8	1	14	LFETISQAMLNAVD	13795
1IRU	VW	HYDROLASE	W	1.8	1.8	1	15	VVTANRMLKQMLFRY	13796
1IWA	IF	LYASE	I	1.8	1.8	1	9	VILERERLD	13797
1IZL	PQ	PHOTOSYNTHESIS	Q	1.8	1.8	1	8	FLGAIAAM	13798
1JD2	2O	HYDROLASE	2	1.8	1.8	1	18	CDVLAKRMANLSQIYTQR	13799
1JD2	MN	HYDROLASE	N	1.8	1.8	1	15	TETAASVFKELCYEN	13800
1JD2	MU	HYDROLASE	M	1.8	1.8	1	14	FGAHMANPLLRKVV	13801
1JEB	AB	OXYGEN STORAGE/TRANSPORT	B	1.8	1.8	1	16	ADEVGGEALGRLLVVY	13802
1JJO	AC	SIGNALING PROTEIN	A	1.8	1.8	1	12	PLSIALAMGMME	13803
1JJO	BD	SIGNALING PROTEIN	B	1.8	1.8	1	12	PLSIALAMGMME	13804
1JJU	AB	ELECTRON TRANSPORT PROTEIN	A	1.8	1.8	1	15	PEDWKHLVNFHLGQF	13805
1JM7	AB	ANTITUMOR	B	1.8	1.8	1	15	AHSRAALDRLEKLLR	13806
1JMU	AB	VIRAL PROTEIN	B	1.8	1.8	1	7	AVAASAL	13807
1JMU	DH	VIRAL PROTEIN	D	1.8	1.8	1	7	PESLNAS	13808
1JNR	AB	OXIDOREDUCTASE	A	1.8	1.8	1	12	LEDYVRYVTLDM	13809
1JOU	AB	BLOOD CLOTTING	A	1.8	1.8	1	5	PRTFG	13810

1JOU	CB	BLOOD CLOTTING	B	1.8	1.8	1	5	AHCLL	13811
1JPW	AD	CELL ADHESION	A	1.8	1.8	1	16	VKFLAITTDCLQILAY	13812
1JY7	CD	OXYGEN STORAGE/TRANSPORT	C	1.8	1.8	1	18	AHAGEYGAEALERMFLSF	13813
1K6L	LM	PHOTOSYNTHESIS	L	1.8	1.8	1	10	WVDWWQWWVK	13814
1K7L	AB	TRANSCRIPTION	B	1.8	1.8	1	10	KILHRLLQEG	13815
1KF6	AB	OXIDOREDUCTASE	A	1.8	1.8	1	16	WAKIRDEMGLAMEEGC	13816
1KFY	AB	OXIDOREDUCTASE	A	1.8	1.8	1	16	WAKIRDEMGLAMEEGC	13817
1KIL	BD	MEMBRANE PROTEIN	B	1.8	1.8	1	39	SEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID	13818
1KIL	BD	MEMBRANE PROTEIN	D	1.8	1.8	1	62	ARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSN KTRIDEANQRATKM	13819
1KN1	AB	ELECTRON TRANSPORT	A	1.8	1.8	1	25	EEMTATCLRDLDYYLRLVTYGIVSG	13820
1KQF	AB	OXIDOREDUCTASE	A	1.8	1.8	1	13	PVGFRWAMEAKNN	13821
1KQF	AB	OXIDOREDUCTASE	B	1.8	1.8	1	6	ACVKTC	13822
1KX4	AB	STRUCTURAL PROTEIN/DNA	B	1.8	1.8	1	11	AMDVVYALKRQ	13823
1KX4	FH	STRUCTURAL PROTEIN/DNA	H	1.8	1.8	1	12	SREIQTAVRLLL	13824
1KYO	LM	OXIDOREDUCTASE/ELECTRON TRANSPORT	M	1.8	1.8	1	21	PHELTESVLPAARYDYAVAEQ	13825
1KYO	MG	OXIDOREDUCTASE/ELECTRON TRANSPORT	G	1.8	1.8	1	10	PIMQTALRRL	13826
1L3E	AB	TRANSCRIPTION	B	1.8	1.8	1	16	AHCASSRQIISHWKNC	13827
1LQ8	GH	BLOOD CLOTTING	G	1.8	1.8	1	14	PVSISMSLAMLSLG	13828
1LWU	AC	BLOOD CLOTTING	C	1.8	1.8	1	46	LEEVRILEQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	13829
1LZW	AB	CHAPERONE	B	1.8	1.8	1	9	QAAYLLRKH	13830
1M1J	BC	BLOOD CLOTTING	B	1.8	1.8	1	13	GCELQTTLLKQEK	13831
1M1J	DF	BLOOD CLOTTING	F	1.8	1.8	1	19	IEQLTQKSKKIIEEIIRYE	13832
1M1Y	IJ	OXIDOREDUCTASE	I	1.8	1.8	1	12	DAWSSRILLEEM	13833
1M45	AB	CELL CYCLE PROTEIN	A	1.8	1.8	1	9	YKKFIEDVL	13834
1MG2	AF	OXIDOREDUCTASE	A	1.8	1.8	1	20	QAQETQGQAAARAAAADLAA	13835
1MVW	P1	CONTRACTILE PROTEIN	1	1.8	1.8	1	12	SVWIGGSILASL	13836
1N34	DE	RIBOSOME	D	1.8	1.8	1	8	EQLVIEFY	13837
1N4Q	EF	TRANSFERASE	E	1.8	1.8	1	16	EKFRDVYDYFRAVLQR	13838
1N52	AB	RNA BINDING PROTEIN	A	1.8	1.8	1	16	PKPKFVREVLEKCMRL	13839
1N86	AB	BLOOD CLOTTING	B	1.8	1.8	1	32	PTNLRVLRSILENLRSKIQKLESDVSAQMEYC	13840
1N86	DE	BLOOD CLOTTING	E	1.8	1.8	1	15	IQKLESDVSAQMEYC	13841
1NCA	LH	HYDROLASE (O-GLYCOSYL)	L	1.8	1.8	1	6	SEQLTS	13842
1NEK	BC	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.8	1.8	1	6	PSFWWN	13843
1NEX	AB	LIGASE, CELL CYCLE	B	1.8	1.8	1	9	FEISLKIFN	13844

1NFD	EF	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)	E	1.8	1.8	1	6	PEELRT	13845
1NIK	AB	TRANSCRIPTION	B	1.8	1.8	1	11	VEGISKLLREH	13846
1NIK	BI	TRANSCRIPTION	B	1.8	1.8	1	7	EILEHIC	13847
1O18	GH	CONTRACTILE PROTEIN	G	1.8	1.8	1	43	AEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNV	13848
1O18	GH	CONTRACTILE PROTEIN	H	1.8	1.8	1	9	EIKNMWAAF	13849
1O94	EF	ELECTRON TRANSPORT	E	1.8	1.8	1	16	AIVVGRILTEVIKKEA	13850
1O94	EF	ELECTRON TRANSPORT	F	1.8	1.8	1	15	PDVFEASVSALIAAH	13851
1OCC	AC	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.8	1.8	1	34	PILYQHLFWFFGHPEVYILILPGFGMISHIVTYY	13852
1OCC	AT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	T	1.8	1.8	1	10	ARTWRFLTFG	13853
1OCC	NQ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.8	1.8	1	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	13854
1OQS	GH	HYDROLASE	G	1.8	1.8	1	13	LFQFGEMILQKTG	13855
1OR7	BF	TRANSCRIPTION	B	1.8	1.8	1	15	VPDVVQEAFIKAYRA	13856
1P22	AB	SIGNALING PROTEIN	A	1.8	1.8	1	10	DHIAENILSY	13857
1P7T	AB	LYASE	A	1.8	1.8	1	10	VQSVQANIAQ	13858
1PIV	13	VIRUS	3	1.8	1.8	1	5	PRLSH	13859
1PON	AB	CALCIUM-BINDING PROTEIN	A	1.8	1.8	1	8	IEELGEIL	13860
1PRC	CL	PHOTOSYNTHETIC REACTION CENTER	C	1.8	1.8	1	18	LSDAYATFALMMSISDSL	13861
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.8	1.8	1	8	STLLGWFG	13862
1PTO	GJ	TOXIN	G	1.8	1.8	1	10	ILAGALATYQ	13863
1Q16	AB	OXIDOREDUCTASE	A	1.8	1.8	1	6	SADWYN	13864
1Q1J	MH	IMMUNE SYSTEM	M	1.8	1.8	1	5	SEELQ	13865
1Q5R	DL	HYDROLASE	L	1.8	1.8	1	23	AGIAIELVRLFAVELEHYEKIEG	13866
1Q90	BD	PHOTOSYNTHESIS	D	1.8	1.8	1	13	WYFYPVFQILRVV	13867
1Q9O	BA	IMMUNE SYSTEM	A	1.8	1.8	1	5	SEQLT	13868
1QGW	AD	PHOTOSYNTHESIS	A	1.8	1.8	1	12	ESDAAKKLQEFI	13869
1R20	AD	HORMONE/GROWTH FACTOR RECEPTOR	A	1.8	1.8	1	21	RQEVEVLREKMFLCLDEYCRR	13870
1R27	AB	OXIDOREDUCTASE	A	1.8	1.8	1	7	EADAKDL	13871
1R4A	CG	PROTEIN TRANSPORT	G	1.8	1.8	1	14	TEFEYLRKVLFEYM	13872
1R5V	CD	SIGNALING PROTEIN	D	1.8	1.8	1	9	RPDAENWNS	13873
1RD8	CB	VIRAL PROTEIN	B	1.8	1.8	1	23	QKSTQNAIDGITNKVNSVIEKMN	13874
1RM6	DF	OXIDOREDUCTASE	F	1.8	1.8	1	16	VKIIKSVETAAAARLC	13875
1RM6	DF	OXIDOREDUCTASE	F	1.8	1.8	1	10	LLDYLRETVG	13876
1RP3	CD	TRANSCRIPTION	C	1.8	1.8	1	8	AKEVAKIL	13877
1RP3	GH	TRANSCRIPTION	G	1.8	1.8	1	8	AKEVAKIL	13878

1RUZ	HI	VIRAL PROTEIN	I	1.8	1.8	1	7	KVKSQLK	13879
1RYP	CK	MULTICATALYTIC PROTEINASE	K	1.8	1.8	1	23	AGDTVQFAEYIQANIQLYSIRED	13880
1S3K	LH	IMMUNE SYSTEM	L	1.8	1.8	1	5	DEQLK	13881
1S70	AB	HYDROLASE	B	1.8	1.8	1	7	AKQKRNE	13882
1SA0	AE	CELL CYCLE	A	1.8	1.8	1	26	YARGHYTIGKEIIDLVLDRIRKLADQ	13883
1SB3	AC	OXIDOREDUCTASE	C	1.8	1.8	1	15	VKIIKSVETAAAARL	13884
1SB3	EF	OXIDOREDUCTASE	F	1.8	1.8	1	15	TPGMIMASEALLRKN	13885
1SCT	AB	OXYGEN TRANSPORT	B	1.8	1.8	1	16	MEGTGLMLMANLFKTS	13886
1SCT	EH	OXYGEN TRANSPORT	H	1.8	1.8	1	15	ADQKDLLRMSWGVLS	13887
1SQB	AB	OXIDOREDUCTASE	A	1.8	1.8	1	8	YAQALQSV	13888
1SUV	AE	METAL TRANSPORT	A	1.8	1.8	1	24	QWLYSARGDFFRATSRLTTDFGNA	13889
1SXJ	BC	REPLICATION	B	1.8	1.8	1	15	YLQLASMLAKIHKLN	13890
1SXJ	CD	REPLICATION	C	1.8	1.8	1	15	WGTAHYTLNKVRSAK	13891
1T4K	AB	IMMUNE SYSTEM	A	1.8	1.8	1	6	SEQLTS	13892
1T6V	LN	HYDROLASE/IMMUNE SYSTEM	N	1.8	1.8	1	5	YALCS	13893
1TIL	AF	TRANSCRIPTION	F	1.8	1.8	1	8	EQFALQAL	13894
1TIL	EF	TRANSCRIPTION	F	1.8	1.8	1	8	PAVKRLFD	13895
1TQE	QX	TRANSCRIPTION/PROTEIN BINDING/DNA	X	1.8	1.8	1	14	TEVKQKLQEFLLSK	13896
1TQY	EF	TRANSFERASE	F	1.8	1.8	1	10	VNTGQISIRH	13897
1U2U	AB	TRANSCRIPTION	B	1.8	1.8	1	26	ALKKRVQALKARNYALKQKVQALRHK	13898
1U35	EF	STRUCTURAL PROTEIN/DNA	F	1.8	1.8	1	11	AMDVVYALKRQ	13899
1USP	AB	OXIDOREDUCTASE	A	1.8	1.8	1	24	PEQLFAAGYAACFQGALGVVSRRQ	13900
1V02	FE	HYDROLASE	F	1.8	1.8	1	24	FLDQQAQERSMDKCLGWFLEPVVR	13901
1V54	BI	OXIDOREDUCTASE	B	1.8	1.8	1	11	LKYFEKWSASM	13902
1V54	OV	OXIDOREDUCTASE	O	1.8	1.8	1	11	LKYFEKWSASM	13903
1V54	QV	OXIDOREDUCTASE	Q	1.8	1.8	1	8	PIQGFSAK	13904
1VF5	NO	PHOTOSYNTHESIS	O	1.8	1.8	1	20	VFPVVIMGTFACIVALSVLD	13905
1VF5	NP	PHOTOSYNTHESIS	N	1.8	1.8	1	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	13906
1VRQ	BD	OXIDOREDUCTASE	B	1.8	1.8	1	7	LERFETG	13907
1VSP	IN	RIBOSOME	I	1.8	1.8	1	5	ELREK	13908
1W2W	MN	ISOMERASE	M	1.8	1.8	1	14	DNGAKYLIDVLQKD	13909
1W5C	AD	PHOTOSYNTHESIS	D	1.8	1.8	1	16	YTKNLLLNEGIRAWMA	13910
1W5C	DE	PHOTOSYNTHESIS	D	1.8	1.8	1	19	LFPCAYLALGGWLTGTTFV	13911
1W5C	DE	PHOTOSYNTHESIS	E	1.8	1.8	1	6	LAYDVF	13912
1W5C	JK	PHOTOSYNTHESIS	J	1.8	1.8	1	14	YLALGGWLTGTTFV	13913
1WCM	AG	TRANSCRIPTION	G	1.8	1.8	1	12	MKQYLKTKLLEE	13914
1WDC	AC	MUSCLE PROTEIN	C	1.8	1.8	1	12	DEDVDEIIKLTD	13915
1WDC	AC	MUSCLE PROTEIN	C	1.8	1.8	1	11	YEDFVKKVMAG	13916
1WQ9	AB	TOXIN	B	1.8	1.8	1	9	FLDVYQRSA	13917

1WR6	AE	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	1.8	1.8	1	12	LEEVNNNVRLLS	13918
1WX5	AB	OXIDOREDUCTASE/METAL TRANSPORT	B	1.8	1.8	1	13	PRAAARAAVDELQ	13919
1WYU	EF	OXIDOREDUCTASE	E	1.8	1.8	1	5	QYIRR	13920
1XFU	AO	LYASE/METAL BINDING PROTEIN	A	1.8	1.8	1	23	EKKRKISIFRGIQAYNEIENVLK	13921
1XFU	BP	LYASE/METAL BINDING PROTEIN	B	1.8	1.8	1	23	EKKRKISIFRGIQAYNEIENVLK	13922
1XFV	FT	LYASE/METAL BINDING PROTEIN	F	1.8	1.8	1	24	QEKKRKISIFRGIQAYNEIENVLK	13923
1XKP	AB	MEMBRANE PROTEIN/CHAPERON	A	1.8	1.8	1	8	IADMAEEV	13924
1XL3	AC	CELL INVASION	A	1.8	1.8	1	9	IYAIWSDLQ	13925
1XLS	BJ	TRANSCRIPTION	B	1.8	1.8	1	23	PVTNICQAADKQLFTLVEWAKRI	13926
1XLS	CK	TRANSCRIPTION	C	1.8	1.8	1	23	PVTNICQAADKQLFTLVEWAKRI	13927
1XLS	GO	TRANSCRIPTION	G	1.8	1.8	1	25	VLPLLTHFADINTFMVQQIIKFTKD	13928
1XM4	AB	HYDROLASE	A	1.8	1.8	1	6	ELALMY	13929
1XMQ	GK	RIBOSOME	K	1.8	1.8	1	18	PYAAQLAALDAAKKAMAY	13930
1XMQ	JN	RIBOSOME	N	1.8	1.8	1	11	RICLRELAHKG	13931
1XQ5	AB	OXYGEN STORAGE/TRANSPORT	A	1.8	1.8	1	16	AEEIGSDALSRMLAVY	13932
1Y56	AB	OXIDOREDUCTASE	B	1.8	1.8	1	15	YEFLREVSYYFTKII	13933
1Y76	AD	TRANSPORT PROTEIN	D	1.8	1.8	1	15	QSQEDISLLLQLVQN	13934
1YE9	LO	OXIDOREDUCTASE	L	1.8	1.8	1	9	DTFWDYVSL	13935
1YHU	EG	OXYGEN STORAGE/TRANSPORT	E	1.8	1.8	1	18	QATLDADLAHLKSQHDPR	13936
1YHU	FH	OXYGEN STORAGE/TRANSPORT	F	1.8	1.8	1	20	PAFRAHATRVLGGLDMCIAL	13937
1YHU	JL	OXYGEN STORAGE/TRANSPORT	J	1.8	1.8	1	23	PAFRAHATRVLGGLDMCIALLDD	13938
1YKK	IJ	OXIDOREDUCTASE	I	1.8	1.8	1	5	VHIGL	13939
1YTZ	TI	CONTRACTILE PROTEIN	T	1.8	1.8	1	26	YLAKADQKRGKKQTARETKKKVLAER	13940
1Z0K	AB	PROTEIN TRANSPORT	A	1.8	1.8	1	10	KSCLLHQFIE	13941
1Z2C	CD	SIGNALING PROTEIN	C	1.8	1.8	1	19	PDSLENIPEKWTPEVKHFC	13942
1Z5S	AD	LIGASE	D	1.8	1.8	1	9	FETAVKKLN	13943
1Z6O	AX	METAL BINDING PROTEIN	A	1.8	1.8	1	16	LSLALYVFDEYLQKTV	13944
1Z7M	DF	TRANSFERASE	F	1.8	1.8	1	6	KSSFKF	13945
1Z7Q	EM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.8	1.8	1	22	AADGDALVKRFKNSVKWYHFDH	13946
1Z7Q	Qk	HYDROLASE/HYDROLASE ACTIVATOR	Q	1.8	1.8	1	10	QVEYALESIS	13947
1Z7Q	YZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.8	1.8	1	15	VAAASKILSNLVYQY	13948
1Z8U	AB	ELECTRON TRANSPORT	B	1.8	1.8	1	18	PVNFKLLSHCLLVTLAAH	13949
1Z8U	CD	ELECTRON TRANSPORT	D	1.8	1.8	1	13	PAVHASLDKFLAS	13950
1ZAV	AX	STRUCTURAL PROTEIN	X	1.8	1.8	1	10	IDEIIEAIEK	13951
1ZBB	ab	STRUCTURAL PROTEIN/DNA	b	1.8	1.8	1	11	AMDVVYALKRQ	13952
1ZBB	AB	STRUCTURAL PROTEIN/DNA	B	1.8	1.8	1	11	AMDVVYALKRQ	13953
1ZBB	gh	STRUCTURAL PROTEIN/DNA	g	1.8	1.8	1	10	VGRVHRLLRK	13954
1ZBB	GH	STRUCTURAL PROTEIN/DNA	G	1.8	1.8	1	10	VGRVHRLLRK	13955

1ZLA	HK	PROTEIN BINDING/VIRUS/DNA	H	1.8	1.8	1	19	ELAKHAVSEGTKAVTKYTS	13956
1ZNV	CD	HYDROLASE/PROTEIN BINDING	C	1.8	1.8	1	15	DVLDVLLEHFVKITE	13957
1ZW3	AB	PROTEIN BINDING	A	1.8	1.8	1	46	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTV	13958
2A1J	AB	DNA BINDING PROTEIN	A	1.8	1.8	1	7	IAELAAL	13959
2A3I	AB	TRANSFERASE	A	1.8	1.8	1	16	AMLVEIISDQLPKVES	13960
2AFH	AB	OXIDOREDUCTASE	A	1.8	1.8	1	6	EKDIVF	13961
2AFH	AB	OXIDOREDUCTASE	B	1.8	1.8	1	11	LWHLRSLVFTD	13962
2AFH	CD	OXIDOREDUCTASE	D	1.8	1.8	1	8	LWHLRSLV	13963
2AK4	FH	IMMUNE SYSTEM	F	1.8	1.8	1	11	VAEQRRAYLEG	13964
2AK4	KN	IMMUNE SYSTEM	K	1.8	1.8	1	11	VAEQRRAYLEG	13965
2B5T	AB	BLOOD CLOTTING	A	1.8	1.8	1	5	PRTFG	13966
2B8K	AF	TRANSFERASE	A	1.8	1.8	1	12	EETRAELSQLCA	13967
2BA1	AD	RNA BINDING PROTEIN	D	1.8	1.8	1	35	RDEVKQAIELAKKGALQIYEMQREAILRRYIEVGE	13968
2BA1	DG	RNA BINDING PROTEIN	G	1.8	1.8	1	21	EKLFDELLDVSINCARKLREK	13969
2BE6	BE	MEMBRANE PROTEIN	B	1.8	1.8	1	15	EEQIAEFKEAFSLFD	13970
2BEX	AC	HYDROLASE/INHIBITOR	A	1.8	1.8	1	14	EEMEDRLQALEKDK	13971
2BRR	HL	IMMUNE SYSTEM	L	1.8	1.8	1	6	SEQLTS	13972
2BS4	DE	OXIDOREDUCTASE	E	1.8	1.8	1	11	PEVAQEVFELD	13973
2BV8	KP	PHOTOSYNTHESIS	K	1.8	1.8	1	8	LSEINRSF	13974
2BV8	OP	PHOTOSYNTHESIS	P	1.8	1.8	1	14	GNKRLDIVNRINSN	13975
2C35	AD	POLYMERASE	A	1.8	1.8	1	15	DEELQQILDDIQTKR	13976
2C7J	AB	ELECTRON TRANSPORT	A	1.8	1.8	1	25	PEGKAKCVRDIDHYLRTISYCCVVG	13977
2C9W	BC	TRANSCRIPTION REGULATION	B	1.8	1.8	1	12	VFELKRIVEGIL	13978
2CLY	AB	HYDROLASE	B	1.8	1.8	1	21	KAVANSLKSWNETLTSRLATL	13979
2CNW	AD	SIGNAL RECOGNITION	D	1.8	1.8	1	14	QNGLEQAKKFHEAV	13980
2CNW	CF	SIGNAL RECOGNITION	C	1.8	1.8	1	9	ARLQEAIGR	13981
2D3G	BP	PROTEIN TRANSPORT	P	1.8	1.8	1	17	QEEEELQLALALSQSEA	13982
2DD4	EI	HYDROLASE	E	1.8	1.8	1	8	HTLFRAYT	13983
2DD4	KC	HYDROLASE	K	1.8	1.8	1	8	HTLFRAYT	13984
2DFS	AC	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	C	1.8	1.8	1	7	EAELQDM	13985
2DFS	MO	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	O	1.8	1.8	1	7	EAELQDM	13986
2DRN	BC	TRANSFERASE	B	1.8	1.8	1	16	LTELLQGYTVEVLRQQ	13987
2DVQ	BQ	TRANSCRIPTION	B	1.8	1.8	1	7	TNCYIYN	13988
2DXB	KC	HYDROLASE	C	1.8	1.8	1	16	DFEILEMAVRELAIEK	13989
2DXB	QU	HYDROLASE	U	1.8	1.8	1	16	DFEILEMAVRELAIEK	13990
2DXB	TR	HYDROLASE	T	1.8	1.8	1	8	HTLFRAYT	13991
2EFC	CB	TRANSPORT PROTEIN	C	1.8	1.8	1	19	EEELDSAGDGLEKYVMTKL	13992
2EHO	IJ	REPLICATION	J	1.8	1.8	1	15	ALYEQNQSDVNEAKS	13993

2EKV	AB	CONTRACTILE PROTEIN	A	1.8	1.8	1	8	RIGLTLIQ	13994
2EKV	AB	CONTRACTILE PROTEIN	B	1.8	1.8	1	8	MEDLKDMF	13995
2EKV	AB	CONTRACTILE PROTEIN	B	1.8	1.8	1	8	FTAFLTLF	13996
2EY4	AE	ISOMERASE/BIOSYNTHETIC PROTEIN	A	1.8	1.8	1	8	EEYFRKAI	13997
2F5Z	FM	OXIDOREDUCTASE/PROTEIN BINDING	F	1.8	1.8	1	6	CEDIAR	13998
2FDB	NR	HORMONE/GROWTH FACTOR/TRANSFERASE	N	1.8	1.8	1	8	TQHVREQS	13999
2FHH	FN	HYDROLASE	N	1.8	1.8	1	23	AAVAVEFARLYAVELEHYEKLEG	14000
2FJ7	BD	STRUCTURAL PROTEIN/DNA	D	1.8	1.8	1	12	SREIQTAVRLLL	14001
2FM8	AC	CHAPERONE/CELL INVASION	A	1.8	1.8	1	22	GEKFSTALNGFYNYLEVFSRSL	14002
2FTK	AE	TRANSFERASE	A	1.8	1.8	1	31	TALTNELIHLLGHSRHDWMNKLQLIKGNLSL	14003
2FUG	12	OXIDOREDUCTASE	1	1.8	1.8	1	17	RRAADRLEQAIKEARAR	14004
2FUG	46	OXIDOREDUCTASE	4	1.8	1.8	1	10	YLQNITYTPR	14005
2FUG	AB	OXIDOREDUCTASE	A	1.8	1.8	1	17	RRAADRLEQAIKEARAR	14006
2FUG	EG	OXIDOREDUCTASE	E	1.8	1.8	1	5	PAEFR	14007
2FYN	KL	OXIDOREDUCTASE	L	1.8	1.8	1	5	RDFLY	14008
2FYN	MR	OXIDOREDUCTASE	M	1.8	1.8	1	11	IGHSIQTWLLG	14009
2FYN	NO	OXIDOREDUCTASE	O	1.8	1.8	1	5	RDFLY	14010
2GC4	IN	OXIDOREDUCTASE, ELECTRON TRANSPORT	I	1.8	1.8	1	20	QAQETQGQAAARAAAADLAA	14011
2GID	AB	TRANSLATION	A	1.8	1.8	1	13	QRFLTQALHYNTG	14012
2GID	HK	TRANSLATION	H	1.8	1.8	1	11	QRFLTQALHYN	14013
2GJE	AD	TRANSLATION/RNA	A	1.8	1.8	1	12	QRFLTQALHYNT	14014
2GJX	AB	HYDROLASE	B	1.8	1.8	1	18	MDDAYDRLTRHRCRMVER	14015
2GJX	EF	HYDROLASE	F	1.8	1.8	1	8	HRCRMVER	14016
2GTL	MO	OXYGEN STORAGE/TRANSPORT	O	1.8	1.8	1	18	PKRIRKAGSLRHRVEELE	14017
2GUZ	OF	CHAPERONE, PROTEIN TRANSPORT	F	1.8	1.8	1	23	FYLQSKVYRAAERLKWELAQREK	14018
2H4C	AB	HYDROLASE	B	1.8	1.8	1	11	ATDRCCFVHDC	14019
2HDN	GH	TRANSLATION	H	1.8	1.8	1	10	HADYVKNMIT	14020
2HGJ	TU	RIBOSOME	T	1.8	1.8	1	29	KARETLFAAGNYAYAHRKRRKRDFRRLWI	14021
2HHF	AB	TRANSFERASE	B	1.8	1.8	1	7	LRSAMRL	14022
2HLD	FG	HYDROLASE	F	1.8	1.8	1	8	QDIIAILG	14023
2HLD	GH	HYDROLASE	G	1.8	1.8	1	5	VPRDL	14024
2HLD	LO	HYDROLASE	L	1.8	1.8	1	14	RSTVAQLVQTLEQH	14025
2HLD	PQ	HYDROLASE	P	1.8	1.8	1	19	YTLANQMLTAMAQGYAAEI	14026
2HOD	DE	BLOOD CLOTTING	E	1.8	1.8	1	15	KIQKLESDVSAQMEY	14027
2HOD	DF	BLOOD CLOTTING	D	1.8	1.8	1	38	KRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRS	14028
2HUE	BC	DNA BINDING PROTEIN	C	1.8	1.8	1	12	AMDVVYALKRQG	14029
2HZM	CB	TRANSCRIPTION	C	1.8	1.8	1	6	PALVFN	14030
2HZS	AD	TRANSCRIPTION	A	1.8	1.8	1	6	PALVFN	14031

2I2R	BF	TRANSPORT PROTEIN	F	1.8	1.8	1	13	VHEKLRWTFNLYD	14032
2I2X	AB	TRANSFERASE	B	1.8	1.8	1	8	EASLKKVL	14033
2I2X	AD	TRANSFERASE	A	1.8	1.8	1	22	TVQCWSETLAYDCALMNTALET	14034
2I2X	ON	TRANSFERASE	O	1.8	1.8	1	22	TVQCWSETLAYDCALMNTALET	14035
2IAN	BT	IMMUNE SYSTEM	B	1.8	1.8	1	10	RPDAEYWNSQ	14036
2IBZ	CD	OXIDOREDUCTASE	C	1.8	1.8	1	15	IELAFSSVEHIMRDV	14037
2IBZ	DH	OXIDOREDUCTASE	H	1.8	1.8	1	22	EEGKALVHHYEECAERVKIQQQ	14038
2IK8	AB	SIGNALING PROTEIN	B	1.8	1.8	1	21	DAAQGKTRTLMEKDSYPRFLK	14039
2INN	AC	OXIDOREDUCTASE	A	1.8	1.8	1	7	PEKYIQA	14040
2INP	AC	OXIDOREDUCTASE	A	1.8	1.8	1	5	KKDIF	14041
2INP	AD	OXIDOREDUCTASE	A	1.8	1.8	1	32	MATVTFGFSAQSDEARHMTLGLEVIKFILEQH	14042
2IPK	AB	IMMUNE SYSTEM	B	1.8	1.8	1	9	RPDAEYWNS	14043
2IV8	AP	ENDOCYTOSIS/REGULATOR	A	1.8	1.8	1	11	RQVFLATWKDI	14044
2IX7	CB	CONTRACTILE PROTEIN/METAL BINDING	B	1.8	1.8	1	9	AAELRHVMT	14045
2J0Q	AC	HYDROLASE	A	1.8	1.8	1	6	HEILEM	14046
2J0Q	AC	HYDROLASE	C	1.8	1.8	1	25	PEGLRVFYYLVQDLKCLVFSLIGLH	14047
2J0Q	AT	HYDROLASE	A	1.8	1.8	1	5	TNKFM	14048
2J0Q	BI	HYDROLASE	B	1.8	1.8	1	5	TNKFM	14049
2J7A	BC	OXIDOREDUCTASE	B	1.8	1.8	1	10	RNEMRALVCG	14050
2J9U	AB	PROTEIN TRANSPORT	B	1.8	1.8	1	7	YELTKSS	14051
2JGZ	AB	TRANSFERASE	B	1.8	1.8	1	15	VKDIYAYLRQLEEEQ	14052
2JIZ	AD	HYDROLASE	A	1.8	1.8	1	7	TELFYKG	14053
2JIZ	KN	HYDROLASE	N	1.8	1.8	1	69	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAA	14054
2JKR	LE	ENDOCYTOSIS	L	1.8	1.8	1	8	TDILATVL	14055
2JU0	AB	METAL BINDING PROTEIN/SIGNALING PROTEIN	A	1.8	1.8	1	11	REDFVKIYKQF	14056
2JU0	AB	METAL BINDING PROTEIN/SIGNALING PROTEIN	A	1.8	1.8	1	10	EKLSWAFELY	14057
2K42	AB	SIGNALING PROTEIN	A	1.8	1.8	1	9	LEAVRQEMR	14058
2K42	AB	SIGNALING PROTEIN	B	1.8	1.8	1	11	VAQRLMQHLAE	14059
2K6T	AB	HORMONE	B	1.8	1.8	1	12	HHFVRALVRVCG	14060
2NPP	DE	SIGNALING PROTEIN,HYDROLASE	D	1.8	1.8	1	10	WRVRYMVADK	14061
2NQB	GH	STRUCTURAL PROTEIN/DNA	G	1.8	1.8	1	10	VGRIHRLLRK	14062
2NTY	BC	SIGNALING PROTEIN	C	1.8	1.8	1	13	VKAVFDAAIKVVL	14063
2NXX	BF	HORMONE/GROWTH FACTOR	B	1.8	1.8	1	9	PGRFAKLLL	14064
2NXX	DH	HORMONE/GROWTH FACTOR	D	1.8	1.8	1	9	PGRFAKLLL	14065
2O01	AB	PHOTOSYNTHESIS	B	1.8	1.8	1	10	FWMLNTIGWV	14066
2OBH	BD	CELL CYCLE	B	1.8	1.8	1	12	DEELQEMIDEAD	14067

2OM0	UV	HORMONE	U	1.8	1.8	1	5	IVEQC	14068
2OT3	AB	PROTEIN TRANSPORT	A	1.8	1.8	1	24	PRDKLACITKCSKHIFNAIKITKN	14069
2OT8	AC	TRANSPORT PROTEIN	A	1.8	1.8	1	18	ISVCNNATWAIGEISIQM	14070
2OV2	EM	PROTEIN BINDING/TRANSFERASE	E	1.8	1.8	1	10	KTCLLISYTT	14071
2P1L	AB	APOPTOSIS	A	1.8	1.8	1	21	WGRIVAFFSFGGALCVESVDK	14072
2P22	AC	TRANSPORT PROTEIN	A	1.8	1.8	1	5	VNSIA	14073
2PF4	AE	HYDROLASE REGULATOR/VIRAL PROTEIN	A	1.8	1.8	1	9	FTSRTSACG	14074
2PF4	BF	HYDROLASE REGULATOR/VIRAL PROTEIN	F	1.8	1.8	1	12	REESLQLMDLLG	14075
2PKG	AD	HYDROLASE REGULATOR/VIRAL PROTEIN	A	1.8	1.8	1	6	KEWAHA	14076
2PKG	AD	HYDROLASE REGULATOR/VIRAL PROTEIN	D	1.8	1.8	1	16	EGTLLLWCDIIGQTTY	14077
2PMS	AC	METAL TRANSPORT, HYDROLASE	C	1.8	1.8	1	40	APLQSKLDAKKAKLSKLEELSDKIDELDAEIAKLEDQLKA	14078
2PMZ	RZ	TRANSLATION, TRANSFERASE	R	1.8	1.8	1	5	EARLR	14079
2PMZ	SX	TRANSLATION, TRANSFERASE	S	1.8	1.8	1	7	IRRASML	14080
2PRG	AC	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	A	1.8	1.8	1	27	VAIRIFQGCQFRSVEAVQEITEYAKSI	14081
2PT7	BG	HYDROLASE/PROTEIN BINDING	B	1.8	1.8	1	15	LSRLMHFARCCASFK	14082
2Q0O	AC	TRANSCRIPTION	A	1.8	1.8	1	9	ASVTANLTG	14083
2Q0O	BD	TRANSCRIPTION	B	1.8	1.8	1	9	ASVTANLTG	14084
2QAR	DE	HYDROLASE REGULATOR	E	1.8	1.8	1	8	KEDFRYRS	14085
2QB0	CB	HYDROLASE REGULATOR	B	1.8	1.8	1	14	GDVLYELLQHILKQ	14086
2QCD	AB	LYASE	A	1.8	1.8	1	12	DYTRAAVRMAEE	14087
2QCD	AB	LYASE	B	1.8	1.8	1	13	DYTRAAVRMAEEH	14088
2QE7	AD	HYDROLASE	D	1.8	1.8	1	10	PAPATTFAHL	14089
2QEJ	AD	IMMUNE SYSTEM	A	1.8	1.8	1	7	LEDLLLG	14090
2QFA	AB	CELL CYCLE/CELL CYCLE/CELL CYCLE	B	1.8	1.8	1	7	WLDYFAL	14091
2QIE	AB	TRANSFERASE	B	1.8	1.8	1	6	EIKDIL	14092
2QJK	EF	ELECTRON TRANSPORT	F	1.8	1.8	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	14093
2QJK	HI	ELECTRON TRANSPORT	I	1.8	1.8	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	14094
2QJP	DE	ELECTRON TRANSPORT	D	1.8	1.8	1	15	VDLAFASVEHIMRNV	14095
2QJP	GH	ELECTRON TRANSPORT	G	1.8	1.8	1	15	VDLAFASVEHIMRNV	14096
2QJY	DE	OXIDOREDUCTASE	D	1.8	1.8	1	15	VDLAFASVEHIMRNV	14097
2QL2	AB	TRANSCRIPTION/DNA	B	1.8	1.8	1	26	RRMKANARERNRMHGLNAALDNLRKV	14098
2QLV	BC	TRANSFERASE/PROTEIN BINDING	C	1.8	1.8	1	12	QYRILKFVALNC	14099
2QM6	CD	TRANSFERASE	D	1.8	1.8	1	5	EMDDF	14100
2QMB	CB	TRANSPORT PROTEIN	C	1.8	1.8	1	18	PVNFKLLGQCFLVVVAIH	14101
2QR1	DE	TRANSFERASE	E	1.8	1.8	1	11	VKTSLSLLTLN	14102

2R6C	AG	REPLICATION	A	1.8	1.8	1	11	LVTVTAELAAS	14103
2R6G	EF	HYDROLASE/TRANSPORT PROTEIN	F	1.8	1.8	1	7	LRVITQN	14104
2RF4	EF	TRANSFERASE	F	1.8	1.8	1	16	TDEVLQFLESFIDEKE	14105
2RI4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.8	1.8	1	18	ENFKLLGNVLVVVLARHH	14106
2UUN	IL	ELECTRON TRANSPORT	I	1.8	1.8	1	8	IDEVNRTF	14107
2UUN	UV	ELECTRON TRANSPORT	V	1.8	1.8	1	13	ANKRLDAVNRITA	14108
2V1S	EL	OXIDOREDUCTASE	E	1.8	1.8	1	25	LKDAEAVQKFFLEEIQLGEELLAQG	14109
2V36	CD	TRANSFERASE	C	1.8	1.8	1	6	AKDVFL	14110
2V55	AB	TRANSFERASE	B	1.8	1.8	1	10	HVATLACVNK	14111
2V7Q	CF	HYDROLASE	C	1.8	1.8	1	7	TELFYKG	14112
2V7Q	DG	HYDROLASE	G	1.8	1.8	1	51	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYE	14113
2VBL	AB	HYDROLASE	A	1.8	1.8	1	12	RWFLDKLVDEIG	14114
2VDB	AB	PROTEIN BINDING	B	1.8	1.8	1	9	DFYFNAINK	14115
2VDW	EF	TRANSFERASE	F	1.8	1.8	1	30	TEFINKFLEFSNRVYEALYYVHSLLYSSMT	14116
2VLH	AB	LYASE	A	1.8	1.8	1	12	GRGAENLLSQLA	14117
2W83	AC	PROTEIN TRANSPORT	A	1.8	1.8	1	6	RPLWRH	14118
2WAQ	AC	TRANSCRIPTION	C	1.8	1.8	1	9	LPRLIEIVD	14119
2WAQ	CK	TRANSCRIPTION	K	1.8	1.8	1	17	RYEIARVISARALQLAM	14120
2WB1	AC	TRANSCRIPTION	C	1.8	1.8	1	13	DLKNLISNKEVLV	14121
2WB1	HK	TRANSCRIPTION	K	1.8	1.8	1	11	HFNEVFISLWQ	14122
2WB1	SO	TRANSCRIPTION	O	1.8	1.8	1	6	ISEVIH	14123
2WDI	FP	RIBOSOME	F	1.8	1.8	1	16	PHLLWEVVRWQLAKRR	14124
2WDI	UV	RIBOSOME	U	1.8	1.8	1	35	RKARETLFAAGNYAYAHRKRRKRDFRRLWIVRINA	14125
2WME	HE	OXIDOREDUCTASE	H	1.8	1.8	1	22	LAETRSVDIVTGADVLEYYAGL	14126
2ZBK	AB	ISOMERASE	A	1.8	1.8	1	12	LMASIIYDALVS	14127
2ZBK	CD	ISOMERASE	C	1.8	1.8	1	10	ASIIYDALVS	14128
2ZCY	BC	HYDROLASE	C	1.8	1.8	1	22	NADSRILIEKARVEAQSHRLTL	14129
2ZCY	GN	HYDROLASE	G	1.8	1.8	1	22	IPDARNAALRAKAEAAEFRYKY	14130
2ZIX	AB	HYDROLASE	A	1.8	1.8	1	5	IKESA	14131
2ZU6	AB	HYDROLASE	A	1.8	1.8	1	7	ADEMLSR	14132
2ZU6	AB	HYDROLASE	A	1.8	1.8	1	10	RRKVDWLTEK	14133
2ZU6	AB	HYDROLASE	B	1.8	1.8	1	6	TNEVAE	14134
2ZU6	FE	HYDROLASE	F	1.8	1.8	1	13	RRKVDWLTEKMHA	14135
2ZVN	EF	SIGNALING PROTEIN/TRANSCRIPTION	F	1.8	1.8	1	84	EDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLK	14136
3A0B	BD	ELECTRON TRANSPORT	D	1.8	1.8	1	17	PVTGLWMSAIGVVGLAL	14137
3B4V	BD	HORMONE REGULATOR COMPLEX	D	1.8	1.8	1	8	KINLLGFL	14138
3BG0	EF	PROTEIN TRANSPORT, HYDROLASE	F	1.8	1.8	1	8	KLIMKERR	14139

3BIM	CK	TRANSCRIPTION REPRESSOR	C	1.8	1.8	1	7	GLFYSIF	14140
3BIM	DL	TRANSCRIPTION REPRESSOR	D	1.8	1.8	1	10	EHVVDTCRKF	14141
3BIM	FN	TRANSCRIPTION REPRESSOR	F	1.8	1.8	1	9	EHVVDTCRK	14142
3BJI	BC	SIGNALING PROTEIN	B	1.8	1.8	1	12	KYHLLLQELVKH	14143
3BO0	AB	RIBOSOME	A	1.8	1.8	1	17	YIAPIIGTIIVFLMVVY	14144
3BOW	AC	HYDROLASE/HYDROLASE INHIBITOR	A	1.8	1.8	1	15	AFELQTILRRVLAKR	14145
3BOW	BC	HYDROLASE/HYDROLASE INHIBITOR	B	1.8	1.8	1	15	ATELMNILNKVVTRH	14146
3BPQ	CD	TOXIN	D	1.8	1.8	1	5	RKSIY	14147
3BZ1	AD	ELECTRON TRANSPORT	D	1.8	1.8	1	28	GLWTFIALHGAFGLIGFMLRQFEIARLV	14148
3BZ1	BD	ELECTRON TRANSPORT	D	1.8	1.8	1	12	IFRFLLFFQGFH	14149
3BZ1	CK	ELECTRON TRANSPORT	C	1.8	1.8	1	26	FPFFVVGVVHLISSAVLGFGGVYHAI	14150
3C1B	CD	STRUCTURAL PROTEIN/DNA	C	1.8	1.8	1	7	EELNKLL	14151
3C7N	AB	CHAPERONE/CHAPERONE	A	1.8	1.8	1	15	DRKNTLEEYIYTLRG	14152
3C8G	CB	TRANSCRIPTION REGULATOR	C	1.8	1.8	1	8	EEIVEYAV	14153
3CHW	AP	STRUCTURAL PROTEIN	P	1.8	1.8	1	7	SSFYVNG	14154
3CJT	CD	TRANSFERASE/RIBOSOMAL PROTEIN	C	1.8	1.8	1	6	AWRRDL	14155
3CWB	CE	OXIDOREDUCTASE	C	1.8	1.8	1	29	GWLIRNLHANGASFFFICIFLHIGRGLYY	14156
3CXH	MG	OXIDOREDUCTASE	G	1.8	1.8	1	10	PIMQTALRRL	14157
3CXH	NE	OXIDOREDUCTASE	N	1.8	1.8	1	10	GNDIVSWLWG	14158
3D24	AB	TRANSCRIPTION	A	1.8	1.8	1	11	LSDQMSVLQSV	14159
3D5B	G4	RIBOSOME	G	1.8	1.8	1	6	NVALPR	14160
3D5D	QZ	RIBOSOME	Q	1.8	1.8	1	15	AQQIEAARVAMVRHF	14161
3D7V	AB	APOPTOSIS	A	1.8	1.8	1	12	ETAFQGMLRKLD	14162
3DBJ	CD	PHOTOSYNTHESIS	D	1.8	1.8	1	13	AITAVINASDVQG	14163
3DBJ	GH	PHOTOSYNTHESIS	H	1.8	1.8	1	13	AITAVINASDVQG	14164
3DHH	AC	OXIDOREDUCTASE	A	1.8	1.8	1	7	IVDRFLA	14165
3DHT	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.8	1.8	1	19	PENFRLLGNMIVIVLGHHL	14166
3DOE	AB	SIGNALING PROTEIN/HYDROLASE	B	1.8	1.8	1	16	FLAFKEMFLDYRAEKE	14167
3DRA	AB	TRANSFERASE	B	1.8	1.8	1	9	KSTKEWLIH	14168
3DTU	AB	OXIDOREDUCTASE	A	1.8	1.8	1	5	LSTSE	14169
3DTU	CD	OXIDOREDUCTASE	C	1.8	1.8	1	5	LSTSE	14170
3DUH	AC	IMMUNE SYSTEM/CYTOKINE	C	1.8	1.8	1	7	PQGLRDN	14171
3DWL	AD	STRUCTURAL PROTEIN	A	1.8	1.8	1	13	PENRENTAEIMFE	14172
3E3Q	AD	IMMUNE SYSTEM	A	1.8	1.8	1	24	AAEYYRAYLEGECVEWLHRYLKNG	14173
3E3Q	UV	IMMUNE SYSTEM	U	1.8	1.8	1	24	AAEYYRAYLEGECVEWLHRYLKNG	14174
3E8U	HL	IMMUNE SYSTEM	L	1.8	1.8	1	7	SEQLTSG	14175
3EDX	CD	HYDROLASE	C	1.8	1.8	1	5	EKTFG	14176
3EIQ	AC	HYDROLASE/ANTITUMOR PROTEIN	A	1.8	1.8	1	10	RRKVDWLTEK	14177
3ESW	AB	HYDROLASE	A	1.8	1.8	1	12	LIKYKDFILSKF	14178

3ETB	HJ	IMMUNE SYSTEM/TOXIN	J	1.8	1.8	1	7	KDIRKIL	14179
3ETR	LN	OXIDOREDUCTASE	L	1.8	1.8	1	10	LLAYLRRKLG	14180
3EX7	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.8	1.8	1	16	EEWKFDTLCDLYDTLT	14181
3EX7	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.8	1.8	1	14	KRKVDWLTEKMREA	14182
3EXG	12	OXIDOREDUCTASE	2	1.8	1.8	1	14	EMGFAGIAVGAAMA	14183
3EXG	AP	OXIDOREDUCTASE	A	1.8	1.8	1	25	VEELKEIDVEVRKEIEDAAQFATAD	14184
3EXH	AD	OXIDOREDUCTASE	D	1.8	1.8	1	7	FNFSMQA	14185
3F1F	FP	RIBOSOME	F	1.8	1.8	1	19	KKVRKKGLAMAVADRAREG	14186
3F5C	AC	TRANSCRIPTION	C	1.8	1.8	1	23	VKYIEGLQWRTQQILTEHIRMMQ	14187
3F8U	AB	IMMUNE SYSTEM/ISOMERASE	A	1.8	1.8	1	17	GHCKNLEPKYKELGEKL	14188
3F9K	MO	VIRAL PROTEIN, RECOMBINATION	O	1.8	1.8	1	10	TEMITTLKKI	14189
3F9K	VW	VIRAL PROTEIN, RECOMBINATION	V	1.8	1.8	1	11	QEVKMVAWWIG	14190
3FAL	AD	SIGNALING PROTEIN	A	1.8	1.8	1	24	LDDQVILLRAGWNELLIASFSHRS	14191
3FAL	CD	SIGNALING PROTEIN	C	1.8	1.8	1	23	PAEVEALREKVYASLEAYCKHKY	14192
3FKS	GI	HYDROLASE	I	1.8	1.8	1	12	YAAYLNVAAQAI	14193
3FKS	SV	HYDROLASE	S	1.8	1.8	1	7	AELFYKG	14194
3G43	CF	METAL BINDING PROTEIN	C	1.8	1.8	1	12	FPEFLTMMARKM	14195
3G43	DF	METAL BINDING PROTEIN	D	1.8	1.8	1	12	EEEIREAFRVFD	14196
3GHG	DE	BLOOD CLOTTING	E	1.8	1.8	1	22	MYLLKDLWQKRQKQVKDNENVV	14197
3GHG	JK	BLOOD CLOTTING	K	1.8	1.8	1	11	GCQLQEALLQQ	14198
3GM1	AE	TRANSFERASE	A	1.8	1.8	1	33	SEECKRQMLTASHTLAVDAKNLLDAVDQAKVLA	14199
3GTM	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.8	1.8	1	6	LSEVMT	14200
3GTU	AB	TRANSFERASE	A	1.8	1.8	1	12	SNAILRYIARKH	14201
3H0L	AB	LIGASE	A	1.8	1.8	1	15	PEVKRRIMLGTFALS	14202
3HGK	DH	TRANSFERASE	D	1.8	1.8	1	7	PEYFIKG	14203
3HOU	MR	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.8	1.8	1	11	EETRAELSQLC	14204
3HRD	EF	OXIDOREDUCTASE	F	1.8	1.8	1	22	RSMVEGQIEGGVTMGQGFVLME	14205
3HRD	FH	OXIDOREDUCTASE	H	1.8	1.8	1	16	IKIHAAVRYAVERCAN	14206
3HRW	CB	OXYGEN TRANSPORT	C	1.8	1.8	1	16	PVNFKLLSHCLLVTLA	14207
3PRO	BD	PRO REGION	D	1.8	1.8	1	11	PQLKFAMQRDL	14208
3PRO	BD	PRO REGION	D	1.8	1.8	1	16	LKQLQSAMEQLDAGAN	14209
1A4Y	AB	COMPLEX (INHIBITOR/NUCLEASE)	B	1.7	1.7	1	12	DRYCESIMRRRG	14210
1AHJ	GH	LYASE	G	1.7	1.7	1	5	WPILG	14211
1AIP	EH	COMPLEX OF TWO ELONGATION FACTORS	H	1.7	1.7	1	18	ELFQNLAKDLAMHIAMMN	14212
1AOI	CD	DNA BINDING PROTEIN/DNA	C	1.7	1.7	1	7	EELNKLL	14213

1APY	AB	HYDROLASE	A	1.7	1.7	1	16	ALDAVESGCAMCEREQ	14214
1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	A	1.7	1.7	1	28	EWAGQLHFWMMFIGSNLIFFPQHFLGRQ	14215
1AWC	AB	TRANSCRIPTION/DNA	B	1.7	1.7	1	8	AFDISIDN	14216
1AYY	AD	HYDROLASE	D	1.7	1.7	1	19	PQQACKEAVERIVKIVNRR	14217
1B33	IO	PHOTOSYNTHESIS	O	1.7	1.7	1	5	LQNTY	14218
1B6C	EB	COMPLEX (ISOMERASE/PROTEIN KINASE)	B	1.7	1.7	1	8	LFDYLNRY	14219
1B8D	AB	PHOTOSYNTHESIS	B	1.7	1.7	1	14	GNKRLDAVNYIVSN	14220
1BCC	AB	OXIDOREDUCTASE	A	1.7	1.7	1	11	QNALEKEVESM	14221
1BCC	AG	OXIDOREDUCTASE	A	1.7	1.7	1	6	YNRIRS	14222
1BCC	DH	OXIDOREDUCTASE	H	1.7	1.7	1	18	EKCVKARERLELCDERVS	14223
1BGY	BR	ELECTRON TRANSPORT	B	1.7	1.7	1	8	RWEVAALQ	14224
1BGY	OS	ELECTRON TRANSPORT	O	1.7	1.7	1	34	HPYITIGQLASVLYFLLILVLMPTAGTIENKLLK	14225
1BX2	AB	IMMUNE SYSTEM	A	1.7	1.7	1	23	AQGALANIAVDKANLEIMTKRSN	14226
1C5B	LH	IMMUNE SYSTEM	L	1.7	1.7	1	6	DEQLKS	14227
1CAX	EB	SEED STORAGE PROTEIN	B	1.7	1.7	1	6	RQVSDL	14228
1CC1	SL	OXIDOREDUCTASE	L	1.7	1.7	1	6	FEQILR	14229
1D4M	34	VIRUS	3	1.7	1.7	1	6	LMEIAE	14230
1D8D	AB	TRANSFERASE	A	1.7	1.7	1	17	EKFRDVYDYFRAVLQRD	14231
1DD4	AC	RIBOSOME	C	1.7	1.7	1	12	LAELVKKLEDKF	14232
1DE4	AC	METAL TRANSPORT INHIBITOR/RECEPTOR	A	1.7	1.7	1	28	SQMWLQLSQSLKGWDHMFTVDFWTIMEN	14233
1DFK	AZ	CONTRACTILE PROTEIN	Z	1.7	1.7	1	11	YEDFVKKVMAG	14234
1DFK	AZ	CONTRACTILE PROTEIN	Z	1.7	1.7	1	18	QDEIDDLKDVFELFDFWD	14235
1DGH	CD	OXIDOREDUCTASE	D	1.7	1.7	1	7	YFAEVEQ	14236
1DHK	AB	COMPLEX (HYDROLASE/INHIBITOR)	A	1.7	1.7	1	13	FKYGAKLGTVVRK	14237
1DQQ	AB	IMMUNE SYSTEM	A	1.7	1.7	1	6	SEQLTS	14238
1E1C	AB	ISOMERASE	B	1.7	1.7	1	13	EEQWEREVEKVLN	14239
1E6E	AB	OXIDOREDUCTASE	A	1.7	1.7	1	21	ITTTMTDSFLTGQILLQDLKA	14240
1E6E	CD	OXIDOREDUCTASE	D	1.7	1.7	1	9	DEENDMLDL	14241
1EF1	AC	MEMBRANE PROTEIN	C	1.7	1.7	1	5	EAEKN	14242
1EF1	BD	MEMBRANE PROTEIN	B	1.7	1.7	1	15	REDAVLEYLKIAQDL	14243
1EM8	CD	GENE REGULATION	D	1.7	1.7	1	5	EHDFF	14244
1EPT	AC	HYDROLASE (SERINE PROTEASE)	C	1.7	1.7	1	9	VNWIQQTIA	14245
1EV1	13	VIRUS	1	1.7	1.7	1	8	AQLRRKLE	14246
1EV1	14	VIRUS	1	1.7	1.7	1	6	IENFLA	14247
1EV1	23	VIRUS	3	1.7	1.7	1	7	LMGEILN	14248
1F3D	LH	IMMUNE SYSTEM	L	1.7	1.7	1	6	SEQLTS	14249
1F3M	AC	TRANSFERASE	C	1.7	1.7	1	11	KELIINEILVM	14250

1F51	AE	TRANSFERASE	E	1.7	1.7	1	12	SGIRILLNEVFN	14251
1F5Q	CB	TRANSFERASE	B	1.7	1.7	1	14	PVLITLACMHLTMN	14252
1F5Q	CB	TRANSFERASE	B	1.7	1.7	1	17	KEELHQCCDLVDIAIVS	14253
1F66	FH	STRUCTURAL PROTEIN/DNA	H	1.7	1.7	1	12	SREIQTAVRLLL	14254
1F6F	AB	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR	A	1.7	1.7	1	7	KAEAINT	14255
1FFT	AC	OXIDOREDUCTASE	A	1.7	1.7	1	18	SFPILTVTVALLTLDRYL	14256
1FFU	BC	HYDROLASE	B	1.7	1.7	1	11	RYIAADAVEAV	14257
1FG9	BD	IMMUNE SYSTEM	D	1.7	1.7	1	5	VCRDG	14258
1FHJ	CB	OXYGEN STORAGE/TRANSPORT	C	1.7	1.7	1	19	PVNFKLLSHCLLVTLACHH	14259
1FNT	ab	HYDROLASE/HYDROLASE ACTIVATOR	a	1.7	1.7	1	21	AADGDALVKRFKNSVKWYHFD	14260
1FNT	Ge	HYDROLASE/HYDROLASE ACTIVATOR	G	1.7	1.7	1	13	FQVEYAVKAVENG	14261
1FQV	CD	LIGASE	C	1.7	1.7	1	10	DELLLGIFSC	14262
1FQV	GH	LIGASE	H	1.7	1.7	1	14	QGTLFELILAANYL	14263
1FS2	CD	LIGASE	C	1.7	1.7	1	11	DELLLGIFSCL	14264
1FSX	AB	OXYGEN STORAGE/TRANSPORT	A	1.7	1.7	1	19	PVNFKLLSHSLLVTLASHL	14265
1FSX	AD	OXYGEN STORAGE/TRANSPORT	A	1.7	1.7	1	19	PVNFKLLSHSLLVTLASHL	14266
1G0U	CJ	HYDROLASE	J	1.7	1.7	1	23	AGDTVQFAEYIQANIQLYSIRED	14267
1G0U	IJ	HYDROLASE	I	1.7	1.7	1	23	ATDVTTLNEMFRYKTNLYKLKEE	14268
1G0U	IJ	HYDROLASE	J	1.7	1.7	1	14	YSGFYTFSLLDHHY	14269
1G0U	WK	HYDROLASE	K	1.7	1.7	1	13	VGELFWKVKEEEG	14270
1G0U	Z1	HYDROLASE	1	1.7	1.7	1	14	FGAHMANPLLRKVV	14271
1G20	AB	OXIDOREDUCTASE	A	1.7	1.7	1	6	ILLEEM	14272
1G20	CD	OXIDOREDUCTASE	C	1.7	1.7	1	6	ILLEEM	14273
1G3I	BI	CHAPERONE/HYDROLASE	I	1.7	1.7	1	18	TADAFTLFELFERKLEMH	14274
1G8K	AB	OXIDOREDUCTASE	A	1.7	1.7	1	5	PYESQ	14275
1G8K	CD	OXIDOREDUCTASE	C	1.7	1.7	1	5	PYESQ	14276
1G8K	EF	OXIDOREDUCTASE	E	1.7	1.7	1	5	PYESQ	14277
1GH0	MN	PHOTOSYNTHESIS	N	1.7	1.7	1	13	TAQIDALSQMVAE	14278
1GH0	OP	PHOTOSYNTHESIS	O	1.7	1.7	1	12	PLTEAVSVADSQ	14279
1GLA	FG	PHOSPHOTRANSFERASE	F	1.7	1.7	1	5	VVFAE	14280
1GLA	FG	PHOSPHOTRANSFERASE	G	1.7	1.7	1	5	IETTE	14281
1GXS	AD	LYASE	D	1.7	1.7	1	10	VSSTRRSLAA	14282
1H1L	CD	OXIDOREDUCTASE	D	1.7	1.7	1	16	QGCVAYFRTYFNRHFK	14283
1H4L	AD	KINASE/KINASE ACTIVATOR	D	1.7	1.7	1	10	SSKMLQINAD	14284
1H4L	BE	KINASE/KINASE ACTIVATOR	E	1.7	1.7	1	9	SSKMLQINA	14285
1HBX	EH	GENE REGULATION	E	1.7	1.7	1	13	ETGKALIQTCLNS	14286
1HH9	AB	IMMUNE SYSTEM/PEPTIDE	A	1.7	1.7	1	5	SEQLT	14287
1HLE	AB	HYDROLASE INHIBITOR (SERINE PROTEINASE)	A	1.7	1.7	1	14	PLSISSALAMIFLG	14288

1HTL	FC	ENTEROTOXIN	C	1.7	1.7	1	30	DTCNEETQNLSTIYLREYQSKVKRQIFSDY	14289
1HV4	AB	OXYGEN STORAGE/TRANSPORT	A	1.7	1.7	1	16	AEEYGAETLERMFTAY	14290
1HV4	GH	OXYGEN STORAGE/TRANSPORT	G	1.7	1.7	1	16	AEEYGAETLERMFTAY	14291
1I3Q	BK	TRANSCRIPTION	K	1.7	1.7	1	12	HTLGNLIRAELL	14292
1I3R	EF	IMMUNE SYSTEM	E	1.7	1.7	1	5	EEFAK	14293
1I7Y	AB	PHOTOSYNTHESIS	B	1.7	1.7	1	14	GNKRLDAVNRITSN	14294
1I84	ST	CONTRACTILE PROTEIN	T	1.7	1.7	1	9	FEDYVEGLR	14295
1IBT	CB	LYASE	C	1.7	1.7	1	13	VLDGIVSYDRAET	14296
1ID3	EC	STRUCTURAL PROTEIN/DNA	C	1.7	1.7	1	10	PRHLQLAIRN	14297
1ID3	GH	STRUCTURAL PROTEIN/DNA	H	1.7	1.7	1	12	AREIQTAVRLIL	14298
1IGT	AB	IMMUNOGLOBULIN	A	1.7	1.7	1	7	SEQLTSG	14299
1IM9	AD	IMMUNE SYSTEM	A	1.7	1.7	1	13	TAAQITQRKWEAA	14300
1IR2	CK	LYASE	C	1.7	1.7	1	21	NAPGAAANRVALEACTQARNE	14301
1IR2	S1	LYASE	S	1.7	1.7	1	21	NAPGAAANRVALEACTQARNE	14302
1IR2	U3	LYASE	U	1.7	1.7	1	21	NAPGAAANRVALEACTQARNE	14303
1IR2	X6	LYASE	X	1.7	1.7	1	14	AKNYGRAVYECLRG	14304
1IR2	Z8	LYASE	Z	1.7	1.7	1	14	AKNYGRAVYECLRG	14305
1IW7	NO	TRANSFERASE	O	1.7	1.7	1	18	KYRLTVVVAKRAQQLLRH	14306
1IWA	CJ	LYASE	C	1.7	1.7	1	5	WTDLL	14307
1IWA	GB	LYASE	G	1.7	1.7	1	9	VILERERLD	14308
1J2J	AB	PROTEIN TRANSPORT	B	1.7	1.7	1	12	EEKSKMLARLLK	14309
1J2J	AB	PROTEIN TRANSPORT	B	1.7	1.7	1	20	PEDLRAANKLIKEMVQEDQK	14310
1J3I	BC	OXIDOREDUCTASE, TRANSFERASE	B	1.7	1.7	1	12	SLDMKYFCAVTT	14311
1JB0	BL	PHOTOSYNTHESIS	B	1.7	1.7	1	17	RGYWQELIETLVWAHER	14312
1JD2	IR	HYDROLASE	R	1.7	1.7	1	19	VEDALYLGKRSILAAAHRD	14313
1JD2	WP	HYDROLASE	W	1.7	1.7	1	22	TADAEILINTARIHAQNYLKTY	14314
1JD2	YS	HYDROLASE	S	1.7	1.7	1	21	AADGDALVKRFKNSVKWYHFD	14315
1JMU	BG	VIRAL PROTEIN	B	1.7	1.7	1	7	PESLNAS	14316
1JMU	FI	VIRAL PROTEIN	F	1.7	1.7	1	7	PESLNAS	14317
1JY7	AB	OXYGEN STORAGE/TRANSPORT	B	1.7	1.7	1	19	PENFRLLGNVLVCVLAHHF	14318
1JY7	AD	OXYGEN STORAGE/TRANSPORT	A	1.7	1.7	1	16	PVNFKLLSHCLLVTLA	14319
1JY7	RS	OXYGEN STORAGE/TRANSPORT	S	1.7	1.7	1	23	PPVQAAYQKVVAGVANALAHKYH	14320
1K6L	MH	PHOTOSYNTHESIS	M	1.7	1.7	1	27	PFHGLSIAFLYGSALLFAMHGATILAV	14321
1KF6	NP	OXIDOREDUCTASE	P	1.7	1.7	1	27	EPVFWGLFGAGGMWSAIIAPVMILLVG	14322
1KFY	NO	OXIDOREDUCTASE	N	1.7	1.7	1	6	YCSEVC	14323
1KFY	NP	OXIDOREDUCTASE	N	1.7	1.7	1	21	PAAAIQQGKVESSKDFLIATL	14324
1KTD	CD	IMMUNE SYSTEM	D	1.7	1.7	1	10	VCRHNYEIFD	14325
1KX4	CD	STRUCTURAL PROTEIN/DNA	C	1.7	1.7	1	10	PRHLQLAVRN	14326
1KYO	CP	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.7	1.7	1	13	PFVGNDIVSWLWG	14327

1KYO	EI	OXIDOREDUCTASE/ELECTRON TRANSPORT	I	1.7	1.7	1	7	SLYKTFF	14328
1L0X	CD	IMMUNE SYSTEM	D	1.7	1.7	1	7	IYFLYEG	14329
1L2I	AC	TRANSCRIPTION RECEPTOR/COACTIVATOR	A	1.7	1.7	1	25	EASMMGLLTNLADRELVHMINWAKR	14330
1L4A	AE	ENDOCYTOSIS/EXOCYTOSIS	E	1.7	1.7	1	22	EKHRKMEEEREEMRQTIRDKYG	14331
1L9J	LM	PHOTOSYNTHESIS	L	1.7	1.7	1	13	IWTHLDWVSNTGY	14332
1LDK	DE	LIGASE	D	1.7	1.7	1	14	QGTLFELILAANYL	14333
1LIA	AL	LIGHT HARVESTING PROTEIN	A	1.7	1.7	1	10	ALDYLINSLS	14334
1LO0	XY	IMMUNE SYSTEM	X	1.7	1.7	1	6	SEQLTS	14335
1LOT	AB	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	A	1.7	1.7	1	16	FTEYKKKLAERLKAKL	14336
1LQ8	CD	BLOOD CLOTTING	C	1.7	1.7	1	14	PVSISMSLAMLSLG	14337
1LQM	EF	HYDROLASE/HYDROLASE INHIBITOR	F	1.7	1.7	1	9	PEEVEEVIG	14338
1LWU	BC	BLOOD CLOTTING	B	1.7	1.7	1	23	SVLEHLRAKMQRMEEAIKTQKEL	14339
1LYW	CB	ASPARTIC PROTEASE	C	1.7	1.7	1	6	IACWIH	14340
1LZW	AB	CHAPERONE	B	1.7	1.7	1	18	LSFQRVLQRAVFHVQSSG	14341
1M1J	BC	BLOOD CLOTTING	C	1.7	1.7	1	12	TGSIEYLIQHIK	14342
1M1Y	AB	OXIDOREDUCTASE	A	1.7	1.7	1	6	EKDIVF	14343
1M1Y	AB	OXIDOREDUCTASE	A	1.7	1.7	1	12	DAWSSRILLEEM	14344
1M1Y	AB	OXIDOREDUCTASE	B	1.7	1.7	1	6	CMAEVI	14345
1M1Y	AB	OXIDOREDUCTASE	B	1.7	1.7	1	11	LWHLRSLVFTD	14346
1M2O	AB	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	1.7	1.7	1	5	RFLLS	14347
1M56	GH	OXIDOREDUCTASE	H	1.7	1.7	1	14	TIVPIVILVAIGAF	14348
1M8Q	GV	CONTRACTILE PROTEIN	V	1.7	1.7	1	12	SVWIGGSILASL	14349
1MG2	EB	OXIDOREDUCTASE	E	1.7	1.7	1	19	AQETQGQAAARAAAADLAA	14350
1MG2	MJ	OXIDOREDUCTASE	M	1.7	1.7	1	20	QAQETQGQAAARAAAADLAA	14351
1MHY	BD	OXIDOREDUCTASE	B	1.7	1.7	1	7	EYEQLSC	14352
1MHY	BD	OXIDOREDUCTASE	D	1.7	1.7	1	7	PQEVHKW	14353
1MJG	CP	OXIDOREDUCTASE	P	1.7	1.7	1	30	VALFREVYHGAITATSYAEILLNQAIRTYG	14354
1MUJ	AB	IMMUNE SYSTEM	A	1.7	1.7	1	7	PEFGQLA	14355
1MUJ	AB	IMMUNE SYSTEM	B	1.7	1.7	1	12	ELGRPDAEYWNS	14356
1N4Q	GH	TRANSFERASE	G	1.7	1.7	1	16	EKFRDVYDYFRAVLQR	14357
1NBW	AB	HYDROLASE	A	1.7	1.7	1	14	FLDAVWWLNEALDR	14358
1NGM	IF	TRANSCRIPTION/DNA	I	1.7	1.7	1	17	DSKLASRKYARIIQKIG	14359
1NH2	CD	TRANSCRIPTION/DNA	D	1.7	1.7	1	22	ASLAMRVLETFDKVVAETLKDN	14360
1NIK	AF	TRANSCRIPTION	F	1.7	1.7	1	17	KYERARILGTRALQISM	14361
1NTK	AB	OXIDOREDUCTASE	A	1.7	1.7	1	19	ESEVLRGKNLLRNALVSHL	14362
1NU7	BD	HYDROLASE/PROTEIN BINDING	D	1.7	1.7	1	16	KTEALELKAKVDLVLG	14363

1NU7	FH	HYDROLASE/PROTEIN BINDING	H	1.7	1.7	1	16	KTEALELKAKVDLVLG	14364
1NVM	CF	LYASE/OXIDOREDUCTASE	C	1.7	1.7	1	12	DLEYIEAVAGEI	14365
1O18	D9	CONTRACTILE PROTEIN	9	1.7	1.7	1	12	SVWIGGSILASL	14366
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	R	1.7	1.7	1	5	PEELG	14367
1OOP	AD	VIRUS	A	1.7	1.7	1	6	VENFLC	14368
1OR7	BF	TRANSCRIPTION	B	1.7	1.7	1	12	QHKVASLVSRYV	14369
1OR7	BF	TRANSCRIPTION	F	1.7	1.7	1	9	KEQLSALMD	14370
1OUU	CD	OXYGEN TRANSPORT	C	1.7	1.7	1	19	PEVHIAVDKFLAAVSAALA	14371
1OXK	EF	SIGNALING PROTEIN	E	1.7	1.7	1	10	WTILNEIISM	14372
1P8D	AC	MEMBRANE PROTEIN/PROTEIN BINDING	C	1.7	1.7	1	10	KILHRLLQEG	14373
1POI	AB	TRANSFERASE	B	1.7	1.7	1	5	LRFMA	14374
1POV	3	VIRUS	3	1.7	1.7	1	5	MEMYR	14375
1PQ1	AB	APOPTOSIS	A	1.7	1.7	1	19	MAAVKQALREAGDEFELRY	14376
1PYT	AC	TERNARY COMPLEX (ZYMOGEN)	A	1.7	1.7	1	11	LQAVKVFLEAH	14377
1PYU	CD	LYASE	D	1.7	1.7	1	6	DEEART	14378
1Q16	AB	OXIDOREDUCTASE	A	1.7	1.7	1	6	KFLDRF	14379
1Q1J	LI	IMMUNE SYSTEM	L	1.7	1.7	1	5	SEELQ	14380
1Q5R	FM	HYDROLASE	M	1.7	1.7	1	7	FTDYLRG	14381
1Q72	LH	IMMUNE SYSTEM	L	1.7	1.7	1	6	SEQLTS	14382
1Q7L	CD	HYDROLASE	C	1.7	1.7	1	11	PSVTLFRQYLR	14383
1Q90	DG	PHOTOSYNTHESIS	D	1.7	1.7	1	13	WYFYPVFQILRVV	14384
1QGW	BD	PHOTOSYNTHESIS	B	1.7	1.7	1	15	TGTAEGVLATSLAKM	14385
1R27	CD	OXIDOREDUCTASE	C	1.7	1.7	1	5	STCLY	14386
1R2B	AC	TRANSCRIPTION	A	1.7	1.7	1	13	EHVVDTCRKFIKA	14387
1R4A	AE	PROTEIN TRANSPORT	E	1.7	1.7	1	12	TKTMAKVITTVL	14388
1R4M	CD	CELL CYCLE	D	1.7	1.7	1	13	KAEVAAEFLNDRV	14389
1R4M	GH	CELL CYCLE	H	1.7	1.7	1	13	KAEVAAEFLNDRV	14390
1R5V	AB	SIGNALING PROTEIN	B	1.7	1.7	1	9	RPDAENWNS	14391
1RE0	AB	PROTEIN TRANSPORT	B	1.7	1.7	1	19	SQQIERIVEAFSSKYSADQ	14392
1RHH	AB	IMMUNE SYSTEM	A	1.7	1.7	1	6	DEQLKS	14393
1RLD	BT	LYASE(CARBON-CARBON)	B	1.7	1.7	1	21	NAPGAVANRVALEACVKARNE	14394
1RM6	AB	OXIDOREDUCTASE	A	1.7	1.7	1	14	PDRITELLDAKEAA	14395
1RM6	BC	OXIDOREDUCTASE	B	1.7	1.7	1	7	PTHRAAA	14396
1RM6	BC	OXIDOREDUCTASE	B	1.7	1.7	1	9	TDLLPNLRR	14397
1RSO	CD	NEUROPEPTIDE/MEMBRANE PROTEIN	D	1.7	1.7	1	13	EKDLDFLHSVFQD	14398
1RU7	IJ	VIRAL PROTEIN	J	1.7	1.7	1	9	NECMESVRN	14399
1RY1	WS	TRANSLATION	W	1.7	1.7	1	17	EQESMARLKKLMTIMDS	14400
1RYP	AG	MULTICATALYTIC PROTEINASE	G	1.7	1.7	1	15	IPAFADRLGQYVQAH	14401

1RYP	BC	MULTICATALYTIC PROTEINASE	C	1.7	1.7	1	22	TADAEILINTARIHAQNYLKTY	14402
1RYP	EL	MULTICATALYTIC PROTEINASE	L	1.7	1.7	1	22	AADCQFWETWLGSQCRLHELRE	14403
1RYP	KL	MULTICATALYTIC PROTEINASE	L	1.7	1.7	1	15	VAAASKILSNLVYQY	14404
1RYP	QX	MULTICATALYTIC PROTEINASE	Q	1.7	1.7	1	22	TADAEILINTARIHAQNYLKTY	14405
1S1C	AY	SIGNALING PROTEIN	A	1.7	1.7	1	9	DRLRPLSYP	14406
1S5E	AD	TRANSERASE,TOXIN	A	1.7	1.7	1	30	TCDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	14407
1S5E	AF	TRANSERASE,TOXIN	F	1.7	1.7	1	20	DSQKKAIERMKDTLRIAYLT	14408
1S5E	BJ	TRANSERASE,TOXIN	B	1.7	1.7	1	29	CDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	14409
1S5L	AD	PHOTOSYNTHESIS	A	1.7	1.7	1	27	GPYQLIIFHFLLGASCYMGRQWELSYR	14410
1S5L	AD	PHOTOSYNTHESIS	D	1.7	1.7	1	27	PFHMMGVAGVLGGALLCAIHGATVENT	14411
1S5L	bd	PHOTOSYNTHESIS	b	1.7	1.7	1	24	TVLSSSIAAVFFAAFVVAGTMWYG	14412
1S5L	DX	PHOTOSYNTHESIS	D	1.7	1.7	1	9	FDILDDWLK	14413
1S6C	AB	TRANSPORT PROTEIN	A	1.7	1.7	1	13	FEDFVTALSILLR	14414
1SA0	BE	CELL CYCLE	B	1.7	1.7	1	8	YTEGAELV	14415
1SB3	EF	OXIDOREDUCTASE	E	1.7	1.7	1	9	TDLLPNLRR	14416
1SFC	JL	TRANSPORT PROTEIN	L	1.7	1.7	1	61	NEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRI DEANQRATKMLG	14417
1SP4	AB	HYDROLASE	A	1.7	1.7	1	5	PTIKE	14418
1SQB	AC	OXIDOREDUCTASE	A	1.7	1.7	1	18	IDDMMFVLQGQWMRLCTS	14419
1T3Q	AB	OXIDOREDUCTASE	A	1.7	1.7	1	10	LADALREVVG	14420
1T3Q	DE	OXIDOREDUCTASE	D	1.7	1.7	1	10	LADALREVVG	14421
1TBQ	HR	COMPLEX (SERINE PROTEASE/INHIBITOR)	R	1.7	1.7	1	9	PCTLNCAKF	14422
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.7	1.7	1	10	YKNKMMVCQV	14423
1TI2	CD	OXIDOREDUCTASE	D	1.7	1.7	1	5	RCAHN	14424
1TI2	KL	OXIDOREDUCTASE	L	1.7	1.7	1	5	RCAHN	14425
1TN6	AB	TRANSFERASE	B	1.7	1.7	1	14	GGYTFCGLAALVIL	14426
1TQY	GH	TRANSFERASE	H	1.7	1.7	1	12	LERAIRLALNDA	14427
1TY4	AC	APOPTOSIS	A	1.7	1.7	1	13	FSPYQDVVRTVGN	14428
1U35	GH	STRUCTURAL PROTEIN/DNA	G	1.7	1.7	1	7	EELNQLL	14429
1UWX	MB	IMMUNE SYSTEM	B	1.7	1.7	1	15	AATAEKVFKQYANDN	14430
1UZD	RM	LYASE	R	1.7	1.7	1	15	AKNYGRAVYECLRGG	14431
1UZD	VW	LYASE	W	1.7	1.7	1	14	DEQIAAQVDYIVAN	14432
1UZH	RM	LYASE	R	1.7	1.7	1	14	AKNYGRAVYECLRG	14433
1V4U	AD	OXYGEN STORAGE/TRANSPORT	D	1.7	1.7	1	20	PDNFRILGDCLTVVIAANLG	14434
1V54	NO	OXIDOREDUCTASE	N	1.7	1.7	1	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	14435
1V54	PT	OXIDOREDUCTASE	P	1.7	1.7	1	23	PWPLTGALSALLMTSGLTMWFHF	14436
1VF5	AB	PHOTOSYNTHESIS	B	1.7	1.7	1	20	VFPVVIMGTFACIVALSVLD	14437
1VF5	AC	PHOTOSYNTHESIS	C	1.7	1.7	1	25	PNRVKWMIAFICLVMLAQLMLILKK	14438

1VF5	NO	PHOTOSYNTHESIS	O	1.7	1.7	1	17	LGVLLMASVPLGLILVP	14439
1VQN	FM	RIBOSOME	F	1.7	1.7	1	9	MHIPELADE	14440
1VS6	L3	RIBOSOME	3	1.7	1.7	1	7	VSKGDLG	14441
1VYT	AE	TRANSPORT PROTEIN	A	1.7	1.7	1	18	EVTDMMQKALFDFLKHRF	14442
1WDC	BC	MUSCLE PROTEIN	C	1.7	1.7	1	18	QDEIDDLKDVFELFDFWD	14443
1WPX	AB	HYDROLASE	A	1.7	1.7	1	15	LERCLGLIESCYDSQ	14444
1WR6	BF	PROTEIN TRANSPORT/SIGNALING PROTEIN	B	1.7	1.7	1	13	LEEVNNNVRLLSE	14445
1WYU	GH	OXIDOREDUCTASE	G	1.7	1.7	1	5	QYIRR	14446
1XLS	FN	TRANSCRIPTION	F	1.7	1.7	1	25	VLPLLTHFADINTFMVQQIIKFTKD	14447
1XLT	EI	OXIDOREDUCTASE	I	1.7	1.7	1	9	AEDAAFIMK	14448
1XS9	AD	TRANSCRIPTION/DNA	D	1.7	1.7	1	13	KKSLTEIKDVLAS	14449
1XTC	CF	TOXIN	F	1.7	1.7	1	6	IAYLTE	14450
1XV9	DH	DNA BINDING PROTEIN	H	1.7	1.7	1	7	KILHRLL	14451
1XXI	DE	TRANSFERASE	D	1.7	1.7	1	10	LRDALSLTDQ	14452
1YA7	AN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.7	1.7	1	23	VGDAQVLVRYMKAELELYRLQRR	14453
1YAG	AG	CONTRACTILE PROTEIN	A	1.7	1.7	1	9	QAVLSLYSS	14454
1YHU	AC	OXYGEN STORAGE/TRANSPORT	A	1.7	1.7	1	18	QATLDADLAHLKSQHDPR	14455
1YHU	AC	OXYGEN STORAGE/TRANSPORT	C	1.7	1.7	1	19	AASRVSAGEEVFAALFKMV	14456
1YHU	IK	OXYGEN STORAGE/TRANSPORT	I	1.7	1.7	1	18	QATLDADLAHLKSQHDPR	14457
1YHU	QS	OXYGEN STORAGE/TRANSPORT	Q	1.7	1.7	1	18	QATLDADLAHLKSQHDPR	14458
1YHU	VX	OXYGEN STORAGE/TRANSPORT	V	1.7	1.7	1	23	PAFRAHATRVLGGLDMCIALLDD	14459
1YNJ	CD	TRANSFERASE	D	1.7	1.7	1	13	YLTRKLVDVAHEI	14460
1YRT	AB	LAYSE, TOXIN	B	1.7	1.7	1	10	YEEFVQMMTA	14461
1Z7Q	AB	HYDROLASE/HYDROLASE ACTIVATOR	B	1.7	1.7	1	14	GPDYRVLVDKSRKV	14462
1Z7Q	EF	HYDROLASE/HYDROLASE ACTIVATOR	F	1.7	1.7	1	18	APDARVLSNYLRQQCNYS	14463
1Z7Q	FG	HYDROLASE/HYDROLASE ACTIVATOR	F	1.7	1.7	1	15	VERAGHLLCDKAQKN	14464
1Z7Q	PW	HYDROLASE/HYDROLASE ACTIVATOR	W	1.7	1.7	1	22	AADTEAVTQLIGSNIELHSLYT	14465
1Z7Q	XL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.7	1.7	1	11	VGELFWKVKEE	14466
1Z7S	34	VIRUS	3	1.7	1.7	1	7	MMELAEI	14467
1ZBB	ef	STRUCTURAL PROTEIN/DNA	f	1.7	1.7	1	11	AMDVVYALKRQ	14468
1ZBB	EF	STRUCTURAL PROTEIN/DNA	F	1.7	1.7	1	11	AMDVVYALKRQ	14469
1ZBB	FH	STRUCTURAL PROTEIN/DNA	F	1.7	1.7	1	27	IYEETRGVLKVFLENVIRDAVTYTEHA	14470
1ZBB	gh	STRUCTURAL PROTEIN/DNA	g	1.7	1.7	1	7	EELNKLL	14471
1ZBD	AB	G PROTEIN	B	1.7	1.7	1	11	EKEIINRVIAR	14472
1ZGL	AB	IMMUNE SYSTEM	A	1.7	1.7	1	20	ALANIAVDKANLEIMTKRSN	14473
1ZRT	DE	OXIDOREDUCTASE/METAL TRANSPORT	D	1.7	1.7	1	30	LVARKQMGLVAMVMLGLLSVMLYLTNKRLW	14474
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.7	1.7	1	12	DEEVDEMIREAD	14475

1ZVV	GJ	TRANSCRIPTION/DNA	G	1.7	1.7	1	17	MYDIGAVAMRLLTKYMN	14476
1ZY8	FM	OXIDOREDUCTASE	M	1.7	1.7	1	9	AARNILEKH	14477
2A9M	LH	IMMUNE SYSTEM	H	1.7	1.7	1	5	GHFYS	14478
2ADF	AL	BLOOD CLOTTING/IMMUNE SYSTEM	A	1.7	1.7	1	13	IGDALGFAVRYLT	14479
2AFH	CD	OXIDOREDUCTASE	C	1.7	1.7	1	7	EKDIVFG	14480
2AQ1	CD	IMMUNE SYSTEM	D	1.7	1.7	1	9	MGNMKYLYD	14481
2AXT	fj	ELECTRON TRANSPORT	j	1.7	1.7	1	22	IVATVAGMGVIVIVGLFFYGAY	14482
2AZE	AB	CELL CYCLE, TRANSCRIPTION	B	1.7	1.7	1	7	CQDLRSI	14483
2B4C	GC	VIRAL PROTEIN/IMMUNE SYSTEM	G	1.7	1.7	1	5	PEIVM	14484
2B5L	AC	PROTEIN BINDING/VIRALPROTEIN	C	1.7	1.7	1	13	YKGVKLAKFGKEN	14485
2B8K	BI	TRANSFERASE	B	1.7	1.7	1	14	WQMLEMLKPCVEDG	14486
2BC4	AB	IMMUNE SYSTEM	B	1.7	1.7	1	9	DTLMQRLRN	14487
2BG9	DE	ION CHANNEL/RECEPTOR	E	1.7	1.7	1	23	KCTLSISVLLAQTIFLFLIAQKV	14488
2BL0	AB	MUSCLE PROTEIN	B	1.7	1.7	1	8	LGSALRSL	14489
2BSK	CD	PROTEIN TRANSPORT	D	1.7	1.7	1	8	SACHRKCV	14490
2BV8	AB	PHOTOSYNTHESIS	B	1.7	1.7	1	13	NTQLDALANMIAE	14491
2BYP	BH	RECEPTOR	H	1.7	1.7	1	6	PRCAWR	14492
2C35	EF	POLYMERASE	E	1.7	1.7	1	13	EVFMKTLNYTARF	14493
2C35	GH	POLYMERASE	G	1.7	1.7	1	13	EVFMKTLNYTARF	14494
2CLY	DE	HYDROLASE	E	1.7	1.7	1	21	KAVANSLKSWNETLTSRLATL	14495
2CNW	AD	SIGNAL RECOGNITION	D	1.7	1.7	1	14	LSATEEILQEVRAS	14496
2D1P	DE	TRANSLATION	D	1.7	1.7	1	11	LGALAEASLTC	14497
2D2M	BC	OXYGEN STORAGE/TRANSPORT	C	1.7	1.7	1	18	SDRRVALAQAVFASLFSR	14498
2DS2	CD	PLANT PROTEIN	D	1.7	1.7	1	16	VCPVLRQAAQQVLQRQ	14499
2DSR	BI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	1.7	1.7	1	7	LRRLEMY	14500
2DXB	KC	HYDROLASE	K	1.7	1.7	1	8	HTLFRAYT	14501
2DXB	NX	HYDROLASE	N	1.7	1.7	1	8	HTLFRAYT	14502
2DZN	CD	PROTEIN BINDING	C	1.7	1.7	1	8	PLFHALAE	14503
2E 32	AB	LIGASE	A	1.7	1.7	1	8	LRWKELVD	14504
2E 32	CD	LIGASE	C	1.7	1.7	1	8	LRWKELVD	14505
2E 32	CD	LIGASE	D	1.7	1.7	1	8	QGTLFELI	14506
2E9X	FG	REPLICATION	G	1.7	1.7	1	11	FYGFGSQLLHF	14507
2EC6	AC	CONTRACTILE PROTEIN	A	1.7	1.7	1	12	YKKLQDQRIGLS	14508
2EHO	BD	REPLICATION	D	1.7	1.7	1	5	LDDIL	14509
2EHO	CD	REPLICATION	C	1.7	1.7	1	15	RIAKLRVSADSFVRQ	14510
2EHO	EG	REPLICATION	E	1.7	1.7	1	12	PAELIERLEQAW	14511
2ES4	AD	HYDROLASE	D	1.7	1.7	1	9	RAVREFFDY	14512
2F2F	DF	TOXIN	D	1.7	1.7	1	5	SEPSN	14513

2F54	DE	IMMUNE SYSTEM	E	1.7	1.7	1	8	EAEISHTQ	14514
2F5Z	JO	OXIDOREDUCTASE/PROTEIN BINDING	O	1.7	1.7	1	7	KEDALKL	14515
2F8N	EF	STRUCTURAL PROTEIN/DNA	F	1.7	1.7	1	11	AMDVVYALKRQ	14516
2F8X	CK	TRANSCRIPTION/DNA	K	1.7	1.7	1	9	PLFLAAREG	14517
2F9D	AP	RNA BINDING PROTEIN	A	1.7	1.7	1	16	TKKKEEQLKLLKEKYG	14518
2FHS	AC	OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN	C	1.7	1.7	1	14	DTVELVMALEEEFD	14519
2FK0	OP	VIRAL PROTEIN	P	1.7	1.7	1	18	DFHDSNVKNLYDKVRLQL	14520
2FR4	AB	IMMUNE SYSTEM/DNA	A	1.7	1.7	1	6	SEQLTS	14521
2FSE	AE	IMMUNE SYSTEM, STRUCTURAL PROTEIN	A	1.7	1.7	1	21	AQGALANIAVDKANLEIMTKR	14522
2FUG	NP	OXIDOREDUCTASE	N	1.7	1.7	1	5	PAEFR	14523
2FUG	VX	OXIDOREDUCTASE	X	1.7	1.7	1	13	KKMAPVMRRVWEQ	14524
2FV4	AB	STRUCTURAL PROTEIN, PROTEIN BINDING	B	1.7	1.7	1	11	NILKLKLYRSL	14525
2FYN	AB	OXIDOREDUCTASE	A	1.7	1.7	1	7	IEEDFNA	14526
2FYN	BC	OXIDOREDUCTASE	C	1.7	1.7	1	5	RDFLY	14527
2FYN	DC	OXIDOREDUCTASE	C	1.7	1.7	1	23	YATAGAGAVATGAAVWPLINQMN	14528
2FYN	GH	OXIDOREDUCTASE	G	1.7	1.7	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	14529
2G2S	AB	LUMINESCENT PROTEIN	A	1.7	1.7	1	6	KGEELF	14530
2G38	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.7	1.7	1	24	EALTVAATEVRRIRDRAIQSDAQV	14531
2GC4	EB	OXIDOREDUCTASE, ELECTRON TRANSPORT	E	1.7	1.7	1	20	QAQETQGQAAARAAAADLAA	14532
2GL7	AC	TRANSCRIPTION	A	1.7	1.7	1	17	QVVVNKAAVMVHQLSKK	14533
2GTL	CD	OXYGEN STORAGE/TRANSPORT	D	1.7	1.7	1	16	VTESLKVKLQWASAFG	14534
2GTL	NO	OXYGEN STORAGE/TRANSPORT	O	1.7	1.7	1	18	PKRIRKAGSLRHRVEELE	14535
2GTP	AD	SIGNALING PROTEIN	D	1.7	1.7	1	13	FRTRESTAKKIKA	14536
2GV5	DF	CELL CYCLE	D	1.7	1.7	1	11	IKNLRRVAKEL	14537
2GV5	EF	CELL CYCLE	E	1.7	1.7	1	13	PLDEIKRAFQLFD	14538
2GWF	EF	HYDROLASE/LIGASE	E	1.7	1.7	1	9	DDSKDTWKK	14539
2H1L	EQ	VIRAL PROTEIN	E	1.7	1.7	1	6	QSRIVE	14540
2H1O	DH	GENE REGULATION/DNA COMPLEX	D	1.7	1.7	1	18	KKKNVLHERMEQSILPLF	14541
2H4Q	AB	HYDROLASE INHIBITOR	A	1.7	1.7	1	15	PWSISSALALTYLAA	14542
2H7D	AB	STRUCTURAL PROTEIN	B	1.7	1.7	1	16	IHDRKEFAKFEEERAR	14543
2HAN	AB	TRANSCRIPTION/DNA	B	1.7	1.7	1	7	MYMRRKC	14544
2HGR	FQ	RIBOSOME	F	1.7	1.7	1	11	YRHLLLEDQRI	14545
2HHH	CN	RIBOSOME	C	1.7	1.7	1	22	KKQYRHLLLEDQRIRGLLEKEL	14546
2HT9	AX	OXIDOREDUCTASE	X	1.7	1.7	1	11	GTENLYFQSME	14547
2HYB	BC	TRANSFERASE	C	1.7	1.7	1	9	SLESCLKFA	14548

2HZS	FI	TRANSCRIPTION	I	1.7	1.7	1	11	VDDVLKFTFTG	14549
2I2R	IM	TRANSPORT PROTEIN	M	1.7	1.7	1	13	VHEKLRWTFNLYD	14550
2I2R	JN	TRANSPORT PROTEIN	N	1.7	1.7	1	13	VHEKLRWTFNLYD	14551
2I2X	KL	TRANSFERASE	L	1.7	1.7	1	8	EASLKKVL	14552
2I2X	MP	TRANSFERASE	M	1.7	1.7	1	22	TVQCWSETLAYDCALMNTALET	14553
2I9L	GH	IMMUNE SYSTEM/VIRAL PROTEIN	G	1.7	1.7	1	7	SEQLTSG	14554
2IAE	DF	HYDROLASE	D	1.7	1.7	1	16	WRVRLAIIEYMPLLAG	14555
2IAN	LN	IMMUNE SYSTEM	L	1.7	1.7	1	14	AVDTYCRHNYGVGE	14556
2INP	AD	OXIDOREDUCTASE	A	1.7	1.7	1	15	TNLLFVPFMSGAAYN	14557
2INP	AF	OXIDOREDUCTASE	A	1.7	1.7	1	19	TFDKYYRPRYEYLAKEAAA	14558
2IVF	AB	OXIDOREDUCTASE	B	1.7	1.7	1	8	TCTVACKN	14559
2IVF	BC	OXIDOREDUCTASE	B	1.7	1.7	1	6	HCVEAC	14560
2J0Q	BF	HYDROLASE	B	1.7	1.7	1	6	HEILEM	14561
2J55	JL	OXIDOREDUCTASE	J	1.7	1.7	1	19	AQETQGQAAARAAAADLAA	14562
2J57	HM	OXIDOREDUCTASE	H	1.7	1.7	1	20	QAQETQGQAAARAAAADLAA	14563
2J7A	MO	OXIDOREDUCTASE	M	1.7	1.7	1	6	CADCHM	14564
2JBA	AB	TRANSCRIPTION	A	1.7	1.7	1	13	PKELVARIKAVMR	14565
2JBL	CL	ELECTRON TRANSPORT	C	1.7	1.7	1	18	LSDAYATFALMMSISDSL	14566
2JIZ	BE	HYDROLASE	E	1.7	1.7	1	12	LATDMGTMQERI	14567
2JIZ	FG	HYDROLASE	F	1.7	1.7	1	8	QDIIAILG	14568
2JKR	EU	ENDOCYTOSIS	E	1.7	1.7	1	5	LASVY	14569
2JM6	AB	APOPTOSIS	B	1.7	1.7	1	21	WGRIVTLISFGAFVAKHLKSV	14570
2JY6	AB	SIGNALING PROTEIN	B	1.7	1.7	1	11	INAAIERLLGS	14571
2K8M	AB	PROTEIN TRANSPORT	B	1.7	1.7	1	6	LDEKMK	14572
2KA4	AB	TRANSCRIPTION REGULATOR	B	1.7	1.7	1	8	EPMEIFRN	14573
2NN6	EF	HYDROLASE/TRANSFERASE	E	1.7	1.7	1	17	LGTEIANTLYRIFNNKS	14574
2NNW	AB	TRANSFERASE	A	1.7	1.7	1	10	PEKVLDQLLK	14575
2NTI	HI	DNA BINDING PROTEIN	H	1.7	1.7	1	13	TITFADIIDELSD	14576
2NVU	AB	PROTEIN TURNOVER, LIGASE	B	1.7	1.7	1	10	PEHCIEYVRM	14577
2NVU	AJ	PROTEIN TURNOVER, LIGASE	A	1.7	1.7	1	9	ENFEEAIKN	14578
2NX5	KN	IMMUNE SYSTEM	K	1.7	1.7	1	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	14579
2NXX	AE	HORMONE/GROWTH FACTOR	A	1.7	1.7	1	9	PGRFAKLLL	14580
2NZD	FH	STRUCTURAL PROTEIN/DNA	F	1.7	1.7	1	11	AMDVVYALKRQ	14581
2NZD	FH	STRUCTURAL PROTEIN/DNA	H	1.7	1.7	1	12	SREIQTAVRLLL	14582
2OCY	AC	ENDOCYTOSIS/EXOCYTOSIS	C	1.7	1.7	1	9	RTITTAYYR	14583
2ODE	AD	SIGNALING PROTEIN	D	1.7	1.7	1	17	TAKLVSKAHRIFEEFVD	14584
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.7	1.7	1	9	DGQKEELIR	14585
2OS8	AC	CONTRACTILE PROTEIN	C	1.7	1.7	1	10	YEEFVKKVMT	14586
2OV2	FN	PROTEIN BINDING/TRANSFERASE	F	1.7	1.7	1	14	LKTVFDEAIRAVLG	14587

2P24	AB	IMMUNE SYSTEM	B	1.7	1.7	1	5	TSLRR	14588
2P58	BC	TRANSPORT PROTEIN/CHAPERONE	C	1.7	1.7	1	9	PRIQTFVNG	14589
2PF4	DF	HYDROLASE REGULATOR/VIRAL PROTEIN	D	1.7	1.7	1	14	WRVRLAIIEYMPLL	14590
2PG1	AL	STRUCTURAL PROTEIN	A	1.7	1.7	1	16	EKDIAAYIKKEFDKKY	14591
2PK9	CB	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	C	1.7	1.7	1	12	DEEQLKLIFDIM	14592
2PL9	CF	SIGNALING PROTIEN	C	1.7	1.7	1	10	KENIIAAAQA	14593
2PMZ	AC	TRANSLATION, TRANSFERASE	C	1.7	1.7	1	8	VVENIIIG	14594
2QA4	AZ	RIBOSOME	Z	1.7	1.7	1	7	GKTVRRS	14595
2QBE	0S	RIBOSOME	S	1.7	1.7	1	7	LVADLIR	14596
2QHO	CD	PROTEIN BINDING/LIGASE	D	1.7	1.7	1	11	EELISQAQVVL	14597
2QHO	CD	PROTEIN BINDING/LIGASE	D	1.7	1.7	1	11	VNLAVNNLLSR	14598
2QJK	BC	ELECTRON TRANSPORT	C	1.7	1.7	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	14599
2QJK	DE	ELECTRON TRANSPORT	D	1.7	1.7	1	7	IEEDFNA	14600
2QJK	GH	ELECTRON TRANSPORT	G	1.7	1.7	1	11	FASVEHIMRNV	14601
2QJK	JI	ELECTRON TRANSPORT	I	1.7	1.7	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	14602
2QJK	KL	ELECTRON TRANSPORT	L	1.7	1.7	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	14603
2QJY	AF	OXIDOREDUCTASE	F	1.7	1.7	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	14604
2QMB	CB	TRANSPORT PROTEIN	B	1.7	1.7	1	18	PENFRLLGDILIIVLAAH	14605
2QR0	WX	IMMUNE SYSTEM	W	1.7	1.7	1	7	DEQLKSG	14606
2QR1	AE	TRANSFERASE	A	1.7	1.7	1	14	FLDLCAMLVCKLFS	14607
2R00	AC	OXIDOREDUCTASE	C	1.7	1.7	1	14	KEEMKMVWETQKIF	14608
2R6G	BF	HYDROLASE/TRANSPORT PROTEIN	F	1.7	1.7	1	11	PFQNFFKITLP	14609
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	1.7	1.7	1	21	FGLAAAIATLIFLLVGALAIV	14610
2RAO	CB	OXYGEN BINDING	B	1.7	1.7	1	7	PWTQRFF	14611
2RHS	AD	LIGASE	A	1.7	1.7	1	10	PDRIAMLKYG	14612
2RHS	CD	LIGASE	C	1.7	1.7	1	15	PLTRTVEEIEDLFLG	14613
2RIV	AB	SIGNALING PROTEIN	A	1.7	1.7	1	14	PVSISAALVMLSFG	14614
2RMS	AB	TRANSCRIPTION	B	1.7	1.7	1	16	EAEMIALAGLLQMSQG	14615
2UZ6	EN	RECEPTOR	N	1.7	1.7	1	7	PPCILNN	14616
2V4J	DE	OXIDOREDUCTASE	D	1.7	1.7	1	15	FVSDIKQEAAYRAAN	14617
2V51	DE	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	D	1.7	1.7	1	9	QAVLSLYAS	14618
2V7Q	AD	HYDROLASE	A	1.7	1.7	1	7	TELFYKG	14619
2V7Q	AG	HYDROLASE	A	1.7	1.7	1	6	AAFAQF	14620
2VDU	DF	TRANSFERASE	F	1.7	1.7	1	5	LPNFF	14621
2VDW	AB	TRANSFERASE	A	1.7	1.7	1	5	ASTME	14622
2VE7	BD	CELL CYCLE	D	1.7	1.7	1	10	LNAAHQEALM	14623
2VGL	AS	PROTEIN TRANSPORT	A	1.7	1.7	1	13	RGLAVFISDIRNC	14624

2VJH	AB	PHOTOSYNTHESIS	B	1.7	1.7	1	12	AELAALKTYIAN	14625
2VJH	AB	PHOTOSYNTHESIS	B	1.7	1.7	1	14	GNKRLDAVNAITSN	14626
2VLH	AB	LYASE	A	1.7	1.7	1	10	TTTRYHQEKN	14627
2VML	KL	PHOTOSYNTHESIS	L	1.7	1.7	1	14	SNKRLDAVNAITGN	14628
2VOF	AB	APOPTOSIS	A	1.7	1.7	1	7	KSYLDDF	14629
2VOY	BE	HYDROLASE	E	1.7	1.7	1	10	FVILLILIAN	14630
2VQ1	AB	IMMUNE SYSTEM	A	1.7	1.7	1	6	SEQLTS	14631
2VQ1	EF	IMMUNE SYSTEM	E	1.7	1.7	1	7	SEQLTSG	14632
2VXV	HL	IMMUNE SYSTEM	L	1.7	1.7	1	7	DEQLKSG	14633
2VYN	DA	OXIDOREDUCTASE	A	1.7	1.7	1	12	RIGRIVFRAAQK	14634
2W2X	AC	SIGNALING PROTEIN/HYDROLASE	A	1.7	1.7	1	10	KTCLLISYTT	14635
2W65	AB	IMMUNE SYSTEM	B	1.7	1.7	1	6	SEQLTS	14636
2W73	FO	METAL BINDING PROTEIN	F	1.7	1.7	1	29	FPEFLTMMARKMKDTDSEEEIREAFRVFD	14637
2WBJ	AB	IMMUNE SYSTEM	A	1.7	1.7	1	22	AQGALANIAVDKANLEIMTKRS	14638
2WH1	GK	RIBOSOME	K	1.7	1.7	1	18	PYAAQLAALDAAKKAMAY	14639
2WIU	CD	TRANSFERASE/TRANSCRIPTION	D	1.7	1.7	1	15	PTQLANAMKLVRQQN	14640
2WME	DC	OXIDOREDUCTASE	C	1.7	1.7	1	13	LDRAADIAVMANF	14641
2WME	FE	OXIDOREDUCTASE	F	1.7	1.7	1	15	TSTGKKVMASASSSS	14642
2Z2S	CD	TRANSCRIPTION	D	1.7	1.7	1	5	SLASV	14643
2Z3R	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.7	1.7	1	20	KVTAMKCFLLELQVISLESG	14644
2Z3R	CB	CYTOKINE/CYTOKINE RECEPTOR	C	1.7	1.7	1	19	ASIHDTVENLIILANNSLS	14645
2Z3R	MP	CYTOKINE/CYTOKINE RECEPTOR	M	1.7	1.7	1	19	ASIHDTVENLIILANNSLS	14646
2ZCK	PL	IMMUNE SYSTEM	P	1.7	1.7	1	10	RKWIKDTIVA	14647
2ZCY	EF	HYDROLASE	E	1.7	1.7	1	12	SQGAKTYLERTL	14648
2ZCY	LM	HYDROLASE	M	1.7	1.7	1	18	PSYIFEYLATVMYQRRSK	14649
2ZCY	OP	HYDROLASE	P	1.7	1.7	1	22	TADAEILINTARIHAQNYLKTY	14650
2ZCY	QX	HYDROLASE	Q	1.7	1.7	1	22	NADSRILIEKARVEAQSHRLTL	14651
2ZCY	ST	HYDROLASE	S	1.7	1.7	1	12	SQGAKTYLERTL	14652
2ZCY	WK	HYDROLASE	K	1.7	1.7	1	19	VEDALYLGKRSILAAAHRD	14653
2ZCY	WK	HYDROLASE	K	1.7	1.7	1	13	VGELFWKVKEEEG	14654
2ZCY	WX	HYDROLASE	X	1.7	1.7	1	13	YSGFYTFSLLDHH	14655
2ZJQ	CI	RIBOSOME	C	1.7	1.7	1	7	SGVLHEV	14656
2ZU6	FE	HYDROLASE	E	1.7	1.7	1	12	ISEAEHCLKELE	14657
2ZVN	GF	SIGNALING PROTEIN/TRANSCRIPTION	F	1.7	1.7	1	84	EDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADIY KADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLK	14658
2ZXX	EF	CELL CYCLE/REPLICATION	E	1.7	1.7	1	5	AFDLI	14659
3A0B	AC	ELECTRON TRANSPORT	C	1.7	1.7	1	19	GPEASQAQAMTFLIRDQKL	14660
3A0B	ac	ELECTRON TRANSPORT	c	1.7	1.7	1	8	ATCFVWFN	14661
3A0B	bd	ELECTRON TRANSPORT	b	1.7	1.7	1	5	GTMWY	14662
3A0B	lm	ELECTRON TRANSPORT	l	1.7	1.7	1	18	RTSLYLGLLLILVLALLF	14663

3A1G	CD	TRANSFERASE	C	1.7	1.7	1	14	SRARIDARIDFESG	14664
3B4V	AD	HORMONE REGULATOR COMPLEX	D	1.7	1.7	1	12	SCHMRQATCFLG	14665
3B4V	FG	HORMONE REGULATOR COMPLEX	G	1.7	1.7	1	12	SCHMRQATCFLG	14666
3B8E	AB	HYDROLASE/TRANSPORT PROTEIN	A	1.7	1.7	1	25	WFCAFPYSLLIFVYDEVRKLIIRRR	14667
3BBN	GI	RIBOSOME	G	1.7	1.7	1	6	KSLAYQ	14668
3BIM	BJ	TRANSCRIPTION REPRESSOR	B	1.7	1.7	1	7	GLFYSIF	14669
3BJI	AD	SIGNALING PROTEIN	A	1.7	1.7	1	21	LREIQQTEEKYTDTLGSIQQH	14670
3BLW	IJ	OXIDOREDUCTASE	J	1.7	1.7	1	16	NLYGDILSDLNSGLSA	14671
3BVH	BC	BLOOD CLOTTING	B	1.7	1.7	1	23	ILENLRSKIQKLESDVSAQMEYC	14672
3BZ1	AD	ELECTRON TRANSPORT	A	1.7	1.7	1	26	SRSLHFFLAAWPVVGVWFTALGISTM	14673
3BZ1	AT	ELECTRON TRANSPORT	T	1.7	1.7	1	21	ETITYVFIFACIIALFFFAIF	14674
3BZ4	CD	IMMUNE SYSTEM	C	1.7	1.7	1	7	SEQLTSG	14675
3BZ4	GB	IMMUNE SYSTEM	G	1.7	1.7	1	6	KDEYER	14676
3C7B	AB	OXIDOREDUCTASE	A	1.7	1.7	1	6	PLLDEL	14677
3C7N	AB	CHAPERONE/CHAPERONE	B	1.7	1.7	1	14	VLTKMKEIAEAYLG	14678
3CDK	CD	TRANSFERASE	C	1.7	1.7	1	13	QGTLAERIRAGGA	14679
3CFB	AB	IMMUNE SYSTEM	A	1.7	1.7	1	6	SEQLTS	14680
3CHW	AP	STRUCTURAL PROTEIN	P	1.7	1.7	1	18	GGLINKKCYEMASHLRRS	14681
3CJI	AC	VIRUS	C	1.7	1.7	1	6	DDYRTG	14682
3CJT	KL	TRANSFERASE/RIBOSOMAL PROTEIN	L	1.7	1.7	1	9	PVGPALGQH	14683
3CL3	AD	VIRAL PROTEIN/SIGNALING PROTEIN	A	1.7	1.7	1	9	PRFLERHLA	14684
3CR3	BD	TRANSFERASE	B	1.7	1.7	1	16	TSELIYAGLEAIQKRG	14685
3CSY	MN	IMMUNE SYSTEM/VIRAL PROTEIN	N	1.7	1.7	1	13	ILNRKAIDFLLQR	14686
3CUE	UX	PROTEIN TRANSPORT	U	1.7	1.7	1	23	QNEEDAKLLYGMIFSLRSITQKL	14687
3CUQ	AB	PROTEIN TRANSPORT	A	1.7	1.7	1	14	TERARQVLEHLLKE	14688
3CWB	BS	OXIDOREDUCTASE	B	1.7	1.7	1	11	SFRITRGIEAV	14689
3CWB	NP	OXIDOREDUCTASE	N	1.7	1.7	1	18	IDDMMFCAQGEWMRLCTS	14690
3CX6	AB	SIGNALING PROTEIN	A	1.7	1.7	1	6	RSERKR	14691
3CXH	CG	OXIDOREDUCTASE	G	1.7	1.7	1	20	EDESYARAYRIIRAHQTELT	14692
3CXH	LN	OXIDOREDUCTASE	N	1.7	1.7	1	5	FRKSN	14693
3CXH	PT	OXIDOREDUCTASE	P	1.7	1.7	1	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	14694
3D2E	AB	CHAPERONE	B	1.7	1.7	1	8	EIAEAYLG	14695
3D54	IL	LIGASE	I	1.7	1.7	1	14	DGIIEGIADYGNSI	14696
3D87	AB	CYTOKINE	A	1.7	1.7	1	32	PWQRLLLRFKILRSLQAFVAVAARVFAHGAAT	14697
3DAW	AB	STRUCTURAL PROTEIN/STRUCTURAL PROTEIN RE	A	1.7	1.7	1	9	QAVLSLYAS	14698
3DAW	AB	STRUCTURAL PROTEIN/STRUCTURAL PROTEIN RE	A	1.7	1.7	1	10	SVWIGGSILA	14699
3DBH	CD	CELL CYCLE	C	1.7	1.7	1	9	DHGQEALES	14700
3DBH	CD	CELL CYCLE	D	1.7	1.7	1	9	YRLTQGVVK	14701

3DBJ	EF	PHOTOSYNTHESIS	E	1.7	1.7	1	25	EEMTATCLRDLDYYLRLVTYGIVAG	14702
3DGC	LR	CYTOKINE/SIGNALING PROTEIN	L	1.7	1.7	1	12	LDLLFMSLRNAC	14703
3DHR	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	1.7	1.7	1	16	VADCGAEALARLLIVY	14704
3DIN	CE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.7	1.7	1	32	EEGRKKFAKYTRRLTLLIGGFQAFFVSFSLAR	14705
3DNL	BC	VIRAL PROTEIN	B	1.7	1.7	1	5	PEIVT	14706
3DQV	CR	LIGASE	C	1.7	1.7	1	16	TELEDLIPEVEEFYKK	14707
3DTP	BD	CONTRACTILE PROTEIN	D	1.7	1.7	1	10	YEELVRMVLS	14708
3DTU	CD	OXIDOREDUCTASE	C	1.7	1.7	1	31	ATWNFVSSLGAFLSFASFLFFLGVIFYTLTR	14709
3DWL	IK	STRUCTURAL PROTEIN	I	1.7	1.7	1	6	REDCIS	14710
3E0J	CD	TRANSFERASE	C	1.7	1.7	1	9	EGEQCSAAH	14711
3E8C	CI	TRANSFERASE	C	1.7	1.7	1	9	MFSHLRRIG	14712
3E8C	DJ	TRANSFERASE	D	1.7	1.7	1	9	MFSHLRRIG	14713
3E8C	FL	TRANSFERASE	F	1.7	1.7	1	18	KAVDWWALGVLIYEMAAG	14714
3EAB	AG	CELL CYCLE	G	1.7	1.7	1	10	MLLQEMADEA	14715
3EH3	AB	OXIDOREDUCTASE	A	1.7	1.7	1	7	TLDYVVH	14716
3EJJ	AX	CYTOKINE/SIGNALING PROTEIN	A	1.7	1.7	1	5	EHCSH	14717
3ETR	AB	OXIDOREDUCTASE	A	1.7	1.7	1	17	FCTPGIVMSMYTLLRNQ	14718
3EUB	AC	OXIDOREDUCTASE	C	1.7	1.7	1	7	AAMQASG	14719
3EZQ	CD	APOPTOSIS	C	1.7	1.7	1	15	SDVDLSKYITTIAGV	14720
3F1E	DE	RIBOSOME	D	1.7	1.7	1	8	EQLVIEFY	14721
3F1F	QZ	RIBOSOME	Q	1.7	1.7	1	15	AQQIEAARVAMVRHF	14722
3F1S	AB	HYDROLASE INHIBITOR/HYDROLASE	B	1.7	1.7	1	5	KDFAE	14723
3F6Z	AB	HYDROLASE	A	1.7	1.7	1	12	LGNWVCAAKFES	14724
3F9K	AC	VIRAL PROTEIN, RECOMBINATION	C	1.7	1.7	1	10	TEMITTLKKI	14725
3FCS	AB	CELL ADHESION/BLOOD CLOTTING	B	1.7	1.7	1	11	LGLMTEKLSQK	14726
3FKS	BF	HYDROLASE	F	1.7	1.7	1	8	AVAEVFTG	14727
3FKS	PR	HYDROLASE	P	1.7	1.7	1	17	PRDLFEYTLANQMLTAM	14728
3FS4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.7	1.7	1	19	PECQAAWQKLVRVVAHALA	14729
3FWC	EF	CELL CYCLE, TRANSCRIPTION	E	1.7	1.7	1	10	ENEFIAICTD	14730
3GCG	AB	SIGNALING PROTEIN/TRANSCRIPTION	B	1.7	1.7	1	8	SIGHFLQS	14731
3GE8	AC	OXIDOREDUCTASE	A	1.7	1.7	1	7	IVDRFLA	14732
3GE8	AE	OXIDOREDUCTASE	A	1.7	1.7	1	22	YPEYVSIQREKDAGAYSVKAAL	14733
3GE8	FE	OXIDOREDUCTASE	E	1.7	1.7	1	11	VEPVIETAEID	14734
3GFK	AB	TRANSCRIPTION/TRANSFERASE	A	1.7	1.7	1	11	IDEIKQILRMT	14735
3GIZ	LH	IMMUNE SYSTEM	L	1.7	1.7	1	7	DEQLKSG	14736
3GTM	AK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	1.7	1.7	1	9	HTLGNLIRA	14737

3GZU	AG	VIRUS	A	1.7	1.7	1	12	FQVANWLHFVNN	14738
3H0L	EF	LIGASE	F	1.7	1.7	1	11	REWVLKIAKLA	14739
3H0L	MN	LIGASE	M	1.7	1.7	1	15	PEVKRRIMLGTFALS	14740
3H4P	Mm	HYDROLASE	M	1.7	1.7	1	12	RARLEAQIYRLT	14741
3HAY	AB	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	1.7	1.7	1	11	EDKIIQVMKEF	14742
3HE6	AC	IMMUNE SYSTEM	A	1.7	1.7	1	29	NQQWEKLQHMFQVYRVSFTRDIQELVKMM	14743
3HEI	KL	TRANSFERASE/SIGNALING PROTEIN	K	1.7	1.7	1	7	SSDFEAR	14744
3HHZ	BL	VIRAL PROTEIN/RNA	L	1.7	1.7	1	11	VVEWLGWFEDQ	14745
3HKZ	AY	TRANSFERASE	A	1.7	1.7	1	10	KRWPSAARRL	14746
3HKZ	BN	TRANSFERASE	N	1.7	1.7	1	6	INEVIH	14747
3HKZ	TZ	TRANSFERASE	Z	1.7	1.7	1	10	MRNTEIWDNL	14748
3HRD	AB	OXIDOREDUCTASE	A	1.7	1.7	1	12	PHYDRGEVAGML	14749
3HRD	BC	OXIDOREDUCTASE	C	1.7	1.7	1	24	VLYKKESVQGVFKKLFVDILDQLE	14750
3HRW	CD	OXYGEN TRANSPORT	D	1.7	1.7	1	16	PENFRLLGNMIVIVLG	14751
9PAI	AB	HYDROLASE INHIBITOR	A	1.7	1.7	1	7	LSALTNI	14752
1A0H	DE	COMPLEX (SERINE PROTEASE/INHIBITOR)	E	1.6	1.6	1	8	KQTAAKLL	14753
1A4J	AB	IMMUNOGLOBULIN	A	1.6	1.6	1	6	DEQLKS	14754
1AHJ	GH	LYASE	H	1.6	1.6	1	16	YYERYVIGVATLMVEK	14755
1AIP	AC	COMPLEX OF TWO ELONGATION FACTORS	A	1.6	1.6	1	17	ELLDLVEMEVRDLLNQY	14756
1AOI	CD	DNA BINDING PROTEIN/DNA	D	1.6	1.6	1	12	SREIQTAVRLLL	14757
1AOI	EF	DNA BINDING PROTEIN/DNA	F	1.6	1.6	1	11	AMDVVYALKRQ	14758
1AQD	AB	COMPLEX (MHC PROTEIN/ANTIGEN)	B	1.6	1.6	1	9	RPDAEYWNS	14759
1BCC	DJ	OXIDOREDUCTASE	D	1.6	1.6	1	13	HTSIRRGFQVYKQ	14760
1BEV	34	VIRUS	4	1.6	1.6	1	6	PSKFTQ	14761
1BFO	AB	ANTIBODY	A	1.6	1.6	1	5	TEQLA	14762
1BGY	PV	ELECTRON TRANSPORT	P	1.6	1.6	1	36	HDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKSR	14763
1BR1	AB	MUSCLE PROTEIN	B	1.6	1.6	1	8	AEIRHVLV	14764
1BX2	AB	IMMUNE SYSTEM	A	1.6	1.6	1	5	EEFGR	14765
1BX2	DE	IMMUNE SYSTEM	D	1.6	1.6	1	5	EEFGR	14766
1BXR	CD	AMIDOTRANSFERASE	C	1.6	1.6	1	19	DKEYQIMRNASMAVLREIG	14767
1C9B	AB	TRANSCRIPTION/DNA	A	1.6	1.6	1	7	FKEICAV	14768
1C9B	EF	TRANSCRIPTION/DNA	E	1.6	1.6	1	7	FKEICAV	14769
1C9B	MN	TRANSCRIPTION/DNA	M	1.6	1.6	1	15	PISVAAAAIYMASQA	14770
1CT8	CD	IMMUNE SYSTEM	C	1.6	1.6	1	6	SEQLTS	14771
1DIO	AB	LYASE	B	1.6	1.6	1	5	ARPKY	14772
1E 08	AD	HYDROGENASE	A	1.6	1.6	1	11	VMEAALRFAYE	14773
1E6E	CD	OXIDOREDUCTASE	C	1.6	1.6	1	21	ITTTMTDSFLTGQILLQDLKA	14774

1E6V	BC	OXIDOREDUCTASE	C	1.6	1.6	1	6	PIRELV	14775
1E6V	BF	OXIDOREDUCTASE	F	1.6	1.6	1	20	EELLQVVQRIHELRTLAGYR	14776
1E6V	EC	OXIDOREDUCTASE	C	1.6	1.6	1	20	EELLQVVQRIHELRTLAGYR	14777
1E6V	EF	OXIDOREDUCTASE	F	1.6	1.6	1	6	PIRELV	14778
1E7P	AB	OXIDOREDUCTASE	A	1.6	1.6	1	8	AIRELAAW	14779
1E7P	DE	OXIDOREDUCTASE	D	1.6	1.6	1	8	AIRELAAW	14780
1E9Y	AB	HYDROLASE	A	1.6	1.6	1	11	PKELDKLMLHY	14781
1EFN	AB	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER)	B	1.6	1.6	1	14	YKAAVDLSHFLKEK	14782
1EM8	AB	GENE REGULATION	B	1.6	1.6	1	5	EHDFF	14783
1EYS	CM	ELECTRON TRANSPORT	M	1.6	1.6	1	15	IFPHLDWTAAFSIRY	14784
1EYS	LM	ELECTRON TRANSPORT	M	1.6	1.6	1	17	HLSWAFAAAIFFYLVLG	14785
1EYX	AB	PHOTOSYNTHESIS	B	1.6	1.6	1	13	GSDLQALRTFISD	14786
1FBI	HX	COMPLEX (ANTIBODY/ANTIGEN)	X	1.6	1.6	1	12	TATANCAKKIVS	14787
1FCD	AC	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	C	1.6	1.6	1	7	AEMLTNN	14788
1FFT	AC	OXIDOREDUCTASE	C	1.6	1.6	1	6	FWIYLM	14789
1FHJ	AD	OXYGEN STORAGE/TRANSPORT	A	1.6	1.6	1	19	PVNFKLLSHCLLVTLACHH	14790
1FIQ	AB	OXIDOREDUCTASE	B	1.6	1.6	1	7	KQVKSVA	14791
1FJ1	CD	IMMUNE SYSTEM	C	1.6	1.6	1	7	SEQLTSG	14792
1FNT	OP	HYDROLASE/HYDROLASE ACTIVATOR	P	1.6	1.6	1	17	TKLLVSEVAKIMQEATQ	14793
1FNT	PW	HYDROLASE/HYDROLASE ACTIVATOR	W	1.6	1.6	1	23	AADTEAVTQLIGSNIELHSLYTS	14794
1FNT	WM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.6	1.6	1	18	VEEVIKLVRDSFTSATER	14795
1FQV	AF	LIGASE	F	1.6	1.6	1	14	AAILKKVIQWCTHH	14796
1FQV	IJ	LIGASE	I	1.6	1.6	1	10	DELLLGIFSC	14797
1FQV	KL	LIGASE	L	1.6	1.6	1	16	KGLLDVTCKTVANMIK	14798
1FS1	AB	LIGASE	B	1.6	1.6	1	15	QGTLFELILAANYLD	14799
1FS2	CD	LIGASE	D	1.6	1.6	1	16	KGLLDVTCKTVANMIK	14800
1FSX	AD	OXYGEN STORAGE/TRANSPORT	D	1.6	1.6	1	20	PENFKLLGNVLVVVLARNFG	14801
1FX0	AB	HYDROLASE	A	1.6	1.6	1	15	LSKQAQAYRQMSLLL	14802
1G0U	1N	HYDROLASE	1	1.6	1.6	1	14	FGAHMANPLLRKVV	14803
1G0U	FN	HYDROLASE	N	1.6	1.6	1	22	AADTQAIADIVQYHLELYTSQY	14804
1G0U	HN	HYDROLASE	N	1.6	1.6	1	22	AADTQAIADIVQYHLELYTSQY	14805
1G0U	IY	HYDROLASE	Y	1.6	1.6	1	19	VEDALYLGKRSILAAAHRD	14806
1G0U	JK	HYDROLASE	K	1.6	1.6	1	15	VAAASKILSNLVYQY	14807
1G0U	V2	HYDROLASE	V	1.6	1.6	1	15	VVSALQMLKQHLFKY	14808
1G20	CD	OXIDOREDUCTASE	C	1.6	1.6	1	7	EKDIVFG	14809
1G73	AC	APOPTOSIS/APOPTOSIS INHIBITOR	C	1.6	1.6	1	8	YEARIFTF	14810
1G73	BD	APOPTOSIS/APOPTOSIS INHIBITOR	D	1.6	1.6	1	8	YEARIFTF	14811
1G8K	CD	OXIDOREDUCTASE	C	1.6	1.6	1	11	PSVAIARHVAG	14812

1GCV	CD	OXYGEN STORAGE/TRANSPORT	C	1.6	1.6	1	19	PDTHCAVDKLLSAICQELS	14813
1GH0	IJ	PHOTOSYNTHESIS	J	1.6	1.6	1	14	SNKRLDVVNRITSN	14814
1GH0	MN	PHOTOSYNTHESIS	N	1.6	1.6	1	14	SNKRLDVVNRITSN	14815
1GH0	MN	PHOTOSYNTHESIS	N	1.6	1.6	1	8	AFTKVVSQ	14816
1GH0	OP	PHOTOSYNTHESIS	P	1.6	1.6	1	14	SNKRLDVVNRITSN	14817
1GO4	EC	CELL CYCLE	E	1.6	1.6	1	25	PTSVARQRLREDHSQLQAECERLRG	14818
1GPW	CD	LYASE/TRANSFERASE	D	1.6	1.6	1	14	KIGRKLLEKVIECS	14819
1GXS	AB	LYASE	A	1.6	1.6	1	19	DDKMAQDTYTFLVKWFERF	14820
1GZS	BC	TOXIN/CELL CYCLE	B	1.6	1.6	1	17	PQQFQLILENIANKYIQ	14821
1H0D	AB	IMMUNE SYSTEM/HYDROLASE	A	1.6	1.6	1	6	SEQLTS	14822
1H0H	AB	DEHYDROGENASE	B	1.6	1.6	1	10	GCQVACKQWH	14823
1H1L	AB	OXIDOREDUCTASE	B	1.6	1.6	1	7	CMAEVIG	14824
1H1L	CD	OXIDOREDUCTASE	C	1.6	1.6	1	6	ERDIVF	14825
1H3O	AB	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	B	1.6	1.6	1	13	VKDVQLHLERQWN	14826
1H4J	AB	OXIDOREDUCTASE	B	1.6	1.6	1	5	PKELN	14827
1H4J	GH	OXIDOREDUCTASE	H	1.6	1.6	1	5	PKELN	14828
1H4L	AD	KINASE/KINASE ACTIVATOR	A	1.6	1.6	1	15	GVPSSALREICLLKE	14829
1H4L	AD	KINASE/KINASE ACTIVATOR	D	1.6	1.6	1	19	DHELQAVLLTCLYLSYSYM	14830
1H4L	BE	KINASE/KINASE ACTIVATOR	E	1.6	1.6	1	20	DHELQAVLLTCLYLSYSYMG	14831
1H6K	BY	NUCLEAR PROTEIN	B	1.6	1.6	1	15	DVMYTTLLIELCKLQ	14832
1H6K	CZ	NUCLEAR PROTEIN	C	1.6	1.6	1	11	FSHSFSALAKF	14833
1HDS	AB	OXYGEN TRANSPORT	A	1.6	1.6	1	18	PAVHANLNKFLANDSTVL	14834
1HEZ	AE	ANTIBODY	E	1.6	1.6	1	17	FEEATAEAYRYADLLAK	14835
1HMV	EF	NUCLEOTIDYLTRANSFERASE	F	1.6	1.6	1	12	KETWETWWTEYW	14836
1HR0	CN	RIBOSOME	C	1.6	1.6	1	18	RHLLLEDQRIRGLLEKEL	14837
1HV4	CD	OXYGEN STORAGE/TRANSPORT	C	1.6	1.6	1	16	AEEYGAETLERMFTAY	14838
1I3R	ED	IMMUNE SYSTEM	E	1.6	1.6	1	22	AQGALANIAVNKANLDVMKERS	14839
1I51	DF	HYDROLASE/HYDROLASE INHIBITOR	F	1.6	1.6	1	8	HADYLLRT	14840
1I7W	AB	CELL ADHESION	A	1.6	1.6	1	12	TRAIPELTKLLN	14841
1I7W	CD	CELL ADHESION	C	1.6	1.6	1	18	DSVLFYAITTLHNLLLHQ	14842
1I94	JN	RIBOSOME	N	1.6	1.6	1	8	LRELAHKG	14843
1IBR	AB	CELL CYCLE, TRANSLATION	B	1.6	1.6	1	13	QVARVAAGLQIKN	14844
1ID3	BD	STRUCTURAL PROTEIN/DNA	D	1.6	1.6	1	11	AREIQTAVRLI	14845
1IR2	X6	LYASE	X	1.6	1.6	1	21	NAPGAAANRVALEACTQARNE	14846
1IRU	BC	HYDROLASE	C	1.6	1.6	1	23	TSDANVLTNELRLIAQRYLLQYQ	14847
1IRU	JZ	HYDROLASE	Z	1.6	1.6	1	19	VEQAYDLARRAIYQATYRD	14848
1IRU	MN	HYDROLASE	M	1.6	1.6	1	22	HGDCLTLTKIIEARLKMYKHSN	14849
1IRU	XL	HYDROLASE	L	1.6	1.6	1	19	VEQAYDLARRAIYQATYRD	14850
1IW7	MN	TRANSFERASE	N	1.6	1.6	1	11	KPFLLKKMEEK	14851

1IWA	EL	LYASE	E	1.6	1.6	1	5	WTDLL	14852
1IWP	AG	LYASE	A	1.6	1.6	1	10	EATELELGMR	14853
1IWP	AG	LYASE	G	1.6	1.6	1	16	HAVARNFRRAAELIAI	14854
1IWP	LM	LYASE	L	1.6	1.6	1	10	GLDIVGALSR	14855
1J1D	DF	CONTRACTILE PROTEIN	D	1.6	1.6	1	15	EEQKNEFKAAFDIFV	14856
1JD2	1U	HYDROLASE	U	1.6	1.6	1	22	AADTQAIADIVQYHLELYTSQY	14857
1JD2	2U	HYDROLASE	2	1.6	1.6	1	22	IPDARNAALRAKAEAAEFRYKY	14858
1JD2	FN	HYDROLASE	F	1.6	1.6	1	22	IPDGRHLVNRGREEAASFKKLY	14859
1JD2	MU	HYDROLASE	M	1.6	1.6	1	19	VQVAEEAIVNAMRVLYYRD	14860
1JD2	TU	HYDROLASE	U	1.6	1.6	1	15	TETAASVFKELCYEN	14861
1JEY	AB	DNA BINDING PROTEIN/DNA	B	1.6	1.6	1	11	FDLLEDIESKI	14862
1JGV	LH	IMMUNE SYSTEM	L	1.6	1.6	1	6	SEQLTS	14863
1JH4	AB	RNA BINDING PROTEIN	A	1.6	1.6	1	19	PESLRSKVDEAVAVLQAHQ	14864
1JJ2	AY	RIBOSOME	Y	1.6	1.6	1	9	VAGKAVMKA	14865
1JJO	DE	SIGNALING PROTEIN	D	1.6	1.6	1	9	FLQMLKMYF	14866
1JMX	BG	OXIDOREDUCTASE	G	1.6	1.6	1	7	LYGCSDP	14867
1JOW	AB	CELL CYCLE/TRANSFERASE	B	1.6	1.6	1	10	IREVAVLRHL	14868
1JPW	BE	CELL ADHESION	B	1.6	1.6	1	15	INVVTCAAGILSNLT	14869
1JRO	CD	OXIDOREDUCTASE	C	1.6	1.6	1	11	TDVSLWVTKAL	14870
1JRO	EF	OXIDOREDUCTASE	F	1.6	1.6	1	13	PEAVLAAVRRAEG	14871
1JY7	AB	OXYGEN STORAGE/TRANSPORT	B	1.6	1.6	1	23	PPVQAAYQKVVAGVANALAHKYH	14872
1JY7	CB	OXYGEN STORAGE/TRANSPORT	C	1.6	1.6	1	16	PVNFKLLSHCLLVTLA	14873
1JY7	CD	OXYGEN STORAGE/TRANSPORT	D	1.6	1.6	1	19	PENFRLLGNVLVCVLAHHF	14874
1JY7	PQ	OXYGEN STORAGE/TRANSPORT	Q	1.6	1.6	1	19	PENFRLLGNVLVCVLAHHF	14875
1K3Z	AD	TRANSCRIPTION	D	1.6	1.6	1	8	PLHLAVEA	14876
1K7L	EF	TRANSCRIPTION	F	1.6	1.6	1	10	KILHRLLQEG	14877
1K8I	AB	IMMUNE SYSTEM	A	1.6	1.6	1	5	EWAQG	14878
1KEN	CT	VIRAL PROTEIN/IMMUNE SYSTEM	C	1.6	1.6	1	8	NQEQTSLY	14879
1KF6	NO	OXIDOREDUCTASE	N	1.6	1.6	1	21	PAAAIQQGKVESSKDFLIATL	14880
1KF6	NP	OXIDOREDUCTASE	N	1.6	1.6	1	21	PAAAIQQGKVESSKDFLIATL	14881
1KFY	AB	OXIDOREDUCTASE	A	1.6	1.6	1	26	TDLLYTIELGHGLNVAECMAHSAMAR	14882
1KFY	NO	OXIDOREDUCTASE	N	1.6	1.6	1	21	PAAAIQQGKVESSKDFLIATL	14883
1KG0	BD	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.6	1.6	1	13	AVDTYCRHNYGVG	14884
1KI1	AB	SIGNALING PROTEIN	B	1.6	1.6	1	13	LSSFILKPMQRVT	14885
1KI1	CD	SIGNALING PROTEIN	D	1.6	1.6	1	13	LSSFILKPMQRVT	14886
1KI6	AB	PHOSPHOTRANSFERASE	B	1.6	1.6	1	10	PQAVLAFVAL	14887
1KN1	AB	ELECTRON TRANSPORT	B	1.6	1.6	1	14	GELRVRAATTIAAN	14888
1KQF	BC	OXIDOREDUCTASE	C	1.6	1.6	1	29	PQMGRILHPFFGIAIFVALMFMFVRFVHH	14889
1KX4	BD	STRUCTURAL PROTEIN/DNA	B	1.6	1.6	1	11	AMDVVYALKRQ	14890
1KX4	GH	STRUCTURAL PROTEIN/DNA	G	1.6	1.6	1	7	EELNKLL	14891

1KYO	OQ	OXIDOREDUCTASE/ELECTRON TRANSPORT	Q	1.6	1.6	1	23	EEGKALVHHYEECAERVKIQQQQ	14892
1L0X	AB	IMMUNE SYSTEM	B	1.6	1.6	1	7	IYFLYEG	14893
1L9B	LC	PHOTOSYNTHESIS	L	1.6	1.6	1	5	WVDWW	14894
1L9B	LM	PHOTOSYNTHESIS	L	1.6	1.6	1	5	ERKYR	14895
1LKY	AB	TRANSCRIPTION	A	1.6	1.6	1	8	KEDFRYRS	14896
1LQ8	AB	BLOOD CLOTTING	A	1.6	1.6	1	7	MQQVENG	14897
1LQM	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.6	1.6	1	6	PLSAHR	14898
1LT4	FA	ENTEROTOXIN	A	1.6	1.6	1	5	IYNRI	14899
1LTX	AB	TRANSFERASE/PROTEIN BINDING	A	1.6	1.6	1	12	ATLWNCRREVLQ	14900
1LWU	DE	BLOOD CLOTTING	D	1.6	1.6	1	13	RIIHLQRRINMQL	14901
1M1E	AB	STRUCTURAL PROTEIN	A	1.6	1.6	1	10	QESKLIILAS	14902
1M1Y	AB	OXIDOREDUCTASE	A	1.6	1.6	1	28	ESIQKKCEEVIAKYKPEWEAVVAKYRPR	14903
1M1Y	IJ	OXIDOREDUCTASE	J	1.6	1.6	1	6	CMAEVI	14904
1M1Y	IJ	OXIDOREDUCTASE	J	1.6	1.6	1	9	KEYQELNFQ	14905
1M1Y	KL	OXIDOREDUCTASE	L	1.6	1.6	1	6	CMAEVI	14906
1M1Y	KL	OXIDOREDUCTASE	L	1.6	1.6	1	8	KEYQELNF	14907
1M2Z	DE	HORMONE/HORMONE ACTIVATOR	D	1.6	1.6	1	11	EMLAEIITNQI	14908
1M56	GI	OXIDOREDUCTASE	G	1.6	1.6	1	9	PVLYQHILW	14909
1MDY	AB	TRANSCRIPTION/DNA	B	1.6	1.6	1	28	ADRRKAATMRERRRLSKVNEAFETLKRS	14910
1MF8	AB	HYDROLASE, LIGASE	B	1.6	1.6	1	8	FEEFCAVV	14911
1MHY	DG	OXIDOREDUCTASE	G	1.6	1.6	1	15	KYEAEAIHIEFRQLY	14912
1MIU	BA	GENE REGULATION/ANTITUMOR PROTEIN	A	1.6	1.6	1	18	SIWVANHYRWIVWKLAAM	14913
1MJE	BA	GENE REGULATION/ANTITUMOR PROTEIN/DNA	A	1.6	1.6	1	8	SLYLTKSS	14914
1MJE	BA	GENE REGULATION/ANTITUMOR PROTEIN/DNA	B	1.6	1.6	1	7	LRAELEK	14915
1MJG	AM	OXIDOREDUCTASE	A	1.6	1.6	1	30	PVNLVFSAIRVALADYTGEHIATDFSDILF	14916
1MK2	AB	TRANSCRIPTION	A	1.6	1.6	1	15	NGPLQWLDKVLTQMG	14917
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	H	1.6	1.6	1	12	DTRDAWVNKIAH	14918
1MNM	BC	TRANSCRIPTION/DNA	B	1.6	1.6	1	11	QEGRNLIQACL	14919
1MTY	BG	MONOOXYGENASE	B	1.6	1.6	1	10	WNESAFSVHA	14920
1MU2	AB	TRANSFERASE	A	1.6	1.6	1	20	GIRLLAQVVQKIGKEALVIW	14921
1MUJ	AB	IMMUNE SYSTEM	A	1.6	1.6	1	22	PQGGLQNIAVVKHNLGVLTKRS	14922
1MVF	AE	IMMUNE SYSTEM	E	1.6	1.6	1	7	ATLMQAL	14923
1MVW	PQ	CONTRACTILE PROTEIN	Q	1.6	1.6	1	9	EIKNMWAAF	14924
1MVW	PR	CONTRACTILE PROTEIN	R	1.6	1.6	1	11	NAEINKILGNP	14925
1N0X	MK	IMMUNE SYSTEM	M	1.6	1.6	1	7	DEQLKSG	14926

1N2D	BC	CELL CYCLE	B	1.6	1.6	1	11	VGDLRYMLTGL	14927
1N4M	BD	CELL CYCLE	B	1.6	1.6	1	5	SKLLN	14928
1N4Q	KL	TRANSFERASE	L	1.6	1.6	1	15	RLTIAFFALSGLDML	14929
1N86	AC	BLOOD CLOTTING	A	1.6	1.6	1	6	IQLLQK	14930
1N95	AB	TRANSFERASE	B	1.6	1.6	1	11	LKSLLQWVTSR	14931
1NBF	BC	HYDROLASE	B	1.6	1.6	1	17	VQELCRVLLDNVENKMK	14932
1NBU	AD	LYASE	A	1.6	1.6	1	15	IETVGAEIADHVMDD	14933
1NEK	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.6	1.6	1	28	LALRLMLQLVIVVALVVYVIYGFVVVWG	14934
1NFD	AB	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)	B	1.6	1.6	1	7	KAEIANK	14935
1NGM	EF	TRANSCRIPTION/DNA	F	1.6	1.6	1	6	TDTYLS	14936
1NGM	IJ	TRANSCRIPTION/DNA	J	1.6	1.6	1	11	ADFLLEQESKR	14937
1NH2	BD	TRANSCRIPTION/DNA	B	1.6	1.6	1	7	REDFENA	14938
1NIK	AB	TRANSCRIPTION	B	1.6	1.6	1	6	AEEEES	14939
1NJ9	AB	IMMUNE SYSTEM	A	1.6	1.6	1	5	SEELE	14940
1O18	MO	CONTRACTILE PROTEIN	M	1.6	1.6	1	10	SAIPEGQFMD	14941
1O94	CD	ELECTRON TRANSPORT	C	1.6	1.6	1	16	AIVVGRILTEVIKKEA	14942
1O96	EF	ELECTRON TRANSFER	F	1.6	1.6	1	14	VDSLGYASSLASKT	14943
1OAO	BC	OXIDOREDUCTASE	B	1.6	1.6	1	30	PVNLVFSAIRVALADYTGEHIATDFSDILF	14944
1OCC	CH	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	H	1.6	1.6	1	20	TRNCWQNYLDFHRCEKAMTA	14945
1OCC	NO	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.6	1.6	1	8	SSLDIVLH	14946
1OED	AE	ION CHANNEL/RECEPTOR	E	1.6	1.6	1	30	KCTLSISVLLAQTIFLFLIAQKVPETSLNV	14947
1OJ5	AB	TRANSCRIPTIONAL COACTIVATOR	B	1.6	1.6	1	10	EQDLTKLLLE	14948
1OR0	AB	HYDROLASE	A	1.6	1.6	1	5	PGRTL	14949
1OR7	AC	TRANSCRIPTION	C	1.6	1.6	1	9	KEQLSALMD	14950
1OR7	BF	TRANSCRIPTION	B	1.6	1.6	1	8	YEEIAAIM	14951
1OXK	EF	SIGNALING PROTEIN	E	1.6	1.6	1	18	LTELDNLGHFLKGSSAAL	14952
1PHN	AB	ELECTRON TRANSPORT	B	1.6	1.6	1	12	AFAKVVAQADAR	14953
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.6	1.6	1	13	IWTHLDWVSNTGY	14954
1PSS	MH	PHOTOSYNTHETIC REACTION CENTER	M	1.6	1.6	1	14	MEGIHRWAIWMAVL	14955
1Q16	AC	OXIDOREDUCTASE	A	1.6	1.6	1	6	KFLDRF	14956
1Q5R	BI	HYDROLASE	I	1.6	1.6	1	7	FTDYLRG	14957
1Q68	AB	MEMBRANE PROTEIN/TRANSFERASE	A	1.6	1.6	1	10	LSQIKRLLSE	14958
1Q9O	DC	IMMUNE SYSTEM	C	1.6	1.6	1	7	SEQLTSG	14959
1Q9W	AB	IMMUNE SYSTEM	A	1.6	1.6	1	6	SEQLTS	14960
1QGW	BD	PHOTOSYNTHESIS	D	1.6	1.6	1	5	SRVVT	14961

1QLE	AC	OXIDOREDUCTASE/IMMUNE SYSTEM	C	1.6	1.6	1	13	AFVMLTGAVAWMK	14962
1QLS	AD	METAL BINDING PROTEIN/INHIBITOR	A	1.6	1.6	1	7	AAFTQNQ	14963
1QPW	AD	OXYGEN TRANSPORT	D	1.6	1.6	1	6	PWTQRF	14964
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	A	1.6	1.6	1	12	AAELRHVMTNLG	14965
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	A	1.6	1.6	1	11	EAELQDMINEV	14966
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	A	1.6	1.6	1	15	DEQIAEFKEAFSLFD	14967
1QVF	AY	RIBOSOME	Y	1.6	1.6	1	9	VAGKAVMKA	14968
1R1K	DA	HORMONE/GROWTH FACTOR RECEPTOR	D	1.6	1.6	1	18	AYVIEDLLHFCRCMYSMM	14969
1R27	AB	OXIDOREDUCTASE	A	1.6	1.6	1	5	STCLY	14970
1R27	CD	OXIDOREDUCTASE	C	1.6	1.6	1	5	EIAKL	14971
1R4M	GH	CELL CYCLE	H	1.6	1.6	1	7	VKKFLER	14972
1R8Q	AE	PROTEIN TRANSPORT/EXCHANGE FACTOR	E	1.6	1.6	1	19	AQKIDRMMEAFAQRYCLCN	14973
1RCO	KT	LYASE	K	1.6	1.6	1	14	AKNYGRAVYECLRG	14974
1RM6	AC	OXIDOREDUCTASE	C	1.6	1.6	1	16	VKIIKSVETAAAARLC	14975
1RYP	DK	MULTICATALYTIC PROTEINASE	K	1.6	1.6	1	23	AGDTVQFAEYIQANIQLYSIRED	14976
1RYP	EF	MULTICATALYTIC PROTEINASE	E	1.6	1.6	1	12	SEGAQAELLNEW	14977
1RYP	GH	MULTICATALYTIC PROTEINASE	H	1.6	1.6	1	15	TETAASVFKELCYEN	14978
1RYP	I2	MULTICATALYTIC PROTEINASE	2	1.6	1.6	1	6	WDFAKD	14979
1RYP	PQ	MULTICATALYTIC PROTEINASE	Q	1.6	1.6	1	22	TADAEILINTARIHAQNYLKTY	14980
1RYP	PX	MULTICATALYTIC PROTEINASE	X	1.6	1.6	1	15	PETFTQLVSSSLYER	14981
1RYP	UV	MULTICATALYTIC PROTEINASE	U	1.6	1.6	1	22	IPDGRHLVNRGREEAASFKKLY	14982
1RZG	CD	IMMUNE SYSTEM	D	1.6	1.6	1	7	DEQLKSG	14983
1S0Y	GJ	LYASE	G	1.6	1.6	1	20	DEQKRALSAGLLRVISEATG	14984
1S5E	AH	TRANSERASE,TOXIN	A	1.6	1.6	1	7	PDEIKQS	14985
1S5L	AD	PHOTOSYNTHESIS	A	1.6	1.6	1	11	INRANLGMEVM	14986
1S5L	OU	PHOTOSYNTHESIS	U	1.6	1.6	1	5	TALVE	14987
1SA0	AB	CELL CYCLE	B	1.6	1.6	1	8	RKLAVNMV	14988
1SB3	BC	OXIDOREDUCTASE	B	1.6	1.6	1	9	TDLLPNLRR	14989
1SCT	GH	OXYGEN TRANSPORT	H	1.6	1.6	1	16	MEGTGLMLMANLFKTS	14990
1SEB	AB	COMPLEX (MHC II/PEPTIDE/TOXIN)	A	1.6	1.6	1	22	AQGALANIAVDKANLEIMTKRS	14991
1SQX	AB	OXIDOREDUCTASE	A	1.6	1.6	1	21	DSQIEKERDVILQELQENDTS	14992
1SR5	BC	HYDROLASE/HYDROLASE INHIBITOR	B	1.6	1.6	1	6	ERELLE	14993
1SXJ	DE	REPLICATION	E	1.6	1.6	1	11	ANIILKELTFS	14994
1T6O	AB	VIRAL PROTEIN	A	1.6	1.6	1	14	EDRKRYLMTLLDDI	14995
1TBQ	KS	COMPLEX (SERINE PROTEASE/INHIBITOR)	S	1.6	1.6	1	9	NCRLECASI	14996
1TI2	IJ	OXIDOREDUCTASE	I	1.6	1.6	1	6	HTARLV	14997
1TII	FC	ENTEROTOXIN	C	1.6	1.6	1	32	CASLTNKLSQHDLADFKKYIKRKFTLMTLLSI	14998

1TO9	AB	BIOSYNTHETIC PROTEIN	A	1.6	1.6	1	9	PTAYSYTSH	14999
1TQY	CD	TRANSFERASE	D	1.6	1.6	1	10	VNTGQISIRH	15000
1TQY	EF	TRANSFERASE	F	1.6	1.6	1	16	AGGLDALGHARRTIRR	15001
1TU3	DH	PROTEIN TRANSPORT	H	1.6	1.6	1	31	LQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	15002
1TUE	FG	REPLICATION	G	1.6	1.6	1	24	IDSQIQYWQLIRWENAIFFAAREH	15003
1TYE	AB	CELL ADHESION	B	1.6	1.6	1	5	DGRLA	15004
1TZN	Hh	TOXIN RECEPTOR/TOXIN	H	1.6	1.6	1	6	WAETMG	15005
1TZN	Ii	TOXIN RECEPTOR/TOXIN	I	1.6	1.6	1	6	WAETMG	15006
1U0N	AD	BLOOD CLOTTING	A	1.6	1.6	1	13	TSEVLKYTLFQIF	15007
1UF2	AD	VIRUS	A	1.6	1.6	1	8	VLVAIYNN	15008
1UYW	LH	IMMUNE SYSTEM	L	1.6	1.6	1	6	SEQLTS	15009
1V29	AB	LYASE	B	1.6	1.6	1	7	PVDYLTS	15010
1V54	AM	OXIDOREDUCTASE	A	1.6	1.6	1	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	15011
1V54	EI	OXIDOREDUCTASE	I	1.6	1.6	1	25	LLARRLRFHIVGAFMVSLGFATFYK	15012
1VRQ	AD	OXIDOREDUCTASE	A	1.6	1.6	1	16	AADVLDWLEEWLQTEW	15013
1VS5	DE	RIBOSOME	D	1.6	1.6	1	16	DYGVQLREKQKVRRIY	15014
1VS6	DP	RIBOSOME	P	1.6	1.6	1	5	LEQEQ	15015
1VSA	IN	RIBOSOME	I	1.6	1.6	1	6	ELREKG	15016
1W5C	GJ	PHOTOSYNTHESIS	J	1.6	1.6	1	16	YTKNLLLNEGIRAWMA	15017
1WDW	AB	LYASE	A	1.6	1.6	1	8	YNPIYRAG	15018
1WR6	CG	PROTEIN TRANSPORT/SIGNALING PROTEIN	C	1.6	1.6	1	13	LEEVNNNVRLLSE	15019
1WYU	AD	OXIDOREDUCTASE	A	1.6	1.6	1	11	EEEIREMLRRV	15020
1XCQ	CM	IMMUNE SYSTEM	M	1.6	1.6	1	10	EAYRYAALHA	15021
1XD2	AC	SIGNALING PROTEIN	C	1.6	1.6	1	17	FSKRRKVAEITGEIQQY	15022
1XL3	BD	CELL INVASION	D	1.6	1.6	1	6	RFYQDL	15023
1XLS	CG	TRANSCRIPTION	C	1.6	1.6	1	23	PAEVEALREKVYASLEAYCKHKY	15024
1XLS	EM	TRANSCRIPTION	E	1.6	1.6	1	25	VLPLLTHFADINTFMVQQIIKFTKD	15025
1XLS	HP	TRANSCRIPTION	H	1.6	1.6	1	25	VLPLLTHFADINTFMVQQIIKFTKD	15026
1XXI	IJ	TRANSFERASE	I	1.6	1.6	1	15	RRMGVEMTLLRALAF	15027
1Y8H	AB	OXYGEN STORAGE/TRANSPORT	A	1.6	1.6	1	16	AGEYGAEALERMFLGF	15028
1YE9	BF	OXIDOREDUCTASE	F	1.6	1.6	1	7	FFAENEQ	15029
1YE9	DH	OXIDOREDUCTASE	H	1.6	1.6	1	8	TDTQISRL	15030
1YHU	JL	OXYGEN STORAGE/TRANSPORT	J	1.6	1.6	1	16	REEFGHFIWSHVFQHS	15031
1YHU	MO	OXYGEN STORAGE/TRANSPORT	M	1.6	1.6	1	18	QATLDADLAHLKSQHDPR	15032
1YHU	RT	OXYGEN STORAGE/TRANSPORT	R	1.6	1.6	1	20	PAFRAHATRVLGGLDMCIAL	15033
1YHU	UW	OXYGEN STORAGE/TRANSPORT	U	1.6	1.6	1	18	QATLDADLAHLKSQHDPR	15034
1YHU	WP	OXYGEN STORAGE/TRANSPORT	P	1.6	1.6	1	16	PDAWSRCFNRITTGMT	15035
1YL4	IU	RIBOSOME	U	1.6	1.6	1	17	GKEQRILAKTIKRARIL	15036
1YNJ	CD	TRANSFERASE	C	1.6	1.6	1	10	AHTLQEMLTI	15037

1YNJ	CD	TRANSFERASE	D	1.6	1.6	1	6	LTDILS	15038
1YNT	CE	IMMUNE SYSTEM	E	1.6	1.6	1	6	AYRYAD	15039
1YOK	AB	TRANSCRIPTION	A	1.6	1.6	1	11	VDDQMKLLQNC	15040
1YR5	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.6	1.6	1	10	YEEFVQMMTA	15041
1YSL	AB	LYASE	A	1.6	1.6	1	24	GPLSNETYIQSFAQVWDEHKKRTG	15042
1YU6	BD	HYDROLASE	B	1.6	1.6	1	14	YSGIVSGIEWATTN	15043
1YUC	AC	TRANSCRIPTION REGULATION	A	1.6	1.6	1	8	LLIEMLHA	15044
1YY8	AB	IMMUNE SYSTEM	A	1.6	1.6	1	6	DEQLKS	15045
1Z0K	AB	PROTEIN TRANSPORT	B	1.6	1.6	1	22	MDEVRTLQENLRQLQDEYDQQQ	15046
1Z7Q	Ef	HYDROLASE/HYDROLASE ACTIVATOR	E	1.6	1.6	1	13	FQVEYSLEAIKLG	15047
1Z7Q	Gh	HYDROLASE/HYDROLASE ACTIVATOR	G	1.6	1.6	1	11	FQVEYAVKAVE	15048
1Z7Q	HN	HYDROLASE/HYDROLASE ACTIVATOR	H	1.6	1.6	1	15	TETAASVFKELCYEN	15049
1Z7Q	JK	HYDROLASE/HYDROLASE ACTIVATOR	K	1.6	1.6	1	14	YSGFYTFSLLDHHY	15050
1Z7Q	JZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.6	1.6	1	19	VEDALYLGKRSILAAAHRD	15051
1Z7Q	KL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.6	1.6	1	15	VAAASKILSNLVYQY	15052
1Z7Q	RY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.6	1.6	1	23	AGDTVQFAEYIQANIQLYSIRED	15053
1Z7Q	ST	HYDROLASE/HYDROLASE ACTIVATOR	T	1.6	1.6	1	18	APDARVLSNYLRQQCNYS	15054
1Z7Q	XL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.6	1.6	1	19	VEDALYLGKRSILAAAHRD	15055
1ZAV	AV	STRUCTURAL PROTEIN	A	1.6	1.6	1	15	PVEAVKIIYNFYKDK	15056
1ZBB	cd	STRUCTURAL PROTEIN/DNA	c	1.6	1.6	1	7	EELNKLL	15057
1ZBB	CD	STRUCTURAL PROTEIN/DNA	C	1.6	1.6	1	7	EELNKLL	15058
1ZBB	GH	STRUCTURAL PROTEIN/DNA	G	1.6	1.6	1	7	EELNKLL	15059
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	C	1.6	1.6	1	7	EELNKLL	15060
1ZOQ	AD	TRANSCRIPTION/TRANSFERASE	D	1.6	1.6	1	13	PQQQQQVLNILKS	15061
1ZOQ	BC	TRANSCRIPTION/TRANSFERASE	C	1.6	1.6	1	13	PQQQQQVLNILKS	15062
1ZQ1	AC	LYASE	A	1.6	1.6	1	8	AEELAKAL	15063
1ZV5	LA	HYDROLASE/IMMUNE SYSTEM	L	1.6	1.6	1	8	VAWRNRCK	15064
1ZY8	BK	OXIDOREDUCTASE	B	1.6	1.6	1	7	CEDIARV	15065
2A45	GH	BLOOD CLOTTING	H	1.6	1.6	1	22	GCQLQEALLQQERPIRNSVDEL	15066
2A5D	AB	PROTEIN TRANSPORT/TRANSFERASE	A	1.6	1.6	1	6	RPLWRH	15067
2ACL	AB	TRANSCRIPTION	B	1.6	1.6	1	8	LLSEIWDV	15068
2ADV	AC	HYDROLASE	A	1.6	1.6	1	14	GADVVAHAHRLMNF	15069
2AFH	AB	OXIDOREDUCTASE	B	1.6	1.6	1	6	CMAEVI	15070
2AGJ	LH	IMMUNE SYSTEM	L	1.6	1.6	1	6	DEQLKS	15071
2AHM	DG	VIRAL PROTEIN, REPLICATION	D	1.6	1.6	1	16	SKLWAQCVQLHNDILL	15072
2AJ3	CD	IMMUNE SYSTEM	C	1.6	1.6	1	7	DEQLKSG	15073
2AK4	AC	IMMUNE SYSTEM	A	1.6	1.6	1	11	VAEQRRAYLEG	15074
2AK4	KB	IMMUNE SYSTEM	K	1.6	1.6	1	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	15075
2AK4	QT	IMMUNE SYSTEM	Q	1.6	1.6	1	11	VAEQRRAYLEG	15076

2AUS	CD	ISOMERASE/STRUCTURAL PROTEIN	C	1.6	1.6	1	12	SHEVVAWIKRIL	15077
2AXT	ad	ELECTRON TRANSPORT	a	1.6	1.6	1	7	WELSYRL	15078
2AXT	ad	ELECTRON TRANSPORT	d	1.6	1.6	1	10	ISQEIRAAED	15079
2AXT	de	ELECTRON TRANSPORT	d	1.6	1.6	1	7	FTRWCQL	15080
2B5L	BD	PROTEIN BINDING/VIRALPROTEIN	D	1.6	1.6	1	12	YKGVKLAKFGKE	15081
2BA0	CF	RNA BINDING PROTEIN	F	1.6	1.6	1	11	IEVGEEMDEIT	15082
2BBM	AB	CALCIUM-BINDING PROTEIN	A	1.6	1.6	1	12	EEEIREAFRVFD	15083
2BNQ	DE	IMMUNE SYSTEM/RECEPTOR	E	1.6	1.6	1	8	EAEISHTQ	15084
2BP7	CB	OXIDOREDUCTASE	C	1.6	1.6	1	9	DHLRRQRQE	15085
2C35	GH	POLYMERASE	G	1.6	1.6	1	11	KFELACLANLC	15086
2CKF	EF	OXIDOREDUCTASE	E	1.6	1.6	1	8	GYHVGWTH	15087
2CNW	BE	SIGNAL RECOGNITION	E	1.6	1.6	1	14	QNGLEQAKKFHEAV	15088
2DBU	AB	TRANSFERASE	A	1.6	1.6	1	16	DALADDLKTYGSEVLP	15089
2DD4	HF	HYDROLASE	H	1.6	1.6	1	8	HTLFRAYT	15090
2DD4	JL	HYDROLASE	L	1.6	1.6	1	10	PNYRRRLVRW	15091
2DF4	BC	LIGASE	C	1.6	1.6	1	7	QELALKN	15092
2DS2	AB	PLANT PROTEIN	B	1.6	1.6	1	12	ALRQCCNQLRQV	15093
2DSQ	AC	PROTEIN BINDING/HORMONE/GROWTH FACTOR	C	1.6	1.6	1	7	LRRLEMY	15094
2DXB	BL	HYDROLASE	B	1.6	1.6	1	8	HTLFRAYT	15095
2DXB	PR	HYDROLASE	R	1.6	1.6	1	10	PNYRRRLVRW	15096
2E9X	AC	REPLICATION	C	1.6	1.6	1	7	LWLAKGL	15097
2E9X	BC	REPLICATION	C	1.6	1.6	1	10	FYGFGSQLLH	15098
2E9X	EG	REPLICATION	G	1.6	1.6	1	7	LWLAKGL	15099
2EHB	AD	SIGNALLING PROTEIN/TRANSFERASE	A	1.6	1.6	1	13	VHEKVKFAFKLYD	15100
2EHO	FH	REPLICATION	H	1.6	1.6	1	8	LWLAKGLF	15101
2EHO	JL	REPLICATION	L	1.6	1.6	1	5	LDDIL	15102
2EJF	BD	LIGASE	B	1.6	1.6	1	19	LPKIVFLGAVGVVETLKEF	15103
2F5Z	AK	OXIDOREDUCTASE/PROTEIN BINDING	A	1.6	1.6	1	7	CEDIARV	15104
2F8N	BD	STRUCTURAL PROTEIN/DNA	D	1.6	1.6	1	12	SREVQTAVRLLL	15105
2F8N	HG	STRUCTURAL PROTEIN/DNA	G	1.6	1.6	1	11	PRHILLAVAND	15106
2F95	AB	MEMBRANE PROTEIN	B	1.6	1.6	1	24	FVGALTVLFGAIAYGEVTAAAATG	15107
2F9D	BQ	RNA BINDING PROTEIN	Q	1.6	1.6	1	6	DEELDA	15108
2FBW	BC	OXIDOREDUCTASE	C	1.6	1.6	1	24	LSQVEQSGVVVLILTLLSSAGIAA	15109
2FBW	BD	OXIDOREDUCTASE	B	1.6	1.6	1	6	PSYWWN	15110
2FBW	OQ	OXIDOREDUCTASE	O	1.6	1.6	1	6	PSYWWN	15111
2FFD	DF	BLOOD CLOTTING	F	1.6	1.6	1	18	NNQKIVNLKEKVAQLEAQ	15112
2FFF	AB	MEMBRANE PROTEIN, TRANSFERASE	B	1.6	1.6	1	22	YLYFTTLAEAQERMYDYLAQRD	15113

2FHS	AC	OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN	A	1.6	1.6	1	14	KDFRKMLAHCEAVT	15114
2FHX	AB	HYDROLASE, METAL BINDING PROTEIN	A	1.6	1.6	1	16	NLGTQTLMDWVAKTMK	15115
2FJ7	CD	STRUCTURAL PROTEIN/DNA	D	1.6	1.6	1	17	LAKHAVSEGTKAVTKYT	15116
2FJ7	EF	STRUCTURAL PROTEIN/DNA	E	1.6	1.6	1	11	VALREIRRYQK	15117
2FJF	OP	IMMUNE SYSTEM	O	1.6	1.6	1	6	DEQLKS	15118
2FK0	EB	VIRAL PROTEIN	B	1.6	1.6	1	52	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDK VRLQL	15119
2FKW	IJ	MEMBRANE PROTEIN, PHOTOSYNTHESIS	I	1.6	1.6	1	9	TWFPAYWQG	15120
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	A	1.6	1.6	1	9	YEEFVQMMT	15121
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	A	1.6	1.6	1	11	TKELGTVMRSL	15122
2FUG	DF	OXIDOREDUCTASE	F	1.6	1.6	1	6	CCAIEM	15123
2FUG	DG	OXIDOREDUCTASE	D	1.6	1.6	1	14	RERETILDLFEWVT	15124
2FUG	J6	OXIDOREDUCTASE	J	1.6	1.6	1	10	FRELIYEWAG	15125
2FUG	JK	OXIDOREDUCTASE	K	1.6	1.6	1	13	AEELWDYLTETLG	15126
2FUG	MO	OXIDOREDUCTASE	M	1.6	1.6	1	9	YLQNITYTP	15127
2FX8	MI	IMMUNE SYSTEM	M	1.6	1.6	1	7	DEQLKSG	15128
2FYM	FE	LYASE	F	1.6	1.6	1	19	ANAILAVSLANAKAAAAAK	15129
2FYN	AF	OXIDOREDUCTASE	F	1.6	1.6	1	23	YATAGAGAVATGAAVWPLINQMN	15130
2FYN	HI	OXIDOREDUCTASE	I	1.6	1.6	1	5	RDFLY	15131
2FYN	MR	OXIDOREDUCTASE	R	1.6	1.6	1	23	YATAGAGAVATGAAVWPLINQMN	15132
2G77	AB	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	A	1.6	1.6	1	11	FIQFAFRWMNC	15133
2GID	AD	TRANSLATION	A	1.6	1.6	1	13	QRFLTQALHYNTG	15134
2GID	PJ	TRANSLATION	P	1.6	1.6	1	7	ALHYNTG	15135
2GL7	AB	TRANSCRIPTION	A	1.6	1.6	1	17	DSVLFYAITTLHNLLLH	15136
2GL7	DE	TRANSCRIPTION	D	1.6	1.6	1	16	INVVTCAAGILSNLTC	15137
2GPV	AG	TRANSCRIPTION	A	1.6	1.6	1	13	WMEILILGVVYRS	15138
2GTL	AM	OXYGEN STORAGE/TRANSPORT	A	1.6	1.6	1	12	YEDRREIRHIWD	15139
2GTL	BM	OXYGEN STORAGE/TRANSPORT	B	1.6	1.6	1	19	DNYFDAFKTAILHVVAAQL	15140
2GTL	CO	OXYGEN STORAGE/TRANSPORT	C	1.6	1.6	1	15	EEDHRIVQKQWDILW	15141
2GTL	EK	OXYGEN STORAGE/TRANSPORT	E	1.6	1.6	1	12	YEDRREIRHIWD	15142
2GTP	BC	SIGNALING PROTEIN	C	1.6	1.6	1	13	FRTRESTAKKIKA	15143
2H1L	GS	VIRAL PROTEIN	G	1.6	1.6	1	16	IQSRIVEWKERLDKEF	15144
2H4P	AB	HYDROLASE INHIBITOR	A	1.6	1.6	1	14	PWSISSALALTYLA	15145
2H4Q	AB	HYDROLASE INHIBITOR	A	1.6	1.6	1	13	IHSGFKELLTAFN	15146

2H9A	AB	OXIDOREDUCTASE	B	1.6	1.6	1	17	IEYSYSIIERMRLGALT	15147
2H9E	HC	HYDROLASE, BLOOD CLOTTING	C	1.6	1.6	1	8	AEDCELDN	15148
2HGP	PV	RIBOSOME	P	1.6	1.6	1	9	YRGLRHRRG	15149
2HHH	DE	RIBOSOME	D	1.6	1.6	1	8	EQLVIEFY	15150
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	A	1.6	1.6	1	5	RSSRA	15151
2HLD	BE	HYDROLASE	B	1.6	1.6	1	15	LSKQAVAYRQLSLLL	15152
2HNT	CF	SERINE PROTEASE	F	1.6	1.6	1	9	KKWIQKVID	15153
2HUE	BC	DNA BINDING PROTEIN	B	1.6	1.6	1	11	PKDIQLARRIR	15154
2HZS	CB	TRANSCRIPTION	C	1.6	1.6	1	6	PALVFN	15155
2HZS	GH	TRANSCRIPTION	H	1.6	1.6	1	8	VSSLMNGL	15156
2I2R	AH	TRANSPORT PROTEIN	A	1.6	1.6	1	5	TEKEF	15157
2I2R	DH	TRANSPORT PROTEIN	H	1.6	1.6	1	14	FEDFVTALSILLRG	15158
2I2X	GH	TRANSFERASE	H	1.6	1.6	1	14	DIGKNIVTALLRAN	15159
2I2X	GH	TRANSFERASE	H	1.6	1.6	1	8	EASLKKVL	15160
2I2X	IJ	TRANSFERASE	I	1.6	1.6	1	14	DKVLRDLMMLSDRY	15161
2I2X	KL	TRANSFERASE	L	1.6	1.6	1	14	DIGKNIVTALLRAN	15162
2I3T	CD	CELL CYCLE	D	1.6	1.6	1	5	FKLIY	15163
2IAE	AB	HYDROLASE	A	1.6	1.6	1	10	FTSRTSACGL	15164
2IAE	DB	HYDROLASE	B	1.6	1.6	1	14	IYPEVVHMFAVNMF	15165
2IAN	BS	IMMUNE SYSTEM	B	1.6	1.6	1	25	KDLLEQRRAAVDTYCRHNYGVGESF	15166
2ICW	AH	IMMUNE SYSTEM	H	1.6	1.6	1	27	VEQIKRNIAILDEIMAKADNDLSYFIS	15167
2IE3	AC	SIGNALING PROTEIN,HYDROLASE	A	1.6	1.6	1	15	VDVKYFAQEALTVLS	15168
2INP	BD	OXIDOREDUCTASE	B	1.6	1.6	1	8	LKDKYQYL	15169
2INP	BD	OXIDOREDUCTASE	B	1.6	1.6	1	5	TRDMA	15170
2INP	BD	OXIDOREDUCTASE	B	1.6	1.6	1	5	KKDIF	15171
2IO1	AB	PROTEIN BINDING, HYDROLASE	A	1.6	1.6	1	7	RGDIQTL	15172
2IZV	BC	TRANSCRIPTION	B	1.6	1.6	1	12	VFELKRIVEGIL	15173
2J0Q	AG	HYDROLASE	G	1.6	1.6	1	12	YKEAQAAMEGLN	15174
2J28	DP	RIBOSOME	P	1.6	1.6	1	6	KQLEQE	15175
2J28	L3	RIBOSOME	3	1.6	1.6	1	6	VRGAAK	15176
2JBL	CM	ELECTRON TRANSPORT	M	1.6	1.6	1	8	WYLWCVKH	15177
2JBL	LM	ELECTRON TRANSPORT	M	1.6	1.6	1	5	YQTIY	15178
2JFA	AP	TRANSCRIPTION	A	1.6	1.6	1	25	EASMMGLLTNLADRELVHMINWAKR	15179
2JKR	AS	ENDOCYTOSIS	A	1.6	1.6	1	14	YTEKQIGYLFISVL	15180
2JKR	EU	ENDOCYTOSIS	E	1.6	1.6	1	18	PMVVANAVAALSEISESH	15181
2JKR	EU	ENDOCYTOSIS	U	1.6	1.6	1	9	FVLIYELLD	15182
2JRI	AC	HYDROLASE/SIGNALING PROTEIN	A	1.6	1.6	1	12	IQVISNALKVWG	15183
2JU0	AB	METAL BINDING PROTEIN/SIGNALING PROTEIN	B	1.6	1.6	1	16	NVAPALVLSSMIMSAI	15184

2KIN	AB	MOTOR PROTEIN	A	1.6	1.6	1	6	EAEILR	15185
2NPI	BD	TRANSCRIPTION	B	1.6	1.6	1	22	KDLYLECISQLGQVVGQRLHLD	15186
2NQB	FH	STRUCTURAL PROTEIN/DNA	F	1.6	1.6	1	11	AMDVVYALKRQ	15187
2NV2	OP	LYASE/TRANSFERASE	O	1.6	1.6	1	10	ERVKRGMAEM	15188
2NY7	HL	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.6	1.6	1	6	DEQLKS	15189
2NYL	AB	HYDROLASE	A	1.6	1.6	1	9	FTSRTSACG	15190
2NYL	AB	HYDROLASE	A	1.6	1.6	1	5	WRVRY	15191
2NZD	EF	STRUCTURAL PROTEIN/DNA	F	1.6	1.6	1	11	AMDVVYALKRQ	15192
2NZD	FH	STRUCTURAL PROTEIN/DNA	F	1.6	1.6	1	28	IYEETRGVLKVFLENVIRDAVTYTEHAK	15193
2O01	HL	PHOTOSYNTHESIS	L	1.6	1.6	1	10	FTGGFFFGGV	15194
2O8F	AB	DNA BINDING PROTEIN/DNA	B	1.6	1.6	1	10	SYGFNAARLA	15195
2OGX	AB	METAL BINDING PROTEIN	A	1.6	1.6	1	13	VRARHVFSVGLDL	15196
2OM0	12	HORMONE	1	1.6	1.6	1	5	IVEQC	15197
2OM0	cd	HORMONE	c	1.6	1.6	1	7	LYQLENY	15198
2OM0	CD	HORMONE	C	1.6	1.6	1	5	IVEQC	15199
2OM0	EF	HORMONE	E	1.6	1.6	1	5	IVEQC	15200
2OM0	gf	HORMONE	g	1.6	1.6	1	7	LYQLENY	15201
2OM0	GH	HORMONE	G	1.6	1.6	1	5	IVEQC	15202
2OM0	KL	HORMONE	K	1.6	1.6	1	5	IVEQC	15203
2OM0	XY	HORMONE	X	1.6	1.6	1	5	IVEQC	15204
2P24	AB	IMMUNE SYSTEM	B	1.6	1.6	1	9	DAEYYNKQY	15205
2P2C	HS	HYDROLASE	S	1.6	1.6	1	8	PLHLAAYD	15206
2PL9	BE	SIGNALING PROTIEN	B	1.6	1.6	1	10	KENIIAAAQA	15207
2PM6	CD	PROTEIN TRANSPORT	C	1.6	1.6	1	14	EVKTEKARVLIASG	15208
2PQK	AB	APOPTOSIS	A	1.6	1.6	1	12	ETAFQGMLRKLD	15209
2PUK	AC	ELECTRON TRANSPORT	A	1.6	1.6	1	19	LSVTAVVIEGLARHKEELG	15210
2PUK	EF	ELECTRON TRANSPORT	E	1.6	1.6	1	6	VPMRER	15211
2PVO	AD	ELECTRON TRANSPORT	D	1.6	1.6	1	6	DDQIEA	15212
2Q86	CD	IMMUNE SYSTEM	D	1.6	1.6	1	7	KAEIANK	15213
2Q97	AT	STRUCTURAL PROTEIN/CELL INVASION	A	1.6	1.6	1	9	QAVLSLYAS	15214
2Q9Q	BC	REPLICATION	B	1.6	1.6	1	18	PEIVECVMEQLEHMEENL	15215
2QHO	AB	PROTEIN BINDING/LIGASE	B	1.6	1.6	1	11	EELISQAQVVL	15216
2QJK	AF	ELECTRON TRANSPORT	F	1.6	1.6	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15217
2QJK	DC	ELECTRON TRANSPORT	D	1.6	1.6	1	9	HSIQTWLLG	15218
2QJP	AF	ELECTRON TRANSPORT	A	1.6	1.6	1	15	QMSFWGATVITGLFG	15219
2QJP	BC	ELECTRON TRANSPORT	C	1.6	1.6	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	15220
2QJY	DC	OXIDOREDUCTASE	C	1.6	1.6	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15221
2QJY	DC	OXIDOREDUCTASE	D	1.6	1.6	1	17	QMSFWGATVITGLFGAI	15222
2QJY	GL	OXIDOREDUCTASE	G	1.6	1.6	1	17	QMSFWGATVITGLFGAI	15223

2QJY	MR	OXIDOREDUCTASE	R	1.6	1.6	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15224
2QJY	PO	OXIDOREDUCTASE	O	1.6	1.6	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15225
2QJY	PO	OXIDOREDUCTASE	P	1.6	1.6	1	17	QMSFWGATVITGLFGAI	15226
2QKI	DF	IMMUNE SYSTEM	F	1.6	1.6	1	5	KYELD	15227
2QL2	CB	TRANSCRIPTION/DNA	C	1.6	1.6	1	21	KLLILQQAVQVILGLEQQVRE	15228
2QR1	AG	TRANSFERASE	A	1.6	1.6	1	7	PHCKREG	15229
2QR1	AG	TRANSFERASE	A	1.6	1.6	1	14	FLDLCAMLVCKLFS	15230
2QTV	BD	PROTEIN TRANSPORT	B	1.6	1.6	1	13	FDEARVELDALFN	15231
2QVS	EB	TRANSFERASE/TRANSFERASE REGULATOR	B	1.6	1.6	1	5	LLFKN	15232
2R6G	AG	HYDROLASE/TRANSPORT PROTEIN	A	1.6	1.6	1	10	KSTLLRMIAG	15233
2R6G	AG	HYDROLASE/TRANSPORT PROTEIN	A	1.6	1.6	1	5	FGLKL	15234
2RAX	AF	CELL CYCLE	F	1.6	1.6	1	38	FLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	15235
2RAX	EB	CELL CYCLE	B	1.6	1.6	1	39	SFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL	15236
2RET	EF	PROTEIN TRANSPORT	F	1.6	1.6	1	16	SQERTARLNELQRALV	15237
2RGN	AB	SIGNALING PROTEIN COMPLEX	B	1.6	1.6	1	11	YFLQELQRCLK	15238
2RHS	AD	LIGASE	D	1.6	1.6	1	16	DRQHKTRTLKETLEGA	15239
2RHS	CD	LIGASE	D	1.6	1.6	1	15	LLPHLIEATAYNVAR	15240
2RI4	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.6	1.6	1	5	PWTQR	15241
2UUN	AB	ELECTRON TRANSPORT	B	1.6	1.6	1	13	ANKRLDAVNRITA	15242
2UUN	EF	ELECTRON TRANSPORT	F	1.6	1.6	1	13	ANKRLDAVNRITA	15243
2UY1	AB	RNA BINDING PROTEIN	A	1.6	1.6	1	14	SRMWDSMIEYEFMV	15244
2UZ1	AB	LYASE	B	1.6	1.6	1	10	IGEFDTLVRK	15245
2UZ1	DC	LYASE	C	1.6	1.6	1	6	GGFTNA	15246
2V46	CN	RIBOSOME	N	1.6	1.6	1	10	RICLRELAHK	15247
2V4J	AC	OXIDOREDUCTASE	C	1.6	1.6	1	8	LKEVYELF	15248
2V4J	AE	OXIDOREDUCTASE	A	1.6	1.6	1	8	FQKLLEVT	15249
2V4J	DB	OXIDOREDUCTASE	D	1.6	1.6	1	8	FQKLLEVT	15250
2V4J	DF	OXIDOREDUCTASE	F	1.6	1.6	1	9	VRILSKNTG	15251
2V5H	DI	TRANSCRIPTION	D	1.6	1.6	1	14	MIPKVDCCIRSLAQ	15252
2V7Q	HI	HYDROLASE	I	1.6	1.6	1	5	EFKAN	15253
2V8F	BC	PROTEIN BINDING	B	1.6	1.6	1	18	GGGLNKKAYSMAKYLRDS	15254
2VDC	CJ	OXIDOREDUCTASE	C	1.6	1.6	1	9	RFAAEILND	15255
2VDU	BE	TRANSFERASE	E	1.6	1.6	1	5	LPNFF	15256
2VGL	AS	PROTEIN TRANSPORT	A	1.6	1.6	1	15	PTFMGLALHCIANVG	15257
2VGX	AB	CHAPERONE	B	1.6	1.6	1	13	EQLYSLAFNQYQS	15258
2VHM	L3	RIBOSOME	3	1.6	1.6	1	6	SKGDLG	15259
2VJH	AB	PHOTOSYNTHESIS	A	1.6	1.6	1	9	GPLDEWGIS	15260
2VL2	AC	OXIDOREDUCTASE	A	1.6	1.6	1	5	VSIFG	15261

2VL2	BC	OXIDOREDUCTASE	B	1.6	1.6	1	11	AFVTGEWGRAH	15262
2VLH	AB	LYASE	B	1.6	1.6	1	16	GRDMEAMAIGLREAMQ	15263
2VML	GH	PHOTOSYNTHESIS	H	1.6	1.6	1	14	SNKRLDAVNAITGN	15264
2VML	GJ	PHOTOSYNTHESIS	J	1.6	1.6	1	25	NRRMAACLRDMEIILRYVSYALLAG	15265
2VML	IJ	PHOTOSYNTHESIS	J	1.6	1.6	1	14	SNKRLDAVNAITGN	15266
2VOF	AB	APOPTOSIS	A	1.6	1.6	1	7	DGFIKKF	15267
2VOF	CD	APOPTOSIS	C	1.6	1.6	1	6	KSYLDD	15268
2VOH	AB	APOPTOSIS	A	1.6	1.6	1	21	QACRVLQRVAFSVQKEVEKNL	15269
2VOY	HK	HYDROLASE	K	1.6	1.6	1	31	GRAIYNNMKQFIRYLISSNVGEVVCIFLTAA	15270
2VVL	FG	OXIDOREDUCTASE	F	1.6	1.6	1	10	SHVWREITRY	15271
2VXT	HL	CYTOKINE	L	1.6	1.6	1	6	SEQLTS	15272
2VXU	HL	IMMUNE SYSTEM	L	1.6	1.6	1	6	SEQLTS	15273
2VYR	AJ	IMMUNE SYSTEM	A	1.6	1.6	1	10	SPLYDMLRKN	15274
2W72	AB	OXYGEN TRANSPORT	B	1.6	1.6	1	21	PPVQAAYQKVVAGVANALAHK	15275
2W73	BL	METAL BINDING PROTEIN	B	1.6	1.6	1	9	YEEFVQMMT	15276
2W73	EM	METAL BINDING PROTEIN	E	1.6	1.6	1	29	FPEFLTMMARKMKDTDSEEEIREAFRVFD	15277
2W80	EF	IMMUNE SYSTEM	E	1.6	1.6	1	6	ENMRRP	15278
2WB1	BN	TRANSCRIPTION	N	1.6	1.6	1	6	RRMLLS	15279
2WB1	WR	TRANSCRIPTION	R	1.6	1.6	1	13	YAFKLLIQELMSM	15280
2WB1	WR	TRANSCRIPTION	W	1.6	1.6	1	6	FAYVMA	15281
2WEL	AD	TRANSFERASE	D	1.6	1.6	1	16	DTDSEEEIREAFRVFD	15282
2WH2	NU	RIBOSOME	U	1.6	1.6	1	5	DLAVR	15283
2WIN	BN	IMMUNE SYSTEM	N	1.6	1.6	1	21	TYYKRTIKISGQKAMYALKSK	15284
2WIN	CD	IMMUNE SYSTEM	C	1.6	1.6	1	7	KGVFVLN	15285
2WIN	KP	IMMUNE SYSTEM	P	1.6	1.6	1	24	FKKMSEAKYQLQKIYNEIDEALKS	15286
2WJV	BE	HYDROLASE	B	1.6	1.6	1	10	HIVNHLVRAK	15287
2WME	FE	OXIDOREDUCTASE	E	1.6	1.6	1	11	LDRAADIAVMA	15288
2WME	FE	OXIDOREDUCTASE	F	1.6	1.6	1	11	LDRAADIAVMA	15289
2YVJ	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.6	1.6	1	17	WSNAQNQGIAVARHLVD	15290
2Z2L	DE	BIOSYNTHETIC PROTEIN	D	1.6	1.6	1	5	MESSL	15291
2Z2S	CD	TRANSCRIPTION	D	1.6	1.6	1	17	DECRARAGALDAVGGSL	15292
2Z3R	GF	CYTOKINE/CYTOKINE RECEPTOR	G	1.6	1.6	1	19	ASIHDTVENLIILANNSLS	15293
2ZCY	IJ	HYDROLASE	J	1.6	1.6	1	13	YSGFYTFSLLDHH	15294
2ZCY	IY	HYDROLASE	Y	1.6	1.6	1	19	VEDALYLGKRSILAAAHRD	15295
2ZCY	RS	HYDROLASE	S	1.6	1.6	1	22	APDARVLSNYLRQQCNYSSLVF	15296
2ZME	AB	PROTEIN TRANSPORT	A	1.6	1.6	1	14	TERARQVLEHLLKE	15297
2ZOE	AB	TOXIN	A	1.6	1.6	1	5	KNFYF	15298
2ZON	AG	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.6	1.6	1	15	LAESYGDTVQVMRTL	15299

2ZU6	DE	HYDROLASE	E	1.6	1.6	1	10	HHELVYEAII	15300
2ZU6	FE	HYDROLASE	E	1.6	1.6	1	8	LKEYLLSG	15301
32C2	AB	IMMUNE SYSTEM	A	1.6	1.6	1	5	SEQLT	15302
3A0B	BD	ELECTRON TRANSPORT	B	1.6	1.6	1	9	VFALLFFFG	15303
3A0B	Bo	ELECTRON TRANSPORT	B	1.6	1.6	1	7	EKLAFYD	15304
3A0B	CK	ELECTRON TRANSPORT	C	1.6	1.6	1	12	GLIVFWAGAMTL	15305
3A0B	df	ELECTRON TRANSPORT	d	1.6	1.6	1	12	YLALGGWLTGTT	15306
3A0B	fj	ELECTRON TRANSPORT	j	1.6	1.6	1	15	MGVIVIVGLFFYGAY	15307
3A0B	LT	ELECTRON TRANSPORT	L	1.6	1.6	1	16	SLYLGLLLILVLALLF	15308
3B9J	JK	OXIDOREDUCTASE	J	1.6	1.6	1	10	TEIGIEMKFK	15309
3BIM	AI	TRANSCRIPTION REPRESSOR	A	1.6	1.6	1	7	GLFYSIF	15310
3BIM	CL	TRANSCRIPTION REPRESSOR	C	1.6	1.6	1	15	HASDVLLNLNRLRSR	15311
3BLW	AB	OXIDOREDUCTASE	A	1.6	1.6	1	15	SMYGTILGNIGAALI	15312
3BLW	IJ	OXIDOREDUCTASE	I	1.6	1.6	1	15	SMYGTILGNIGAALI	15313
3BZ1	AD	ELECTRON TRANSPORT	D	1.6	1.6	1	10	ISQEIRAAED	15314
3BZ1	HX	ELECTRON TRANSPORT	X	1.6	1.6	1	29	PSLKGFFIGLLSGAVVLGLTFAVLIAISQ	15315
3C1B	EF	STRUCTURAL PROTEIN/DNA	E	1.6	1.6	1	12	PKDIQLARRIRG	15316
3C1B	GH	STRUCTURAL PROTEIN/DNA	G	1.6	1.6	1	10	PRHLQLAVRN	15317
3C72	AB	TRANSFERASE	A	1.6	1.6	1	26	KRLEREQKLKLYQSATQAVFQKRQAG	15318
3C7B	AB	OXIDOREDUCTASE	A	1.6	1.6	1	8	IENEVVKL	15319
3C7K	AB	SIGNALING PROTEIN	B	1.6	1.6	1	12	HETRELTKTNLQ	15320
3C8G	CB	TRANSCRIPTION REGULATOR	B	1.6	1.6	1	11	IDVALRLIYAL	15321
3C91	CJ	HYDROLASE	J	1.6	1.6	1	22	VGDAQVLVRYMKAELELYRLQR	15322
3CDK	CD	TRANSFERASE	C	1.6	1.6	1	10	KIFERQFLSG	15323
3CF4	AG	OXIDOREDUCTASE	A	1.6	1.6	1	35	MKGHNGREFFLRVITGTACHAAHGRHLLDHLIEKY	15324
3CFK	JB	IMMUNE SYSTEM	J	1.6	1.6	1	7	DEQLKSG	15325
3CHX	AB	MEMBRANE PROTEIN	B	1.6	1.6	1	5	WPAIA	15326
3CHX	EF	MEMBRANE PROTEIN	F	1.6	1.6	1	5	WPAIA	15327
3CHX	IJ	MEMBRANE PROTEIN	J	1.6	1.6	1	5	WPAIA	15328
3CIP	AG	STRUCTURAL PROTEIN	A	1.6	1.6	1	9	QAVLSLYAS	15329
3CJH	CJ	PROTEIN TRANSPORT	C	1.6	1.6	1	15	ELVNKISENCFEKCL	15330
3CJI	AB	VIRUS	A	1.6	1.6	1	6	FNFYSL	15331
3CJT	MN	TRANSFERASE/RIBOSOMAL PROTEIN	N	1.6	1.6	1	8	VGPALGQH	15332
3CM8	AB	RNA BINDING PROTEIN/TRANSFERASE	A	1.6	1.6	1	22	PQLEGFSAESRKLLLIVQALRD	15333
3CUE	SV	PROTEIN TRANSPORT	S	1.6	1.6	1	24	NLAIQIADNFLRKVYCLYSDYVMK	15334
3CWB	NO	OXIDOREDUCTASE	N	1.6	1.6	1	8	AGYFVEHL	15335
3CXH	NP	OXIDOREDUCTASE	P	1.6	1.6	1	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	15336
3CXH	QS	OXIDOREDUCTASE	Q	1.6	1.6	1	17	VEEFFHLQHYLDTATAP	15337
3D69	LH	IMMUNE SYSTEM	L	1.6	1.6	1	6	SEELQA	15338
3D85	CD	IMMUNE SYSTEM/CYTOKINE	C	1.6	1.6	1	7	PQGLRDN	15339

3DA7	GH	PROTEIN BINDING	G	1.6	1.6	1	7	KSEAQAL	15340
3DAC	AB	CELL CYCLE	A	1.6	1.6	1	10	SPLYEMLKRN	15341
3DBJ	AB	PHOTOSYNTHESIS	A	1.6	1.6	1	25	EEMTATCLRDLDYYLRLVTYGIVAG	15342
3DCT	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	A	1.6	1.6	1	25	AEENFLILTEMATNHVQVLVEFTKK	15343
3DGG	AB	IMMUNE SYSTEM	A	1.6	1.6	1	5	SEQLT	15344
3DHR	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	1.6	1.6	1	20	PENFRLLGDILVIILAAHFG	15345
3DHW	EG	MEMBRANE PROTEIN/HYDROLASE	E	1.6	1.6	1	5	LLPEA	15346
3DIN	AC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	A	1.6	1.6	1	26	VEFKKETYYMFDEMMRRINDTIANYV	15347
3DL8	HF	PROTEIN TRANSPORT	F	1.6	1.6	1	21	LTKATYWLGALFLVLALLLSV	15348
3DQV	DY	LIGASE	D	1.6	1.6	1	18	TELEDLIPEVEEFYKKNH	15349
3DRA	AB	TRANSFERASE	A	1.6	1.6	1	14	HHVWSYRKWLVDTF	15350
3DUH	BD	IMMUNE SYSTEM/CYTOKINE	D	1.6	1.6	1	7	PQGLRDN	15351
3DWL	IK	STRUCTURAL PROTEIN	K	1.6	1.6	1	8	KFMQFLMG	15352
3DXA	AJ	IMMUNE SYSTEM	A	1.6	1.6	1	29	PEYWDRETQISKTNTQTYRENLRTALRYY	15353
3DXA	FJ	IMMUNE SYSTEM	F	1.6	1.6	1	29	PEYWDRETQISKTNTQTYRENLRTALRYY	15354
3E0J	AB	TRANSFERASE	A	1.6	1.6	1	9	EGEQCSAAH	15355
3E7S	AB	OXIDOREDUCTASE	A	1.6	1.6	1	5	WAWIV	15356
3EDX	CD	HYDROLASE	C	1.6	1.6	1	8	EKELLDSY	15357
3EJJ	AX	CYTOKINE/SIGNALING PROTEIN	A	1.6	1.6	1	18	PNANATERLQELSNNLNS	15358
3EOA	AB	IMMUNE SYSTEM/CELL ADHESION	A	1.6	1.6	1	5	DEQLK	15359
3EUB	JK	OXIDOREDUCTASE	K	1.6	1.6	1	7	KQVKSVA	15360
3EUB	KL	OXIDOREDUCTASE	L	1.6	1.6	1	8	PEKIRNAC	15361
3EUB	ST	OXIDOREDUCTASE	T	1.6	1.6	1	9	EIGIEMKFK	15362
3EUB	SU	OXIDOREDUCTASE	S	1.6	1.6	1	10	LLAYLRRKLG	15363
3EX7	EH	HYDROLASE/RNA BINDING PROTEIN/RNA	E	1.6	1.6	1	27	PEGLRVFYYLVQDLKCLVFSLIGLHFK	15364
3EXG	CD	OXIDOREDUCTASE	C	1.6	1.6	1	13	GQIFEAYNMAALW	15365
3EXG	GH	OXIDOREDUCTASE	G	1.6	1.6	1	13	GQIFEAYNMAALW	15366
3EXH	AB	OXIDOREDUCTASE	B	1.6	1.6	1	14	EMGFAGIAVGAAMA	15367
3EXH	AD	OXIDOREDUCTASE	D	1.6	1.6	1	5	VAQYD	15368
3EZQ	AB	APOPTOSIS	A	1.6	1.6	1	15	SDVDLSKYITTIAGV	15369
3EZQ	GH	APOPTOSIS	G	1.6	1.6	1	15	SDVDLSKYITTIAGV	15370
3EZQ	IJ	APOPTOSIS	I	1.6	1.6	1	15	SDVDLSKYITTIAGV	15371
3F9K	IK	VIRAL PROTEIN, RECOMBINATION	K	1.6	1.6	1	15	MDSRLQRIHAEIKNS	15372
3FBI	CD	TRANSCRIPTION	C	1.6	1.6	1	5	PYVKF	15373
3FBI	CD	TRANSCRIPTION	C	1.6	1.6	1	5	ALDYL	15374
3FFC	AG	IMMUNE SYSTEM	A	1.6	1.6	1	29	PEYWDRNTQIFKTNTQTDRESLRNLRGYY	15375

3FGC	AD	OXIDOREDUCTASE	D	1.6	1.6	1	18	NAQRKEYAGLYHEVAQAH	15376
3FKS	DG	HYDROLASE	G	1.6	1.6	1	18	IKNIEKITKTMKIVASTR	15377
3FKU	EB	VIRAL PROTEIN/IMMUNE SYSTEM	E	1.6	1.6	1	10	YEELKHLLSR	15378
3FKU	KH	VIRAL PROTEIN/IMMUNE SYSTEM	K	1.6	1.6	1	10	YEELKHLLSR	15379
3FLO	CD	TRANSFERASE	C	1.6	1.6	1	15	LDELFLKLFTPILKT	15380
3FWC	BD	CELL CYCLE, TRANSCRIPTION	D	1.6	1.6	1	11	KSQIQQYLVES	15381
3FWC	MN	CELL CYCLE, TRANSCRIPTION	M	1.6	1.6	1	12	YHELKVAMKALG	15382
3G43	DF	METAL BINDING PROTEIN	D	1.6	1.6	1	12	DEEVDEMIREAD	15383
3G6J	AB	IMMUNE SYSTEM	A	1.6	1.6	1	7	KGVFVLN	15384
3G9K	LS	HYDROLASE	L	1.6	1.6	1	9	LDLAKPRIY	15385
3GBM	HL	VIRAL PROTEIN / IMMUNE SYSTEM	L	1.6	1.6	1	6	SEELQA	15386
3GE8	AB	OXIDOREDUCTASE	A	1.6	1.6	1	8	LEGALKYM	15387
3GE8	DG	OXIDOREDUCTASE	D	1.6	1.6	1	7	IVDRFLA	15388
3GHG	GH	BLOOD CLOTTING	G	1.6	1.6	1	16	LKDYEDQQKQLEQVIA	15389
3GLH	IJ	TRANSFERASE	I	1.6	1.6	1	15	RRMGVEMTLLRALAF	15390
3H0L	AB	LIGASE	A	1.6	1.6	1	11	IIAPSEASSNL	15391
3H0L	DE	LIGASE	D	1.6	1.6	1	19	YLKAQKVRRLITNDFLKAF	15392
3H0L	GH	LIGASE	G	1.6	1.6	1	15	PEVKRRIMLGTFALS	15393
3H0L	VW	LIGASE	V	1.6	1.6	1	15	PEVKRRIMLGTFALS	15394
3HE7	CD	IMMUNE SYSTEM	D	1.6	1.6	1	8	EAEISHTQ	15395
3HGK	DF	TRANSFERASE	D	1.6	1.6	1	7	PEYFIKG	15396
3HH2	BC	SIGNALING PROTEIN/CYTOKINE	C	1.6	1.6	1	10	DNTLFKWMIF	15397
3HKI	DE	HYDROLASE	D	1.6	1.6	1	5	EKTFG	15398
3HKZ	AC	TRANSFERASE	A	1.6	1.6	1	9	DVNRIFERV	15399
3HKZ	HK	TRANSFERASE	K	1.6	1.6	1	10	HFNEVFISLW	15400
3HOU	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.6	1.6	1	8	EGTALSRL	15401
3HOU	DG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	D	1.6	1.6	1	17	EARLVIKEALVERRRAF	15402
3HOU	MD	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.6	1.6	1	8	PEEVRAIS	15403
3HOY	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	1.6	1.6	1	12	HTLGNLIRAELL	15404
3HPG	AH	TRANSFERASE	A	1.6	1.6	1	15	GQEFRVQTMKWYAMF	15405
3HRW	AB	OXYGEN TRANSPORT	B	1.6	1.6	1	10	VGGEALGRLL	15406
4RUB	BT	LYASE(CARBON-CARBON)	B	1.6	1.6	1	21	NAPGAVANRVALEACVKARNE	15407
7CEI	AB	IMMUNE SYSTEM	B	1.6	1.6	1	9	RNNNDRMKV	15408
1A9W	AE	OXYGEN TRANSPORT	E	1.5	1.5	1	16	VEEAGGEALGRLLVVY	15409
1A9W	AF	OXYGEN TRANSPORT	F	1.5	1.5	1	20	PENFKLLGNVMVIILATHFG	15410
1AD0	CD	IMMUNOGLOBULIN	C	1.5	1.5	1	7	DEQLKSG	15411

1AHJ	AB	LYASE	A	1.5	1.5	1	5	WPILG	15412
1AHJ	AB	LYASE	B	1.5	1.5	1	7	PRHYMMT	15413
1AHJ	EF	LYASE	E	1.5	1.5	1	5	WPILG	15414
1AJS	AB	AMINOTRANSFERASE	B	1.5	1.5	1	15	GTGALRIGAEFLARW	15415
1AJS	AB	AMINOTRANSFERASE	B	1.5	1.5	1	12	PVVRKVEQRIAN	15416
1AL0	1F	VIRUS	1	1.5	1.5	1	13	RSRARRCVEACVY	15417
1AQD	GH	COMPLEX (MHC PROTEIN/ANTIGEN)	H	1.5	1.5	1	10	RPDAEYWNSQ	15418
1AW8	BE	DECARBOXYLASE	E	1.5	1.5	1	5	AAAHC	15419
1AZZ	BC	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.5	1.5	1	9	LDWIQTQTG	15420
1B33	HI	PHOTOSYNTHESIS	H	1.5	1.5	1	13	PGELDRIKSFVSS	15421
1B33	LO	PHOTOSYNTHESIS	L	1.5	1.5	1	7	TPIEEIG	15422
1B35	AC	VIRUS	C	1.5	1.5	1	6	LSRVLS	15423
1BB1	BC	DE NOVO PROTEIN DESIGN	B	1.5	1.5	1	33	KIAAIKEEQAAIEEEIQAIKEEIAAIKYLIAQI	15424
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.5	1.5	1	8	RDVQMALH	15425
1BGY	CF	ELECTRON TRANSPORT	C	1.5	1.5	1	33	HPYITIGQLASVLYFLLILVLMPTAGTIENKLL	15426
1BGY	JK	ELECTRON TRANSPORT	J	1.5	1.5	1	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	15427
1BJ1	LH	COMPLEX (ANTIBODY/ANTIGEN)	L	1.5	1.5	1	7	DEQLKSG	15428
1C9B	QR	TRANSCRIPTION/DNA	Q	1.5	1.5	1	7	FKEICAV	15429
1CC1	SL	OXIDOREDUCTASE	L	1.5	1.5	1	11	VNVGRLVRSYD	15430
1CDL	CG	CALCIUM-BINDING PROTEIN	C	1.5	1.5	1	12	DEEVDEMIREAD	15431
1CLO	LH	IMMUNOGLOBULIN	L	1.5	1.5	1	6	SEQLTS	15432
1CT8	AB	IMMUNE SYSTEM	A	1.5	1.5	1	6	SEQLTS	15433
1D3B	AB	RNA BINDING PROTEIN	A	1.5	1.5	1	8	PIKVLHEA	15434
1D4M	14	VIRUS	1	1.5	1.5	1	6	VENFLG	15435
1DFL	BW	CONTRACTILE PROTEIN	B	1.5	1.5	1	13	QDQRIGLSVIQRN	15436
1DII	BD	OXIDOREDUCTASE	D	1.5	1.5	1	14	GKNLYDKVCGHCHK	15437
1DIO	AG	LYASE	G	1.5	1.5	1	7	LENVLSN	15438
1DKF	AB	HORMONE/GROWTH FACTOR RECEPTOR	A	1.5	1.5	1	15	RLPALRSIGLKCLEH	15439
1DOW	AB	CELL ADHESION	A	1.5	1.5	1	18	RAARALLSAVTRLLILAD	15440
1E3A	AB	ANTIBIOTIC RESISTANCE	A	1.5	1.5	1	6	KQFNTF	15441
1E7P	BC	OXIDOREDUCTASE	B	1.5	1.5	1	6	GTKIMR	15442
1E7P	EF	OXIDOREDUCTASE	E	1.5	1.5	1	6	GTKIMR	15443
1E7P	HI	OXIDOREDUCTASE	H	1.5	1.5	1	6	GTKIMR	15444
1E7P	KL	OXIDOREDUCTASE	K	1.5	1.5	1	6	GTKIMR	15445
1EF1	AC	MEMBRANE PROTEIN	A	1.5	1.5	1	7	QRVLEQH	15446
1EJH	AE	TRANSLATION	A	1.5	1.5	1	15	DLDRFWLETLLCLIG	15447
1EJM	EB	HYDROLASE/INHIBITOR	B	1.5	1.5	1	8	AEDCLRTC	15448

1EQZ	GH	STRUCTURAL PROTEIN/DNA	H	1.5	1.5	1	11	AMDVVYALKRQ	15449
1EYS	MH	ELECTRON TRANSPORT	M	1.5	1.5	1	13	AAEGAALFWRWTM	15450
1F3D	JK	IMMUNE SYSTEM	J	1.5	1.5	1	5	SEQLT	15451
1F66	BD	STRUCTURAL PROTEIN/DNA	D	1.5	1.5	1	12	SREIQTAVRLLL	15452
1F80	CF	TRANSFERASE	C	1.5	1.5	1	23	EARKNEFLAGRFAAKEAFSKAFG	15453
1FDH	AG	OXYGEN TRANSPORT	A	1.5	1.5	1	21	PAVHASLDKFLASVSTVLTSK	15454
1FHJ	AD	OXYGEN STORAGE/TRANSPORT	D	1.5	1.5	1	20	PENFKLLGNVLVCVLAHHFG	15455
1FHJ	CB	OXYGEN STORAGE/TRANSPORT	B	1.5	1.5	1	20	PENFKLLGNVLVCVLAHHFG	15456
1FL5	LH	IMMUNE SYSTEM	L	1.5	1.5	1	6	DEQLKS	15457
1FNT	BI	HYDROLASE/HYDROLASE ACTIVATOR	I	1.5	1.5	1	23	AADTEAVTQLIGSNIELHSLYTS	15458
1FNT	Ub	HYDROLASE/HYDROLASE ACTIVATOR	b	1.5	1.5	1	20	ISDMQHIERLLKDLVTENAY	15459
1FOE	AB	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	A	1.5	1.5	1	12	KYPLLLRELFAL	15460
1FQV	EF	LIGASE	E	1.5	1.5	1	10	DELLLGIFSC	15461
1FYZ	BD	OXIDOREDUCTASE	D	1.5	1.5	1	12	KSARLAVEGLWQ	15462
1FYZ	DF	OXIDOREDUCTASE	F	1.5	1.5	1	21	DYLWIEAKLEEKVAVLKARAF	15463
1G0U	1N	HYDROLASE	N	1.5	1.5	1	6	SGSTFI	15464
1G0U	H1	HYDROLASE	H	1.5	1.5	1	9	SLAAMAVLE	15465
1G0U	LM	HYDROLASE	L	1.5	1.5	1	21	AADGDALVKRFKNSVKWYHFD	15466
1G0U	VM	HYDROLASE	V	1.5	1.5	1	9	SLAAMAVLE	15467
1G0U	WX	HYDROLASE	W	1.5	1.5	1	22	ATDVTTLNEMFRYKTNLYKLKE	15468
1G20	CB	OXIDOREDUCTASE	C	1.5	1.5	1	16	FDGFAIFARDMDMTLN	15469
1G20	CD	OXIDOREDUCTASE	C	1.5	1.5	1	12	GYEFEEFVKRIK	15470
1G8K	AB	OXIDOREDUCTASE	A	1.5	1.5	1	11	PSVAIARHVAG	15471
1G8K	GH	OXIDOREDUCTASE	G	1.5	1.5	1	11	PSVAIARHVAG	15472
1G9M	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.5	1.5	1	7	DEQLKSG	15473
1GCV	CB	OXYGEN STORAGE/TRANSPORT	C	1.5	1.5	1	7	PGSKSYF	15474
1GH0	AB	PHOTOSYNTHESIS	B	1.5	1.5	1	14	SNKRLDVVNRITSN	15475
1GH0	SR	PHOTOSYNTHESIS	S	1.5	1.5	1	17	DAAVEANSYLDYAINAL	15476
1GH0	UP	PHOTOSYNTHESIS	P	1.5	1.5	1	16	ASTIVSNAARSLFAEQ	15477
1GH0	WT	PHOTOSYNTHESIS	T	1.5	1.5	1	25	SRRMAACLRDMEIILRYVTYAVFAG	15478
1GO3	EF	TRANSFERASE	F	1.5	1.5	1	8	LDDLRAIY	15479
1H1L	AB	OXIDOREDUCTASE	A	1.5	1.5	1	6	ERDIVF	15480
1H1L	AB	OXIDOREDUCTASE	A	1.5	1.5	1	12	DAWASRILLEEM	15481
1H1L	CB	OXIDOREDUCTASE	C	1.5	1.5	1	16	YDGFAIFARDMDMTLN	15482
1H5R	AB	TRANSFERASE	A	1.5	1.5	1	19	HQSLIEASNFIATIEERQG	15483
1H5R	CB	TRANSFERASE	C	1.5	1.5	1	8	PEEIAFRK	15484
1H5R	CB	TRANSFERASE	C	1.5	1.5	1	10	NYGQYLYKMT	15485
1H6K	AX	NUCLEAR PROTEIN	A	1.5	1.5	1	15	DVMYTTLLIELCKLQ	15486
1H6K	AX	NUCLEAR PROTEIN	A	1.5	1.5	1	17	TTCVDRFINWFSHHLSN	15487

1H6K	CZ	NUCLEAR PROTEIN	C	1.5	1.5	1	15	DVMYTTLLIELCKLQ	15488
1HBM	DB	METHANOGENESIS	D	1.5	1.5	1	12	EDQAETLKAEVG	15489
1HC9	AC	TOXIN/PEPTIDE	A	1.5	1.5	1	5	CSSRG	15490
1HMV	AB	NUCLEOTIDYLTRANSFERASE	A	1.5	1.5	1	21	DVKQLTEAVQKITTESIVIWG	15491
1HMV	CD	NUCLEOTIDYLTRANSFERASE	C	1.5	1.5	1	21	DVKQLTEAVQKITTESIVIWG	15492
1HMV	CD	NUCLEOTIDYLTRANSFERASE	D	1.5	1.5	1	18	VNDIQKLVGKLNWASQIY	15493
1HMV	EF	NUCLEOTIDYLTRANSFERASE	E	1.5	1.5	1	21	DVKQLTEAVQKITTESIVIWG	15494
1HMV	GH	NUCLEOTIDYLTRANSFERASE	G	1.5	1.5	1	21	DVKQLTEAVQKITTESIVIWG	15495
1HR0	LQ	RIBOSOME	L	1.5	1.5	1	8	INQLVRKG	15496
1HR8	EF	HYDROLASE	E	1.5	1.5	1	11	GRAMAETLELL	15497
1HR8	EF	HYDROLASE	F	1.5	1.5	1	11	QQGIELEIENI	15498
1HV4	CB	OXYGEN STORAGE/TRANSPORT	C	1.5	1.5	1	19	PVNFKFLGHCFLVVVAIHH	15499
1HVU	AE	TRANSFERASE/RNA	A	1.5	1.5	1	5	FRKYT	15500
1HVU	DB	TRANSFERASE/RNA	D	1.5	1.5	1	5	FRKYT	15501
1HYR	AC	IMMUNE SYSTEM	C	1.5	1.5	1	20	DRETRDLTGNGKDLRMTLAH	15502
1I3O	DF	APOPTOSIS	F	1.5	1.5	1	8	HADYLLRT	15503
1I51	CD	HYDROLASE/HYDROLASE INHIBITOR	C	1.5	1.5	1	16	TDKDAEALFKCFRSLG	15504
1I7W	CD	CELL ADHESION	C	1.5	1.5	1	8	DDAELATR	15505
1IAI	LH	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)	L	1.5	1.5	1	7	SEQLTSG	15506
1IB1	DH	SIGNALING PROTEIN/TRANSFERASE	H	1.5	1.5	1	17	AAGVFEIEREAFISVSG	15507
1IBL	CN	RIBOSOME	N	1.5	1.5	1	11	RICLRELAHKG	15508
1IBR	CD	CELL CYCLE, TRANSLATION	D	1.5	1.5	1	18	RLELEAAQKFLERAAVEN	15509
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.5	1.5	1	9	YEEFVQMMT	15510
1IR2	HP	LYASE	P	1.5	1.5	1	14	DEQIAAQVDYIVAN	15511
1IR2	S1	LYASE	S	1.5	1.5	1	10	PELAAACEVW	15512
1IRE	AB	LYASE	B	1.5	1.5	1	6	PAEYLE	15513
1IRU	AI	HYDROLASE	I	1.5	1.5	1	23	AADTDMTTQLISSNLELHSLSTG	15514
1IRU	BJ	HYDROLASE	J	1.5	1.5	1	14	PYTLMSMVANLLYE	15515
1IRU	PX	HYDROLASE	P	1.5	1.5	1	23	GPDYRVLVHRARKLAQQYYLVYQ	15516
1IRU	QY	HYDROLASE	Y	1.5	1.5	1	17	PTAAANFTRRNLADCLR	15517
1IRU	RY	HYDROLASE	Y	1.5	1.5	1	22	AGDTVQFAEYIQKNVQLYKMRN	15518
1IRU	WN	HYDROLASE	N	1.5	1.5	1	15	YGAYLAQPLLREVLE	15519
1IW7	AC	TRANSFERASE	A	1.5	1.5	1	5	AEKHG	15520
1IW7	AC	TRANSFERASE	C	1.5	1.5	1	14	KREVEVLRRAEKLG	15521
1IW7	BD	TRANSFERASE	D	1.5	1.5	1	7	EEALAAH	15522
1IW7	MP	TRANSFERASE	P	1.5	1.5	1	12	AMVLKLRKGLID	15523
1IW7	NO	TRANSFERASE	O	1.5	1.5	1	12	EDRLQKEMERIY	15524
1IWA	ED	LYASE	D	1.5	1.5	1	13	DEQIKKQIDYMIS	15525

1IWP	AG	LYASE	G	1.5	1.5	1	7	LEKVLSG	15526
1IWP	LM	LYASE	L	1.5	1.5	1	17	EDIASNILNMLRQRVTG	15527
1J1D	AC	CONTRACTILE PROTEIN	A	1.5	1.5	1	11	PEELQEMIDEV	15528
1J7V	LR	CYTOKINE/RECEPTOR	L	1.5	1.5	1	8	KTFFQMKD	15529
1J9C	TL	BLOOD CLOTTING	T	1.5	1.5	1	7	TDEIVKD	15530
1JB0	AF	PHOTOSYNTHESIS	A	1.5	1.5	1	18	RGYWQELIESIVWAHNKL	15531
1JD2	EF	HYDROLASE	E	1.5	1.5	1	15	VERAGHLLCDKAQKN	15532
1JD2	EF	HYDROLASE	F	1.5	1.5	1	22	IPDGRHLVNRGREEAASFKKLY	15533
1JD2	JR	HYDROLASE	J	1.5	1.5	1	13	YSGFYTFSLLDHH	15534
1JD2	JR	HYDROLASE	J	1.5	1.5	1	18	TEEGLDLLKLCVQELEKR	15535
1JD2	PK	HYDROLASE	K	1.5	1.5	1	11	QTFAYGVLDSN	15536
1JD2	TN	HYDROLASE	T	1.5	1.5	1	14	FGAHMANPLLRKVV	15537
1JD2	WX	HYDROLASE	X	1.5	1.5	1	13	FQVEYALEAVKRG	15538
1JEY	AB	DNA BINDING PROTEIN/DNA	B	1.5	1.5	1	19	PFEQAKKVITMFVQRQVFA	15539
1JEY	AB	DNA BINDING PROTEIN/DNA	B	1.5	1.5	1	7	QHIWNML	15540
1JNR	AB	OXIDOREDUCTASE	A	1.5	1.5	1	21	EDLVADYARHVDGTVHLFEKW	15541
1JNR	CD	OXIDOREDUCTASE	C	1.5	1.5	1	21	EDLVADYARHVDGTVHLFEKW	15542
1JSU	AB	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.5	1.5	1	17	LQLVGTAAMLLASKFEE	15543
1JY7	PQ	OXYGEN STORAGE/TRANSPORT	P	1.5	1.5	1	19	PAVHASLDKFLASVSTVLT	15544
1JY7	RQ	OXYGEN STORAGE/TRANSPORT	R	1.5	1.5	1	16	PVNFKLLSHCLLVTLA	15545
1JY7	WX	OXYGEN STORAGE/TRANSPORT	W	1.5	1.5	1	16	PVNFKLLSHCLLVTLA	15546
1K5D	AB	SIGNALING PROTEIN/SIGNALING ACTIVATOR	A	1.5	1.5	1	7	YEHDLEV	15547
1K5D	GH	SIGNALING PROTEIN/SIGNALING ACTIVATOR	G	1.5	1.5	1	12	KPFLWLARKLIG	15548
1K6L	LH	PHOTOSYNTHESIS	L	1.5	1.5	1	5	ERKYR	15549
1K6L	LM	PHOTOSYNTHESIS	M	1.5	1.5	1	17	HTAWAFLSAIWLWMVLG	15550
1K7L	CD	TRANSCRIPTION	C	1.5	1.5	1	8	PLLQEIYR	15551
1KEG	LH	IMMUNE SYSTEM/DNA	L	1.5	1.5	1	6	SEQLTS	15552
1KF6	MN	OXIDOREDUCTASE	N	1.5	1.5	1	7	PAQMAKY	15553
1KF6	ND	OXIDOREDUCTASE	D	1.5	1.5	1	20	GKWVFYGLAAILTVVTLIGV	15554
1KF6	OP	OXIDOREDUCTASE	O	1.5	1.5	1	26	PEPIIKSLWAVTVVATIVILFVALYW	15555
1KFU	LS	HYDROLASE	S	1.5	1.5	1	11	IDTCRSMVAVM	15556
1KFY	AB	OXIDOREDUCTASE	A	1.5	1.5	1	13	TGFHMLHTLFQTS	15557
1KFY	AB	OXIDOREDUCTASE	B	1.5	1.5	1	12	PAAITLAHRYNE	15558
1KFY	BD	OXIDOREDUCTASE	D	1.5	1.5	1	25	VFWGLFGAGGMWSAIIAPVMILLVG	15559
1KKQ	AE	TRANSCRIPTION	E	1.5	1.5	1	7	EAIIRKA	15560
1KLI	LH	HYDROLASE	H	1.5	1.5	1	6	RTFSER	15561
1KTK	AE	IMMUNE SYSTEM	A	1.5	1.5	1	10	VKSDLLYAYT	15562

1KX4	BD	STRUCTURAL PROTEIN/DNA	D	1.5	1.5	1	12	SREIQTAVRLLL	15563
1KX4	EC	STRUCTURAL PROTEIN/DNA	E	1.5	1.5	1	11	TVALREIRRYQ	15564
1KX4	EF	STRUCTURAL PROTEIN/DNA	F	1.5	1.5	1	11	AMDVVYALKRQ	15565
1KYO	AC	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.5	1.5	1	5	FRKSN	15566
1KYO	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.5	1.5	1	15	IELAFSSVEHIMRDV	15567
1KYO	DI	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.5	1.5	1	19	HASIRRGYQVYREVCAACH	15568
1KYO	NE	OXIDOREDUCTASE/ELECTRON TRANSPORT	E	1.5	1.5	1	30	KGRSYAYFMVGAMGLLSSAGAKSTVETFIS	15569
1KYO	RS	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.5	1.5	1	21	EDESYARAYRIIRAHQTELTH	15570
1KZ7	CD	SIGNALING PROTEIN	C	1.5	1.5	1	21	AEDLQEALSSILGILKAVNDS	15571
1L5G	AB	CELL ADHESION	B	1.5	1.5	1	11	VNLYQNYSELI	15572
1L9J	RS	PHOTOSYNTHESIS	S	1.5	1.5	1	26	MEGIHRWAIWMAVLVTLTGGIGILLS	15573
1LB1	EF	SIGNALING PROTEIN	E	1.5	1.5	1	39	EEESLAILRRHVMNELLDTERAYVEELLCVLEGYAAEMD	15574
1LIA	AB	LIGHT HARVESTING PROTEIN	A	1.5	1.5	1	9	GPLDEWGIA	15575
1LQ8	EF	BLOOD CLOTTING	E	1.5	1.5	1	14	PVSISMSLAMLSLG	15576
1LQS	SM	IMMUNE SYSTEM	M	1.5	1.5	1	5	KPTLQ	15577
1LT4	DA	ENTEROTOXIN	A	1.5	1.5	1	30	DTCNEETQNLSTIYLREYQSKVKRQIFSDY	15578
1LVC	AD	LYASE	A	1.5	1.5	1	6	SAEFIK	15579
1M1Y	AB	OXIDOREDUCTASE	A	1.5	1.5	1	6	CPIGLI	15580
1M1Y	KL	OXIDOREDUCTASE	K	1.5	1.5	1	6	EKDIVF	15581
1M1Y	KL	OXIDOREDUCTASE	L	1.5	1.5	1	11	LWHLRSLVFTD	15582
1M63	AB	HYDROLASE/ISOMERASE	B	1.5	1.5	1	8	FEEFCAVV	15583
1M63	EF	HYDROLASE/ISOMERASE	F	1.5	1.5	1	5	EEFCA	15584
1MI5	AE	IMMUNE SYSTEM	A	1.5	1.5	1	29	PEYWDRNTQIFKTNTQTDRESLRNLRGYY	15585
1MJG	DP	OXIDOREDUCTASE	D	1.5	1.5	1	30	PVNLVFSAIRVALADYTGEHIATDFSDILF	15586
1MMO	BG	OXIDOREDUCTASE (MONOOXYGENASE)	B	1.5	1.5	1	10	WNESAFSVHA	15587
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	H	1.5	1.5	1	6	EVDFRH	15588
1MVW	MO	CONTRACTILE PROTEIN	O	1.5	1.5	1	10	ASQVGDIARA	15589
1MZN	EF	TRANSCRIPTION	E	1.5	1.5	1	22	PVTNICQAADKQLFTLVEWAKR	15590
1N1J	AB	DNA BINDING PROTEIN	A	1.5	1.5	1	11	GEDILFAMSTL	15591
1N2D	AC	CELL CYCLE	A	1.5	1.5	1	10	YKKFIEDVLR	15592
1N4Q	AB	TRANSFERASE	A	1.5	1.5	1	15	YQVWHHRRVLVEWLK	15593
1N4Q	AB	TRANSFERASE	A	1.5	1.5	1	17	PYLIAFLVDIYEDMLEN	15594
1N4Q	CD	TRANSFERASE	C	1.5	1.5	1	15	YQVWHHRRVLVEWLK	15595

1N4Q	CD	TRANSFERASE	C	1.5	1.5	1	17	PYLIAFLVDIYEDMLEN	15596
1N4Q	EF	TRANSFERASE	E	1.5	1.5	1	15	YQVWHHRRVLVEWLK	15597
1N4Q	IJ	TRANSFERASE	I	1.5	1.5	1	15	YQVWHHRRVLVEWLK	15598
1N4Q	KL	TRANSFERASE	K	1.5	1.5	1	15	YQVWHHRRVLVEWLK	15599
1N73	EF	BLOOD CLOTTING	F	1.5	1.5	1	5	TTANK	15600
1NBU	BC	LYASE	B	1.5	1.5	1	15	IETVGAEIADHVMDD	15601
1NBW	CD	HYDROLASE	C	1.5	1.5	1	15	FLDAVWWLNEALDRG	15602
1NEK	BD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.5	1.5	1	27	GVHDFILVRATAIVLTLYIIYMVGFFA	15603
1NEX	AB	LIGASE, CELL CYCLE	B	1.5	1.5	1	5	LITSL	15604
1NF5	CD	TRANSFERASE/TRANSFERASE	C	1.5	1.5	1	12	LLEWACVLFHTS	15605
1NSN	HS	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)	S	1.5	1.5	1	12	HLRKSEAQAKKE	15606
1NT2	AB	RNA BINDING PROTEIN	B	1.5	1.5	1	20	MARFLAAKLAIAAKIDYFRG	15607
1O96	EF	ELECTRON TRANSFER	E	1.5	1.5	1	11	STGISVASYLN	15608
1O96	QZ	ELECTRON TRANSFER	Q	1.5	1.5	1	11	STGISVASYLN	15609
1OCC	AT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.5	1.5	1	17	YMGMVWAMMSIGFLGFI	15610
1OCC	NG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.5	1.5	1	17	YMGMVWAMMSIGFLGFI	15611
1OEY	DM	IMMUNE SYSTEM	M	1.5	1.5	1	6	DEDVAL	15612
1OL5	AB	TRANSFERASE/CELL CYCLE	A	1.5	1.5	1	21	EQRTATYITELANALSYCHSK	15613
1OSP	LH	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN)	L	1.5	1.5	1	6	SEQLTS	15614
1OYV	BI	HYDROLASE	B	1.5	1.5	1	14	YSGIVSGIEWATTN	15615
1P4E	BD	DNA BINDING PROTEIN/RECOMBINATION/DNA	B	1.5	1.5	1	12	PKVLVRQFVERF	15616
1P7T	AB	LYASE	B	1.5	1.5	1	17	RATLRISSQHIANWLRH	15617
1P8D	BD	MEMBRANE PROTEIN/PROTEIN BINDING	B	1.5	1.5	1	8	PLLSEIWD	15618
1PIV	34	VIRUS	4	1.5	1.5	1	6	PSKFTE	15619
1Q16	AB	OXIDOREDUCTASE	A	1.5	1.5	1	7	LLMLTLG	15620
1Q90	BC	PHOTOSYNTHESIS	B	1.5	1.5	1	17	QVGYWAVKIVTGVPDAI	15621
1QLE	AB	OXIDOREDUCTASE/IMMUNE SYSTEM	A	1.5	1.5	1	5	LSTTE	15622
1QVF	FL	RIBOSOME	L	1.5	1.5	1	15	QIAELMWHRMQEWRN	15623
1QVF	RU	RIBOSOME	U	1.5	1.5	1	24	PAEREAELDDLKTELLNARAVQAA	15624
1R1K	DA	HORMONE/GROWTH FACTOR RECEPTOR	A	1.5	1.5	1	19	RLPALRSISLKSFEHLFFF	15625
1R27	AB	OXIDOREDUCTASE	A	1.5	1.5	1	18	RSQIIRIAREFADNADKT	15626
1R4M	CD	CELL CYCLE	C	1.5	1.5	1	5	LVLPG	15627

1R4M	CD	CELL CYCLE	D	1.5	1.5	1	9	YRLTQGVVK	15628
1R4M	EF	CELL CYCLE	E	1.5	1.5	1	5	LVLPG	15629
1R4M	GH	CELL CYCLE	G	1.5	1.5	1	5	LVLPG	15630
1R4M	GH	CELL CYCLE	H	1.5	1.5	1	9	YRLTQGVVK	15631
1R4P	AD	TOXIN	D	1.5	1.5	1	13	WNLQPLLQSAQLT	15632
1R8U	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	B	1.5	1.5	1	19	AHCASSRQIISHWKNCTRH	15633
1RD8	EB	VIRAL PROTEIN	E	1.5	1.5	1	8	YEELREQL	15634
1RH5	AB	PROTEIN TRANSPORT	A	1.5	1.5	1	19	YIAPIIGTIIVFLMVVYAE	15635
1RHI	14	VIRUS	1	1.5	1.5	1	5	VESFL	15636
1RI8	AB	IMMUNE SYSTEM/HYDROLASE	B	1.5	1.5	1	8	VAWRNRCK	15637
1RIW	AC	HYDROLASE/BLOOD CLOTTING	A	1.5	1.5	1	8	ERELLESY	15638
1RU7	KJ	VIRAL PROTEIN	J	1.5	1.5	1	52	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEK VKSQL	15639
1RUZ	LM	VIRAL PROTEIN	M	1.5	1.5	1	7	KVKSQLK	15640
1RYP	GH	MULTICATALYTIC PROTEINASE	G	1.5	1.5	1	22	IPDGRHLVNRGREEAASFKKLY	15641
1RYP	I2	MULTICATALYTIC PROTEINASE	2	1.5	1.5	1	14	FGAHMANPLLRKVV	15642
1RYP	JK	MULTICATALYTIC PROTEINASE	K	1.5	1.5	1	14	YSGFYTFSLLDHHY	15643
1RYP	XY	MULTICATALYTIC PROTEINASE	Y	1.5	1.5	1	13	YSGFYTFSLLDHH	15644
1RZR	AS	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	S	1.5	1.5	1	10	RPATTLVQAA	15645
1S5L	HX	PHOTOSYNTHESIS	X	1.5	1.5	1	30	SLKGFFIGLLSGAVVLGLTFAVLIAISQID	15646
1S5L	hx	PHOTOSYNTHESIS	x	1.5	1.5	1	30	SLKGFFIGLLSGAVVLGLTFAVLIAISQID	15647
1SCT	CB	OXYGEN TRANSPORT	B	1.5	1.5	1	15	ADQKDLLRMSWGVLS	15648
1SQB	AC	OXIDOREDUCTASE	A	1.5	1.5	1	7	YNRIRSG	15649
1SQB	BI	OXIDOREDUCTASE	B	1.5	1.5	1	19	NPDVQAAKNKLKAGYLMSV	15650
1SQB	DH	OXIDOREDUCTASE	H	1.5	1.5	1	20	TEELLDFLHARDHCVAHKLF	15651
1SQX	CD	OXIDOREDUCTASE	D	1.5	1.5	1	6	SYIVRA	15652
1SQX	CE	OXIDOREDUCTASE	C	1.5	1.5	1	29	GWIIRYMHANGASMFFICLYMHVGRGLYY	15653
1SXJ	BC	REPLICATION	C	1.5	1.5	1	6	IDVVRN	15654
1SY9	AB	CALCIUM-BINDING PROTEIN	A	1.5	1.5	1	12	TKELGTVMRSLG	15655
1SY9	AB	CALCIUM-BINDING PROTEIN	A	1.5	1.5	1	15	EEQIAEFKEAFSLFD	15656
1SYX	AB	TRANSLATION/IMMUNE SYSTEM	A	1.5	1.5	1	17	KQEMVDIIETVYRGARK	15657
1TB6	LH	HYDROLASE/BLOOD CLOTTING	H	1.5	1.5	1	9	KKWIQKVID	15658
1TCO	AB	COMPLEX (HYDROLASE/ISOMERASE)	B	1.5	1.5	1	13	NGELFQVLKMMVG	15659
1TFO	AB	TOXIN/TOXIN INHIBITOR	A	1.5	1.5	1	7	RKQLDKK	15660
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	1.5	1.5	1	16	QRLVQNCLWTLRNLSD	15661
1TI2	IJ	OXIDOREDUCTASE	I	1.5	1.5	1	14	ACEIRALARQWAKK	15662
1TI2	IJ	OXIDOREDUCTASE	J	1.5	1.5	1	6	RCAHNC	15663

1TIL	EF	TRANSCRIPTION	E	1.5	1.5	1	23	MDELTEIKTVVSEAVTNAIIHGY	15664
1TPX	AC	UNKNOWN FUNCTION	A	1.5	1.5	1	24	QNNFVHDCVNITVKQHTVTTTTKG	15665
1TQE	RY	TRANSCRIPTION/PROTEIN BINDING/DNA	Y	1.5	1.5	1	14	TEVKQKLQEFLLSK	15666
1TU3	AF	PROTEIN TRANSPORT	A	1.5	1.5	1	8	HSLAPMYY	15667
1TU3	CH	PROTEIN TRANSPORT	C	1.5	1.5	1	5	APMYY	15668
1TY4	AC	APOPTOSIS	A	1.5	1.5	1	7	TIFEKKH	15669
1TZI	BV	IMMUNE SYSTEM	V	1.5	1.5	1	8	FMDVYQRS	15670
1U35	AB	STRUCTURAL PROTEIN/DNA	B	1.5	1.5	1	11	AMDVVYALKRQ	15671
1U35	AG	STRUCTURAL PROTEIN/DNA	A	1.5	1.5	1	11	TVALREIRRYQ	15672
1U35	FH	STRUCTURAL PROTEIN/DNA	F	1.5	1.5	1	11	AMDVVYALKRQ	15673
1U5T	AB	TRANSPORT PROTEIN	A	1.5	1.5	1	18	VNDFYYEVCLKVIEICRQ	15674
1U6G	AC	LIGASE	A	1.5	1.5	1	16	KSRYMELYTHVYNYCT	15675
1U6G	AC	LIGASE	C	1.5	1.5	1	12	KQEFEKQDELKR	15676
1U6G	AC	LIGASE	C	1.5	1.5	1	15	KDFRFMATNDLMTEL	15677
1U9I	ED	CIRCADIAN CLOCK PROTEIN	E	1.5	1.5	1	18	NNAFRQFVIGVTGYAKQE	15678
1UF2	AI	VIRUS	A	1.5	1.5	1	15	EHDVVNAQRENRIFY	15679
1UHL	AB	DNA BINDING PROTEIN	B	1.5	1.5	1	12	MFPRMLMKLVSL	15680
1UM4	LH	IMMUNE SYSTEM	L	1.5	1.5	1	7	DEQLKSG	15681
1UM9	AD	OXIDOREDUCTASE	D	1.5	1.5	1	5	DKLYL	15682
1UWE	UV	ANTIBODY	U	1.5	1.5	1	7	AEQLASG	15683
1UZD	BC	LYASE	B	1.5	1.5	1	21	NAPGAAANRVALEACTQARNE	15684
1UZD	BC	LYASE	B	1.5	1.5	1	10	PELAAACEVW	15685
1UZH	BC	LYASE	B	1.5	1.5	1	10	PELAAACEVW	15686
1UZH	BF	LYASE	B	1.5	1.5	1	14	AKNYGRAVYECLRG	15687
1UZH	OM	LYASE	O	1.5	1.5	1	14	AKNYGRAVYECLRG	15688
1V54	CG	OXIDOREDUCTASE	C	1.5	1.5	1	23	PWPLTGALSALLMTSGLTMWFHF	15689
1V54	DE	OXIDOREDUCTASE	D	1.5	1.5	1	12	ASQKALKEKEKA	15690
1V54	DM	OXIDOREDUCTASE	D	1.5	1.5	1	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	15691
1V54	NP	OXIDOREDUCTASE	P	1.5	1.5	1	33	VYGSTFFVATGFHGLHVIIGSTFLIVCFFRQLK	15692
1V7N	IX	IMMUNE SYSTEM/CYTOKINE	X	1.5	1.5	1	15	LLGQLSGQVRLLLGA	15693
1V7N	LH	IMMUNE SYSTEM/CYTOKINE	L	1.5	1.5	1	7	SEQLTSG	15694
1V9U	13	VIRUS/RECEPTOR	1	1.5	1.5	1	5	LESFL	15695
1VRS	BE	OXIDOREDUCTASE	E	1.5	1.5	1	13	VASKEFEKYTFSD	15696
1W1I	DH	HYDROLASE	H	1.5	1.5	1	18	RDAIKRIAYEFVEMKAKD	15697
1W2B	KN	RIBOSOME	K	1.5	1.5	1	7	VREIDEN	15698
1W72	DI	IMMUNE SYSTEM	D	1.5	1.5	1	29	PEYWDQETRNMKAHSQTDRANLGTLRGYY	15699
1W98	AB	TRANSFERASE	B	1.5	1.5	1	18	RETFYLAQDFFDRYMATQ	15700
1WCM	AB	TRANSCRIPTION	A	1.5	1.5	1	12	EETRAELSQLCA	15701
1WDW	CD	LYASE	C	1.5	1.5	1	13	KTIQESHYRALKN	15702

1WDW	CD	LYASE	D	1.5	1.5	1	15	LKDAINEALRDWVAT	15703
1WDW	EF	LYASE	E	1.5	1.5	1	13	KTIQESHYRALKN	15704
1WYU	AB	OXIDOREDUCTASE	B	1.5	1.5	1	5	AEDLI	15705
1X86	EF	SIGNALING PROTEIN/MEMBRANE PROTEIN	E	1.5	1.5	1	30	PCEIKRQEVINELFYTERAHVRTLKVLDQV	15706
1X86	GH	SIGNALING PROTEIN/MEMBRANE PROTEIN	G	1.5	1.5	1	22	NFVNQAVKEAENKQRLEDYQRR	15707
1XCQ	GO	IMMUNE SYSTEM	O	1.5	1.5	1	12	ATAEAYRYAALH	15708
1XFU	CQ	LYASE/METAL BINDING PROTEIN	C	1.5	1.5	1	13	SAEFIKNLSSIRR	15709
1XFU	FT	LYASE/METAL BINDING PROTEIN	F	1.5	1.5	1	8	LTEIKKQI	15710
1XFV	ES	LYASE/METAL BINDING PROTEIN	S	1.5	1.5	1	13	SEEEIREAFRVFD	15711
1XFV	FT	LYASE/METAL BINDING PROTEIN	T	1.5	1.5	1	10	YEEFVQMMTA	15712
1XKP	AC	MEMBRANE PROTEIN/CHAPERON	C	1.5	1.5	1	10	LALLEHLIPQ	15713
1XLS	GO	TRANSCRIPTION	O	1.5	1.5	1	9	ALLRYLLDK	15714
1XME	AB	OXIDOREDUCTASE	A	1.5	1.5	1	25	YYQGLTLHGVLNAIVFTQLFAQAIM	15715
1XME	AC	OXIDOREDUCTASE	A	1.5	1.5	1	24	PAFVAPVLGLLGFIPGGAGGIVNA	15716
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	B	1.5	1.5	1	17	DVVKESVNELSEKAKTD	15717
1XPK	DC	TRANSFERASE	C	1.5	1.5	1	9	AAVQIHNLL	15718
1XV9	BF	DNA BINDING PROTEIN	B	1.5	1.5	1	25	VLPLVTHFADINTFMVLQVIKFTKD	15719
1XV9	BF	DNA BINDING PROTEIN	F	1.5	1.5	1	7	KILHRLL	15720
1Y74	CB	TRANSPORT PROTEIN	C	1.5	1.5	1	20	RFCSAIREVYEQLYDTLDIT	15721
1Y76	CB	TRANSPORT PROTEIN	B	1.5	1.5	1	15	QSQEDISLLLQLVQN	15722
1Y76	CB	TRANSPORT PROTEIN	B	1.5	1.5	1	13	IEDLFSSLKHIQH	15723
1Y8R	BC	LIGASE	B	1.5	1.5	1	15	RAARNHVNRMCLAAD	15724
1YA7	EK	HYDROLASE/HYDROLASE ACTIVATOR	E	1.5	1.5	1	23	VADARVLVDFARISAQQEKVTYG	15725
1YCP	LH	COMPLEX (SERINE PROTEASE/PEPTIDE)	L	1.5	1.5	1	5	FEKKQ	15726
1YCR	AB	COMPLEX (ONCOGENE PROTEIN/PEPTIDE)	A	1.5	1.5	1	15	MKEVLFYLGQYIMTK	15727
1YE9	DH	OXIDOREDUCTASE	H	1.5	1.5	1	10	PLLQGRLFSY	15728
1YE9	IP	OXIDOREDUCTASE	P	1.5	1.5	1	8	FFAENEQA	15729
1YE9	LM	OXIDOREDUCTASE	M	1.5	1.5	1	18	PLLQGRLFSYTDTQISRL	15730
1YHN	AB	PROTEIN TRANSPORT	B	1.5	1.5	1	28	QILQERNELKAKVFLLKEELAYFQRELL	15731
1YHU	QS	OXYGEN STORAGE/TRANSPORT	S	1.5	1.5	1	18	IPTLESMLDHLAGQHAVR	15732
1YHU	UX	OXYGEN STORAGE/TRANSPORT	U	1.5	1.5	1	16	MLERAKVKDEWAKAYG	15733
1YNK	LH	IMMUNE SYSTEM	L	1.5	1.5	1	6	SEQLTS	15734
1YR5	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.5	1.5	1	11	EAELQDMINEV	15735
1Z0K	CD	PROTEIN TRANSPORT	C	1.5	1.5	1	11	KSCLLHQFIEK	15736
1Z7Q	BI	HYDROLASE/HYDROLASE ACTIVATOR	I	1.5	1.5	1	22	AADTEAVTQLIGSNIELHSLYT	15737

1Z7Q	FM	HYDROLASE/HYDROLASE ACTIVATOR	F	1.5	1.5	1	18	APDARVLSNYLRQQCNYS	15738
1Z7Q	Hb	HYDROLASE/HYDROLASE ACTIVATOR	H	1.5	1.5	1	5	EYEQL	15739
1Z7Q	XY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.5	1.5	1	14	YSGFYTFSLLDHHY	15740
1Z7Z	13	VIRUS/RECEPTOR	1	1.5	1.5	1	5	LVSIN	15741
1ZAV	AY	STRUCTURAL PROTEIN	Y	1.5	1.5	1	15	VSELAELVKKLEDKF	15742
1ZBB	ec	STRUCTURAL PROTEIN/DNA	e	1.5	1.5	1	13	TVALREIRRYQKS	15743
1ZBB	EC	STRUCTURAL PROTEIN/DNA	E	1.5	1.5	1	13	TVALREIRRYQKS	15744
1ZGL	DE	IMMUNE SYSTEM	E	1.5	1.5	1	8	RPDAEYWN	15745
1ZGL	DF	IMMUNE SYSTEM	D	1.5	1.5	1	21	GALANIAVDKANLEIMTKRSN	15746
1ZGL	JL	IMMUNE SYSTEM	J	1.5	1.5	1	20	ALANIAVDKANLEIMTKRSN	15747
1ZGL	KL	IMMUNE SYSTEM	K	1.5	1.5	1	8	RPDAEYWN	15748
1ZLA	AG	PROTEIN BINDING/VIRUS/DNA	A	1.5	1.5	1	11	TVALREIRRYQ	15749
1ZLA	EF	PROTEIN BINDING/VIRUS/DNA	F	1.5	1.5	1	11	AMDVVYALKRQ	15750
1ZLI	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.5	1.5	1	5	ECVSK	15751
1ZOQ	AC	TRANSCRIPTION/TRANSFERASE	A	1.5	1.5	1	13	TCLRALVEMARVG	15752
1ZV8	IF	VIRAL PROTEIN	I	1.5	1.5	1	48	QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS	15753
1ZW3	AB	PROTEIN BINDING	A	1.5	1.5	1	24	TAPVSAVQAAVSNLVRVGKETVQT	15754
2A45	HI	BLOOD CLOTTING	H	1.5	1.5	1	22	GCQLQEALLQQERPIRNSVDEL	15755
2A45	JK	BLOOD CLOTTING	J	1.5	1.5	1	25	CRMKGLIDEVNQDFTNRINKLKNSL	15756
2A79	AB	MEMBRANE PROTEIN	A	1.5	1.5	1	14	SMEIMEAYSVARQF	15757
2AA1	CD	OXYGEN STORAGE/TRANSPORT	D	1.5	1.5	1	20	PDNFKLLADCLTIVVAARFG	15758
2AAB	LH	IMMUNE SYSTEM	L	1.5	1.5	1	6	SEQLTS	15759
2ACL	EF	TRANSCRIPTION	E	1.5	1.5	1	18	GAIFDRVLTELVSKMRDM	15760
2ADG	AB	IMMUNE SYSTEM	A	1.5	1.5	1	6	SEQLTS	15761
2AFH	AB	OXIDOREDUCTASE	A	1.5	1.5	1	8	SRILLEEM	15762
2AFH	CB	OXIDOREDUCTASE	C	1.5	1.5	1	16	FDGFAIFARDMDMTLN	15763
2AFH	CD	OXIDOREDUCTASE	C	1.5	1.5	1	9	EKARKDRNK	15764
2AFH	CD	OXIDOREDUCTASE	C	1.5	1.5	1	8	SRILLEEM	15765
2AI0	NJ	IMMUNE SYSTEM	N	1.5	1.5	1	6	SEQLTS	15766
2AJ3	EF	IMMUNE SYSTEM	E	1.5	1.5	1	7	DEQLKSG	15767
2AJZ	AB	IMMUNE SYSTEM	A	1.5	1.5	1	5	SEQLT	15768
2AK4	FH	IMMUNE SYSTEM	F	1.5	1.5	1	13	LCVEWLRRYLENG	15769
2AKW	AB	LIGASE	A	1.5	1.5	1	16	PITLMERELVEIFRAL	15770
2AKW	AB	LIGASE	B	1.5	1.5	1	13	EEDLVEEVARIQG	15771
2AXT	ad	ELECTRON TRANSPORT	a	1.5	1.5	1	5	ICVAY	15772
2AXT	ad	ELECTRON TRANSPORT	d	1.5	1.5	1	13	IFRFLLFFQGFHN	15773
2AXT	DE	ELECTRON TRANSPORT	D	1.5	1.5	1	7	FTRWCQL	15774
2B59	AB	HYDROLASE/STRUCTURAL PROTEIN	A	1.5	1.5	1	8	IAGYKETG	15775
2B7Y	CD	LECTIN	D	1.5	1.5	1	5	LKDVV	15776

2B87	AB	PROTEIN BINDING	B	1.5	1.5	1	14	SLQVVAFINSLRDD	15777
2BCX	AB	CALCIUM BINDING PROTEIN	A	1.5	1.5	1	12	DEEVDEMIREAD	15778
2BE7	AD	TRANSFERASE	A	1.5	1.5	1	7	AARLASE	15779
2BG9	AB	ION CHANNEL/RECEPTOR	A	1.5	1.5	1	29	MTLSISVLLSLTVFLLVIVELIPSTSSAV	15780
2BPA	13	VIRUS/DNA	1	1.5	1.5	1	16	KHLFQGYLNIYNNYFK	15781
2BRU	AC	OXIDOREDUCTASE	C	1.5	1.5	1	9	MNVLLAEAK	15782
2BS4	DE	OXIDOREDUCTASE	E	1.5	1.5	1	13	IFIVLNMIRETYD	15783
2BTV	AF	VIRUS	A	1.5	1.5	1	5	MQRRF	15784
2BYP	CI	RECEPTOR	I	1.5	1.5	1	6	PRCAWR	15785
2C0L	AB	TRANSPORT PROTEIN/RECEPTOR	A	1.5	1.5	1	15	ENIWSTLRLALSMLG	15786
2C9W	AC	TRANSCRIPTION REGULATION	A	1.5	1.5	1	10	TRLKDYLEEY	15787
2CCI	AB	CELL CYCLE	B	1.5	1.5	1	18	NETLHLAVNYIDRFLSSM	15788
2CKF	CD	OXIDOREDUCTASE	C	1.5	1.5	1	17	TLESDDGENMSSATYVN	15789
2CLY	DE	HYDROLASE	E	1.5	1.5	1	12	LVDDFEKKFNAL	15790
2CMY	AB	HYDROLASE	B	1.5	1.5	1	10	ELLRRCLDNC	15791
2CNW	CF	SIGNAL RECOGNITION	C	1.5	1.5	1	18	EEDLKATLREIRRALMDA	15792
2CZV	AD	HYDROLASE	D	1.5	1.5	1	17	KDEVKELIWKSSLEVLG	15793
2D0O	AB	CHAPERONE	A	1.5	1.5	1	7	GVLVSNR	15794
2DD4	AC	HYDROLASE	C	1.5	1.5	1	10	PNYRRRLVRW	15795
2DD4	GI	HYDROLASE	G	1.5	1.5	1	5	QKDLW	15796
2DFK	AB	CELL CYCLE	A	1.5	1.5	1	25	IDGFLLTPVQKICKYPLQLAELLKY	15797
2DFS	AE	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	E	1.5	1.5	1	7	EAELQDM	15798
2DFS	MN	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	N	1.5	1.5	1	11	AAELRHVMTNL	15799
2DFX	EI	HYDROLASE	E	1.5	1.5	1	10	QKIRGQMPER	15800
2DXB	AC	HYDROLASE	A	1.5	1.5	1	5	QKDLW	15801
2DXB	AC	HYDROLASE	C	1.5	1.5	1	10	PNYRRRLVRW	15802
2DXB	DF	HYDROLASE	D	1.5	1.5	1	5	QKDLW	15803
2DXB	GI	HYDROLASE	I	1.5	1.5	1	10	PNYRRRLVRW	15804
2DXB	MO	HYDROLASE	O	1.5	1.5	1	10	PNYRRRLVRW	15805
2DXB	PR	HYDROLASE	P	1.5	1.5	1	5	QKDLW	15806
2DXB	VX	HYDROLASE	V	1.5	1.5	1	5	QKDLW	15807
2DXB	VX	HYDROLASE	X	1.5	1.5	1	10	PNYRRRLVRW	15808
2E 32	AB	LIGASE	A	1.5	1.5	1	10	EPLLLRVLAE	15809
2E 74	AB	PHOTOSYNTHESIS	B	1.5	1.5	1	12	VPLGLILVPFIE	15810
2EC6	AB	CONTRACTILE PROTEIN	A	1.5	1.5	1	12	YKKLQDQRIGLS	15811
2EC6	AC	CONTRACTILE PROTEIN	C	1.5	1.5	1	5	VCRCL	15812
2EFC	AB	TRANSPORT PROTEIN	B	1.5	1.5	1	10	KSSLVLRFVK	15813
2EHB	AD	SIGNALLING PROTEIN/TRANSFERASE	A	1.5	1.5	1	11	IDEWKDFVSLN	15814

2EHO	JL	REPLICATION	J	1.5	1.5	1	7	LIRELHR	15815
2EHO	KL	REPLICATION	K	1.5	1.5	1	17	DTRIAKLRVSADSFVRQ	15816
2EKV	AC	CONTRACTILE PROTEIN	A	1.5	1.5	1	9	RQKLMEATS	15817
2EQ9	KL	OXIDOREDUCTASE	L	1.5	1.5	1	11	PAARKLARELG	15818
2F5Z	IO	OXIDOREDUCTASE/PROTEIN BINDING	I	1.5	1.5	1	6	CEDIAR	15819
2F8N	AG	STRUCTURAL PROTEIN/DNA	A	1.5	1.5	1	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	15820
2FD6	LH	IMMUNE SYSTEM, HYDROLASE	L	1.5	1.5	1	7	SEQLTSG	15821
2FF6	GA	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	A	1.5	1.5	1	9	QAVLSLYAS	15822
2FHH	1T	HYDROLASE	T	1.5	1.5	1	23	AAVAVEFARLYAVELEHYEKLEG	15823
2FHH	ML	HYDROLASE	L	1.5	1.5	1	23	AAVAVEFARLYAVELEHYEKLEG	15824
2FHH	SJ	HYDROLASE	J	1.5	1.5	1	23	AAVAVEFARLYAVELEHYEKLEG	15825
2FHJ	AD	TRANSFERASE	D	1.5	1.5	1	17	QPAGLQAAEAAVDAIKG	15826
2FHJ	BD	TRANSFERASE	B	1.5	1.5	1	17	QPAGLQAAEAAVDAIKG	15827
2FHJ	BD	TRANSFERASE	D	1.5	1.5	1	17	QPAGLQAAEAAVDAIKG	15828
2FJ7	AB	STRUCTURAL PROTEIN/DNA	A	1.5	1.5	1	8	EIRRYQKS	15829
2FJ7	EF	STRUCTURAL PROTEIN/DNA	E	1.5	1.5	1	11	PKDIQLARRIR	15830
2FNJ	BC	PROTEIN TRANSPORT/SIGNALING PROTEIN	B	1.5	1.5	1	12	VFELKRIVEGIL	15831
2FOI	BC	OXIDOREDUCTASE	C	1.5	1.5	1	13	FIDYAIEYSEKYA	15832
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	A	1.5	1.5	1	12	AAELRHVMTNLG	15833
2FR4	LH	IMMUNE SYSTEM/DNA	L	1.5	1.5	1	6	SEQLTS	15834
2FUG	46	OXIDOREDUCTASE	4	1.5	1.5	1	6	FEKTME	15835
2FUG	VY	OXIDOREDUCTASE	V	1.5	1.5	1	14	RERETILDLFEWVT	15836
2FYN	GL	OXIDOREDUCTASE	G	1.5	1.5	1	17	QMSFWGATVITGLFGAI	15837
2FYN	MN	OXIDOREDUCTASE	N	1.5	1.5	1	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	15838
2FYN	PO	OXIDOREDUCTASE	O	1.5	1.5	1	23	YATAGAGAVATGAAVWPLINQMN	15839
2G9H	AC	IMMUNE SYSTEM	A	1.5	1.5	1	22	AQGALANIAVDKANLEIMTKRS	15840
2GFB	CD	IMMUNOGLOBULIN	C	1.5	1.5	1	6	SEQLTS	15841
2GHO	CD	TRANSFERASE	C	1.5	1.5	1	10	FRVLVKELQA	15842
2GID	GB	TRANSLATION	G	1.5	1.5	1	12	QRFLTQALHYNT	15843
2GJX	AB	HYDROLASE	A	1.5	1.5	1	18	LTFAYERLSHFRCELLRR	15844
2GJX	DB	HYDROLASE	D	1.5	1.5	1	15	SVLDEAFQRYRDLLF	15845
2GL7	DE	TRANSCRIPTION	D	1.5	1.5	1	10	YKNKMMVCQV	15846
2GS0	AB	TRANSCRIPTION	B	1.5	1.5	1	10	PDDIEQWFTE	15847
2GTL	IL	OXYGEN STORAGE/TRANSPORT	L	1.5	1.5	1	19	PEFGAHSQRVLSGLDITIS	15848
2GTL	KL	OXYGEN STORAGE/TRANSPORT	L	1.5	1.5	1	16	VTESLKVKLQWASAFG	15849
2GUZ	AB	CHAPERONE, PROTEIN TRANSPORT	A	1.5	1.5	1	8	SKEALQIL	15850
2GUZ	OF	CHAPERONE, PROTEIN TRANSPORT	O	1.5	1.5	1	15	KKKLKEVHRKIMLAN	15851

2GV5	AC	CELL CYCLE	A	1.5	1.5	1	11	IKNLRRVAKEL	15852
2GWF	CF	HYDROLASE/LIGASE	F	1.5	1.5	1	7	RRYYENY	15853
2GZD	BC	PROTEIN TRANSPORT	C	1.5	1.5	1	19	KDTHIRELEDYIDNLLVRV	15854
2H1P	LH	COMPLEX (ANTIBODY/PEPTIDE)	L	1.5	1.5	1	6	SEQLTS	15855
2H4M	BD	PROTEIN TRANSPORT	B	1.5	1.5	1	18	DFMIVALDLLSGLAEGLG	15856
2H67	AB	HORMONE/GROWTH FACTOR	B	1.5	1.5	1	12	SDLVEALYLVCG	15857
2H7V	AC	SIGNALING PROTEIN	C	1.5	1.5	1	45	SETYGFLNRLAEAKITLSQQLNTLQQQQESAKAQLSILINRSGSW	15858
2H9A	AB	OXIDOREDUCTASE	A	1.5	1.5	1	18	ISEGLFYQTQIRRLAIKK	15859
2HDN	EF	TRANSLATION	F	1.5	1.5	1	7	ALKALEG	15860
2HDN	KL	TRANSLATION	L	1.5	1.5	1	7	ALKALEG	15861
2HGR	MQ	RIBOSOME	Q	1.5	1.5	1	11	RICLRELAHKG	15862
2HHH	DE	RIBOSOME	E	1.5	1.5	1	11	AVPRAILELAG	15863
2HLD	AD	HYDROLASE	A	1.5	1.5	1	15	LSKQAVAYRQLSLLL	15864
2HLD	JM	HYDROLASE	M	1.5	1.5	1	9	PAPATTFAH	15865
2HLD	TW	HYDROLASE	T	1.5	1.5	1	15	LSKQAVAYRQLSLLL	15866
2HLD	Y1	HYDROLASE	Y	1.5	1.5	1	63	EYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNR TRQAVITNELVDIITG	15867
2HOD	HI	BLOOD CLOTTING	H	1.5	1.5	1	6	NIPTNL	15868
2HRP	MN	COMPLEX (IMMUNOGLOBULIN/PEPTIDE)	M	1.5	1.5	1	6	SEQLTS	15869
2HTM	BF	BIOSYNTHETIC PROTEIN	B	1.5	1.5	1	12	FGVMREAIAAAK	15870
2HVY	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	1.5	1.5	1	8	EEYFRKAI	15871
2HYI	AC	HYDROLASE/RNA BINDING PROTEIN/RNA	A	1.5	1.5	1	25	GLRVFYYLVQDLKCLVFSLIGLHFK	15872
2I2P	DE	RIBOSOME	E	1.5	1.5	1	5	AMRAV	15873
2I2R	KO	TRANSPORT PROTEIN	O	1.5	1.5	1	12	EDTFKQIYAQFF	15874
2I2X	AB	TRANSFERASE	A	1.5	1.5	1	9	KEVFDYAVL	15875
2I2X	AB	TRANSFERASE	B	1.5	1.5	1	16	DALMVGMGVVIRLYDE	15876
2I2X	CB	TRANSFERASE	B	1.5	1.5	1	8	EASLKKVL	15877
2I2X	EF	TRANSFERASE	F	1.5	1.5	1	20	DLIDDALMVGMGVVIRLYDE	15878
2I2X	EH	TRANSFERASE	E	1.5	1.5	1	22	TVQCWSETLAYDCALMNTALET	15879
2I9L	AB	IMMUNE SYSTEM/VIRAL PROTEIN	A	1.5	1.5	1	7	SEQLTSG	15880
2I9L	CD	IMMUNE SYSTEM/VIRAL PROTEIN	C	1.5	1.5	1	7	SEQLTSG	15881
2IAE	AB	HYDROLASE	B	1.5	1.5	1	11	LGLRAYIRKQI	15882
2IAM	BP	IMMUNE SYSTEM	B	1.5	1.5	1	15	AAVDTYCRHNYGVGE	15883
2IAN	PR	IMMUNE SYSTEM	P	1.5	1.5	1	22	AQGALANIAVDKANLEIMTKRS	15884
2IBI	AB	HYDROLASE	A	1.5	1.5	1	16	AQEFLRFLLDGLHNEV	15885
2IBZ	DI	OXIDOREDUCTASE	D	1.5	1.5	1	19	HASIRRGYQVYREVCAACH	15886
2IBZ	HG	OXIDOREDUCTASE	H	1.5	1.5	1	17	VEEFFHLQHYLDTATAP	15887

2ICE	DE	IMMUNE SYSTEM	D	1.5	1.5	1	7	KGVFVLN	15888
2ICW	BC	IMMUNE SYSTEM	B	1.5	1.5	1	13	AVDTYCRHNYGVG	15889
2INN	BD	OXIDOREDUCTASE	D	1.5	1.5	1	8	NAKIAGDA	15890
2INP	AC	OXIDOREDUCTASE	A	1.5	1.5	1	6	PEKYIQ	15891
2INP	BD	OXIDOREDUCTASE	D	1.5	1.5	1	13	AALDESKAYWMDD	15892
2IX7	CA	CONTRACTILE PROTEIN/METAL BINDING	A	1.5	1.5	1	11	DEEVDEMIREA	15893
2J0Q	BI	HYDROLASE	B	1.5	1.5	1	11	VGEDIRKLDYG	15894
2J1K	IB	VIRUS/RECEPTOR	I	1.5	1.5	1	6	HTWKLC	15895
2J28	TX	RIBOSOME	X	1.5	1.5	1	7	LREQFNL	15896
2J5G	AD	HYDROLASE	D	1.5	1.5	1	11	TLNLRYTRVAL	15897
2J7A	PR	OXIDOREDUCTASE	P	1.5	1.5	1	5	CADCH	15898
2J9D	BE	MEMBRANE TRANSPORT	B	1.5	1.5	1	11	LEIVKKALSDA	15899
2JDQ	BD	PROTEIN TRANSPORT	B	1.5	1.5	1	16	LTMTRNAVWALSNLCR	15900
2JEL	LH	COMPLEX (ANTIBODY/ANTIGEN)	L	1.5	1.5	1	7	SEQLTSG	15901
2JGB	AB	TRANSLATION	B	1.5	1.5	1	9	RKFLMECRN	15902
2JIZ	CD	HYDROLASE	D	1.5	1.5	1	6	RAIAEL	15903
2JKR	AB	ENDOCYTOSIS	A	1.5	1.5	1	8	TDILATVL	15904
2JKR	EM	ENDOCYTOSIS	E	1.5	1.5	1	16	PDLRDRGYIYWRLLST	15905
2JKR	LI	ENDOCYTOSIS	I	1.5	1.5	1	20	NLAYLEAIHNFVEVLNEYFH	15906
2JU0	AB	METAL BINDING PROTEIN/SIGNALING PROTEIN	A	1.5	1.5	1	12	FEEFITVLSTTS	15907
2KIN	AB	MOTOR PROTEIN	A	1.5	1.5	1	17	QEQVYNACAKQIVKDVL	15908
2NS8	AH	TRANSCRIPTION	A	1.5	1.5	1	17	EKQYETLENQLAFLTQQ	15909
2NS8	CF	TRANSCRIPTION	C	1.5	1.5	1	31	LENALYALSAVGHFTLGSVLEDQEHQVAKEE	15910
2NTI	GI	DNA BINDING PROTEIN	G	1.5	1.5	1	11	SSVKKILSKAS	15911
2NTY	BD	SIGNALING PROTEIN	B	1.5	1.5	1	20	SALALSNAITNLAASIFGEQ	15912
2NU9	DI	LIGASE	D	1.5	1.5	1	12	CKDSILEAIDAG	15913
2NUU	AI	TRANSPORT PROTEIN/SIGNALING PROTEIN	A	1.5	1.5	1	7	EEQEREG	15914
2NUU	BG	TRANSPORT PROTEIN/SIGNALING PROTEIN	B	1.5	1.5	1	7	EEQEREG	15915
2NUU	CH	TRANSPORT PROTEIN/SIGNALING PROTEIN	C	1.5	1.5	1	7	EEQEREG	15916
2NV2	IJ	LYASE/TRANSFERASE	I	1.5	1.5	1	10	ERVKRGMAEM	15917
2NVU	BC	PROTEIN TURNOVER, LIGASE	B	1.5	1.5	1	15	IIARRWINGMLISLL	15918
2NYL	AB	HYDROLASE	B	1.5	1.5	1	18	RAYIRKQINNIFYRFIYE	15919
2NZ1	AD	VIRAL PROTEIN/CYTOKINE	A	1.5	1.5	1	9	TCPCYYKYS	15920
2NZ1	BE	VIRAL PROTEIN/CYTOKINE	B	1.5	1.5	1	9	TCPCYYKYS	15921
2NZD	EC	STRUCTURAL PROTEIN/DNA	E	1.5	1.5	1	13	TVALREIRRYQKS	15922

2O26	EU	CYTOKINE/SIGNALING PROTEIN	E	1.5	1.5	1	22	SHCWLRDMVIQLSLSLTTLLDK	15923
2O60	AB	METAL BINDING PROTEIN	A	1.5	1.5	1	11	TKELGTVMRSL	15924
2O60	AB	METAL BINDING PROTEIN	A	1.5	1.5	1	11	EAELQDMINEV	15925
2O97	AB	DNA BINDING PROTEIN	B	1.5	1.5	1	11	KSQLIDKIAAG	15926
2ODY	AB	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	B	1.5	1.5	1	9	KKWIQKVID	15927
2OF5	DJ	APOPTOSIS	J	1.5	1.5	1	8	WPAVALHL	15928
2OM0	ab	HORMONE	a	1.5	1.5	1	5	IVEQC	15929
2OM0	eh	HORMONE	e	1.5	1.5	1	7	LYQLENY	15930
2OM0	ID	HORMONE	I	1.5	1.5	1	7	LYQLENY	15931
2OM0	Q2	HORMONE	Q	1.5	1.5	1	7	LYQLENY	15932
2OM0	ST	HORMONE	S	1.5	1.5	1	5	IVEQC	15933
2OM0	UY	HORMONE	U	1.5	1.5	1	7	LYQLENY	15934
2ONK	DE	MEMBRANE PROTEIN	E	1.5	1.5	1	10	EMELIHLVES	15935
2OTJ	AZ	RIBOSOME	Z	1.5	1.5	1	9	PGGKTVRRS	15936
2OZB	AB	RNA BINDING PROTEIN/RNA	B	1.5	1.5	1	21	RRKAARLVAAKCTLAARVDSF	15937
2P1N	AB	SIGNALING PROTEIN	A	1.5	1.5	1	8	EEEEEVRR	15938
2P1N	AB	SIGNALING PROTEIN	B	1.5	1.5	1	8	KSWYEIER	15939
2P22	CD	TRANSPORT PROTEIN	D	1.5	1.5	1	9	NVEELLRRI	15940
2PBD	AV	STRUCTURAL PROTEIN	A	1.5	1.5	1	12	SVWIGGSILASL	15941
2PBI	AB	SIGNALING PROTEIN	A	1.5	1.5	1	14	AFLQKIEALVKDMQ	15942
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	H	1.5	1.5	1	9	GKYAKEKED	15943
2PKQ	OR	OXIDOREDUCTASE	R	1.5	1.5	1	13	RIGRNFLRCWHGR	15944
2PKQ	OR	OXIDOREDUCTASE	R	1.5	1.5	1	10	VKQASHLLKY	15945
2PMZ	GW	TRANSLATION, TRANSFERASE	W	1.5	1.5	1	16	RYEIARVISARALQLA	15946
2PMZ	QR	TRANSLATION, TRANSFERASE	Q	1.5	1.5	1	11	EEAIAEAKEIM	15947
2PMZ	SY	TRANSLATION, TRANSFERASE	Y	1.5	1.5	1	6	INEVIH	15948
2PMZ	TU	TRANSLATION, TRANSFERASE	U	1.5	1.5	1	5	LQRTY	15949
2PQK	AB	APOPTOSIS	A	1.5	1.5	1	11	KSLSRVMIHVF	15950
2PUK	AB	ELECTRON TRANSPORT	A	1.5	1.5	1	8	KEAEVKNT	15951
2Q9Q	FH	REPLICATION	F	1.5	1.5	1	31	LKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	15952
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	B	1.5	1.5	1	11	DNERSDIFDAM	15953
2QE7	AE	HYDROLASE	A	1.5	1.5	1	9	VFYLHSRLL	15954
2QE7	CD	HYDROLASE	C	1.5	1.5	1	9	VFYLHSRLL	15955
2QHO	EF	PROTEIN BINDING/LIGASE	F	1.5	1.5	1	11	EELISQAQVVL	15956
2QHO	GH	PROTEIN BINDING/LIGASE	H	1.5	1.5	1	11	EELISQAQVVL	15957
2QHO	GH	PROTEIN BINDING/LIGASE	H	1.5	1.5	1	11	VNLAVNNLLSR	15958
2QHR	HL	IMMUNE SYSTEM/VIRAL PROTEIN	L	1.5	1.5	1	6	SEELKE	15959
2QI9	AF	MEMBRANE PROTEIN	A	1.5	1.5	1	7	SVDLRQL	15960

2QI9	BD	MEMBRANE PROTEIN	B	1.5	1.5	1	7	EISARQL	15961
2QJK	DC	ELECTRON TRANSPORT	D	1.5	1.5	1	17	QMSFWGATVITGLFGAI	15962
2QJK	GL	ELECTRON TRANSPORT	G	1.5	1.5	1	17	QMSFWGATVITGLFGAI	15963
2QJK	GL	ELECTRON TRANSPORT	L	1.5	1.5	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15964
2QJK	QR	ELECTRON TRANSPORT	R	1.5	1.5	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15965
2QJY	AF	OXIDOREDUCTASE	A	1.5	1.5	1	17	QMSFWGATVITGLFGAI	15966
2QJY	GL	OXIDOREDUCTASE	L	1.5	1.5	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	15967
2QJY	JI	OXIDOREDUCTASE	J	1.5	1.5	1	33	NATLNRFFSLHYLLPFVIAALVAIHIWAFHSTG	15968
2QJY	MR	OXIDOREDUCTASE	M	1.5	1.5	1	17	QMSFWGATVITGLFGAI	15969
2QJY	PO	OXIDOREDUCTASE	P	1.5	1.5	1	33	NATLNRFFSLHYLLPFVIAALVAIHIWAFHSTG	15970
2QMB	AB	TRANSPORT PROTEIN	B	1.5	1.5	1	16	VADCGAEALARLLIVY	15971
2QMB	CD	TRANSPORT PROTEIN	D	1.5	1.5	1	15	FRLLGDILIIVLAAH	15972
2QR0	MN	IMMUNE SYSTEM	M	1.5	1.5	1	7	DEQLKSG	15973
2QR1	CE	TRANSFERASE	C	1.5	1.5	1	14	FLDLCAMLVCKLFS	15974
2QRV	AB	TRANSFERASE/TRANSFERASE REGULATOR	B	1.5	1.5	1	10	EDLDVASRFL	15975
2QY0	AD	HYDROLASE	D	1.5	1.5	1	8	VEELMKLG	15976
2R00	AC	OXIDOREDUCTASE	A	1.5	1.5	1	15	KEEMKMVWETQKIFN	15977
2R6G	EF	HYDROLASE/TRANSPORT PROTEIN	E	1.5	1.5	1	18	MSAFWYAVRTAVINAASG	15978
2R6G	EF	HYDROLASE/TRANSPORT PROTEIN	F	1.5	1.5	1	9	FERAQEVLL	15979
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	F	1.5	1.5	1	13	VLFPLVCTIAIAF	15980
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	G	1.5	1.5	1	16	SLVALYALFDRLGEYI	15981
2RAO	AD	OXYGEN BINDING	D	1.5	1.5	1	20	PENFRLLGNVLVIVLSHHFG	15982
2REX	CD	SIGNALING PROTEIN/LIPOPROTEIN	C	1.5	1.5	1	5	LQHYK	15983
2RHS	AD	LIGASE	A	1.5	1.5	1	16	MSDLKGTLELVAKKLF	15984
2RI4	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.5	1.5	1	18	ENFKLLGNVLVVVLARHH	15985
2RI4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	1.5	1.5	1	19	PAVHASLDKFLANVSTVLT	15986
2RI4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	1.5	1.5	1	19	PENFKLLGNVLVVVLARHH	15987
2UUN	CD	ELECTRON TRANSPORT	C	1.5	1.5	1	12	PLTDAVSTADSQ	15988
2UXN	AB	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	B	1.5	1.5	1	9	FQAISDVIG	15989
2UYL	AB	IMMUNE SYSTEM	A	1.5	1.5	1	7	SEQLTSG	15990
2UZ1	AB	LYASE	A	1.5	1.5	1	10	IGEFDTLVRK	15991
2UZ6	AO	RECEPTOR	O	1.5	1.5	1	7	PPCILNN	15992
2UZ6	FT	RECEPTOR	T	1.5	1.5	1	7	PPCILNN	15993
2UZ6	GP	RECEPTOR	P	1.5	1.5	1	7	PPCILNN	15994
2UZ6	HR	RECEPTOR	R	1.5	1.5	1	7	PPCILNN	15995

2V17	HL	IMMUNE SYSTEM	L	1.5	1.5	1	7	SEQLTSG	15996
2V46	FR	RIBOSOME	R	1.5	1.5	1	16	AKEQRILAKTIKRARI	15997
2V4J	AE	OXIDOREDUCTASE	A	1.5	1.5	1	8	ITEYRKRH	15998
2V7Q	FG	HYDROLASE	F	1.5	1.5	1	28	SEHYDVARGVQKILQDYKSLQDIIAILG	15999
2V7Q	GI	HYDROLASE	G	1.5	1.5	1	10	FGDASVIALE	16000
2V8S	EV	PROTEIN TRANSPORT	E	1.5	1.5	1	13	GQLMGEIAKATFM	16001
2VBO	AB	HYDROLASE	A	1.5	1.5	1	12	RWFLDKLVDEIG	16002
2VE7	BD	CELL CYCLE	B	1.5	1.5	1	14	KLESLEAKNRALNE	16003
2VE7	BD	CELL CYCLE	D	1.5	1.5	1	7	KLERLEK	16004
2VGL	BM	PROTEIN TRANSPORT	B	1.5	1.5	1	14	IYVKLEKLDIMIRL	16005
2VJE	CD	LIGASE	D	1.5	1.5	1	5	QNLLK	16006
2VJM	AB	TRANSFERASE	B	1.5	1.5	1	7	NVAQCSG	16007
2VML	ED	PHOTOSYNTHESIS	D	1.5	1.5	1	25	NRRMAACLRDMEIILRYVSYALLAG	16008
2VML	EF	PHOTOSYNTHESIS	F	1.5	1.5	1	14	SNKRLDAVNAITGN	16009
2VOG	AB	APOPTOSIS	A	1.5	1.5	1	5	KSYLD	16010
2VOH	AB	APOPTOSIS	A	1.5	1.5	1	10	WEDGFIKKFE	16011
2VOY	CH	HYDROLASE	C	1.5	1.5	1	5	LMVLK	16012
2VPD	AB	GENE REGULATION	A	1.5	1.5	1	10	ETAYGLLTAE	16013
2VUS	GO	TRANSCRIPTION	O	1.5	1.5	1	11	NACGLFLKLHG	16014
2W2X	AD	SIGNALING PROTEIN/HYDROLASE	A	1.5	1.5	1	9	DRLRPLSYP	16015
2WAQ	BC	TRANSCRIPTION	B	1.5	1.5	1	13	YAFKLLIQELMSM	16016
2WAQ	CK	TRANSCRIPTION	K	1.5	1.5	1	10	HFNEVFISLW	16017
2WB1	AB	TRANSCRIPTION	A	1.5	1.5	1	16	RTSQSGYMQRRLINAL	16018
2WB1	WR	TRANSCRIPTION	W	1.5	1.5	1	6	PDEIRK	16019
2WD7	AC	OXIDOREDUCTASE	A	1.5	1.5	1	27	VETQVAELIGTNAIAPFLLTMSFAQRQ	16020
2WIN	JQ	IMMUNE SYSTEM	Q	1.5	1.5	1	24	FKKMSEAKYQLQKIYNEIDEALKS	16021
2WME	FE	OXIDOREDUCTASE	E	1.5	1.5	1	15	TSTGKKVMASASSSS	16022
2YVC	CF	CELL ADHESION	C	1.5	1.5	1	21	LRINKRILALCMGNHELYMRR	16023
2Z2T	BD	VIRAL PROTEIN/INHIBITOR	B	1.5	1.5	1	34	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARI	16024
2Z2T	BD	VIRAL PROTEIN/INHIBITOR	D	1.5	1.5	1	31	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK	16025
2Z3R	IL	CYTOKINE/CYTOKINE RECEPTOR	I	1.5	1.5	1	20	ASIHDTVENLIILANNSLSS	16026
2Z91	CD	IMMUNE SYSTEM	D	1.5	1.5	1	6	SEQLTS	16027
2ZBK	EF	ISOMERASE	E	1.5	1.5	1	10	ASIIYDALVS	16028
2ZCY	H0	HYDROLASE	0	1.5	1.5	1	6	WDFAKD	16029
2ZCY	MN	HYDROLASE	M	1.5	1.5	1	20	ISDMQHIERLLKDLVTENAY	16030
2ZCY	VM	HYDROLASE	M	1.5	1.5	1	6	WDFAKD	16031
2ZCY	Z0	HYDROLASE	0	1.5	1.5	1	18	PSYIFEYLATVMYQRRSK	16032
2ZHX	EF	HYDROLASE/HYDROLASE INHIBITOR	F	1.5	1.5	1	9	PEEVEEVIG	16033
2ZHX	KL	HYDROLASE/HYDROLASE INHIBITOR	K	1.5	1.5	1	10	RDASTLKPML	16034
2ZJQ	GN	RIBOSOME	N	1.5	1.5	1	8	LADIAARE	16035

2ZJQ	HM	RIBOSOME	H	1.5	1.5	1	6	RELRDR	16036
2ZKR	nq	RIBOSOMAL PROTEIN/RNA	n	1.5	1.5	1	9	YYARKRLVI	16037
2ZME	BD	PROTEIN TRANSPORT	D	1.5	1.5	1	17	VDTRQKQLAAWCSLVLS	16038
2ZU6	AB	HYDROLASE	A	1.5	1.5	1	19	RELAQQIQKVVMALGDYMG	16039
2ZXE	AB	HYDROLASE/TRANSPORT PROTEIN	A	1.5	1.5	1	7	WVEQETY	16040
3A0B	ad	ELECTRON TRANSPORT	a	1.5	1.5	1	20	GPYQLIIFHFLLGASCYMGR	16041
3A0B	CZ	ELECTRON TRANSPORT	C	1.5	1.5	1	11	HLISSAVLGFG	16042
3A0B	cz	ELECTRON TRANSPORT	z	1.5	1.5	1	17	ALVILSFVMVIGVPVAY	16043
3A0B	fj	ELECTRON TRANSPORT	f	1.5	1.5	1	17	TLAVPTIFFLGAIAAMQ	16044
3A0B	LM	ELECTRON TRANSPORT	L	1.5	1.5	1	16	SLYLGLLLILVLALLF	16045
3A0B	LM	ELECTRON TRANSPORT	M	1.5	1.5	1	15	LVPSVFLIILYVQTE	16046
3B63	NM	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	N	1.5	1.5	1	16	KANREKMTQIMFETFN	16047
3BCQ	CB	TRANSPORT PROTEIN/OXYGEN BINDING	C	1.5	1.5	1	19	PANFKILSHNLLVVLAQQF	16048
3BIM	DL	TRANSCRIPTION REPRESSOR	D	1.5	1.5	1	7	GLFYSIF	16049
3BIM	FM	TRANSCRIPTION REPRESSOR	F	1.5	1.5	1	15	HASDVLLNLNRLRSR	16050
3BLW	AB	OXIDOREDUCTASE	B	1.5	1.5	1	16	NLYGDILSDLNSGLSA	16051
3BLW	KL	OXIDOREDUCTASE	L	1.5	1.5	1	16	NLYGDILSDLNSGLSA	16052
3BLW	OP	OXIDOREDUCTASE	O	1.5	1.5	1	15	SMYGTILGNIGAALI	16053
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.5	1.5	1	11	QHIYSMIIRRY	16054
3BPN	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.5	1.5	1	16	ITLQEIIKTLNSLTEQ	16055
3BRV	AD	TRANSFERASE/TRANSCRIPTION	A	1.5	1.5	1	22	EELVAEAHNLCTLLENAIQDTV	16056
3BUA	BF	DNA BINDING PROTEIN	B	1.5	1.5	1	16	PLESAINVLEMIKTEF	16057
3BUZ	AB	TOXIN/STRUCTURAL PROTEIN	A	1.5	1.5	1	6	DYQIES	16058
3BXK	AB	MEMBRANE PROTEIN, SIGNALING PROTEIN	A	1.5	1.5	1	15	EEQIAEFKEAFSLFD	16059
3BXK	CD	MEMBRANE PROTEIN, SIGNALING PROTEIN	C	1.5	1.5	1	12	DEEVDEMIREAD	16060
3BZ1	AC	ELECTRON TRANSPORT	C	1.5	1.5	1	19	GPEASQAQAMTFLIRDQKL	16061
3BZ1	AD	ELECTRON TRANSPORT	D	1.5	1.5	1	12	LLCAIHGATVEN	16062
3BZ4	EF	IMMUNE SYSTEM	E	1.5	1.5	1	6	SEQLTS	16063
3BZL	BD	MEMBRANE PROTEIN, PROTEIN TRANSPORT	D	1.5	1.5	1	13	AKALQIIKLAELY	16064
3C5Z	EF	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	F	1.5	1.5	1	5	EAEIS	16065
3C91	FM	HYDROLASE	M	1.5	1.5	1	22	VGDAQVLVRYMKAELELYRLQR	16066
3C91	QX	HYDROLASE	X	1.5	1.5	1	22	VGDAQVLVRYMKAELELYRLQR	16067
3CF4	AG	OXIDOREDUCTASE	A	1.5	1.5	1	5	PHSSK	16068
3CF4	AG	OXIDOREDUCTASE	A	1.5	1.5	1	13	WQEAIPMMAKACI	16069

3CF6	ER	SIGNALING PROTEIN/GTP-BINDING PROTEIN	E	1.5	1.5	1	13	KFKKFYAEFESLM	16070
3CFK	AB	IMMUNE SYSTEM	A	1.5	1.5	1	7	DEQLKSG	16071
3CFK	GI	IMMUNE SYSTEM	G	1.5	1.5	1	7	DEQLKSG	16072
3CHX	EF	MEMBRANE PROTEIN	F	1.5	1.5	1	8	LADLVGFH	16073
3CLE	LH	IMMUNE SYSTEM	L	1.5	1.5	1	6	SEQLTS	16074
3CUE	CE	PROTEIN TRANSPORT	C	1.5	1.5	1	17	TQVLQYIYSHIYVKYVS	16075
3CUE	SV	PROTEIN TRANSPORT	V	1.5	1.5	1	14	NILCGVLKGSLEMV	16076
3CVH	HL	IMMUNE SYSTEM	L	1.5	1.5	1	6	SEQLTS	16077
3CWB	OF	OXIDOREDUCTASE	O	1.5	1.5	1	19	PWEVTDLQPQLKVDKAVAF	16078
3CWB	PR	OXIDOREDUCTASE	P	1.5	1.5	1	23	WNFGSLLAVCLMTQILTGLLLAM	16079
3CWB	PR	OXIDOREDUCTASE	P	1.5	1.5	1	29	GWLIRNLHANGASFFFICIFLHIGRGLYY	16080
3CXH	CP	OXIDOREDUCTASE	C	1.5	1.5	1	22	KLLGVITMFAAILVLLVLPFTD	16081
3CXH	NE	OXIDOREDUCTASE	N	1.5	1.5	1	33	NPTIQRFFALHYLVPFIIAAMVIMHLMALHIHG	16082
3CXH	NE	OXIDOREDUCTASE	N	1.5	1.5	1	22	KLLGVITMFAAILVLLVLPFTD	16083
3D24	AB	TRANSCRIPTION	A	1.5	1.5	1	23	AVATLCDLFDREIVVTISWAKSI	16084
3D2E	CD	CHAPERONE	D	1.5	1.5	1	18	KRAVRRLRTACERAKRTL	16085
3D4U	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.5	1.5	1	5	ECVSK	16086
3D5A	BH	RIBOSOME	B	1.5	1.5	1	9	AIAVREARK	16087
3D6N	AB	HYDROLASE/TRANSFERASE	A	1.5	1.5	1	7	EVSALLG	16088
3DBH	AB	CELL CYCLE	A	1.5	1.5	1	5	LVLPG	16089
3DBH	CD	CELL CYCLE	C	1.5	1.5	1	14	ATGTEILKNLVLPG	16090
3DBH	FK	CELL CYCLE	F	1.5	1.5	1	13	IIARRWINGMLIS	16091
3DCG	AB	LIGASE/VIRAL PROTEIN	A	1.5	1.5	1	12	VFELKRIVEGIL	16092
3DGE	AD	TRANSFERASE/SIGNALING PROTEIN	A	1.5	1.5	1	32	LSTLKEFLEVIIDQSNHLENLLNELLDFSRLE	16093
3DHR	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.5	1.5	1	20	PENFRLLGDILVIILAAHFG	16094
3DHR	EH	OXYGEN STORAGE, OXYGEN TRANSPORT	H	1.5	1.5	1	20	PENFRLLGDILVIILAAHFG	16095
3DIN	BF	MEMBRANE PROTEIN, PROTEIN TRANSPORT	B	1.5	1.5	1	26	VEFKKETYYMFDEMMRRINDTIANYV	16096
3DIN	CE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.5	1.5	1	7	TVLSTMS	16097
3DIN	FH	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	1.5	1.5	1	7	TVLSTMS	16098
3DL8	GE	PROTEIN TRANSPORT	G	1.5	1.5	1	28	FILITVLTLVAGTMFLVWIADRITEKGI	16099
3DL8	HF	PROTEIN TRANSPORT	H	1.5	1.5	1	28	FILITVLTLVAGTMFLVWIADRITEKGI	16100
3DNL	GI	VIRAL PROTEIN	G	1.5	1.5	1	10	VEQMHEDIIS	16101
3DQV	AC	LIGASE	C	1.5	1.5	1	22	EEENEGIVQLRILRTQEAIIQI	16102
3DTP	AE	CONTRACTILE PROTEIN	E	1.5	1.5	1	12	KNDIRATFDSLG	16103

3DTU	CD	OXIDOREDUCTASE	C	1.5	1.5	1	18	GHLWNVMITGHGILMMFF	16104
3DUF	EF	OXIDOREDUCTASE/TRANSFERASE	E	1.5	1.5	1	10	FNLKEQYEIY	16105
3DVE	AB	MEMBRANE PROTEIN	A	1.5	1.5	1	11	TKELGTVMRSL	16106
3DWL	IK	STRUCTURAL PROTEIN	I	1.5	1.5	1	19	FRNTLHFHIKASKAYMHQR	16107
3DWL	IK	STRUCTURAL PROTEIN	K	1.5	1.5	1	8	EIERILVR	16108
3DXA	AE	IMMUNE SYSTEM	A	1.5	1.5	1	29	PEYWDRETQISKTNTQTYRENLRTALRYY	16109
3DZU	AD	TRANSCRIPTION/DNA	D	1.5	1.5	1	5	REFLK	16110
3E0J	EF	TRANSFERASE	E	1.5	1.5	1	9	EGEQCSAAH	16111
3EA5	AB	TRANSPORT PROTEIN	B	1.5	1.5	1	18	QNIRLTSETQLKKLSNDN	16112
3EA5	CD	TRANSPORT PROTEIN	C	1.5	1.5	1	12	KPFLWLARKLIG	16113
3EB6	AB	APOPTOSIS, LIGASE	B	1.5	1.5	1	16	MALKRIHKELNDLARD	16114
3EDX	EF	HYDROLASE	E	1.5	1.5	1	5	EKTFG	16115
3EIQ	AC	HYDROLASE/ANTITUMOR PROTEIN	A	1.5	1.5	1	15	RELAQQIQKVVMALG	16116
3ENO	AC	HYDROLASE/UNKNOWN FUNCTION	C	1.5	1.5	1	23	SSALRGTVNSYLRWIKAAIDVIE	16117
3EQS	AB	LIGASE	A	1.5	1.5	1	11	HRKIYTMIYRN	16118
3ERC	AD	TRANSCRIPTION, TRANSFERASE/DNA, RNA	D	1.5	1.5	1	11	ENVLSSDILDL	16119
3EUB	23	OXIDOREDUCTASE	3	1.5	1.5	1	9	EIGIEMKFK	16120
3EUB	34	OXIDOREDUCTASE	4	1.5	1.5	1	8	PEKIRNAC	16121
3EUB	BC	OXIDOREDUCTASE	C	1.5	1.5	1	8	PEKIRNAC	16122
3EX7	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.5	1.5	1	12	DIRILRDIEQYY	16123
3EXG	36	OXIDOREDUCTASE	6	1.5	1.5	1	12	VKDIIFAIKKTL	16124
3EXG	36	OXIDOREDUCTASE	6	1.5	1.5	1	7	FNFSMQA	16125
3EXG	MN	OXIDOREDUCTASE	M	1.5	1.5	1	13	GQIFEAYNMAALW	16126
3EXG	SR	OXIDOREDUCTASE	R	1.5	1.5	1	7	FNFSMQA	16127
3EXH	EC	OXIDOREDUCTASE	E	1.5	1.5	1	17	AQVPLGAGIALACKYNG	16128
3EZQ	KL	APOPTOSIS	K	1.5	1.5	1	15	SDVDLSKYITTIAGV	16129
3F3P	AD	STRUCTURAL PROTEIN	D	1.5	1.5	1	6	SAEYLQ	16130
3FH6	FG	TRANSPORT PROTEIN	F	1.5	1.5	1	14	KAVYRVLLILPYAV	16131
3FH6	HI	TRANSPORT PROTEIN	H	1.5	1.5	1	14	KAVYRVLLILPYAV	16132
3FHI	AB	TRANSFERASE	A	1.5	1.5	1	18	KAVDWWALGVLIYEMAAG	16133
3FIE	AC	HYDROLASE, TOXIN/PROTEIN TRANSPORT	A	1.5	1.5	1	13	PAGEVLLQEISYA	16134
3FIH	KG	RIBOSOME	K	1.5	1.5	1	15	PFAAQVAAERCADAV	16135
3FKS	AE	HYDROLASE	E	1.5	1.5	1	15	TREGNDLYREMKETG	16136
3FKS	FG	HYDROLASE	F	1.5	1.5	1	8	QDIIAILG	16137
3FKS	GI	HYDROLASE	G	1.5	1.5	1	22	VPRDLFEYTLANQMLTAMAQGY	16138
3FKU	GH	VIRAL PROTEIN/IMMUNE SYSTEM	H	1.5	1.5	1	18	DFHDSNVKNLYDKVRLQL	16139
3FWB	BC	CELL CYCLE, TRANSCRIPTION	C	1.5	1.5	1	16	NYELISNELKARLLQE	16140

3G43	BE	METAL BINDING PROTEIN	B	1.5	1.5	1	11	EEIREAFRVFD	16141
3GE8	AB	OXIDOREDUCTASE	A	1.5	1.5	1	16	WAAIAAKHFFDDIITG	16142
3GE8	BH	OXIDOREDUCTASE	H	1.5	1.5	1	11	VEPVIETAEID	16143
3GE8	DF	OXIDOREDUCTASE	D	1.5	1.5	1	5	YELTR	16144
3GE8	DF	OXIDOREDUCTASE	D	1.5	1.5	1	7	IVDRFLA	16145
3GGR	AC	CELL CYCLE	C	1.5	1.5	1	8	SEGLREAF	16146
3GJF	AH	IMMUNE SYSTEM	A	1.5	1.5	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	16147
3GJX	CA	PROTEIN TRANSPORT	A	1.5	1.5	1	22	TEIFKICLEYWNHLAAELYRES	16148
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.5	1.5	1	23	PQVCAKLFGNIQKVVNFWLLHNG	16149
3GTM	BI	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.5	1.5	1	14	WQMLEMLKPCVEDG	16150
3GTM	CL	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.5	1.5	1	11	DEFIAHRLGLI	16151
3H0L	BC	LIGASE	C	1.5	1.5	1	7	REKALMN	16152
3H0L	WX	LIGASE	X	1.5	1.5	1	7	REKALMN	16153
3H32	AC	BLOOD CLOTTING	A	1.5	1.5	1	44	EVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRG	16154
3H87	BC	TOXIN/ANTITOXIN	C	1.5	1.5	1	8	PELMRQAW	16155
3HHL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.5	1.5	1	10	KEVFAQFRAN	16156
3HHZ	AK	VIRAL PROTEIN/RNA	K	1.5	1.5	1	10	VVEWLGWFED	16157
3HHZ	DN	VIRAL PROTEIN/RNA	N	1.5	1.5	1	11	VVEWLGWFEDQ	16158
3HKZ	BL	TRANSFERASE	L	1.5	1.5	1	13	HTLGNLIAGTLRR	16159
3HKZ	DL	TRANSFERASE	L	1.5	1.5	1	5	EIKGL	16160
3HKZ	IJ	TRANSFERASE	J	1.5	1.5	1	5	RLLDN	16161
3HKZ	OV	TRANSFERASE	O	1.5	1.5	1	7	IRRASML	16162
3HKZ	QR	TRANSFERASE	R	1.5	1.5	1	8	EDVRAILA	16163
3HOU	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.5	1.5	1	11	TLFCCLLRSRL	16164
3HOU	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.5	1.5	1	7	LIEKFLR	16165
3HOU	MQ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.5	1.5	1	11	TLFCCLLRSRL	16166
3HOU	NO	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.5	1.5	1	6	QSSIDR	16167
3HOU	PS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	P	1.5	1.5	1	9	PFEVAQLGS	16168
3HOU	PS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	P	1.5	1.5	1	7	ADEAKTL	16169

3HOY	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.5	1.5	1	10	YCCRRMILTH	16170
3HPG	FK	TRANSFERASE	F	1.5	1.5	1	15	GQEFRVQTMKWYAMF	16171
3PRO	BD	PRO REGION	D	1.5	1.5	1	17	PTQLPQYLQTEKLARTQ	16172
3UBP	AC	HYDROLASE	A	1.5	1.5	1	19	YPEAVAIITSFIMEGARDG	16173
4RUB	BT	LYASE(CARBON-CARBON)	B	1.5	1.5	1	9	IQVERDKLN	16174
4RUB	DV	LYASE(CARBON-CARBON)	D	1.5	1.5	1	8	IQVERDKL	16175
7FAB	LH	IMMUNOGLOBULIN	L	1.5	1.5	1	6	SEELQA	16176
1NOV	CF	VIRUS	C	1.4	1.4	1	14	EYALAAYRKIARDI	16177
1A0H	DE	COMPLEX (SERINE PROTEASE/INHIBITOR)	E	1.4	1.4	1	8	RPVCKAST	16178
1A9W	AF	OXYGEN TRANSPORT	A	1.4	1.4	1	19	PVNFKLLSHCLLVTLAAHL	16179
1A9W	CE	OXYGEN TRANSPORT	C	1.4	1.4	1	19	PVNFKLLSHCLLVTLAAHL	16180
1AGR	AE	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	E	1.4	1.4	1	16	EENIDFWISCEEYKKI	16181
1AJS	AB	AMINOTRANSFERASE	A	1.4	1.4	1	11	ENHNGVFTTAG	16182
1AOI	GH	DNA BINDING PROTEIN/DNA	G	1.4	1.4	1	10	VGRVHRLLRK	16183
1AON	GU	COMPLEX (GROEL/GROES)	G	1.4	1.4	1	13	GEALATLVVNTMR	16184
1AW8	AB	DECARBOXYLASE	B	1.4	1.4	1	6	DEEART	16185
1B33	ED	PHOTOSYNTHESIS	D	1.4	1.4	1	25	TRRYAACIRDLDYYLRYATYAMLAG	16186
1B8D	AB	PHOTOSYNTHESIS	B	1.4	1.4	1	12	SDLQSLKSFIND	16187
1B9X	AB	SIGNALING PROTEIN	A	1.4	1.4	1	5	LSQIT	16188
1BDJ	AB	COMPLEX (CHEMOTAXIS/TRANSFERASE)	B	1.4	1.4	1	16	WRHDVEVLKAWVAKAT	16189
1BEV	12	VIRUS	2	1.4	1.4	1	5	FDRTM	16190
1BGX	TL	COMPLEX (POLYMERASE/INHIBITOR)	T	1.4	1.4	1	25	VAYLRALSLEVAEEIARLEAEVFRL	16191
1BGY	AC	ELECTRON TRANSPORT	A	1.4	1.4	1	6	YNRIRS	16192
1BGY	CF	ELECTRON TRANSPORT	C	1.4	1.4	1	22	PLSQCLFWALVADLLTLTWIGG	16193
1BGY	CG	ELECTRON TRANSPORT	C	1.4	1.4	1	33	HPYITIGQLASVLYFLLILVLMPTAGTIENKLL	16194
1BGY	MN	ELECTRON TRANSPORT	M	1.4	1.4	1	10	ALEKEVESMG	16195
1BGY	MU	ELECTRON TRANSPORT	M	1.4	1.4	1	20	DSQIEKERDVILQELQENDT	16196
1BH8	AB	TRANSCRIPTION REGULATION COMPLEX	B	1.4	1.4	1	13	EEQLNRYEMYRRS	16197
1BH8	AB	TRANSCRIPTION REGULATION COMPLEX	B	1.4	1.4	1	9	KAAIKRLIQ	16198
1BI4	AB	DNA INTEGRATION	B	1.4	1.4	1	14	AGERIVDIIATDIQ	16199
1BJO	AB	AMINOTRANSFERASE	A	1.4	1.4	1	17	TFAWYLSGLVFKWLKAN	16200
1BJO	AB	AMINOTRANSFERASE	B	1.4	1.4	1	17	TFAWYLSGLVFKWLKAN	16201
1BVY	AF	OXIDOREDUCTASE	A	1.4	1.4	1	13	KNWKKAHNILLPS	16202
1BVY	AF	OXIDOREDUCTASE	F	1.4	1.4	1	16	TAEGTARDLADIAMSK	16203

1C0G	SA	CONTRACTILE PROTEIN	A	1.4	1.4	1	9	QAVLSLYAS	16204
1C4Z	AD	LIGASE	A	1.4	1.4	1	11	RKEFVNLYSDY	16205
1CDL	DH	CALCIUM-BINDING PROTEIN	D	1.4	1.4	1	12	AAELRHVMTNLG	16206
1CGI	EI	SERINE PROTEASE/INHIBITOR COMPLEX	E	1.4	1.4	1	9	NTNCKKYWG	16207
1D2Z	AB	APOPTOSIS	B	1.4	1.4	1	12	FSAADFVALDFL	16208
1D9K	BC	IMMUNE SYSTEM	C	1.4	1.4	1	22	PQGGLQNIATGKHNLEILTKRS	16209
1D9K	CP	IMMUNE SYSTEM	C	1.4	1.4	1	22	PQGGLQNIATGKHNLEILTKRS	16210
1DEE	EF	IMMUNE SYSTEM	E	1.4	1.4	1	6	DEQLKS	16211
1DGR	BM	PLANT PROTEIN	B	1.4	1.4	1	8	YDEIEQTL	16212
1DGR	CY	PLANT PROTEIN	Y	1.4	1.4	1	8	GEEVEELL	16213
1DII	AC	OXIDOREDUCTASE	C	1.4	1.4	1	14	GKNLYDKVCGHCHK	16214
1DIO	AG	LYASE	A	1.4	1.4	1	11	GLEVVKALAQG	16215
1DIO	AG	LYASE	G	1.4	1.4	1	5	LANKH	16216
1DIO	LM	LYASE	L	1.4	1.4	1	11	LIDHFIARYGI	16217
1DKF	AB	HORMONE/GROWTH FACTOR RECEPTOR	A	1.4	1.4	1	7	RFAKLLL	16218
1DQQ	CD	IMMUNE SYSTEM	C	1.4	1.4	1	6	SEQLTS	16219
1E6V	AC	OXIDOREDUCTASE	C	1.4	1.4	1	11	DVAENRRKYMN	16220
1E6V	DF	OXIDOREDUCTASE	F	1.4	1.4	1	11	DVAENRRKYMN	16221
1E6Y	AB	OXIDOREDUCTASE	B	1.4	1.4	1	12	KVEGTAVGFSFF	16222
1E7P	BC	OXIDOREDUCTASE	B	1.4	1.4	1	14	LQSKIAYLRRKMVS	16223
1E7P	HI	OXIDOREDUCTASE	H	1.4	1.4	1	14	LQSKIAYLRRKMVS	16224
1E7P	KL	OXIDOREDUCTASE	K	1.4	1.4	1	14	LQSKIAYLRRKMVS	16225
1E9Y	AB	HYDROLASE	A	1.4	1.4	1	5	VASMI	16226
1EER	AB	COMPLEX (CYTOKINE/RECEPTOR)	A	1.4	1.4	1	5	FYAWK	16227
1EFN	CD	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER)	D	1.4	1.4	1	15	YKAAVDLSHFLKEKG	16228
1EFP	CD	ELECTRON TRANSPORT	D	1.4	1.4	1	11	ATGQMLAAILG	16229
1EFU	AB	COMPLEX (TWO ELONGATION FACTORS)	B	1.4	1.4	1	11	MMDCKKALTEA	16230
1EIY	AB	LIGASE/RNA	B	1.4	1.4	1	9	PVSIRKTAR	16231
1ES7	CD	CYTOKINE	D	1.4	1.4	1	7	SDFQCKD	16232
1EV1	13	VIRUS	1	1.4	1.4	1	6	IENFLA	16233
1F45	AB	CYTOKINE/CYTPKINE	B	1.4	1.4	1	5	TVEAC	16234
1F60	AB	TRANSLATION	A	1.4	1.4	1	12	KSTTTGHLIYKC	16235
1F66	CD	STRUCTURAL PROTEIN/DNA	D	1.4	1.4	1	12	SREIQTAVRLLL	16236
1F66	FD	STRUCTURAL PROTEIN/DNA	F	1.4	1.4	1	11	AMDVVYALKRQ	16237
1F66	GH	STRUCTURAL PROTEIN/DNA	H	1.4	1.4	1	12	SREIQTAVRLLL	16238
1F93	BF	TRANSCRIPTION	B	1.4	1.4	1	10	RVALQAEKLD	16239

1FE8	IM	IMMUNE SYSTEM	M	1.4	1.4	1	6	SEQLTS	16240
1FH5	LH	IMMUNE SYSTEM	L	1.4	1.4	1	7	SEQLTSG	16241
1FM6	UV	TRANSCRIPTION	U	1.4	1.4	1	24	LDDQVILLRAGWNELLIASFSHRS	16242
1FNT	AI	HYDROLASE/HYDROLASE ACTIVATOR	I	1.4	1.4	1	23	AADTEAVTQLIGSNIELHSLYTS	16243
1FNT	DK	HYDROLASE/HYDROLASE ACTIVATOR	D	1.4	1.4	1	17	RILIEKARVEAQSHRLT	16244
1FNT	Ja	HYDROLASE/HYDROLASE ACTIVATOR	a	1.4	1.4	1	11	LIMPFLDNQVN	16245
1FNT	Ok	HYDROLASE/HYDROLASE ACTIVATOR	O	1.4	1.4	1	14	YQVEYAFKATNQTN	16246
1FNT	QY	HYDROLASE/HYDROLASE ACTIVATOR	Q	1.4	1.4	1	22	TADAEILINTARIHAQNYLKTY	16247
1FNT	RY	HYDROLASE/HYDROLASE ACTIVATOR	R	1.4	1.4	1	17	RILIEKARVEAQSHRLT	16248
1FOE	AB	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	A	1.4	1.4	1	5	LESYL	16249
1FOE	EF	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	E	1.4	1.4	1	5	LESYL	16250
1FQV	KL	LIGASE	K	1.4	1.4	1	9	LPELLKVSG	16251
1FQV	OP	LIGASE	P	1.4	1.4	1	8	PEEIRKTF	16252
1FS1	AB	LIGASE	A	1.4	1.4	1	8	KRWYRLAS	16253
1FS2	CB	LIGASE	C	1.4	1.4	1	9	VSTLHGILS	16254
1G0U	BJ	HYDROLASE	J	1.4	1.4	1	23	AGDTVQFAEYIQANIQLYSIRED	16255
1G0U	HZ	HYDROLASE	H	1.4	1.4	1	18	KEEAIKLASDAIQAGIWN	16256
1G0U	IZ	HYDROLASE	Z	1.4	1.4	1	13	ASLIMPFLDNQVN	16257
1G0U	RZ	HYDROLASE	R	1.4	1.4	1	22	TADARSMIEHARTAAVTHNLYY	16258
1G0U	T2	HYDROLASE	2	1.4	1.4	1	22	AADTQAIADIVQYHLELYTSQY	16259
1G0U	T2	HYDROLASE	T	1.4	1.4	1	22	IPDGRHLVNRGREEAASFKKLY	16260
1G0U	WK	HYDROLASE	K	1.4	1.4	1	19	VEDALYLGKRSILAAAHRD	16261
1G20	CD	OXIDOREDUCTASE	C	1.4	1.4	1	9	EKARKDRNK	16262
1G20	CH	OXIDOREDUCTASE	H	1.4	1.4	1	8	IMEMAAEA	16263
1G3I	CJ	CHAPERONE/HYDROLASE	J	1.4	1.4	1	18	TADAFTLFELFERKLEMH	16264
1G3I	XQ	CHAPERONE/HYDROLASE	Q	1.4	1.4	1	13	ADAFTLFELFERK	16265
1G3N	AB	CELL CYCLE, SIGNALING PROTEIN	B	1.4	1.4	1	10	PEIARRLLLR	16266
1G3N	EF	CELL CYCLE, SIGNALING PROTEIN	F	1.4	1.4	1	9	VIHDAARAG	16267
1G8K	EF	OXIDOREDUCTASE	E	1.4	1.4	1	11	PSVAIARHVAG	16268
1G8K	GH	OXIDOREDUCTASE	G	1.4	1.4	1	5	PYESQ	16269
1GG2	BG	COMPLEX (GTP-BINDING/TRANSDUCER)	B	1.4	1.4	1	7	LSQITNN	16270
1GGI	MJ	IMMUNOGLOBULIN	M	1.4	1.4	1	6	SEQLTS	16271
1GH0	CD	PHOTOSYNTHESIS	D	1.4	1.4	1	14	SNKRLDVVNRITSN	16272
1GH0	QT	PHOTOSYNTHESIS	Q	1.4	1.4	1	17	DAAVEANSYLDYAINAL	16273
1GH0	ST	PHOTOSYNTHESIS	T	1.4	1.4	1	14	SNKRLDVVNRITSN	16274
1GH0	WX	PHOTOSYNTHESIS	X	1.4	1.4	1	14	SNKRLDVVNRITSN	16275
1GK0	CD	HYDROLASE	D	1.4	1.4	1	8	REQVEAAV	16276

1GO4	FB	CELL CYCLE	F	1.4	1.4	1	30	PTSVARQRLREDHSQLQAECERLRGLLRAM	16277
1GUA	AB	COMPLEX (GTP-BINDING/ATP-BINDING)	A	1.4	1.4	1	10	KSALTVQFVQ	16278
1H1L	AD	OXIDOREDUCTASE	A	1.4	1.4	1	16	YDGFAIFARDMDMTLN	16279
1H1V	GA	ACTIN-BINDING	A	1.4	1.4	1	12	SVWIGGSILASL	16280
1H2R	SL	OXIDOREDUCTASE	S	1.4	1.4	1	8	GCSESVLR	16281
1H4L	BE	KINASE/KINASE ACTIVATOR	E	1.4	1.4	1	13	PHYFTQVFSDLKN	16282
1H6K	CZ	NUCLEAR PROTEIN	Z	1.4	1.4	1	12	RADAENAMRYIN	16283
1HBX	AG	GENE REGULATION	A	1.4	1.4	1	27	KLRRYTTFSKRKTGIMKKAYELSTLTG	16284
1HLU	AP	COMPLEX (ACETYLATION/ACTIN-BINDING)	A	1.4	1.4	1	9	VDIRKDLYA	16285
1HQM	CE	TRANSCRIPTION	C	1.4	1.4	1	14	IEGRNAAYQAIIKG	16286
1HR8	CD	HYDROLASE	C	1.4	1.4	1	11	GRAMAETLELL	16287
1I3Q	AB	TRANSCRIPTION	A	1.4	1.4	1	21	PQVCAKLFGNIQKVVNFWLLH	16288
1I3Q	BC	TRANSCRIPTION	C	1.4	1.4	1	13	LAMANSLRRVMIA	16289
1I3R	EF	IMMUNE SYSTEM	F	1.4	1.4	1	14	EVDTVCRHNYEIFD	16290
1I7W	AB	CELL ADHESION	A	1.4	1.4	1	17	QVVVNKAAVMVHQLSKK	16291
1I7Z	AB	IMMUNE SYSTEM	A	1.4	1.4	1	6	DEQLKS	16292
1IBL	CE	RIBOSOME	C	1.4	1.4	1	15	VRRAIKQAVQRVMES	16293
1IBT	AF	LYASE	F	1.4	1.4	1	17	GRRKAMAKSIAECGQDA	16294
1ICF	AB	HYDROLASE	A	1.4	1.4	1	19	CWAFSATGALEGQMFRKTG	16295
1ID3	EC	STRUCTURAL PROTEIN/DNA	E	1.4	1.4	1	13	TVALREIRRFQKS	16296
1IQD	AB	IMMUNE SYSTEM/BLOOD CLOTTING	A	1.4	1.4	1	6	DEQLKS	16297
1IR2	CK	LYASE	C	1.4	1.4	1	10	PELAAACEVW	16298
1IR2	FN	LYASE	F	1.4	1.4	1	10	PELAAACEVW	16299
1IR2	HP	LYASE	H	1.4	1.4	1	10	PELAAACEVW	16300
1IR2	U3	LYASE	U	1.4	1.4	1	10	PELAAACEVW	16301
1IR2	X6	LYASE	X	1.4	1.4	1	10	PELAAACEVW	16302
1IR2	Z8	LYASE	Z	1.4	1.4	1	10	PELAAACEVW	16303
1IRU	AI	HYDROLASE	A	1.4	1.4	1	23	TADSRSQVQRARYEAANWKYKYG	16304
1IRU	CK	HYDROLASE	K	1.4	1.4	1	17	PTAAANFTRRNLADCLR	16305
1IRU	I2	HYDROLASE	I	1.4	1.4	1	11	SLAAMAVFEDK	16306
1IRU	QY	HYDROLASE	Y	1.4	1.4	1	22	AGDTVQFAEYIQKNVQLYKMRN	16307
1IW7	BC	TRANSFERASE	B	1.4	1.4	1	17	FGVTLGNPLRRILLSSI	16308
1IW7	CD	TRANSFERASE	D	1.4	1.4	1	23	MEKTARLLDALKYYGFTFSTTSG	16309
1IWA	AP	LYASE	A	1.4	1.4	1	21	IQAGATANRVALEAMILARNE	16310
1IWA	GD	LYASE	G	1.4	1.4	1	18	WRERYLFTMEAVNKASAA	16311
1IWA	ON	LYASE	N	1.4	1.4	1	14	DEQIKKQIDYMISK	16312
1IWP	AE	LYASE	E	1.4	1.4	1	19	VRPKFMAKAALFHIKETKH	16313

1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.4	1.4	1	12	FPEFLTMMARKM	16314
1IZL	EF	PHOTOSYNTHESIS	E	1.4	1.4	1	5	ALFIA	16315
1IZL	JN	PHOTOSYNTHESIS	J	1.4	1.4	1	18	QLGVAGVFGGALFCAMHG	16316
1J1D	AC	CONTRACTILE PROTEIN	A	1.4	1.4	1	12	EEELSDLFRMFD	16317
1J1D	DF	CONTRACTILE PROTEIN	D	1.4	1.4	1	8	IYKAAVEQ	16318
1J1E	DE	CONTRACTILE PROTEIN	D	1.4	1.4	1	12	EEELSDLFRMFD	16319
1JB0	IL	PHOTOSYNTHESIS	L	1.4	1.4	1	27	ANLGGLISGIALILVATACLAAYGLVS	16320
1JD2	HS	HYDROLASE	S	1.4	1.4	1	19	VEEVIKLVRDSFTSATERH	16321
1JEB	AD	OXYGEN STORAGE/TRANSPORT	D	1.4	1.4	1	20	PENFRLLGNMIVIVLGHHLG	16322
1JEB	CB	OXYGEN STORAGE/TRANSPORT	B	1.4	1.4	1	20	PENFRLLGNMIVIVLGHHLG	16323
1JEB	CD	OXYGEN STORAGE/TRANSPORT	C	1.4	1.4	1	19	PVNFKLLSHCLLVTLAARF	16324
1JJO	CF	SIGNALING PROTEIN	C	1.4	1.4	1	9	FLQMLKMYF	16325
1JMU	CD	VIRAL PROTEIN	C	1.4	1.4	1	5	PGMLN	16326
1JMU	EF	VIRAL PROTEIN	E	1.4	1.4	1	5	PGMLN	16327
1JPW	CF	CELL ADHESION	C	1.4	1.4	1	17	EKLLWTTSRVLKVLSVC	16328
1JRO	GH	OXIDOREDUCTASE	H	1.4	1.4	1	9	HRAARIAAR	16329
1JSU	BC	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.4	1.4	1	8	VAEFVYIT	16330
1JTG	CD	HYDROLASE	C	1.4	1.4	1	6	PVTEKH	16331
1JXP	BD	VIRAL PROTEIN COMPLEX	B	1.4	1.4	1	11	LLGCIITSLTG	16332
1JY7	CD	OXYGEN STORAGE/TRANSPORT	D	1.4	1.4	1	23	PPVQAAYQKVVAGVANALAHKYH	16333
1JY7	PS	OXYGEN STORAGE/TRANSPORT	P	1.4	1.4	1	16	PVNFKLLSHCLLVTLA	16334
1JY7	RS	OXYGEN STORAGE/TRANSPORT	S	1.4	1.4	1	19	PENFRLLGNVLVCVLAHHF	16335
1JY7	UV	OXYGEN STORAGE/TRANSPORT	V	1.4	1.4	1	19	PENFRLLGNVLVCVLAHHF	16336
1JY7	WX	OXYGEN STORAGE/TRANSPORT	W	1.4	1.4	1	18	AHAGEYGAEALERMFLSF	16337
1K5D	AB	SIGNALING PROTEIN/SIGNALING ACTIVATOR	A	1.4	1.4	1	12	KPFLWLARKLIG	16338
1K7L	CD	TRANSCRIPTION	C	1.4	1.4	1	23	LNDQVTLLKYGVYEAIFAMLSSV	16339
1KCS	LH	IMMUNE SYSTEM	L	1.4	1.4	1	6	SEQLSS	16340
1KF6	MN	OXIDOREDUCTASE	N	1.4	1.4	1	13	LLDALGYIKDNLA	16341
1KF9	AB	HORMONE/GROWTH FACTOR	A	1.4	1.4	1	28	LSRLADNAWLRADRLNQLAFDTYQEFEE	16342
1KF9	DE	HORMONE/GROWTH FACTOR	D	1.4	1.4	1	28	LSRLADNAWLRADRLNQLAFDTYQEFEE	16343
1KFY	OP	OXIDOREDUCTASE	O	1.4	1.4	1	13	PEAWAGFVDFLQN	16344
1KTK	BF	IMMUNE SYSTEM	B	1.4	1.4	1	6	DLLYAY	16345
1KXP	AD	CONTRACTILE PROTEIN/PROTEIN BINDING	D	1.4	1.4	1	16	FTEYKKKLAERLKAKL	16346
1KYO	AC	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.4	1.4	1	7	YMRIRSD	16347

1KYO	DE	OXIDOREDUCTASE/ELECTRON TRANSPORT	E	1.4	1.4	1	30	KGRSYAYFMVGAMGLLSSAGAKSTVETFIS	16348
1KYO	OP	OXIDOREDUCTASE/ELECTRON TRANSPORT	P	1.4	1.4	1	31	KGRSYAYFMVGAMGLLSSAGAKSTVETFISS	16349
1KZ7	AB	SIGNALING PROTEIN	B	1.4	1.4	1	19	PSSFENVKEKWVPEITHHC	16350
1L9B	MH	PHOTOSYNTHESIS	M	1.4	1.4	1	5	MEGIH	16351
1L9J	RS	PHOTOSYNTHESIS	S	1.4	1.4	1	12	TAAERAALFWRW	16352
1LIA	KL	LIGHT HARVESTING PROTEIN	L	1.4	1.4	1	14	GNKRLDAVNYIVSN	16353
1LK3	MI	IMMUNE SYSTEM	M	1.4	1.4	1	6	TEQLAT	16354
1LKY	EF	TRANSCRIPTION	F	1.4	1.4	1	8	KEDFRYRS	16355
1LNU	AB	SUGAR BINDING PROTEIN	B	1.4	1.4	1	9	GRPDAEYWN	16356
1LO4	LH	IMMUNE SYSTEM	L	1.4	1.4	1	6	SEQLTS	16357
1LOT	AB	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	A	1.4	1.4	1	11	AMDVFVCTYFM	16358
1LQ8	AB	BLOOD CLOTTING	A	1.4	1.4	1	14	PVSISMSLAMLSLG	16359
1LQS	RL	IMMUNE SYSTEM	L	1.4	1.4	1	14	ATRLQDLRVTFHRV	16360
1LVC	CF	LYASE	F	1.4	1.4	1	7	EFKEAFS	16361
1LWU	DE	BLOOD CLOTTING	E	1.4	1.4	1	10	QKEIENRYKE	16362
1LWU	GF	BLOOD CLOTTING	F	1.4	1.4	1	46	LEEVRILEQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	16363
1LWU	GH	BLOOD CLOTTING	H	1.4	1.4	1	6	ENRYKE	16364
1LYW	CD	ASPARTIC PROTEASE	D	1.4	1.4	1	7	DVFIGRY	16365
1M1E	AB	STRUCTURAL PROTEIN	A	1.4	1.4	1	15	INVVTCAAGILSNLT	16366
1M1J	EF	BLOOD CLOTTING	F	1.4	1.4	1	7	CGIADFF	16367
1M1Y	AB	OXIDOREDUCTASE	B	1.4	1.4	1	8	KEYQELNF	16368
1M2Z	DE	HORMONE/HORMONE ACTIVATOR	E	1.4	1.4	1	9	ALLRYLLDK	16369
1M45	AB	CELL CYCLE PROTEIN	A	1.4	1.4	1	8	DAEVDELL	16370
1M8Q	AC	CONTRACTILE PROTEIN	C	1.4	1.4	1	9	EDFVEGLRV	16371
1M8Q	AC	CONTRACTILE PROTEIN	C	1.4	1.4	1	10	DFKEAFLLFD	16372
1M8Q	GI	CONTRACTILE PROTEIN	I	1.4	1.4	1	8	EAFVKHIM	16373
1MIO	AB	MOLYBDENUM-IRON PROTEIN	A	1.4	1.4	1	6	ESDIVF	16374
1MIO	CD	MOLYBDENUM-IRON PROTEIN	C	1.4	1.4	1	6	CPVGLI	16375
1MIO	CD	MOLYBDENUM-IRON PROTEIN	D	1.4	1.4	1	6	CLSETL	16376
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	C	1.4	1.4	1	10	WNESAFSVHA	16377
1MTY	BG	MONOOXYGENASE	G	1.4	1.4	1	12	DTRDAWVNKIAH	16378
1MTY	CH	MONOOXYGENASE	C	1.4	1.4	1	10	WNESAFSVHA	16379
1MTY	DB	MONOOXYGENASE	B	1.4	1.4	1	10	AVPKAEWTNG	16380
1MTY	DG	MONOOXYGENASE	G	1.4	1.4	1	15	KWEAEKIHIGFRQAY	16381
1MTY	EC	MONOOXYGENASE	C	1.4	1.4	1	9	AVPKAEWTN	16382

1MXE	AE	METAL BINDING PROTEIN	A	1.4	1.4	1	11	EAELQDMINEV	16383
1MZN	CD	TRANSCRIPTION	C	1.4	1.4	1	22	PVTNICQAADKQLFTLVEWAKR	16384
1N1J	AB	DNA BINDING PROTEIN	B	1.4	1.4	1	9	RNDIAMAIT	16385
1N4M	AC	CELL CYCLE	A	1.4	1.4	1	15	AFDFYKVIESFIKAE	16386
1N4M	BD	CELL CYCLE	B	1.4	1.4	1	19	REMIKHLERCEHRIMESLA	16387
1N4Q	GH	TRANSFERASE	G	1.4	1.4	1	15	YQVWHHRRVLVEWLK	16388
1N52	AB	RNA BINDING PROTEIN	B	1.4	1.4	1	10	RADAENAMRY	16389
1N5W	DE	OXIDOREDUCTASE	E	1.4	1.4	1	7	VEDIRFT	16390
1N95	AB	TRANSFERASE	A	1.4	1.4	1	17	EKFRDVYDYFRAVLQRD	16391
1NBU	BC	LYASE	C	1.4	1.4	1	13	YVRLASRAAEIVA	16392
1NEK	BC	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.4	1.4	1	27	FEAGKRSAKISFVITVVLSLLAGVLVW	16393
1NEX	CD	LIGASE, CELL CYCLE	D	1.4	1.4	1	9	FEISLKIFN	16394
1NF3	AC	SIGNALING PROTEIN	A	1.4	1.4	1	10	KTCLLISYTT	16395
1NGM	EF	TRANSCRIPTION/DNA	E	1.4	1.4	1	6	LKTVAL	16396
1NGM	EF	TRANSCRIPTION/DNA	F	1.4	1.4	1	11	ADFLLEQESKR	16397
1NHG	AC	OXIDOREDUCTASE	A	1.4	1.4	1	5	HASQK	16398
1NHG	BD	OXIDOREDUCTASE	B	1.4	1.4	1	23	MSSAKAALESDTRVLAYHLGRNY	16399
1NI4	AB	OXIDOREDUCTASE	B	1.4	1.4	1	9	FAGIAVGAA	16400
1NIK	BJ	TRANSCRIPTION	J	1.4	1.4	1	7	LIEKFLR	16401
1NLW	DE	TRANSCRIPTION/DNA	D	1.4	1.4	1	25	RSTHNEMEKNRRAHLRLSLEKLKGL	16402
1NTK	AB	OXIDOREDUCTASE	B	1.4	1.4	1	19	NPDVQAAKNKLKAGYLMSV	16403
1NTK	AB	OXIDOREDUCTASE	B	1.4	1.4	1	15	SEGFLDEVGSQALAA	16404
1NTK	CF	OXIDOREDUCTASE	C	1.4	1.4	1	22	PLSQCLFWALVADLLTLTWIGG	16405
1NTK	DH	OXIDOREDUCTASE	H	1.4	1.4	1	10	PLTTVREQCE	16406
1NVM	CF	LYASE/OXIDOREDUCTASE	F	1.4	1.4	1	12	HVQNEALLRQAK	16407
1NVM	EF	LYASE/OXIDOREDUCTASE	E	1.4	1.4	1	11	KQHIEYARNLG	16408
1NX0	BD	HYDROLASE	B	1.4	1.4	1	21	FEEFKYLWNNIKKWQAIYKQF	16409
1NZY	AB	LYASE	A	1.4	1.4	1	16	THLQVMAKERFHAGWM	16410
1O0P	AB	RNA BINDING PROTEIN	A	1.4	1.4	1	16	DEEYEEIVEDVRDECS	16411
1OCC	BI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	B	1.4	1.4	1	10	LKYFEKWSAS	16412
1OCC	OV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	O	1.4	1.4	1	10	LKYFEKWSAS	16413
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	1.4	1.4	1	12	ASQKALKEKEKA	16414
1OCC	QX	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	1.4	1.4	1	7	PIQGFSA	16415
1OE9	AB	ATPASE/MYOSIN	B	1.4	1.4	1	9	GAELRHVLT	16416
1OEY	AJ	IMMUNE SYSTEM	J	1.4	1.4	1	6	DEDVAL	16417

1OJ5	AB	TRANSCRIPTIONAL COACTIVATOR	A	1.4	1.4	1	13	WEDLVRKCIYAFF	16418
1OQS	EF	HYDROLASE	E	1.4	1.4	1	13	LFQFGEMILQKTG	16419
1OR0	CD	HYDROLASE	D	1.4	1.4	1	7	QIERVSR	16420
1OUU	AB	OXYGEN TRANSPORT	A	1.4	1.4	1	19	PEVHIAVDKFLAAVSAALA	16421
1OUU	CD	OXYGEN TRANSPORT	C	1.4	1.4	1	18	GNFKILSHNILVTLAIHF	16422
1OUU	CD	OXYGEN TRANSPORT	D	1.4	1.4	1	19	PEIQATWQKFMKVVVAAMG	16423
1OXK	AB	SIGNALING PROTEIN	A	1.4	1.4	1	18	LTELDNLGHFLKGSSAAL	16424
1OXK	GH	SIGNALING PROTEIN	G	1.4	1.4	1	18	LTELDNLGHFLKGSSAAL	16425
1OXK	KL	SIGNALING PROTEIN	K	1.4	1.4	1	10	WTILNEIISM	16426
1OXK	KL	SIGNALING PROTEIN	L	1.4	1.4	1	14	HVNQEVIKRMLNLE	16427
1P16	BD	TRANSFERASE	B	1.4	1.4	1	12	LPKRLGYITENV	16428
1P22	AB	SIGNALING PROTEIN	B	1.4	1.4	1	14	KGLLDVTCKTVANM	16429
1P4E	AC	DNA BINDING PROTEIN/RECOMBINATION/DNA	A	1.4	1.4	1	12	PKVLVRQFVERF	16430
1P4E	AD	DNA BINDING PROTEIN/RECOMBINATION/DNA	D	1.4	1.4	1	12	PKVLVRQFVERF	16431
1PG7	WX	IMMUNE SYSTEM	W	1.4	1.4	1	6	SEELKT	16432
1PGR	EF	CYTOKINE	E	1.4	1.4	1	25	GPTLDTLQLDVADFATTIWQQMEEL	16433
1PID	AB	HORMONE	B	1.4	1.4	1	12	SHLVEALYLVCG	16434
1PMA	IW	PROTEASE	I	1.4	1.4	1	15	IENLVKRVADQMQQY	16435
1POI	CD	TRANSFERASE	D	1.4	1.4	1	15	NVRFVGFEINEYLHK	16436
1PSS	MH	PHOTOSYNTHETIC REACTION CENTER	M	1.4	1.4	1	8	STLLGWFG	16437
1Q1J	MI	IMMUNE SYSTEM	M	1.4	1.4	1	5	SEELQ	16438
1Q86	C1	RIBOSOME	1	1.4	1.4	1	9	VAGKAVMKA	16439
1QHH	BC	HYDROLASE	B	1.4	1.4	1	7	DLSLLRI	16440
1QPW	AB	OXYGEN TRANSPORT	A	1.4	1.4	1	18	PSVHASLDKFLANVSTVL	16441
1QPW	AB	OXYGEN TRANSPORT	B	1.4	1.4	1	16	VDEVGGEALGRLLVVY	16442
1QUQ	CD	DNA-BINDING PROTEIN	D	1.4	1.4	1	14	LGLYNEAVKIIHDF	16443
1R2B	AD	TRANSCRIPTION	A	1.4	1.4	1	15	HASDVLLNLNRLRSR	16444
1R4M	AB	CELL CYCLE	A	1.4	1.4	1	5	LVLPG	16445
1R4M	BI	CELL CYCLE	B	1.4	1.4	1	15	IIARRWINGMLISLL	16446
1R4M	CD	CELL CYCLE	C	1.4	1.4	1	8	DHGQEALE	16447
1R4M	EF	CELL CYCLE	F	1.4	1.4	1	9	YRLTQGVVK	16448
1R4M	GH	CELL CYCLE	G	1.4	1.4	1	8	DHGQEALE	16449
1R4P	AF	TOXIN	A	1.4	1.4	1	7	QFLYTTG	16450
1R5W	AF	SIGNALING PROTEIN	A	1.4	1.4	1	23	AQGALANIAVDKANLDVMKERSN	16451
1R6O	AC	HYDROLASE	C	1.4	1.4	1	11	MEFVIDVLQKF	16452
1RCO	EM	LYASE	E	1.4	1.4	1	15	CEDMMKRAVFARELG	16453
1RCO	HC	LYASE	H	1.4	1.4	1	15	CEDMMKRAVFARELG	16454
1RCO	KT	LYASE	K	1.4	1.4	1	15	CEDMMKRAVFARELG	16455

1RCO	OI	LYASE	O	1.4	1.4	1	15	CEDMMKRAVFARELG	16456
1RCO	RS	LYASE	R	1.4	1.4	1	15	CEDMMKRAVFARELG	16457
1RH5	AC	PROTEIN TRANSPORT	A	1.4	1.4	1	19	FKEKLKWTGIVLVLYFIMG	16458
1RM6	BC	OXIDOREDUCTASE	B	1.4	1.4	1	6	LEAIAE	16459
1RM6	DE	OXIDOREDUCTASE	E	1.4	1.4	1	22	VKYRRRVLLAISRKVVDQLWEA	16460
1RP3	AB	TRANSCRIPTION	A	1.4	1.4	1	21	KRAEAYIKLRIKGAIYDYLRS	16461
1RP3	GH	TRANSCRIPTION	G	1.4	1.4	1	22	PKRAEAYIKLRIKGAIYDYLRS	16462
1RU7	CF	VIRAL PROTEIN	F	1.4	1.4	1	22	QKSTQNAINGITNKVNSVIEKM	16463
1RU7	ED	VIRAL PROTEIN	D	1.4	1.4	1	52	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQL	16464
1RUY	LI	VIRAL PROTEIN	I	1.4	1.4	1	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	16465
1RYP	GH	MULTICATALYTIC PROTEINASE	H	1.4	1.4	1	22	AADTQAIADIVQYHLELYTSQY	16466
1RYP	QY	MULTICATALYTIC PROTEINASE	Y	1.4	1.4	1	22	GDTVQFAEYIQANIQLYSIRED	16467
1RYP	S1	MULTICATALYTIC PROTEINASE	1	1.4	1.4	1	22	AADGDALVKRFKNSVKWYHFDH	16468
1RYP	TU	MULTICATALYTIC PROTEINASE	T	1.4	1.4	1	11	SQGAKTYLERT	16469
1RYP	UV	MULTICATALYTIC PROTEINASE	V	1.4	1.4	1	22	AADTQAIADIVQYHLELYTSQY	16470
1RYP	XL	MULTICATALYTIC PROTEINASE	L	1.4	1.4	1	13	VGELFWKVKEEEG	16471
1RYP	XY	MULTICATALYTIC PROTEINASE	Y	1.4	1.4	1	17	PQAVSSFVRQELAKSIR	16472
1RZ7	LH	IMMUNE SYSTEM	L	1.4	1.4	1	6	DEQLKS	16473
1RZI	MN	IMMUNE SYSTEM	M	1.4	1.4	1	5	DEQLK	16474
1RZR	AD	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	D	1.4	1.4	1	7	VARGLAS	16475
1S5E	BN	TRANSERASE,TOXIN	B	1.4	1.4	1	29	CDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	16476
1S5L	AC	PHOTOSYNTHESIS	C	1.4	1.4	1	19	GPEASQAQAMTFLIRDQKL	16477
1S5L	AD	PHOTOSYNTHESIS	D	1.4	1.4	1	16	VAAIFRFLLFFQGFHN	16478
1S5L	at	PHOTOSYNTHESIS	t	1.4	1.4	1	8	ETITYVFI	16479
1S5L	DM	PHOTOSYNTHESIS	D	1.4	1.4	1	9	ISQEIRAAE	16480
1S5L	LT	PHOTOSYNTHESIS	T	1.4	1.4	1	8	ETITYVFI	16481
1SB0	AB	TRANSCRIPTION	A	1.4	1.4	1	20	RDEYYHLLAEKIYKIQKELE	16482
1SEB	EF	COMPLEX (MHC II/PEPTIDE/TOXIN)	E	1.4	1.4	1	22	AQGALANIAVDKANLEIMTKRS	16483
1SHZ	AF	SIGNALING PROTEIN	A	1.4	1.4	1	22	RPTIYSNVIKGMRVLVDAREKL	16484
1SQX	AC	OXIDOREDUCTASE	A	1.4	1.4	1	7	YNRIRSG	16485
1SQX	AI	OXIDOREDUCTASE	A	1.4	1.4	1	21	DSQIEKERDVILQELQENDTS	16486
1SQX	ED	OXIDOREDUCTASE	E	1.4	1.4	1	35	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMS	16487
1SV0	BD	TRANSCRIPTION	D	1.4	1.4	1	15	RADVWKWLINMAVSE	16488
1SYX	CD	TRANSLATION/IMMUNE SYSTEM	C	1.4	1.4	1	17	KQEMVDIIETVYRGARK	16489
1T03	LH	TRANSFERASE/ANTIBODY/DNA	L	1.4	1.4	1	7	SEQLTSG	16490
1T0Q	AB	OXIDOREDUCTASE	A	1.4	1.4	1	6	PERYKN	16491
1TFO	AB	TOXIN/TOXIN INHIBITOR	B	1.4	1.4	1	15	AIEFSERICVERRRL	16492

1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.4	1.4	1	16	VVVNKAAVMVHQLSKK	16493
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.4	1.4	1	10	REGLLAIFKS	16494
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.4	1.4	1	14	EDITEPAICALRHL	16495
1TI2	AB	OXIDOREDUCTASE	A	1.4	1.4	1	5	PETNS	16496
1TIL	AF	TRANSCRIPTION	A	1.4	1.4	1	9	MGFTIMENF	16497
1TU3	AG	PROTEIN TRANSPORT	G	1.4	1.4	1	33	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	16498
1TX4	AB	COMPLEX (GTPASE ACTIVATN/PROTO-ONCOGENE)	A	1.4	1.4	1	10	NTNLAVVFGP	16499
1TY4	BD	APOPTOSIS	B	1.4	1.4	1	7	TIFEKKH	16500
1TYG	BA	BIOSYNTHETIC PROTEIN	A	1.4	1.4	1	15	AEEAVRIARLAKASG	16501
1TZN	Hh	TOXIN RECEPTOR/TOXIN	h	1.4	1.4	1	16	IHEGLKLANEQIQKAG	16502
1TZN	Ii	TOXIN RECEPTOR/TOXIN	i	1.4	1.4	1	16	IHEGLKLANEQIQKAG	16503
1U0N	AB	BLOOD CLOTTING	A	1.4	1.4	1	11	FVRYVQGLKKK	16504
1U6H	AB	CELL ADHESION	A	1.4	1.4	1	18	RTIESILEPVAQQISHLV	16505
1UCY	LE	COMPLEX (SERINE PROTEASE/COAGULATION)	L	1.4	1.4	1	7	EKELFES	16506
1UEX	AC	TOXIN/BLOOD CLOTTING	C	1.4	1.4	1	11	FVRYVQGLKKK	16507
1UJ3	AB	IMMUNE SYSTEM/BLOOD CLOTTING	A	1.4	1.4	1	6	DEQLKS	16508
1UJW	AB	TRANSPORT PROTEIN/HYDROLASE	B	1.4	1.4	1	32	QAKAVQVYNSRKSELDAANKTLADAIAEIKQF	16509
1UZD	AI	LYASE	I	1.4	1.4	1	14	DEQIAAQVDYIVAN	16510
1UZD	OT	LYASE	T	1.4	1.4	1	14	DEQIAAQVDYIVAN	16511
1UZD	VW	LYASE	V	1.4	1.4	1	21	NAPGAAANRVALEACTQARNE	16512
1UZH	RM	LYASE	R	1.4	1.4	1	10	PELAAACEVW	16513
1V02	BE	HYDROLASE	E	1.4	1.4	1	24	FLDQQAQERSMDKCLGWFLEPVVR	16514
1V54	CJ	OXIDOREDUCTASE	J	1.4	1.4	1	8	VAEKQKLF	16515
1V54	PW	OXIDOREDUCTASE	W	1.4	1.4	1	8	VAEKQKLF	16516
1V54	TU	OXIDOREDUCTASE	U	1.4	1.4	1	14	ISWVSTWDDRRAEG	16517
1V9U	13	VIRUS/RECEPTOR	1	1.4	1.4	1	6	IRRKFE	16518
1VCB	HF	TRANSCRIPTION	H	1.4	1.4	1	7	GTIKAML	16519
1VF5	CG	PHOTOSYNTHESIS	G	1.4	1.4	1	7	VLGLVFA	16520
1VF5	FH	PHOTOSYNTHESIS	F	1.4	1.4	1	26	EMLYAALLSFGLIFVGWGLGVLLLKI	16521
1VF5	NP	PHOTOSYNTHESIS	P	1.4	1.4	1	25	PNRVKWMIAFICLVMLAQLMLILKK	16522
1VF5	ST	PHOTOSYNTHESIS	S	1.4	1.4	1	26	EMLYAALLSFGLIFVGWGLGVLLLKI	16523
1VS5	JN	RIBOSOME	N	1.4	1.4	1	9	IKVREAAMR	16524
1VSP	RW	RIBOSOME	W	1.4	1.4	1	16	SPVELEKLVREKKREL	16525
1W5C	AD	PHOTOSYNTHESIS	A	1.4	1.4	1	24	GPYQLIIFHFLLGASCYMGRQWEL	16526
1W5C	AD	PHOTOSYNTHESIS	A	1.4	1.4	1	26	PFHQLGVAGVFGGALFCAMHGSLVTS	16527

1W5C	AD	PHOTOSYNTHESIS	D	1.4	1.4	1	18	PFHMMGVAGVLGGALLCA	16528
1W5C	GJ	PHOTOSYNTHESIS	G	1.4	1.4	1	26	PFHQLGVAGVFGGALFCAMHGSLVTS	16529
1W5C	GJ	PHOTOSYNTHESIS	J	1.4	1.4	1	18	PFHMMGVAGVLGGALLCA	16530
1W5C	JK	PHOTOSYNTHESIS	K	1.4	1.4	1	6	LAYDVF	16531
1W7P	CD	PROTEIN TRANSPORT	C	1.4	1.4	1	22	SLTRRQQISTWIDIISQYCKTK	16532
1WDC	AB	MUSCLE PROTEIN	B	1.4	1.4	1	9	DKELTAMLK	16533
1WR6	AE	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	1.4	1.4	1	6	DGDREL	16534
1WR6	BF	PROTEIN TRANSPORT/SIGNALING PROTEIN	B	1.4	1.4	1	6	DGDREL	16535
1X3Z	AB	HYDROLASE	A	1.4	1.4	1	21	DDEIYQLACRDEQEQIELIRG	16536
1X75	BC	ISOMERASE/SIGNALING PROTEIN	C	1.4	1.4	1	14	ENDIKNAINLMFWG	16537
1XFU	DR	LYASE/METAL BINDING PROTEIN	R	1.4	1.4	1	10	YEEFVQMMTA	16538
1XFV	FT	LYASE/METAL BINDING PROTEIN	F	1.4	1.4	1	7	GYLSDYY	16539
1XKM	AD	ANTIBIOTIC	D	1.4	1.4	1	19	LIEARKYLEQLHRKLKNCK	16540
1XKP	AB	MEMBRANE PROTEIN/CHAPERON	B	1.4	1.4	1	19	LPLLHQAFEQLLRLQQEVL	16541
1XLS	BJ	TRANSCRIPTION	J	1.4	1.4	1	7	ALLRYLL	16542
1XOF	AB	DE NOVO PROTEIN	A	1.4	1.4	1	9	EAEKLLRDA	16543
1XQS	BD	CHAPERONE	B	1.4	1.4	1	22	EAEQAADQQEREGALELLADLC	16544
1XTC	CG	TOXIN	G	1.4	1.4	1	12	MKDTLRIAYLTE	16545
1XV9	AB	DNA BINDING PROTEIN	A	1.4	1.4	1	22	LPALRSIGLKCLEHLFFFKLIG	16546
1Y64	AB	STRUCTURAL PROTEIN	B	1.4	1.4	1	7	PSVVEFL	16547
1Y76	AD	TRANSPORT PROTEIN	A	1.4	1.4	1	20	PLFNQILTLQQSIKQLKGQL	16548
1YA7	EO	HYDROLASE/HYDROLASE ACTIVATOR	E	1.4	1.4	1	12	FQVEYAREAVKK	16549
1YA7	GN	HYDROLASE/HYDROLASE ACTIVATOR	G	1.4	1.4	1	15	IENLVKRVADQMQQY	16550
1YE9	AE	OXIDOREDUCTASE	E	1.4	1.4	1	13	PYIRERVVDQLAH	16551
1YE9	DG	OXIDOREDUCTASE	D	1.4	1.4	1	9	FPDFVHAVK	16552
1YE9	IM	OXIDOREDUCTASE	M	1.4	1.4	1	13	FHRRELWEAIEAG	16553
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	I	1.4	1.4	1	21	DRKVAMGFLAATILIVVMAMS	16554
1YHU	FG	OXYGEN STORAGE/TRANSPORT	F	1.4	1.4	1	15	PLQRLKVKRQWAEAY	16555
1YHU	KD	OXYGEN STORAGE/TRANSPORT	D	1.4	1.4	1	16	PDAWSRCFNRITTGMT	16556
1YKK	KL	OXIDOREDUCTASE	L	1.4	1.4	1	6	KTSIAR	16557
1YNJ	CD	TRANSFERASE	D	1.4	1.4	1	5	FRQNL	16558
1YNT	AB	IMMUNE SYSTEM	A	1.4	1.4	1	5	SEQLT	16559
1Z0J	AB	PROTEIN TRANSPORT	A	1.4	1.4	1	9	RALAPMYYR	16560
1Z5X	UE	HORMONE/GROWTH FACTOR RECEPTOR	E	1.4	1.4	1	21	GWKVEKIQEIYIEALKAYVEN	16561
1Z6O	JT	METAL BINDING PROTEIN	T	1.4	1.4	1	13	EALGEFIFDKKLL	16562
1Z7M	AE	TRANSFERASE	E	1.4	1.4	1	6	KSSFKF	16563

1Z7Q	AG	HYDROLASE/HYDROLASE ACTIVATOR	A	1.4	1.4	1	21	IPDARNAALRAKAEAAEFRYK	16564
1Z7Q	Ai	HYDROLASE/HYDROLASE ACTIVATOR	A	1.4	1.4	1	10	YQVEYAFKAT	16565
1Z7Q	Ai	HYDROLASE/HYDROLASE ACTIVATOR	i	1.4	1.4	1	20	LGVAVQHAVLKIIDELEIKT	16566
1Z7Q	BJ	HYDROLASE/HYDROLASE ACTIVATOR	B	1.4	1.4	1	17	TKLLVSEVAKIMQEATQ	16567
1Z7Q	Ja	HYDROLASE/HYDROLASE ACTIVATOR	J	1.4	1.4	1	9	SDQLFGMCE	16568
1Z7Q	JZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.4	1.4	1	11	VGELFWKVKEE	16569
1Z7Q	OU	HYDROLASE/HYDROLASE ACTIVATOR	O	1.4	1.4	1	21	IPDARNAALRAKAEAAEFRYK	16570
1Z7Q	Sa	HYDROLASE/HYDROLASE ACTIVATOR	a	1.4	1.4	1	15	INSAARNIQHLLYGK	16571
1Z7Q	UV	HYDROLASE/HYDROLASE ACTIVATOR	U	1.4	1.4	1	22	IPDGRHLVNRGREEAASFKKLY	16572
1Z7Q	VN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.4	1.4	1	7	FGAHMAN	16573
1Z7Q	WN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.4	1.4	1	18	VQVAEEAIVNAMRVLYYR	16574
1Z7Q	XY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.4	1.4	1	17	PQAVSSFVRQELAKSIR	16575
1ZBB	BD	STRUCTURAL PROTEIN/DNA	D	1.4	1.4	1	12	SREIQTAVRLLL	16576
1ZBB	cd	STRUCTURAL PROTEIN/DNA	c	1.4	1.4	1	10	PRHLQLAVRN	16577
1ZC4	AD	SIGNALING PROTEIN	A	1.4	1.4	1	11	AAIRDNYFRSG	16578
1ZC4	AD	SIGNALING PROTEIN	D	1.4	1.4	1	26	AKIKREWLEVLEETKRALSDKRRREQ	16579
1ZGL	AC	IMMUNE SYSTEM	A	1.4	1.4	1	20	ALANIAVDKANLEIMTKRSN	16580
1ZGL	EF	IMMUNE SYSTEM	E	1.4	1.4	1	13	AVDTYCRHNYGVG	16581
1ZGL	JK	IMMUNE SYSTEM	K	1.4	1.4	1	8	RPDAEYWN	16582
1ZLA	EC	PROTEIN BINDING/VIRUS/DNA	E	1.4	1.4	1	11	TVALREIRRYQ	16583
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	G	1.4	1.4	1	7	EELNKLL	16584
1ZNV	AD	HYDROLASE/PROTEIN BINDING	D	1.4	1.4	1	9	RNNNDRMKV	16585
1ZOY	AB	OXIDOREDUCTASE	A	1.4	1.4	1	12	PGISETAMIFAG	16586
1ZRT	CD	OXIDOREDUCTASE/METAL TRANSPORT	D	1.4	1.4	1	30	LVARKQMGLVAMVMLGLLSVMLYLTNKRLW	16587
1ZRT	PQ	OXIDOREDUCTASE/METAL TRANSPORT	Q	1.4	1.4	1	30	LVARKQMGLVAMVMLGLLSVMLYLTNKRLW	16588
1ZUN	AB	TRANSFERASE	A	1.4	1.4	1	12	ELDIWQYIYLEG	16589
1ZY8	FM	OXIDOREDUCTASE	F	1.4	1.4	1	7	CEDIARV	16590
2A1D	AB	HYDROLASE	B	1.4	1.4	1	8	KQTAAKLL	16591
2A1T	DR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.4	1.4	1	6	IQHLAG	16592
2A40	AB	STRUCTURAL PROTEIN	B	1.4	1.4	1	11	VAVGKLLDYLN	16593
2A45	JK	BLOOD CLOTTING	K	1.4	1.4	1	21	GCQLQEALLQQERPIRNSVDE	16594
2A45	JL	BLOOD CLOTTING	J	1.4	1.4	1	25	CRMKGLIDEVNQDFTNRINKLKNSL	16595
2A5Y	AB	APOPTOSIS	B	1.4	1.4	1	6	STFDLF	16596
2AA1	AB	OXYGEN STORAGE/TRANSPORT	B	1.4	1.4	1	20	PDNFKLLADCLTIVVAARFG	16597
2ACL	EF	TRANSCRIPTION	F	1.4	1.4	1	10	REDQIALLKT	16598
2AFH	AB	OXIDOREDUCTASE	B	1.4	1.4	1	14	SYGKFIQRDTLHKG	16599
2AFH	AF	OXIDOREDUCTASE	A	1.4	1.4	1	6	EKDIVF	16600

2AFH	CD	OXIDOREDUCTASE	C	1.4	1.4	1	29	ESIQKKCEEVIAKYKPEWEAVVAKYRPRL	16601
2AHM	BG	VIRAL PROTEIN, REPLICATION	G	1.4	1.4	1	68	EVVLKKLKKSLNVAKSEFDRDAAMQRKLEKMADQAMTQMYKQARS EDKRAKVTSAMQTMLFTMLRKLD	16602
2AHM	DE	VIRAL PROTEIN, REPLICATION	E	1.4	1.4	1	23	EDKRAKVTSAMQTMLFTMLRKLD	16603
2AK4	AC	IMMUNE SYSTEM	A	1.4	1.4	1	13	LCVEWLRRYLENG	16604
2AQ1	AB	IMMUNE SYSTEM	B	1.4	1.4	1	8	QSKYLMMY	16605
2AQ1	CD	IMMUNE SYSTEM	D	1.4	1.4	1	8	QSKYLMMY	16606
2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	A	1.4	1.4	1	5	PEEIR	16607
2AUS	CD	ISOMERASE/STRUCTURAL PROTEIN	C	1.4	1.4	1	8	EEYIRKAI	16608
2AXT	av	ELECTRON TRANSPORT	a	1.4	1.4	1	16	WADIINRANLGMEVMH	16609
2AXT	DE	ELECTRON TRANSPORT	E	1.4	1.4	1	6	LAYDVF	16610
2AXT	FJ	ELECTRON TRANSPORT	J	1.4	1.4	1	22	IVATVAGMGVIVIVGLFFYGAY	16611
2B4J	AC	VIRAL PROTEIN, RECOMBINATION	C	1.4	1.4	1	17	SMDSRLQRIHAEIKNSL	16612
2B8K	AB	TRANSFERASE	A	1.4	1.4	1	12	EETRAELSQLCA	16613
2BA0	AD	RNA BINDING PROTEIN	A	1.4	1.4	1	6	VPRVIG	16614
2BA1	BE	RNA BINDING PROTEIN	E	1.4	1.4	1	35	RDEVKQAIELAKKGALQIYEMQREAILRRYIEVGE	16615
2BAP	BD	SIGNALING PROTEIN	B	1.4	1.4	1	17	PNMMIDAAKLLSALCIL	16616
2BBV	BE	VIRUS/RNA	B	1.4	1.4	1	14	EVALQEYRTVARSL	16617
2BE6	BE	MEMBRANE PROTEIN	B	1.4	1.4	1	12	EAELQDMINEVD	16618
2BEC	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	A	1.4	1.4	1	8	GDRIIESF	16619
2BO9	CD	HYDROLASE	C	1.4	1.4	1	17	WISQATAIWTARKIVSD	16620
2BOV	AB	TRANSFERASE	B	1.4	1.4	1	13	KSEKEAIVSYTKS	16621
2BP7	AF	OXIDOREDUCTASE	F	1.4	1.4	1	12	VYVAQVAAEESG	16622
2BR2	MX	HYDROLASE	X	1.4	1.4	1	29	PDEFRQAFDLAVKGINIIYNLEREALKSK	16623
2BSK	CF	PROTEIN TRANSPORT	F	1.4	1.4	1	20	KGESVCLDRCVSKYLDIHER	16624
2BSK	CF	PROTEIN TRANSPORT	F	1.4	1.4	1	5	KKLTE	16625
2BSK	EB	PROTEIN TRANSPORT	B	1.4	1.4	1	7	SACHRKC	16626
2BSK	EF	PROTEIN TRANSPORT	F	1.4	1.4	1	8	SACHRKCV	16627
2BTV	AC	VIRUS	A	1.4	1.4	1	14	DDMFNALLPDLIAG	16628
2BTV	AC	VIRUS	C	1.4	1.4	1	19	ANVMEILGIAINRYNGLTL	16629
2BV8	AB	PHOTOSYNTHESIS	B	1.4	1.4	1	12	AFAKVVAQADAR	16630
2BV8	OP	PHOTOSYNTHESIS	P	1.4	1.4	1	12	AFAKVVAQADAR	16631
2C35	EF	POLYMERASE	E	1.4	1.4	1	11	KFELACLANLC	16632
2C4F	HL	HYDROLASE	H	1.4	1.4	1	10	RTFSERTLAF	16633
2C7J	AB	ELECTRON TRANSPORT	A	1.4	1.4	1	15	RARAGLEAARAFANN	16634
2CCI	CD	CELL CYCLE	D	1.4	1.4	1	15	KKQVLRMEHLVLKVL	16635
2CG5	AB	TRANSFERASE/HYDROLASE	A	1.4	1.4	1	8	IPEFFHIM	16636
2CLY	DE	HYDROLASE	E	1.4	1.4	1	22	EFLTQSKTRIQEYEKELEKMRN	16637

2CNW	CF	SIGNAL RECOGNITION	C	1.4	1.4	1	12	AREQLRLLGEKV	16638
2CNW	CF	SIGNAL RECOGNITION	F	1.4	1.4	1	14	EEVLEELEMALLAA	16639
2CZV	AC	HYDROLASE	A	1.4	1.4	1	11	PRDLISLGVVI	16640
2D1P	BC	TRANSLATION	C	1.4	1.4	1	7	FAALLRL	16641
2D1P	EF	TRANSLATION	F	1.4	1.4	1	7	FAALLRL	16642
2D7C	AD	PROTEIN TRANSPORT	D	1.4	1.4	1	23	AIQKQEEINFRLQDYIDRIIVAI	16643
2D7C	BC	PROTEIN TRANSPORT	C	1.4	1.4	1	23	AIQKQEEINFRLQDYIDRIIVAI	16644
2D9Q	AB	SIGNALING PROTEIN/CYTOKINE	A	1.4	1.4	1	24	QSFLLKCLEQVRKIQGDGAALQEK	16645
2DD4	DF	HYDROLASE	D	1.4	1.4	1	5	QKDLW	16646
2DD4	EF	HYDROLASE	E	1.4	1.4	1	9	AEERRRKQN	16647
2DD4	HL	HYDROLASE	L	1.4	1.4	1	10	PNYRRRLVRW	16648
2DD4	KL	HYDROLASE	K	1.4	1.4	1	7	QTVYLGM	16649
2DFK	AB	CELL CYCLE	A	1.4	1.4	1	12	HLDACMELSKLM	16650
2DFK	CD	CELL CYCLE	C	1.4	1.4	1	12	KYPLQLAELLKY	16651
2DFS	AB	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	B	1.4	1.4	1	11	AAELRHVMTNL	16652
2DFS	AC	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	C	1.4	1.4	1	8	DEEVDEMI	16653
2DFS	AD	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	D	1.4	1.4	1	8	DEEVDEMI	16654
2DFS	AF	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	F	1.4	1.4	1	10	EAELQDMINE	16655
2DFS	AG	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	G	1.4	1.4	1	11	AAELRHVMTNL	16656
2DFS	MP	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	P	1.4	1.4	1	9	LGTVMRSLG	16657
2DFS	MS	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	S	1.4	1.4	1	11	AAELRHVMTNL	16658
2DQF	EF	IMMUNE SYSTEM/HYDROLASE	F	1.4	1.4	1	12	TASVNCAKKIVS	16659
2DSQ	BI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	1.4	1.4	1	7	LRRLEMY	16660
2DXB	DF	HYDROLASE	F	1.4	1.4	1	10	PNYRRRLVRW	16661
2DXB	QU	HYDROLASE	Q	1.4	1.4	1	8	HTLFRAYT	16662
2DYM	GH	PROTEIN TURNOVER/PROTEIN TURNOVER	G	1.4	1.4	1	11	HMNDIKQLLWN	16663
2E 74	AB	PHOTOSYNTHESIS	A	1.4	1.4	1	23	ELTWISGVILAVITVSFGVTGYS	16664
2E5L	DE	RIBOSOME	D	1.4	1.4	1	16	DYAVRLREKQKLRRIY	16665
2EC6	AB	CONTRACTILE PROTEIN	B	1.4	1.4	1	10	IEYIKDLLEN	16666
2EFC	AD	TRANSPORT PROTEIN	D	1.4	1.4	1	10	KSSLVLRFVK	16667

2EG4	AB	TRANSFERASE	A	1.4	1.4	1	8	MHEWLQEG	16668
2EHO	AB	REPLICATION	B	1.4	1.4	1	5	ALYEQ	16669
2EHO	AC	REPLICATION	A	1.4	1.4	1	14	RIRYVLSSYLRCRL	16670
2EHO	CD	REPLICATION	C	1.4	1.4	1	9	LTKLLLNHA	16671
2EHO	CD	REPLICATION	D	1.4	1.4	1	12	RGLFQTGQKGLN	16672
2EHO	EF	REPLICATION	F	1.4	1.4	1	12	ALYEQNQSDVNE	16673
2EHO	EG	REPLICATION	G	1.4	1.4	1	10	GTFLTQALNH	16674
2EHO	IJ	REPLICATION	I	1.4	1.4	1	10	PEELAFAREF	16675
2EJF	AC	LIGASE	A	1.4	1.4	1	7	TNEFAKT	16676
2EKV	AC	CONTRACTILE PROTEIN	C	1.4	1.4	1	9	YEDLMKKVM	16677
2EQ9	JL	OXIDOREDUCTASE	J	1.4	1.4	1	14	AGELIAEAALALEM	16678
2EQB	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.4	1.4	1	6	FITTIG	16679
2EQB	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.4	1.4	1	11	RTITTAYYRGA	16680
2ERJ	EH	IMMUNE SYSTEM/CYTOKINE	H	1.4	1.4	1	9	LKPLEEVLN	16681
2F5Z	JO	OXIDOREDUCTASE/PROTEIN BINDING	J	1.4	1.4	1	7	CEDIARV	16682
2F8N	DK	STRUCTURAL PROTEIN/DNA	D	1.4	1.4	1	12	SREVQTAVRLLL	16683
2F8N	DK	STRUCTURAL PROTEIN/DNA	K	1.4	1.4	1	10	PRHLQLAIRN	16684
2F93	AB	MEMBRANE PROTEIN	A	1.4	1.4	1	28	SGIKSLYVRLRNLTVILWAIYPFIWLLG	16685
2F9I	AB	TRANSFERASE	B	1.4	1.4	1	8	RRVIEQTI	16686
2FBJ	LH	IMMUNOGLOBULIN	L	1.4	1.4	1	7	SEQLTSG	16687
2FBW	NO	OXIDOREDUCTASE	N	1.4	1.4	1	14	TGHSLLHTLYGRSL	16688
2FEP	AS	TRANSCRIPTION	A	1.4	1.4	1	17	IFYSELARGIEDIATMY	16689
2FFD	DF	BLOOD CLOTTING	F	1.4	1.4	1	6	QEIYNS	16690
2FGW	LH	IMMUNOGLOBULIN	L	1.4	1.4	1	6	DEQLKS	16691
2FHJ	CD	TRANSFERASE	D	1.4	1.4	1	19	EDELKEQLLDRIGQCVMTA	16692
2FJ7	AB	STRUCTURAL PROTEIN/DNA	A	1.4	1.4	1	12	PKDIQLARRIRG	16693
2FK0	ED	VIRAL PROTEIN	D	1.4	1.4	1	23	KESTQKAIDGVTNKVNSIIDKMN	16694
2FKW	MN	MEMBRANE PROTEIN, PHOTOSYNTHESIS	M	1.4	1.4	1	26	PAIGIPALLGSVTVIAILVHLAILSH	16695
2FOI	AC	OXIDOREDUCTASE	A	1.4	1.4	1	5	HASQK	16696
2FOT	AC	METAL BINDING, STRUCTURAL PROTEIN	A	1.4	1.4	1	12	EAELQDMINEVD	16697
2FRV	AB	OXIDOREDUCTASE	A	1.4	1.4	1	9	VDELILDVI	16698
2FRV	CD	OXIDOREDUCTASE	C	1.4	1.4	1	9	VDELILDVI	16699
2FRV	EF	OXIDOREDUCTASE	E	1.4	1.4	1	9	VDELILDVI	16700
2FRV	GH	OXIDOREDUCTASE	G	1.4	1.4	1	9	VDELILDVI	16701
2FRV	GJ	OXIDOREDUCTASE	G	1.4	1.4	1	15	PMNFVGTVVHLLTKG	16702
2FRV	IJ	OXIDOREDUCTASE	I	1.4	1.4	1	9	VDELILDVI	16703
2FRV	SL	OXIDOREDUCTASE	S	1.4	1.4	1	9	VDELILDVI	16704
2FTK	BF	TRANSFERASE	F	1.4	1.4	1	12	GLQALDIVTKER	16705

2FUG	BC	OXIDOREDUCTASE	B	1.4	1.4	1	11	PTEVMGVASFY	16706
2FUG	KL	OXIDOREDUCTASE	K	1.4	1.4	1	11	PTEVMGVASFY	16707
2FUG	MP	OXIDOREDUCTASE	M	1.4	1.4	1	14	RERETILDLFEWVT	16708
2FUG	VX	OXIDOREDUCTASE	V	1.4	1.4	1	10	YLQNITYTPR	16709
2FYL	AB	SURFACE ACTIVE PROTEIN	A	1.4	1.4	1	13	EKLNQLWEKAQRL	16710
2FYM	DE	LYASE	D	1.4	1.4	1	19	ANAILAVSLANAKAAAAAK	16711
2FYN	AF	OXIDOREDUCTASE	A	1.4	1.4	1	17	QMSFWGATVITGLFGAI	16712
2FYN	DC	OXIDOREDUCTASE	D	1.4	1.4	1	17	QMSFWGATVITGLFGAI	16713
2FYN	GL	OXIDOREDUCTASE	L	1.4	1.4	1	23	YATAGAGAVATGAAVWPLINQMN	16714
2FYN	PO	OXIDOREDUCTASE	P	1.4	1.4	1	17	QMSFWGATVITGLFGAI	16715
2GAG	AB	OXIDOREDUCTASE	B	1.4	1.4	1	16	LGDVRESVRRVEANKL	16716
2GCO	AB	SIGNALING PROTEIN	A	1.4	1.4	1	14	VREVFEMATRAGLQ	16717
2GHO	BD	TRANSFERASE	B	1.4	1.4	1	11	VVEIILNLKEL	16718
2GHO	CD	TRANSFERASE	D	1.4	1.4	1	7	PEKIRSW	16719
2GID	PK	TRANSLATION	P	1.4	1.4	1	6	QRFLTQ	16720
2GJZ	AB	IMMUNE SYSTEM	A	1.4	1.4	1	7	SEQLTSG	16721
2GJZ	LH	IMMUNE SYSTEM	L	1.4	1.4	1	7	SEQLTSG	16722
2GL7	DE	TRANSCRIPTION	D	1.4	1.4	1	15	EDITEPAICALRHLT	16723
2GTL	EF	OXYGEN STORAGE/TRANSPORT	F	1.4	1.4	1	16	VLEGLKVKSEWGRAYG	16724
2GTL	EH	OXYGEN STORAGE/TRANSPORT	H	1.4	1.4	1	14	PDMLAAQLAHLKVQ	16725
2GUZ	ID	CHAPERONE, PROTEIN TRANSPORT	D	1.4	1.4	1	15	MDKINNRFNYLFEVN	16726
2GW4	CD	LUMINESCENT PROTEIN	D	1.4	1.4	1	5	YFKQS	16727
2H7V	BD	SIGNALING PROTEIN	D	1.4	1.4	1	28	FSDIGSLVRAHKHLETLLEVLVTLSQQG	16728
2H9A	AB	OXIDOREDUCTASE	A	1.4	1.4	1	5	RHDKR	16729
2H9G	LH	IMMUNE SYSTEM/APOTOSIS	L	1.4	1.4	1	6	DEQLKS	16730
2HDN	AB	TRANSLATION	B	1.4	1.4	1	7	ALKALEG	16731
2HDN	CD	TRANSLATION	D	1.4	1.4	1	7	ALKALEG	16732
2HDN	GH	TRANSLATION	H	1.4	1.4	1	7	ALKALEG	16733
2HDN	IJ	TRANSLATION	J	1.4	1.4	1	7	ALKALEG	16734
2HIK	LN	REPLICATION	N	1.4	1.4	1	13	SDGFKSAISEVST	16735
2HLD	DG	HYDROLASE	G	1.4	1.4	1	53	LKEVEMRLKSIKNIEKITKTMKIVASTRLSKAEKAKISAKKMDEAEQLFYKNA	16736
2HLD	UX	HYDROLASE	U	1.4	1.4	1	15	LSKQAVAYRQLSLLL	16737
2HLD	XY	HYDROLASE	X	1.4	1.4	1	8	QDIIAILG	16738
2HTM	AE	BIOSYNTHETIC PROTEIN	A	1.4	1.4	1	6	NTAIAE	16739
2HYB	BC	TRANSFERASE	B	1.4	1.4	1	7	RDSLEAR	16740
2HYB	HI	TRANSFERASE	H	1.4	1.4	1	7	RDSLEAR	16741
2HYI	IJ	HYDROLASE/RNA BINDING PROTEIN/RNA	I	1.4	1.4	1	11	VGEDIRKLDYG	16742
2I2P	CN	RIBOSOME	N	1.4	1.4	1	11	RIKVREAAMRG	16743

2I2R	JN	TRANSPORT PROTEIN	N	1.4	1.4	1	8	HVDVFFQK	16744
2I2X	AD	TRANSFERASE	D	1.4	1.4	1	8	EASLKKVL	16745
2I2X	OP	TRANSFERASE	P	1.4	1.4	1	8	EASLKKVL	16746
2I9L	EF	IMMUNE SYSTEM/VIRAL PROTEIN	E	1.4	1.4	1	7	SEQLTSG	16747
2IAE	AC	HYDROLASE	C	1.4	1.4	1	11	FHDLMELFRIG	16748
2IAM	AB	IMMUNE SYSTEM	A	1.4	1.4	1	21	QGALANIAVDKANLEIMTKRS	16749
2IAN	DE	IMMUNE SYSTEM	E	1.4	1.4	1	6	EAEISH	16750
2IAN	FG	IMMUNE SYSTEM	F	1.4	1.4	1	21	QGALANIAVDKANLEIMTKRS	16751
2IAN	PQ	IMMUNE SYSTEM	P	1.4	1.4	1	22	AQGALANIAVDKANLEIMTKRS	16752
2IBF	AD	CELL ADHESION, STRUCTURAL PROTEIN	A	1.4	1.4	1	29	MEDLVTYTKNLGPGMTKMAKMIDERQQEL	16753
2IBZ	EX	OXIDOREDUCTASE	E	1.4	1.4	1	8	PHEIQEAN	16754
2ICW	AB	IMMUNE SYSTEM	B	1.4	1.4	1	9	RPDAEYWNS	16755
2ICW	DH	IMMUNE SYSTEM	H	1.4	1.4	1	27	VEQIKRNIAILDEIMAKADNDLSYFIS	16756
2IFQ	CB	OXIDOREDUCTASE	B	1.4	1.4	1	12	KEKLEATINELV	16757
2IHB	AB	SIGNALING PROTEIN	A	1.4	1.4	1	10	RSERKKWIHC	16758
2INP	BE	OXIDOREDUCTASE	B	1.4	1.4	1	21	PDTFDKYYRPRYEYLAKEAAA	16759
2IO5	BC	CHAPERONE/STRUCTURAL PROTEIN	C	1.4	1.4	1	12	AMDVVYALKRQG	16760
2IPU	LH	IMMUNE SYSTEM	L	1.4	1.4	1	6	SEQLTS	16761
2IVF	AB	OXIDOREDUCTASE	A	1.4	1.4	1	6	FNNNLY	16762
2J0Q	BI	HYDROLASE	B	1.4	1.4	1	12	DIRILRDIEQYY	16763
2J57	GK	OXIDOREDUCTASE	G	1.4	1.4	1	20	QAQETQGQAAARAAAADLAA	16764
2J57	IN	OXIDOREDUCTASE	I	1.4	1.4	1	20	QAQETQGQAAARAAAADLAA	16765
2J57	JL	OXIDOREDUCTASE	J	1.4	1.4	1	20	QAQETQGQAAARAAAADLAA	16766
2J7A	HI	OXIDOREDUCTASE	H	1.4	1.4	1	10	RNEMRALVCG	16767
2J7A	MO	OXIDOREDUCTASE	M	1.4	1.4	1	5	RNEMR	16768
2J8S	AE	MEMBRANE PROTEIN	A	1.4	1.4	1	8	QEKAQALG	16769
2J8S	BD	MEMBRANE PROTEIN	D	1.4	1.4	1	13	DLGKKLLEAARAG	16770
2JBA	AB	TRANSCRIPTION	B	1.4	1.4	1	14	PKELVARIKAVMRR	16771
2JBL	LM	ELECTRON TRANSPORT	L	1.4	1.4	1	5	GWWLD	16772
2JDQ	AE	PROTEIN TRANSPORT	A	1.4	1.4	1	15	LTMTRNAVWALSNLC	16773
2JGD	AB	OXIDOREDUCTASE	B	1.4	1.4	1	10	GVVQETLNMS	16774
2JIZ	CG	HYDROLASE	G	1.4	1.4	1	70	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAAL	16775
2JIZ	IL	HYDROLASE	I	1.4	1.4	1	15	LSKQAVAYRQMSLLL	16776
2JIZ	IN	HYDROLASE	N	1.4	1.4	1	69	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAA	16777
2JXC	AB	ENDOCYTOSIS/PROTEIN BINDING	A	1.4	1.4	1	9	GDKVKPVLL	16778
2JXC	AB	ENDOCYTOSIS/PROTEIN BINDING	A	1.4	1.4	1	16	RDEFAVAMFLVYCALE	16779
2NPP	DE	SIGNALING PROTEIN,HYDROLASE	E	1.4	1.4	1	18	LRAYIRKQINNIFYRFIY	16780

2NQB	EC	STRUCTURAL PROTEIN/DNA	E	1.4	1.4	1	13	TVALREIRRYQKS	16781
2NQB	EF	STRUCTURAL PROTEIN/DNA	E	1.4	1.4	1	12	PKDIQLARRIRG	16782
2NQB	GH	STRUCTURAL PROTEIN/DNA	G	1.4	1.4	1	7	EELNKLL	16783
2NTI	GH	DNA BINDING PROTEIN	G	1.4	1.4	1	15	ESVLNVIAADVTLVG	16784
2NTY	AC	SIGNALING PROTEIN	A	1.4	1.4	1	19	EHKVLDLKNRIEASVVIWK	16785
2NTY	AC	SIGNALING PROTEIN	A	1.4	1.4	1	30	VGQAVLESYSRILESLAYTVMSRIEDVLYT	16786
2NTY	AC	SIGNALING PROTEIN	A	1.4	1.4	1	20	QDRQARWKKEIDWLLSVTDH	16787
2NUU	EK	TRANSPORT PROTEIN/SIGNALING PROTEIN	E	1.4	1.4	1	20	LLGACSGAIAGLVGVTPACG	16788
2NUU	FK	TRANSPORT PROTEIN/SIGNALING PROTEIN	F	1.4	1.4	1	7	EEQEREG	16789
2NV2	MN	LYASE/TRANSFERASE	M	1.4	1.4	1	11	AEQAKIAEEAG	16790
2NVU	AB	PROTEIN TURNOVER, LIGASE	A	1.4	1.4	1	24	SGKYIKLQNVYREKAKKDAAAVGN	16791
2NX5	KP	IMMUNE SYSTEM	K	1.4	1.4	1	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	16792
2NZ1	XY	VIRAL PROTEIN/CYTOKINE	X	1.4	1.4	1	9	TCPCYYKYS	16793
2NZD	GH	STRUCTURAL PROTEIN/DNA	G	1.4	1.4	1	7	EELNKLL	16794
2O01	AB	PHOTOSYNTHESIS	A	1.4	1.4	1	7	SLMFLFS	16795
2O60	AB	METAL BINDING PROTEIN	A	1.4	1.4	1	12	FPEFLTMMARKM	16796
2O8A	AI	HYDROLASE/INHIBITOR	I	1.4	1.4	1	8	EMNILATL	16797
2O8A	BJ	HYDROLASE/INHIBITOR	J	1.4	1.4	1	14	IKLARQLISKDLHD	16798
2O8A	BJ	HYDROLASE/INHIBITOR	J	1.4	1.4	1	8	EMNILATL	16799
2O8F	AB	DNA BINDING PROTEIN/DNA	A	1.4	1.4	1	16	TFMAEMLETASILRSA	16800
2O8F	AB	DNA BINDING PROTEIN/DNA	B	1.4	1.4	1	7	HSLVEDY	16801
2ODE	AB	SIGNALING PROTEIN	B	1.4	1.4	1	15	EENLEFWLACEEFKK	16802
2OM0	3T	HORMONE	3	1.4	1.4	1	7	LYQLENY	16803
2OM0	ib	HORMONE	i	1.4	1.4	1	7	LYQLENY	16804
2ONK	BD	MEMBRANE PROTEIN	D	1.4	1.4	1	13	PLRVFFTVSLPLS	16805
2OQ1	AB	TRANSFERASE	A	1.4	1.4	1	11	RAEAEEHLKLA	16806
2OT8	AC	TRANSPORT PROTEIN	A	1.4	1.4	1	14	ALVRSITCWTLSRY	16807
2OTJ	FM	RIBOSOME	M	1.4	1.4	1	15	QLAELQWQRQQEWRN	16808
2OTJ	KU	RIBOSOME	U	1.4	1.4	1	9	SKCENNADL	16809
2OV2	GO	PROTEIN BINDING/TRANSFERASE	G	1.4	1.4	1	10	KTCLLISYTT	16810
2OZB	AB	RNA BINDING PROTEIN/RNA	A	1.4	1.4	1	9	HLPLLCEDK	16811
2OZB	DE	RNA BINDING PROTEIN/RNA	E	1.4	1.4	1	21	RRKAARLVAAKCTLAARVDSF	16812
2P1L	EF	APOPTOSIS	E	1.4	1.4	1	5	YRRAF	16813
2P22	CD	TRANSPORT PROTEIN	C	1.4	1.4	1	18	RILESKYVASWQDYHSEF	16814
2P5T	AB	TRANSCRIPTION REGULATOR	B	1.4	1.4	1	19	QVEKEMLQVGEKRLNELLE	16815
2P5T	GH	TRANSCRIPTION REGULATOR	G	1.4	1.4	1	32	PVEDYELTLKIEIVKERGANLLSRLYRYQDSQ	16816
2PBD	AP	STRUCTURAL PROTEIN	A	1.4	1.4	1	9	IDIRKDLYA	16817

2PF4	BH	HYDROLASE REGULATOR/VIRAL PROTEIN	B	1.4	1.4	1	19	YAIREAATSNLKKLVEKFG	16818
2PG1	CJ	STRUCTURAL PROTEIN	C	1.4	1.4	1	16	EKDIAAYIKKEFDKKY	16819
2PMZ	AB	TRANSLATION, TRANSFERASE	A	1.4	1.4	1	11	EEAIAEAKEIM	16820
2PMZ	AC	TRANSLATION, TRANSFERASE	A	1.4	1.4	1	5	RFRGN	16821
2PMZ	BN	TRANSLATION, TRANSFERASE	N	1.4	1.4	1	6	INEVIH	16822
2PMZ	CK	TRANSLATION, TRANSFERASE	K	1.4	1.4	1	16	RYEIARVISARALQLA	16823
2PMZ	DL	TRANSLATION, TRANSFERASE	D	1.4	1.4	1	7	IRRASML	16824
2PON	AB	APOPTOSIS INHIBITOR	B	1.4	1.4	1	22	WGRIVAFFSFGGALCVESVDKE	16825
2PQN	AB	APOPTOSIS	A	1.4	1.4	1	14	PQQLEILRQQVVSE	16826
2PRG	AC	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	A	1.4	1.4	1	8	PLLQEIYK	16827
2PUK	AB	ELECTRON TRANSPORT	A	1.4	1.4	1	6	VPMRER	16828
2PUK	EF	ELECTRON TRANSPORT	E	1.4	1.4	1	8	KEAEVKNT	16829
2PV2	CF	ISOMERASE	C	1.4	1.4	1	7	GIFAQAL	16830
2PVO	AC	ELECTRON TRANSPORT	C	1.4	1.4	1	17	GPSKAMAPKYEKLAEEY	16831
2PXY	AD	IMMUNE SYSTEM	D	1.4	1.4	1	22	LERTRAELDTVCRYNYEETEVP	16832
2Q26	AB	VIRUS/RNA	B	1.4	1.4	1	7	MWERVKS	16833
2Q26	CD	VIRUS/RNA	D	1.4	1.4	1	6	VKSIIK	16834
2QAD	AB	VIRAL PROTEIN/IMMUNE SYSTEM	A	1.4	1.4	1	5	PEIVT	16835
2QE7	BF	HYDROLASE	B	1.4	1.4	1	9	VFYLHSRLL	16836
2QEX	AZ	RIBOSOME	Z	1.4	1.4	1	9	PGGKTVRRS	16837
2QIE	KJ	TRANSFERASE	J	1.4	1.4	1	6	EIKDIL	16838
2QJ9	BD	CYTOKINE/RECEPTOR	B	1.4	1.4	1	13	NHAIVQTLVNSVN	16839
2QJK	AF	ELECTRON TRANSPORT	A	1.4	1.4	1	17	QMSFWGATVITGLFGAI	16840
2QJK	JI	ELECTRON TRANSPORT	J	1.4	1.4	1	9	HSIQTWLLG	16841
2QJK	MO	ELECTRON TRANSPORT	M	1.4	1.4	1	24	IWGVVLAFCLVLQIVTGIVLAMHY	16842
2QJK	PO	ELECTRON TRANSPORT	P	1.4	1.4	1	17	QMSFWGATVITGLFGAI	16843
2QJP	EF	ELECTRON TRANSPORT	F	1.4	1.4	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	16844
2QJY	GH	OXIDOREDUCTASE	G	1.4	1.4	1	22	PMFKIYFWLLAADFVILTWVGA	16845
2QLV	EF	TRANSFERASE/PROTEIN BINDING	F	1.4	1.4	1	11	QYRILKFVALN	16846
2QMB	AD	TRANSPORT PROTEIN	A	1.4	1.4	1	19	PVNFKLLGQCFLVVVAIHH	16847
2QMU	AC	TRANSLATION	A	1.4	1.4	1	16	KEEALSQYRQIKQFTK	16848
2QNA	AB	TRANSPORT PROTEIN	A	1.4	1.4	1	19	GGVQEDALMAVSTLVEVLG	16849
2QOY	FR	RIBOSOME	R	1.4	1.4	1	17	AKYQRQLARAIKRARYL	16850
2QOY	GK	RIBOSOME	K	1.4	1.4	1	14	PFAAQVAAERCADA	16851
2QQP	AF	VIRUS	F	1.4	1.4	1	13	PSVIKGIAQQAVG	16852
2QR0	KL	IMMUNE SYSTEM	K	1.4	1.4	1	7	DEQLKSG	16853
2QR0	MP	IMMUNE SYSTEM	P	1.4	1.4	1	8	FMDVYQRS	16854
2QSH	AX	DNA BINDING PROTEIN/DNA	X	1.4	1.4	1	13	VEDLLSLRQVVSG	16855

2QVS	EB	TRANSFERASE/TRANSFERASE REGULATOR	E	1.4	1.4	1	8	MFSHLRRI	16856
2R6C	AG	REPLICATION	A	1.4	1.4	1	11	VSYLSELADAV	16857
2R9R	GH	MEMBRANE PROTEIN, TRANSPORT PROTEIN	G	1.4	1.4	1	14	SMEIMEAYSVARQF	16858
2REX	AB	SIGNALING PROTEIN/LIPOPROTEIN	A	1.4	1.4	1	5	LQHYK	16859
2RGN	DE	SIGNALING PROTEIN COMPLEX	D	1.4	1.4	1	22	TENIRFVFAAVKDTILQLNLKE	16860
2RHK	BC	VIRAL PROTEIN/NUCLEAR PROTEIN	C	1.4	1.4	1	5	KHWLR	16861
2RHS	AB	LIGASE	A	1.4	1.4	1	6	VRFLEQ	16862
2SIV	AF	ENVELOPE GLYCOPROTEIN	F	1.4	1.4	1	31	QEWERKVDFLEENITALLEEAQIQQEKNMYE	16863
2SIV	CB	ENVELOPE GLYCOPROTEIN	B	1.4	1.4	1	33	QEWERKVDFLEENITALLEEAQIQQEKNMYELQ	16864
2UUN	AD	ELECTRON TRANSPORT	A	1.4	1.4	1	8	IDEVNRTF	16865
2UUN	GJ	ELECTRON TRANSPORT	G	1.4	1.4	1	8	IDEVNRTF	16866
2UVP	AD	UNKNOWN FUNCTION	A	1.4	1.4	1	12	ANLSLATIEMTY	16867
2UYL	MN	IMMUNE SYSTEM	M	1.4	1.4	1	6	SEQLTS	16868
2UYL	XY	IMMUNE SYSTEM	X	1.4	1.4	1	6	SEQLTS	16869
2UZ1	DC	LYASE	C	1.4	1.4	1	10	IGEFDTLVRK	16870
2UZ1	DC	LYASE	D	1.4	1.4	1	10	IGEFDTLVRK	16871
2UZ6	FP	RECEPTOR	P	1.4	1.4	1	7	PPCILNN	16872
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	B	1.4	1.4	1	9	FQAISDVIG	16873
2V4I	EH	TRANSFERASE	H	1.4	1.4	1	11	WGRVAMAIGKC	16874
2V6X	AB	PROTEIN TRANSPORT	B	1.4	1.4	1	6	QNLVSN	16875
2V7Q	DG	HYDROLASE	D	1.4	1.4	1	28	SEHYDVARGVQKILQDYKSLQDIIAILG	16876
2V7Q	FJ	HYDROLASE	F	1.4	1.4	1	28	SEHYDVARGVQKILQDYKSLQDIIAILG	16877
2V7Q	GI	HYDROLASE	I	1.4	1.4	1	5	YWRQA	16878
2V7Q	HI	HYDROLASE	I	1.4	1.4	1	5	YWRQA	16879
2V8S	EV	PROTEIN TRANSPORT	E	1.4	1.4	1	10	ERVVTSAREH	16880
2VDO	AB	CELL ADHESION/IMMUNE SYSTEM	B	1.4	1.4	1	10	VNLYQNYSEL	16881
2VGL	BM	PROTEIN TRANSPORT	B	1.4	1.4	1	15	NYVVQEAIVVIRDIF	16882
2VGX	AB	CHAPERONE	A	1.4	1.4	1	8	FQALCVLD	16883
2VLH	AB	LYASE	B	1.4	1.4	1	10	TTTRYHQEKN	16884
2VOY	HI	HYDROLASE	I	1.4	1.4	1	7	ALEVAEK	16885
2VPE	CD	GENE REGULATION	C	1.4	1.4	1	5	DTCMA	16886
2VUS	DL	TRANSCRIPTION	D	1.4	1.4	1	14	RQAASLIRVAAAVG	16887
2VUS	GO	TRANSCRIPTION	G	1.4	1.4	1	14	RQAASLIRVAAAVG	16888
2VZD	BD	CELL ADHESION	B	1.4	1.4	1	9	AFDTLFDHA	16889
2W2X	AC	SIGNALING PROTEIN/HYDROLASE	A	1.4	1.4	1	7	LKTVFDE	16890
2W73	BL	METAL BINDING PROTEIN	B	1.4	1.4	1	29	FPEFLTMMARKMKDTDSEEEIREAFRVFD	16891
2WAQ	BD	TRANSCRIPTION	B	1.4	1.4	1	11	IEQLQNEILKY	16892
2WAQ	BN	TRANSCRIPTION	B	1.4	1.4	1	6	RSSVER	16893

2WB1	AB	TRANSCRIPTION	A	1.4	1.4	1	8	KEEAQQIL	16894
2WB1	AB	TRANSCRIPTION	A	1.4	1.4	1	6	FAYVMA	16895
2WB1	AK	TRANSCRIPTION	A	1.4	1.4	1	11	EEAIAEAKEIM	16896
2WB1	WY	TRANSCRIPTION	W	1.4	1.4	1	5	PSAAR	16897
2WB1	YZ	TRANSCRIPTION	Y	1.4	1.4	1	19	IEAAREIIIREISKVLAEQ	16898
2WBE	BC	STRUCTURAL PROTEIN	B	1.4	1.4	1	23	EMEFTEAESNMNDLVSEYQQYQD	16899
2WEL	AD	TRANSFERASE	D	1.4	1.4	1	8	YEEFVQMM	16900
2WIN	AB	IMMUNE SYSTEM	B	1.4	1.4	1	5	WEKFG	16901
2WJV	AD	HYDROLASE	D	1.4	1.4	1	6	QLAANH	16902
2Z2S	EF	TRANSCRIPTION	E	1.4	1.4	1	11	ASQAEECAQDV	16903
2Z2S	EF	TRANSCRIPTION	F	1.4	1.4	1	10	DALLTAYAAG	16904
2Z2S	GH	TRANSCRIPTION	G	1.4	1.4	1	10	QENARLGRAI	16905
2ZC5	CD	BIOSYNTHETIC PROTEIN	D	1.4	1.4	1	16	DNYLKEVINQVEEETG	16906
2ZCY	AH	HYDROLASE	A	1.4	1.4	1	5	YKRIY	16907
2ZCY	H0	HYDROLASE	0	1.4	1.4	1	14	FGAHMANPLLRKVV	16908
2ZCY	JY	HYDROLASE	Y	1.4	1.4	1	19	VEDALYLGKRSILAAAHRD	16909
2ZCY	T1	HYDROLASE	1	1.4	1.4	1	15	TETAASVFKELCYEN	16910
2ZHX	KL	HYDROLASE/HYDROLASE INHIBITOR	L	1.4	1.4	1	9	PEEVEEVIG	16911
2ZIX	AB	HYDROLASE	A	1.4	1.4	1	5	AYLAL	16912
2ZIX	AB	HYDROLASE	A	1.4	1.4	1	6	ARQLMQ	16913
2ZNV	DC	HYDROLASE/SIGNALING PROTEIN	C	1.4	1.4	1	13	IENVKAKIQDKEG	16914
2ZNW	BZ	IMMUNE SYSTEM/HYDROLASE	Z	1.4	1.4	1	5	SRWWC	16915
2ZSH	AB	HORMONE RECEPTOR	A	1.4	1.4	1	6	IESRTV	16916
3A0B	bd	ELECTRON TRANSPORT	b	1.4	1.4	1	9	PRGWFTFAH	16917
3A0B	kz	ELECTRON TRANSPORT	k	1.4	1.4	1	9	AIFDPLVDV	16918
3A0B	LT	ELECTRON TRANSPORT	T	1.4	1.4	1	9	TITYVFIFA	16919
3BBN	CN	RIBOSOME	N	1.4	1.4	1	10	GHILREMVHT	16920
3BBO	ST	RIBOSOME	S	1.4	1.4	1	26	LVSAHRDRDRQKRDFRRLWITRINAA	16921
3BG0	EF	PROTEIN TRANSPORT, HYDROLASE	F	1.4	1.4	1	10	TEKLYKEVRQ	16922
3BIM	CK	TRANSCRIPTION REPRESSOR	C	1.4	1.4	1	9	EHVVDTCRK	16923
3BIM	GP	TRANSCRIPTION REPRESSOR	G	1.4	1.4	1	15	HASDVLLNLNRLRSR	16924
3BJI	AD	SIGNALING PROTEIN	A	1.4	1.4	1	11	KYHLLLQELVK	16925
3BL2	AC	VIRAL PROTEIN/APOPTOSIS	A	1.4	1.4	1	5	YGPAL	16926
3BLW	GH	OXIDOREDUCTASE	G	1.4	1.4	1	15	SMYGTILGNIGAALI	16927
3BLW	KL	OXIDOREDUCTASE	K	1.4	1.4	1	11	VDNASMQAVAK	16928
3BLW	MN	OXIDOREDUCTASE	M	1.4	1.4	1	15	SMYGTILGNIGAALI	16929
3BRW	BD	GTP BINDING PROTEIN	B	1.4	1.4	1	6	EKFAKL	16930
3BU8	AC	DNA BINDING PROTEIN	A	1.4	1.4	1	17	YGDFRQIRDIMQALLVR	16931
3BZ4	AB	IMMUNE SYSTEM	A	1.4	1.4	1	7	SEQLTSG	16932
3C7B	AB	OXIDOREDUCTASE	A	1.4	1.4	1	10	LQPCFEDLGN	16933

3C91	SZ	HYDROLASE	S	1.4	1.4	1	23	VADARVLVDFARISAQQEKVTYG	16934
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.4	1.4	1	9	DALFNELVK	16935
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	A	1.4	1.4	1	22	QKELSKYSTHLHLAEDCMKHYQ	16936
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	B	1.4	1.4	1	33	DEFFEQVEEIRGFIDKIAENVEEVKRKHSAILA	16937
3CHX	AB	MEMBRANE PROTEIN	B	1.4	1.4	1	12	TTDWMFLTLLFL	16938
3CHX	BC	MEMBRANE PROTEIN	B	1.4	1.4	1	14	AVLGGYHIHFMLTA	16939
3CHX	BC	MEMBRANE PROTEIN	C	1.4	1.4	1	5	PSHII	16940
3CHX	EF	MEMBRANE PROTEIN	E	1.4	1.4	1	8	TIIGYAVT	16941
3CHX	FG	MEMBRANE PROTEIN	F	1.4	1.4	1	14	AVLGGYHIHFMLTA	16942
3CHX	FG	MEMBRANE PROTEIN	G	1.4	1.4	1	5	PSHII	16943
3CHX	IJ	MEMBRANE PROTEIN	I	1.4	1.4	1	8	TIIGYAVT	16944
3CHX	JK	MEMBRANE PROTEIN	J	1.4	1.4	1	14	AVLGGYHIHFMLTA	16945
3CHX	JK	MEMBRANE PROTEIN	K	1.4	1.4	1	5	PSHII	16946
3CSY	ML	IMMUNE SYSTEM/VIRAL PROTEIN	L	1.4	1.4	1	13	ILNRKAIDFLLQR	16947
3CUE	IK	PROTEIN TRANSPORT	I	1.4	1.4	1	17	TQVLQYIYSHIYVKYVS	16948
3CUE	NP	PROTEIN TRANSPORT	N	1.4	1.4	1	23	AGDFETKLSDYGHNIGIRLLELL	16949
3CW2	FN	TRANSLATION	F	1.4	1.4	1	6	LSQYRQ	16950
3CWB	CE	OXIDOREDUCTASE	C	1.4	1.4	1	23	WNFGSLLAVCLMTQILTGLLLAM	16951
3CXH	AC	OXIDOREDUCTASE	A	1.4	1.4	1	7	YMRIRSD	16952
3CXH	BR	OXIDOREDUCTASE	B	1.4	1.4	1	21	PHELTESVLPAARYDYAVAEQ	16953
3CXH	BR	OXIDOREDUCTASE	R	1.4	1.4	1	21	YLLPYILEAEAAAKEKDELDN	16954
3CXH	LM	OXIDOREDUCTASE	L	1.4	1.4	1	11	LGEAFKKIDAI	16955
3CXH	MG	OXIDOREDUCTASE	G	1.4	1.4	1	21	YLLPYILEAEAAAKEKDELDN	16956
3CXH	OP	OXIDOREDUCTASE	P	1.4	1.4	1	32	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSM	16957
3CXH	OQ	OXIDOREDUCTASE	Q	1.4	1.4	1	23	EEGKALVHHYEECAERVKIQQQQ	16958
3D24	AB	TRANSCRIPTION	A	1.4	1.4	1	9	KLFLEMLEA	16959
3D54	EH	LIGASE	E	1.4	1.4	1	14	DGIIEGIADYGNSI	16960
3D5A	DE	RIBOSOME	D	1.4	1.4	1	8	EQLVIEFY	16961
3D5D	G4	RIBOSOME	G	1.4	1.4	1	6	NVALPR	16962
3D85	AB	IMMUNE SYSTEM/CYTOKINE	A	1.4	1.4	1	6	DEQLKS	16963
3DBH	AB	CELL CYCLE	A	1.4	1.4	1	9	ATGTEILKN	16964
3DBH	EF	CELL CYCLE	E	1.4	1.4	1	22	NYQVEEDIGKLKSCLTGFLQEY	16965
3DF0	AB	HYDROLASE	A	1.4	1.4	1	7	ILFKIFK	16966
3DHH	AE	OXIDOREDUCTASE	A	1.4	1.4	1	31	AISVAIMLTFSFETGFTNMQFLGLAADAAEA	16967
3DHR	GF	OXYGEN STORAGE, OXYGEN TRANSPORT	F	1.4	1.4	1	20	PENFRLLGDILVIILAAHFG	16968
3DHW	AC	MEMBRANE PROTEIN/HYDROLASE	A	1.4	1.4	1	27	LLPEALPGLVNAATITLITLVGYSAMG	16969
3DIF	CD	IMMUNE SYSTEM	C	1.4	1.4	1	6	SEQLTS	16970
3DIN	FG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	1.4	1.4	1	22	GTSALIAVGVALDIIQQMETHM	16971

3DKN	AB	PROTEIN TRANSPORT/RNA	A	1.4	1.4	1	18	VMSSAFVGFLATIANFIG	16972
3DKN	AB	PROTEIN TRANSPORT/RNA	B	1.4	1.4	1	20	DFNQKIEQLKEFIEECRRVW	16973
3DNL	BC	VIRAL PROTEIN	B	1.4	1.4	1	13	RAKWNNTLKQIAS	16974
3DNL	EF	VIRAL PROTEIN	E	1.4	1.4	1	13	RAKWNNTLKQIAS	16975
3DNL	HI	VIRAL PROTEIN	H	1.4	1.4	1	13	RAKWNNTLKQIAS	16976
3DTP	BF	CONTRACTILE PROTEIN	F	1.4	1.4	1	6	IFGDRI	16977
3DW8	DE	HYDROLASE	D	1.4	1.4	1	6	ELLPFL	16978
3DXA	KN	IMMUNE SYSTEM	K	1.4	1.4	1	29	PEYWDRETQISKTNTQTYRENLRTALRYY	16979
3DXA	KO	IMMUNE SYSTEM	K	1.4	1.4	1	29	PEYWDRETQISKTNTQTYRENLRTALRYY	16980
3DZU	AD	TRANSCRIPTION/DNA	A	1.4	1.4	1	7	RFAKLLL	16981
3E8C	DJ	TRANSFERASE	D	1.4	1.4	1	18	KAVDWWALGVLIYEMAAG	16982
3E8C	EK	TRANSFERASE	E	1.4	1.4	1	18	KAVDWWALGVLIYEMAAG	16983
3EDQ	CD	HYDROLASE	C	1.4	1.4	1	15	TDVDAANLRETFRNL	16984
3EDX	AB	HYDROLASE	B	1.4	1.4	1	11	KRWIQKVIDQF	16985
3EH3	AC	OXIDOREDUCTASE	A	1.4	1.4	1	36	PTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLR	16986
3EH3	BC	OXIDOREDUCTASE	C	1.4	1.4	1	14	KGALAVILVLTLTI	16987
3EIQ	DC	HYDROLASE/ANTITUMOR PROTEIN	C	1.4	1.4	1	15	VQARAALDKATVLLS	16988
3EJB	EF	OXIDOREDUCTASE/LIPID TRANSPORT	F	1.4	1.4	1	28	RKALTEGNIMAVQAMAYFKELIQKRKRH	16989
3EJJ	AX	CYTOKINE/SIGNALING PROTEIN	A	1.4	1.4	1	12	NGHLKVLQQLID	16990
3EUH	BF	CELL CYCLE	F	1.4	1.4	1	14	ELDMMVGKILCYLY	16991
3EXG	ED	OXIDOREDUCTASE	E	1.4	1.4	1	17	GVAYRTREEIQEVRSKS	16992
3EXG	IL	OXIDOREDUCTASE	L	1.4	1.4	1	6	KILEDN	16993
3EXG	KL	OXIDOREDUCTASE	L	1.4	1.4	1	14	EMGFAGIAVGAAMA	16994
3EXG	ST	OXIDOREDUCTASE	S	1.4	1.4	1	13	GQIFEAYNMAALW	16995
3EXG	U6	OXIDOREDUCTASE	U	1.4	1.4	1	24	VEELKEIDVEVRKEIEDAAQFATA	16996
3EXH	EF	OXIDOREDUCTASE	E	1.4	1.4	1	13	GQIFEAYNMAALW	16997
3EYF	CD	IMMUNE SYSTEM	C	1.4	1.4	1	7	DEQLKSG	16998
3EZQ	GH	APOPTOSIS	H	1.4	1.4	1	5	QNRSG	16999
3F02	AC	HYDROLASE INHIBITOR	A	1.4	1.4	1	15	PLSIALAMGMMELGA	17000
3F02	BD	HYDROLASE INHIBITOR	B	1.4	1.4	1	15	PLSIALAMGMMELGA	17001
3F1F	QZ	RIBOSOME	Z	1.4	1.4	1	12	LVEFDKVFRQAS	17002
3F1F	W5	RIBOSOME	W	1.4	1.4	1	9	PRKVRLVVD	17003
3F9K	EG	VIRAL PROTEIN, RECOMBINATION	G	1.4	1.4	1	10	TEMITTLKKI	17004
3F9K	QS	VIRAL PROTEIN, RECOMBINATION	S	1.4	1.4	1	10	TEMITTLKKI	17005
3FDO	AB	CELL CYCLE	A	1.4	1.4	1	16	VKEVMHYLGQYIMVKQ	17006
3FH9	AB	OXYGEN TRANSPORT	B	1.4	1.4	1	20	PENFRLLGNVLVCVLARHFG	17007
3FHI	AB	TRANSFERASE	B	1.4	1.4	1	6	ELALIY	17008
3FKS	BF	HYDROLASE	F	1.4	1.4	1	10	GNDLYREMKE	17009
3FKS	CD	HYDROLASE	C	1.4	1.4	1	12	LKLFLAQYREVA	17010
3FKS	CD	HYDROLASE	D	1.4	1.4	1	15	TREGNDLYREMKETG	17011

3FKS	CF	HYDROLASE	F	1.4	1.4	1	8	PAPATTFA	17012
3FKS	LO	HYDROLASE	L	1.4	1.4	1	14	RSTVAQLVQTLEQH	17013
3FKS	PR	HYDROLASE	P	1.4	1.4	1	14	FQESALIADKLLSV	17014
3FKS	SV	HYDROLASE	V	1.4	1.4	1	10	PAPATTFAHL	17015
3FKS	UX	HYDROLASE	U	1.4	1.4	1	15	LSKQAVAYRQLSLLL	17016
3FKS	VY	HYDROLASE	Y	1.4	1.4	1	28	LKEVEMRLKSIKNIEKITKTMKIVASTR	17017
3FKU	CD	VIRAL PROTEIN/IMMUNE SYSTEM	C	1.4	1.4	1	10	YEELKHLLSR	17018
3FLO	AB	TRANSFERASE	A	1.4	1.4	1	15	LDELFLKLFTPILKT	17019
3FLO	CD	TRANSFERASE	D	1.4	1.4	1	18	RELMETGRSVVQKYLNDC	17020
3FMO	AB	ONCOPROTEIN/HYDROLASE	B	1.4	1.4	1	8	PGTVLDWC	17021
3FS4	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.4	1.4	1	19	PVNFKLLGQCFLVVVAIHH	17022
3FS4	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.4	1.4	1	20	PENFRLLGDILIIVLAAHFT	17023
3FXD	CD	UNKNOWN FUNCTION	D	1.4	1.4	1	15	IISPVKDCILTVAKA	17024
3G3B	GF	HYDROLASE/IMMUNE SYSTEM	F	1.4	1.4	1	11	RCELAAAMKRH	17025
3G43	DE	METAL BINDING PROTEIN	D	1.4	1.4	1	11	EAELQDMINEV	17026
3G43	DF	METAL BINDING PROTEIN	D	1.4	1.4	1	15	EEQIAEFKEAFSLFD	17027
3G6D	HA	IMMUNE SYSTEM	A	1.4	1.4	1	17	TALRELIEELVNITQNQ	17028
3G9V	AB	CYTOKINE/CYTOKINE RECEPTOR	B	1.4	1.4	1	17	PYITNRTFMLAKEASLA	17029
3GE8	AC	OXIDOREDUCTASE	A	1.4	1.4	1	14	WGRCWDVITENVLN	17030
3GHG	DF	BLOOD CLOTTING	D	1.4	1.4	1	43	LRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIK	17031
3GHG	EF	BLOOD CLOTTING	E	1.4	1.4	1	14	VEAVSQTSSSSFQY	17032
3GJX	BA	PROTEIN TRANSPORT	A	1.4	1.4	1	22	YLDMLNVYKCLSENISAAIQAN	17033
3GJX	FD	PROTEIN TRANSPORT	D	1.4	1.4	1	20	DEQNFIQNLSLFLCTFLKEH	17034
3GKW	HL	IMMUNE SYSTEM, ANTITUMOR PROTEIN	L	1.4	1.4	1	6	DEQLKS	17035
3GLH	DE	TRANSFERASE	D	1.4	1.4	1	10	LRDALSLTDQ	17036
3GLI	AE	TRANSFERASE/DNA	A	1.4	1.4	1	25	PVILLRTLQRELLLLVNLKRQSAHT	17037
3GLI	DE	TRANSFERASE/DNA	D	1.4	1.4	1	17	PTDIQLYYQTLLIGRKE	17038
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.4	1.4	1	17	VAHLIECLLSKVAALSG	17039
3GTM	AS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.4	1.4	1	10	FINIAQMSAC	17040
3GZ1	BP	CHAPERONE	B	1.4	1.4	1	13	TPVFHTGQCQLRL	17041
3H0L	DE	LIGASE	D	1.4	1.4	1	11	IIAPSEASSNL	17042
3H0L	GH	LIGASE	G	1.4	1.4	1	13	IFEMYARTRDEGF	17043
3H0L	HI	LIGASE	I	1.4	1.4	1	7	REKALMN	17044
3H0L	SU	LIGASE	S	1.4	1.4	1	6	SIPTYY	17045
3H2V	BF	CELL ADHESION	B	1.4	1.4	1	20	DIIAAAKRMALLMAEMSRLV	17046

3H2V	DG	CELL ADHESION	D	1.4	1.4	1	9	DEESEQATE	17047
3H32	DF	BLOOD CLOTTING	D	1.4	1.4	1	41	VLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSC	17048
3H4P	Ab	HYDROLASE	b	1.4	1.4	1	6	LYKMRT	17049
3H6P	BD	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	D	1.4	1.4	1	23	YQGWQTQWNQALEDLVRAYQSMS	17050
3HAE	PT	IMMUNE SYSTEM	P	1.4	1.4	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	17051
3HAX	CD	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	D	1.4	1.4	1	10	AHLPPLCEEK	17052
3HE6	AC	IMMUNE SYSTEM	A	1.4	1.4	1	12	SWLDLPIKVLNA	17053
3HHZ	CM	VIRAL PROTEIN/RNA	C	1.4	1.4	1	6	YNQARV	17054
3HKZ	AB	TRANSFERASE	A	1.4	1.4	1	9	YMQRRLINA	17055
3HKZ	AB	TRANSFERASE	B	1.4	1.4	1	13	YAFKLLIQELMSM	17056
3HKZ	IJ	TRANSFERASE	J	1.4	1.4	1	7	PRNTYQS	17057
3HKZ	MJ	TRANSFERASE	M	1.4	1.4	1	8	VVENIIIG	17058
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.4	1.4	1	8	PEEVRAIS	17059
3HOY	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.4	1.4	1	21	VLLDEEYKQLVKDRKFLREVF	17060
3HPG	AH	TRANSFERASE	A	1.4	1.4	1	11	ESTQLLMKYLG	17061
3HRD	AB	OXIDOREDUCTASE	A	1.4	1.4	1	8	REESTTVS	17062
3HRD	AD	OXIDOREDUCTASE	A	1.4	1.4	1	7	SLEKVMG	17063
3HRD	EF	OXIDOREDUCTASE	E	1.4	1.4	1	8	REESTTVS	17064
3HRD	EF	OXIDOREDUCTASE	E	1.4	1.4	1	13	GPAVITRATVHCM	17065
3HRW	AB	OXYGEN TRANSPORT	A	1.4	1.4	1	19	PAVHASLDKFLASVSTVLT	17066
3HRZ	BC	IMMUNE SYSTEM	B	1.4	1.4	1	5	PRAKG	17067
3HS0	HD	IMMUNE SYSTEM	D	1.4	1.4	1	7	KGSCERD	17068
3UBP	AC	HYDROLASE	A	1.4	1.4	1	22	PAEKEKLQIFLASELLLRRKAR	17069
3UBP	AC	HYDROLASE	A	1.4	1.4	1	5	VPEMI	17070
1A6T	AB	IMMUNOGLOBULIN	A	1.3	1.3	1	6	SEQLTS	17071
1A81	AH	COMPLEX (TRANSFERASE/PEPTIDE)	A	1.3	1.3	1	16	FEDLKENLIREYVKQT	17072
1A9W	AE	OXYGEN TRANSPORT	A	1.3	1.3	1	19	PAVHASLDKFLASVSTVLT	17073
1A9W	AE	OXYGEN TRANSPORT	A	1.3	1.3	1	19	PVNFKLLSHCLLVTLAAHL	17074
1AD0	AB	IMMUNOGLOBULIN	A	1.3	1.3	1	7	DEQLKSG	17075
1AGR	DH	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	H	1.3	1.3	1	14	DEAQKKIFNLMEKD	17076
1AHJ	CD	LYASE	C	1.3	1.3	1	6	KDCLIG	17077
1AHJ	EF	LYASE	F	1.3	1.3	1	9	QDELESLAG	17078
1AIP	BC	COMPLEX OF TWO ELONGATION FACTORS	C	1.3	1.3	1	18	ELFQNLAKDLAMHIAMMN	17079

1AM4	AD	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)	D	1.3	1.3	1	6	DRLRPL	17080
1AOI	GH	DNA BINDING PROTEIN/DNA	H	1.3	1.3	1	12	SREIQTAVRLLL	17081
1AVO	AN	PROTEASOME ACTIVATOR	N	1.3	1.3	1	6	FEKLKK	17082
1AVZ	BC	COMPLEX (MYRISTYLATION/TRANSFERASE)	B	1.3	1.3	1	15	YKAAVDLSHFLKEKG	17083
1AYY	AD	HYDROLASE	A	1.3	1.3	1	10	DGALEFALSQ	17084
1AZZ	BD	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.3	1.3	1	9	NADCDAVYG	17085
1B33	DN	PHOTOSYNTHESIS	N	1.3	1.3	1	12	NWFREQQRIQKM	17086
1B33	LK	PHOTOSYNTHESIS	K	1.3	1.3	1	25	TRRYAACIRDLDYYLRYATYAMLAG	17087
1B4U	AB	DIOXYGENASE	A	1.3	1.3	1	10	QEEYAQMMID	17088
1B8D	KL	PHOTOSYNTHESIS	L	1.3	1.3	1	6	SVLDDR	17089
1BAF	LH	IMMUNOGLOBULIN	L	1.3	1.3	1	6	SEQLTS	17090
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	A	1.3	1.3	1	15	GHYVPELSQLVHRSK	17091
1BGY	DF	ELECTRON TRANSPORT	F	1.3	1.3	1	20	ENLYDDRVFRIKRALDLSMR	17092
1BGY	MO	ELECTRON TRANSPORT	M	1.3	1.3	1	6	YNRIRS	17093
1BGY	VW	ELECTRON TRANSPORT	V	1.3	1.3	1	31	TSTFALTIVVGALFFERAFDQGADAIYEHIN	17094
1BI8	AB	COMPLEX (KINASE/INHIBITOR)	B	1.3	1.3	1	10	VQEVRRLLHR	17095
1BI8	CD	COMPLEX (KINASE/INHIBITOR)	D	1.3	1.3	1	10	VQEVRRLLHR	17096
1BJ1	JK	COMPLEX (ANTIBODY/ANTIGEN)	J	1.3	1.3	1	6	DEQLKS	17097
1C5D	LH	IMMUNE SYSTEM	L	1.3	1.3	1	7	TEQLATG	17098
1C9B	QR	TRANSCRIPTION/DNA	R	1.3	1.3	1	8	LEGLVLTH	17099
1CB7	AB	ISOMERASE	B	1.3	1.3	1	5	AYTRQ	17100
1CB7	CD	ISOMERASE	C	1.3	1.3	1	6	GEIDCK	17101
1CC1	SL	OXIDOREDUCTASE	S	1.3	1.3	1	14	EMALAHMYEIAEKF	17102
1CDL	BF	CALCIUM-BINDING PROTEIN	B	1.3	1.3	1	11	AAELRHVMTNL	17103
1CE1	LH	ANTIBODY	L	1.3	1.3	1	7	DEQLKSG	17104
1CF7	AB	TRANSCRIPTION/DNA	B	1.3	1.3	1	16	LRHFSMKVCEKVQRKG	17105
1CKK	AB	CALMODULIN-PEPTIDE COMPLEX	A	1.3	1.3	1	6	MMARKM	17106
1CKN	AB	CAPPING ENZYME	B	1.3	1.3	1	12	PTIIKDHLKKAN	17107
1CL7	LH	IMMUNE SYSTEM	L	1.3	1.3	1	7	SEQLTSG	17108
1CPC	AB	LIGHT HARVESTING PROTEIN	B	1.3	1.3	1	12	AFAKVVSQADAR	17109
1CPC	KL	LIGHT HARVESTING PROTEIN	L	1.3	1.3	1	13	GSQIDALSALVAD	17110
1CZ8	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	DEQLKS	17111
1D4M	13	VIRUS	3	1.3	1.3	1	7	LLGEILN	17112
1D8D	AB	TRANSFERASE	B	1.3	1.3	1	14	GGYTFCGLAALVIL	17113
1D8D	AB	TRANSFERASE	B	1.3	1.3	1	23	VTSIEQAKVEEKIQEVFSSYKFN	17114
1D9K	EH	IMMUNE SYSTEM	H	1.3	1.3	1	18	LERTRAELDTVCRHNYEK	17115

1DCE	AB	TRANSFERASE	A	1.3	1.3	1	14	FHCWDYRRFVAAQA	17116
1DD4	BC	RIBOSOME	B	1.3	1.3	1	9	LKEAKDLVE	17117
1DE4	AC	METAL TRANSPORT INHIBITOR/RECEPTOR	C	1.3	1.3	1	7	RADIKEM	17118
1DFB	LH	IMMUNOGLOBULIN	L	1.3	1.3	1	6	DEQLKS	17119
1DKG	AD	COMPLEX (HSP24/HSP70)	A	1.3	1.3	1	18	KAEMENLRRRTELDIEKA	17120
1DML	CD	DNA BINDING PROTEIN/TRANSFERASE	D	1.3	1.3	1	9	DVAARLRAA	17121
1DX5	AM	SERINE PROTEINASE	M	1.3	1.3	1	11	KKWIQKVIDQF	17122
1E1C	CD	ISOMERASE	C	1.3	1.3	1	13	AARRFEELAAKAG	17123
1E3D	CD	HYDROGENASE	D	1.3	1.3	1	10	PRDAQHFTQR	17124
1E6Y	DE	OXIDOREDUCTASE	E	1.3	1.3	1	12	KVEGTAVGFSFF	17125
1E6Y	EF	OXIDOREDUCTASE	E	1.3	1.3	1	15	IGTVIESVVRRAIEA	17126
1E7P	BC	OXIDOREDUCTASE	B	1.3	1.3	1	5	ACHDV	17127
1E7P	HI	OXIDOREDUCTASE	H	1.3	1.3	1	5	ACHDV	17128
1E7P	KL	OXIDOREDUCTASE	K	1.3	1.3	1	5	ACHDV	17129
1EAY	AC	SIGNAL TRANSDUCTION COMPLEX	A	1.3	1.3	1	10	KENIIAAAQA	17130
1EBD	AC	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)	C	1.3	1.3	1	10	PSVRKYAREK	17131
1EFU	AB	COMPLEX (TWO ELONGATION FACTORS)	B	1.3	1.3	1	14	EELVKHIAMHVAAS	17132
1EFU	CD	COMPLEX (TWO ELONGATION FACTORS)	C	1.3	1.3	1	18	EELLELVEMEVRELLSQY	17133
1EM8	AB	GENE REGULATION	B	1.3	1.3	1	10	PLVSDVLRAL	17134
1EO2	AB	OXIDOREDUCTASE	B	1.3	1.3	1	5	KTSVL	17135
1EP3	AB	OXIDOREDUCTASE	B	1.3	1.3	1	5	VCEDG	17136
1EQZ	CD	STRUCTURAL PROTEIN/DNA	C	1.3	1.3	1	11	TVALREIRRYQ	17137
1EQZ	EF	STRUCTURAL PROTEIN/DNA	E	1.3	1.3	1	7	EELNKLL	17138
1ETZ	AB	IMMUNE SYSTEM	A	1.3	1.3	1	6	SEELET	17139
1EV1	13	VIRUS	3	1.3	1.3	1	7	LMGEILN	17140
1EV1	34	VIRUS	4	1.3	1.3	1	6	PGKFTE	17141
1EXB	AE	METAL TRANSPORT	A	1.3	1.3	1	15	REKVEVQLPELFHKI	17142
1EYX	AB	PHOTOSYNTHESIS	A	1.3	1.3	1	16	HEAVVKEAGDACFGKY	17143
1EZX	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.3	1.3	1	14	PVSIATAFAMLSLG	17144
1F3J	AP	IMMUNE SYSTEM	A	1.3	1.3	1	22	PQGGLQNIAAEKHNLGILTKRS	17145
1F51	CG	TRANSFERASE	C	1.3	1.3	1	31	ALTNELIHLLGHSRHDWMNKLQLIKGNLSLQ	17146
1F66	FH	STRUCTURAL PROTEIN/DNA	F	1.3	1.3	1	11	AMDVVYALKRQ	17147
1F66	GH	STRUCTURAL PROTEIN/DNA	G	1.3	1.3	1	7	EELDSLI	17148
1F6M	FH	OXIDOREDUCTASE	H	1.3	1.3	1	12	KGQLKEFLDANL	17149
1F93	CH	TRANSCRIPTION	H	1.3	1.3	1	13	QLQTELLAALLES	17150
1F99	KN	PHOTOSYNTHESIS	K	1.3	1.3	1	8	LEEINRTF	17151

1F9E	CD	APOPTOSIS	C	1.3	1.3	1	15	THLDAGALTTTFEEL	17152
1F9E	EF	APOPTOSIS	E	1.3	1.3	1	15	THLDAGALTTTFEEL	17153
1F9E	GH	APOPTOSIS	G	1.3	1.3	1	15	THLDAGALTTTFEEL	17154
1F9E	IJ	APOPTOSIS	I	1.3	1.3	1	15	THLDAGALTTTFEEL	17155
1F9E	KL	APOPTOSIS	K	1.3	1.3	1	15	THLDAGALTTTFEEL	17156
1FAI	LH	IMMUNOGLOBULIN	L	1.3	1.3	1	6	SEQLTS	17157
1FBV	AC	LIGASE	A	1.3	1.3	1	9	QEQYELYCE	17158
1FE8	JN	IMMUNE SYSTEM	N	1.3	1.3	1	5	SEQLT	17159
1FFU	DE	HYDROLASE	E	1.3	1.3	1	7	KEDARFI	17160
1FLC	AB	HYDROLASE	B	1.3	1.3	1	24	KGFEKIGNDIQILKSSINIAIEKL	17161
1FNT	Ci	HYDROLASE/HYDROLASE ACTIVATOR	C	1.3	1.3	1	10	QVEYALESIS	17162
1FNT	OU	HYDROLASE/HYDROLASE ACTIVATOR	O	1.3	1.3	1	22	IPDARNAALRAKAEAAEFRYKY	17163
1FNT	OV	HYDROLASE/HYDROLASE ACTIVATOR	V	1.3	1.3	1	20	AADTQAIADIVQYHLELYTS	17164
1FNT	OW	HYDROLASE/HYDROLASE ACTIVATOR	W	1.3	1.3	1	23	AADTEAVTQLIGSNIELHSLYTS	17165
1FNT	WN	HYDROLASE/HYDROLASE ACTIVATOR	W	1.3	1.3	1	9	SLAAMAVLE	17166
1FNT	WX	HYDROLASE/HYDROLASE ACTIVATOR	X	1.3	1.3	1	18	PEDLFETISQALLNAADR	17167
1FNT	XL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.3	1.3	1	19	VEDALYLGKRSILAAAHRD	17168
1FOE	CD	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	C	1.3	1.3	1	5	LESYL	17169
1FOE	EF	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	E	1.3	1.3	1	36	KKVLFSLGGSFLYYADRFKLYSAFCASHTKVPKVLV	17170
1FPP	BA	PRENYLTRANSFERASE	B	1.3	1.3	1	15	QIVATDVCQFLELCQ	17171
1FPP	BA	PRENYLTRANSFERASE	B	1.3	1.3	1	10	LKSLLQWVTS	17172
1FPT	LH	COMPLEX (ANTIBODY/PV-1 FRAGMENT)	L	1.3	1.3	1	5	YKVSN	17173
1FQV	IJ	LIGASE	J	1.3	1.3	1	16	KGLLDVTCKTVANMIK	17174
1FSX	AB	OXYGEN STORAGE/TRANSPORT	B	1.3	1.3	1	21	PVLQADFQKVVAGVANALAHR	17175
1FXT	AB	LIGASE	A	1.3	1.3	1	14	LKSALISLQALLQS	17176
1FYZ	DF	OXIDOREDUCTASE	F	1.3	1.3	1	6	EVDFRH	17177
1G0U	1N	HYDROLASE	N	1.3	1.3	1	22	AADTQAIADIVQYHLELYTSQY	17178
1G0U	BI	HYDROLASE	B	1.3	1.3	1	23	TADAEILINTARIHAQNYLKTYN	17179
1G0U	DL	HYDROLASE	D	1.3	1.3	1	22	TADARSMIEHARTAAVTHNLYY	17180
1G0U	H1	HYDROLASE	1	1.3	1.3	1	6	WDFAKD	17181
1G0U	OV	HYDROLASE	V	1.3	1.3	1	22	AADTEAVTQLIGSNIELHSLYT	17182
1G0U	RY	HYDROLASE	R	1.3	1.3	1	22	TADARSMIEHARTAAVTHNLYY	17183
1G0U	S1	HYDROLASE	1	1.3	1.3	1	20	ISDMQHIERLLKDLVTENAY	17184
1G0U	VM	HYDROLASE	M	1.3	1.3	1	19	VQVAEEAIVNAMRVLYYRD	17185
1G0Y	RI	IMMUNE SYSTEM	I	1.3	1.3	1	7	WEESNAY	17186
1G20	AB	OXIDOREDUCTASE	A	1.3	1.3	1	9	EKARKDRNK	17187
1G20	AB	OXIDOREDUCTASE	B	1.3	1.3	1	15	QQNMKDGLQNCKATY	17188

1G20	AD	OXIDOREDUCTASE	A	1.3	1.3	1	16	FDGFAIFARDMDMTLN	17189
1G20	AD	OXIDOREDUCTASE	D	1.3	1.3	1	16	LDWTDEFLMKVSEISG	17190
1G20	CB	OXIDOREDUCTASE	B	1.3	1.3	1	16	LDWTDEFLMKVSEISG	17191
1G20	CD	OXIDOREDUCTASE	C	1.3	1.3	1	6	ISEIEL	17192
1G20	CD	OXIDOREDUCTASE	D	1.3	1.3	1	6	CMAEVI	17193
1G3N	AB	CELL CYCLE, SIGNALING PROTEIN	B	1.3	1.3	1	9	NELASAAAR	17194
1G3N	EG	CELL CYCLE, SIGNALING PROTEIN	G	1.3	1.3	1	13	CEDRIFYNILEIE	17195
1GH0	CF	PHOTOSYNTHESIS	C	1.3	1.3	1	8	IDEINRTF	17196
1GH0	IL	PHOTOSYNTHESIS	L	1.3	1.3	1	25	SRRMAACLRDMEIILRYVTYAVFAG	17197
1GH0	KH	PHOTOSYNTHESIS	H	1.3	1.3	1	25	SRRMAACLRDMEIILRYVTYAVFAG	17198
1GH0	KH	PHOTOSYNTHESIS	K	1.3	1.3	1	8	IDEINRTF	17199
1GH0	ST	PHOTOSYNTHESIS	S	1.3	1.3	1	10	TGPMDEYLIA	17200
1GH0	WT	PHOTOSYNTHESIS	W	1.3	1.3	1	8	IDEINRTF	17201
1GK0	AB	HYDROLASE	B	1.3	1.3	1	8	REQVEAAV	17202
1GXS	CD	LYASE	C	1.3	1.3	1	19	DDKMAQDTYTFLVKWFERF	17203
1H1L	AB	OXIDOREDUCTASE	A	1.3	1.3	1	16	EGQMAAIIAKYRPRLE	17204
1H1L	CB	OXIDOREDUCTASE	B	1.3	1.3	1	16	LAATDELLMTVSQLSG	17205
1H8B	AB	STRUCTURAL PROTEIN	A	1.3	1.3	1	9	YAAFSSALY	17206
1HBH	AB	OXYGEN CARRIER	B	1.3	1.3	1	16	YDDIGPKALSRCLIVY	17207
1HBH	AD	OXYGEN CARRIER	A	1.3	1.3	1	19	PANFKILNHCILVVISTMF	17208
1HBX	EH	GENE REGULATION	E	1.3	1.3	1	26	KLRRYTTFSKRKTGIMKKAYELSTLT	17209
1HE1	AD	SIGNALING PROTEIN	D	1.3	1.3	1	9	DRLRPLSYP	17210
1HE1	BC	SIGNALING PROTEIN	C	1.3	1.3	1	9	DRLRPLSYP	17211
1HMV	AB	NUCLEOTIDYLTRANSFERASE	B	1.3	1.3	1	18	VNDIQKLVGKLNWASQIY	17212
1HV4	CB	OXYGEN STORAGE/TRANSPORT	B	1.3	1.3	1	6	PWTQRF	17213
1I1A	AC	IMMUNE SYSTEM	A	1.3	1.3	1	12	PETDIVGNLWMK	17214
1I1R	AB	CYTOKINE	B	1.3	1.3	1	20	MELLTKTLGWDIQEELNKLT	17215
1I2M	CD	CELL CYCLE	C	1.3	1.3	1	5	QEKFG	17216
1I3O	BE	APOPTOSIS	E	1.3	1.3	1	5	FFVLG	17217
1I7W	AB	CELL ADHESION	B	1.3	1.3	1	6	KAADSD	17218
1I7W	CD	CELL ADHESION	C	1.3	1.3	1	15	WPLIKATVGLIRNLA	17219
1ID3	FD	STRUCTURAL PROTEIN/DNA	F	1.3	1.3	1	9	DVVYALKRQ	17220
1IGT	CD	IMMUNOGLOBULIN	C	1.3	1.3	1	7	SEQLTSG	17221
1IND	LH	IMMUNOGLOBULIN	L	1.3	1.3	1	6	SEELET	17222
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.3	1.3	1	14	FPEFLTMMARKMKD	17223
1IR2	BJ	LYASE	B	1.3	1.3	1	14	AKNYGRAVYECLRG	17224
1IR2	BJ	LYASE	B	1.3	1.3	1	10	PELAAACEVW	17225
1IR2	DL	LYASE	D	1.3	1.3	1	10	PELAAACEVW	17226
1IR2	EM	LYASE	E	1.3	1.3	1	10	PELAAACEVW	17227

1IR2	GO	LYASE	G	1.3	1.3	1	14	AKNYGRAVYECLRG	17228
1IR2	GO	LYASE	G	1.3	1.3	1	21	NAPGAAANRVALEACTQARNE	17229
1IR2	GO	LYASE	G	1.3	1.3	1	10	PELAAACEVW	17230
1IR2	T2	LYASE	T	1.3	1.3	1	10	PELAAACEVW	17231
1IR2	V4	LYASE	V	1.3	1.3	1	10	PELAAACEVW	17232
1IR2	Y7	LYASE	Y	1.3	1.3	1	10	PELAAACEVW	17233
1IR2	Z8	LYASE	8	1.3	1.3	1	14	DEQIAAQVDYIVAN	17234
1IRU	AB	HYDROLASE	B	1.3	1.3	1	23	GPDYRVLVHRARKLAQQYYLVYQ	17235
1IRU	CK	HYDROLASE	K	1.3	1.3	1	22	AGDTVQFAEYIQKNVQLYKMRN	17236
1IRU	OP	HYDROLASE	P	1.3	1.3	1	23	GPDYRVLVHRARKLAQQYYLVYQ	17237
1IRU	T2	HYDROLASE	2	1.3	1.3	1	18	PRAIHSWLTRAMYSRRSK	17238
1IRU	VW	HYDROLASE	V	1.3	1.3	1	23	AADTQAVADAVTYQLGFHSIELN	17239
1IRU	WM	HYDROLASE	W	1.3	1.3	1	18	EEEAKNLVSEAIAAGIFN	17240
1IW7	CD	TRANSFERASE	D	1.3	1.3	1	16	VGIVAAQSIGEPGTQL	17241
1IW7	KM	TRANSFERASE	K	1.3	1.3	1	5	AEKHG	17242
1IW7	NO	TRANSFERASE	O	1.3	1.3	1	11	AETWAMKELLT	17243
1IWA	MJ	LYASE	J	1.3	1.3	1	14	DEQIKKQIDYMISK	17244
1IWA	OJ	LYASE	O	1.3	1.3	1	21	IQAGATANRVALEAMILARNE	17245
1IYJ	AB	GENE REGULATION/ANTITUMOR PROTEIN	B	1.3	1.3	1	18	PERVLLQLKYRYDVEIDN	17246
1IYJ	CD	GENE REGULATION/ANTITUMOR PROTEIN	D	1.3	1.3	1	6	LQAAVG	17247
1J1D	DF	CONTRACTILE PROTEIN	D	1.3	1.3	1	12	TKELGKVMRMLG	17248
1J1D	EF	CONTRACTILE PROTEIN	E	1.3	1.3	1	22	QTEREKKKKILAERRKVLAIDH	17249
1J1E	AB	CONTRACTILE PROTEIN	A	1.3	1.3	1	8	YDEFLEFM	17250
1JB0	AB	PHOTOSYNTHESIS	B	1.3	1.3	1	32	KEAIISHLSWVSLFLGFHTLGLYVHNDVVVAF	17251
1JB0	AF	PHOTOSYNTHESIS	F	1.3	1.3	1	29	DFLIPSVLFLYIAGWIGWVGRAYLIAVRN	17252
1JBU	HL	HYDROLASE	H	1.3	1.3	1	10	RTFSERTLAF	17253
1JD2	1U	HYDROLASE	1	1.3	1.3	1	21	IPDGRHLVNRGREEAASFKKL	17254
1JD2	EM	HYDROLASE	M	1.3	1.3	1	18	PSYIFEYLATVMYQRRSK	17255
1JD2	GH	HYDROLASE	G	1.3	1.3	1	18	CDVLAKRMANLSQIYTQR	17256
1JMU	AB	VIRAL PROTEIN	A	1.3	1.3	1	5	PGMLN	17257
1JMU	CD	VIRAL PROTEIN	D	1.3	1.3	1	12	MQSVVKLLDDQL	17258
1JMX	AG	OXIDOREDUCTASE	G	1.3	1.3	1	5	MMSTY	17259
1JNH	EF	IMMUNE SYSTEM	E	1.3	1.3	1	6	SEELET	17260
1JNL	LH	IMMUNE SYSTEM	L	1.3	1.3	1	7	SEQLTSG	17261
1JNR	AB	OXIDOREDUCTASE	A	1.3	1.3	1	23	SSGSFTEGRIAAKAAVRFILEQK	17262
1JOW	AB	CELL CYCLE/TRANSFERASE	A	1.3	1.3	1	12	ATDFLIPLCNAL	17263
1JPS	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	DEQLKS	17264
1JY2	OS	BLOOD CLOTTING	O	1.3	1.3	1	28	GCKLQDTLVRQERPIRKSIEDLRNTVDS	17265

1JY7	AB	OXYGEN STORAGE/TRANSPORT	A	1.3	1.3	1	19	PAVHASLDKFLASVSTVLT	17266
1JY7	UV	OXYGEN STORAGE/TRANSPORT	U	1.3	1.3	1	19	PAVHASLDKFLASVSTVLT	17267
1JY7	WX	OXYGEN STORAGE/TRANSPORT	X	1.3	1.3	1	19	PENFRLLGNVLVCVLAHHF	17268
1K6L	LH	PHOTOSYNTHESIS	H	1.3	1.3	1	22	LLEEDKICGYVAGGLMYAAPKR	17269
1K8I	AB	IMMUNE SYSTEM	B	1.3	1.3	1	10	ESLIHRLQNG	17270
1KC5	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEQLTS	17271
1KF6	AB	OXIDOREDUCTASE	A	1.3	1.3	1	5	HTVAA	17272
1KF6	MN	OXIDOREDUCTASE	M	1.3	1.3	1	16	WAKIRDEMGLAMEEGC	17273
1KF9	DC	HORMONE/GROWTH FACTOR	D	1.3	1.3	1	6	RSVFAN	17274
1KFA	MI	IMMUNE SYSTEM	M	1.3	1.3	1	6	SEQLTS	17275
1KFY	BD	OXIDOREDUCTASE	B	1.3	1.3	1	21	PAAAIQQGKVESSKDFLIATL	17276
1KG0	AD	VIRAL PROTEIN/IMMUNE SYSTEM	A	1.3	1.3	1	22	AQGALANIAVDKANLEIMTKRS	17277
1KI6	AB	PHOSPHOTRANSFERASE	B	1.3	1.3	1	16	NVFAWALDVLAKRLRS	17278
1KKQ	DH	TRANSCRIPTION	D	1.3	1.3	1	18	QCTSVETVTELTEFAKAI	17279
1KQS	AY	RIBOSOME	Y	1.3	1.3	1	9	VAGKAVMKA	17280
1KX4	CD	STRUCTURAL PROTEIN/DNA	C	1.3	1.3	1	7	EELNKLL	17281
1KXP	AD	CONTRACTILE PROTEIN/PROTEIN BINDING	A	1.3	1.3	1	9	QAVLSLYAS	17282
1KXP	AD	CONTRACTILE PROTEIN/PROTEIN BINDING	A	1.3	1.3	1	11	IHETTYNSIMK	17283
1KYO	CP	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.3	1.3	1	15	QMSHWGATVITNLFS	17284
1KYO	NE	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	1.3	1.3	1	15	QMSHWGATVITNLFS	17285
1KYO	OR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.3	1.3	1	21	EDESYARAYRIIRAHQTELTH	17286
1L2I	AC	TRANSCRIPTION RECEPTOR/COACTIVATOR	A	1.3	1.3	1	11	LHDQVHLLECA	17287
1L4A	BD	ENDOCYTOSIS/EXOCYTOSIS	D	1.3	1.3	1	29	IGNLRNMAIDMGNEIGSQNRQVDRIQQKA	17288
1L7T	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEQLTS	17289
1L9B	LM	PHOTOSYNTHESIS	L	1.3	1.3	1	13	IWTHLDWVSNTGY	17290
1L9J	MH	PHOTOSYNTHESIS	M	1.3	1.3	1	7	ELEQIAD	17291
1L9J	RS	PHOTOSYNTHESIS	R	1.3	1.3	1	13	IWTHLDWVSNTGY	17292
1LIA	AB	LIGHT HARVESTING PROTEIN	B	1.3	1.3	1	14	GNKRLDAVNYIVSN	17293
1LKY	CD	TRANSCRIPTION	D	1.3	1.3	1	14	GDVLYELLQHILKQ	17294
1LKY	EF	TRANSCRIPTION	F	1.3	1.3	1	14	GDVLYELLQHILKQ	17295
1LOT	AB	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	B	1.3	1.3	1	9	QAVLSLYAS	17296
1LP9	EF	IMMUNE SYSTEM	F	1.3	1.3	1	7	KAEIANK	17297
1LQM	CD	HYDROLASE/HYDROLASE INHIBITOR	D	1.3	1.3	1	9	PEEVEEVIG	17298

1LRW	CD	OXIDOREDUCTASE	D	1.3	1.3	1	5	PAELS	17299
1LT4	HA	ENTEROTOXIN	H	1.3	1.3	1	20	DSQKKAIERMKDTLRITYLT	17300
1LVC	AD	LYASE	D	1.3	1.3	1	12	AAELRHVMTNLG	17301
1LWU	AB	BLOOD CLOTTING	A	1.3	1.3	1	13	RIIHLQRRINMQL	17302
1LWU	JC	BLOOD CLOTTING	C	1.3	1.3	1	46	LEEVRILEQIGVSHDAQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	17303
1M1Y	IJ	OXIDOREDUCTASE	I	1.3	1.3	1	6	EKDIVF	17304
1M1Y	IJ	OXIDOREDUCTASE	I	1.3	1.3	1	6	CPIGLI	17305
1M1Y	JN	OXIDOREDUCTASE	J	1.3	1.3	1	13	KRWKKAVDAILAA	17306
1M63	AB	HYDROLASE/ISOMERASE	B	1.3	1.3	1	10	KEQKLRFAFR	17307
1M8Q	PR	CONTRACTILE PROTEIN	R	1.3	1.3	1	8	EAFVKHIM	17308
1M93	AC	VIRAL PROTEIN	A	1.3	1.3	1	14	PPSISSVLTILYYG	17309
1M93	BC	VIRAL PROTEIN	B	1.3	1.3	1	10	DTNFKKWSDS	17310
1MDU	AB	STRUCTURAL PROTEIN	B	1.3	1.3	1	9	QAVLSLYAS	17311
1MHY	DG	OXIDOREDUCTASE	D	1.3	1.3	1	8	LSEVIAEG	17312
1MIO	CB	MOLYBDENUM-IRON PROTEIN	C	1.3	1.3	1	13	DAWEMDRVLEKIG	17313
1MJG	CO	OXIDOREDUCTASE	C	1.3	1.3	1	36	AWTIVARNVGLMILTGAAAHCEHGNHIAHALVEMAE	17314
1MJG	DP	OXIDOREDUCTASE	D	1.3	1.3	1	36	AWTIVARNVGLMILTGAAAHCEHGNHIAHALVEMAE	17315
1MTY	CH	MONOOXYGENASE	H	1.3	1.3	1	13	DTRDAWVNKIAHV	17316
1MVW	PR	CONTRACTILE PROTEIN	R	1.3	1.3	1	10	DFKEAFLLFD	17317
1MWA	AH	IMMUNE SYSTEM	H	1.3	1.3	1	10	EAERLRAYLE	17318
1MWN	BY	STRUCTURAL PROTEIN	B	1.3	1.3	1	12	QEVVDKVMETLD	17319
1N0X	LH	IMMUNE SYSTEM	L	1.3	1.3	1	5	DEQLK	17320
1N2D	AC	CELL CYCLE	A	1.3	1.3	1	10	DAEVDELLKG	17321
1N4Q	IJ	TRANSFERASE	I	1.3	1.3	1	17	PYLIAFLVDIYEDMLEN	17322
1N4Q	IJ	TRANSFERASE	J	1.3	1.3	1	15	RLTIAFFALSGLDML	17323
1N52	AB	RNA BINDING PROTEIN	A	1.3	1.3	1	15	DVMYTTLLIELCKLQ	17324
1NB3	BJ	HYDROLASE	B	1.3	1.3	1	12	PSQAFEYIRYNK	17325
1NEX	CB	LIGASE, CELL CYCLE	B	1.3	1.3	1	12	FNSLNLKLSQKY	17326
1NH2	AC	TRANSCRIPTION/DNA	A	1.3	1.3	1	19	EDDSKLASRKYARIIQKIG	17327
1NI4	AB	OXIDOREDUCTASE	B	1.3	1.3	1	9	VGAEICARI	17328
1NIK	AB	TRANSCRIPTION	A	1.3	1.3	1	11	EETRAELSQLC	17329
1NIK	AE	TRANSCRIPTION	A	1.3	1.3	1	10	EIIQNAQRDA	17330
1NIK	CJ	TRANSCRIPTION	C	1.3	1.3	1	11	DEFIAHRLGLI	17331
1NIK	CJ	TRANSCRIPTION	J	1.3	1.3	1	11	WESYLNLLQED	17332
1NJ9	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEELET	17333
1NL0	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEELQA	17334
1NTK	AI	OXIDOREDUCTASE	A	1.3	1.3	1	20	DSQIEKERDVILQELQENDT	17335
1NTK	CD	OXIDOREDUCTASE	C	1.3	1.3	1	15	TTTAFSSVTHICRDV	17336
1NTK	CD	OXIDOREDUCTASE	D	1.3	1.3	1	9	YRHLVGVCY	17337

1NTK	CF	OXIDOREDUCTASE	C	1.3	1.3	1	34	HPYITIGQLASVLYFLLILVLMPTAGTIENKLLK	17338
1NZY	CB	LYASE	B	1.3	1.3	1	16	THLQVMAKERFHAGWM	17339
1O18	DF	CONTRACTILE PROTEIN	F	1.3	1.3	1	10	DFKEAFLLFD	17340
1O94	BE	ELECTRON TRANSPORT	B	1.3	1.3	1	21	GEWSYHRDYRETQITKLLKKN	17341
1O96	EF	ELECTRON TRANSFER	E	1.3	1.3	1	16	EWDDFSLEEAMKIKES	17342
1O96	EF	ELECTRON TRANSFER	E	1.3	1.3	1	16	AIVVGRILTEVIKKEA	17343
1OED	BC	ION CHANNEL/RECEPTOR	B	1.3	1.3	1	27	FYIVYTIIPCILISILAILVFYLPPDA	17344
1OOP	AC	VIRUS	A	1.3	1.3	1	6	VENFLC	17345
1OVL	AB	TRANSCRIPTION	A	1.3	1.3	1	11	ISAFSCIAALA	17346
1OVL	DF	TRANSCRIPTION	F	1.3	1.3	1	11	AIIDKLFLDTL	17347
1OW3	AB	GENE REGULATION/SIGNALING PROTEIN	A	1.3	1.3	1	14	LHLPAVILKTFLRE	17348
1OW7	AD	TRANSFERASE	A	1.3	1.3	1	19	KVYENVTGLVKAVIEMSSK	17349
1OW7	CF	TRANSFERASE	C	1.3	1.3	1	28	HREIEMAQKLLNSDLGELINKMKLAQQY	17350
1OXK	AD	SIGNALING PROTEIN	D	1.3	1.3	1	12	GLLSTKMIRRDL	17351
1P22	AB	SIGNALING PROTEIN	B	1.3	1.3	1	9	AAILKKVIQ	17352
1PC8	AB	HYDROLASE	A	1.3	1.3	1	14	NPILWRARQYINSG	17353
1PG7	YZ	IMMUNE SYSTEM	Y	1.3	1.3	1	6	SEELKT	17354
1PIV	34	VIRUS	3	1.3	1.3	1	6	MMELAE	17355
1PMA	LY	PROTEASE	L	1.3	1.3	1	23	VADARVLVDFARISAQQEKVTYG	17356
1POI	AB	TRANSFERASE	A	1.3	1.3	1	10	RRFRKWFEAG	17357
1PRC	LH	PHOTOSYNTHETIC REACTION CENTER	L	1.3	1.3	1	28	GFWQAITVCALGAFISWMLREVEISRKL	17358
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.3	1.3	1	7	EIEQITD	17359
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.3	1.3	1	16	HTAWAFLSAIWLWMVL	17360
1PTO	EF	TOXIN	E	1.3	1.3	1	13	PMEVMLRAVFMQQ	17361
1PTO	IJ	TOXIN	J	1.3	1.3	1	12	PMEVMLRAVFMQ	17362
1PTO	KL	TOXIN	K	1.3	1.3	1	12	PMEVMLRAVFMQ	17363
1PYT	AB	TERNARY COMPLEX (ZYMOGEN)	A	1.3	1.3	1	15	VQSLLDEEQEQMFAS	17364
1PYT	BD	TERNARY COMPLEX (ZYMOGEN)	B	1.3	1.3	1	18	WITQATGVWFAKKFTEDY	17365
1PZ5	AB	IMMUNE SYSTEM	A	1.3	1.3	1	7	SEQLTSG	17366
1PZL	AB	TRANSCRIPTION	A	1.3	1.3	1	21	IADVCESMKEQLLVLVEWAKY	17367
1Q16	AB	OXIDOREDUCTASE	A	1.3	1.3	1	14	KRLMKMWREAKALH	17368
1Q16	AB	OXIDOREDUCTASE	A	1.3	1.3	1	18	RSQIIRIAREFADNADKT	17369
1Q16	AB	OXIDOREDUCTASE	A	1.3	1.3	1	5	STCLY	17370
1Q16	BC	OXIDOREDUCTASE	B	1.3	1.3	1	5	IDDYY	17371
1Q1J	LH	IMMUNE SYSTEM	L	1.3	1.3	1	5	SEELQ	17372
1Q5Q	EM	HYDROLASE	M	1.3	1.3	1	14	FDGKANRLASMVRG	17373
1Q5R	AI	HYDROLASE	I	1.3	1.3	1	23	AGIAIELVRLFAVELEHYEKIEG	17374
1Q5R	EL	HYDROLASE	L	1.3	1.3	1	7	FTDYLRG	17375
1Q5R	EM	HYDROLASE	E	1.3	1.3	1	19	GRSLANAYAQTLGTIFTEQ	17376

1Q7L	AB	HYDROLASE	A	1.3	1.3	1	5	MELFV	17377
1Q7L	CD	HYDROLASE	C	1.3	1.3	1	5	MELFV	17378
1Q90	DG	PHOTOSYNTHESIS	D	1.3	1.3	1	22	PIATILFLLGTLVAVWLGIGST	17379
1QFU	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.3	1.3	1	7	KIQLTSG	17380
1QLE	CD	OXIDOREDUCTASE/IMMUNE SYSTEM	C	1.3	1.3	1	28	PVVRIGLQYGFILFIMSEVMFFVAWFWA	17381
1R1R	AD	OXIDOREDUCTASE	D	1.3	1.3	1	7	TDDLSNF	17382
1R1R	CF	OXIDOREDUCTASE	F	1.3	1.3	1	7	TDDLSNF	17383
1R20	AD	HORMONE/GROWTH FACTOR RECEPTOR	A	1.3	1.3	1	6	RFAALL	17384
1R27	CD	OXIDOREDUCTASE	C	1.3	1.3	1	18	RSQIIRIAREFADNADKT	17385
1R3I	HC	MEMBRANE PROTEIN	C	1.3	1.3	1	10	YPRALWWSVE	17386
1R4A	BF	PROTEIN TRANSPORT	F	1.3	1.3	1	12	TKTMAKVITTVL	17387
1R4M	AB	CELL CYCLE	A	1.3	1.3	1	5	DRQLR	17388
1R4P	AD	TOXIN	A	1.3	1.3	1	7	QFLYTTG	17389
1R6O	AC	HYDROLASE	A	1.3	1.3	1	17	QELELSLNMAFARAREH	17390
1R6O	AD	HYDROLASE	D	1.3	1.3	1	11	MEFVIDVLQKF	17391
1R8Q	BF	PROTEIN TRANSPORT/EXCHANGE FACTOR	F	1.3	1.3	1	19	AQKIDRMMEAFAQRYCLCN	17392
1RCO	BW	LYASE	B	1.3	1.3	1	15	CEDMMKRAVFARELG	17393
1RCO	LF	LYASE	L	1.3	1.3	1	15	CEDMMKRAVFARELG	17394
1RGI	GA	CONTRACTILE PROTEIN	A	1.3	1.3	1	9	QAVLSLYAS	17395
1RGI	GA	CONTRACTILE PROTEIN	G	1.3	1.3	1	18	QDESGAAAIFTVQLDDYL	17396
1RM6	DF	OXIDOREDUCTASE	F	1.3	1.3	1	8	RDEIKAAL	17397
1RM6	DF	OXIDOREDUCTASE	F	1.3	1.3	1	9	KLQAAFHEK	17398
1RP3	GD	TRANSCRIPTION	D	1.3	1.3	1	13	DEKVVKGLIEFFT	17399
1RU7	EB	VIRAL PROTEIN	B	1.3	1.3	1	22	QKSTQNAINGITNKVNSVIEKM	17400
1RUY	HK	VIRAL PROTEIN	K	1.3	1.3	1	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	17401
1RUZ	HM	VIRAL PROTEIN	H	1.3	1.3	1	10	YEELREQLSS	17402
1RUZ	JK	VIRAL PROTEIN	K	1.3	1.3	1	7	KVKSQLK	17403
1RV6	WX	HORMONE/GROWTH FACTOR/RECEPTOR	W	1.3	1.3	1	8	FQEVWGRS	17404
1RYP	AH	MULTICATALYTIC PROTEINASE	H	1.3	1.3	1	22	AADTQAIADIVQYHLELYTSQY	17405
1RYP	FN	MULTICATALYTIC PROTEINASE	N	1.3	1.3	1	20	ISDMQHIERLLKDLVTENAY	17406
1RYP	H2	MULTICATALYTIC PROTEINASE	2	1.3	1.3	1	19	VQVAEEAIVNAMRVLYYRD	17407
1RYP	I1	MULTICATALYTIC PROTEINASE	1	1.3	1.3	1	18	VEEVIKLVRDSFTSATER	17408
1RYP	MN	MULTICATALYTIC PROTEINASE	M	1.3	1.3	1	22	AADGDALVKRFKNSVKWYHFDH	17409
1RYP	ST	MULTICATALYTIC PROTEINASE	T	1.3	1.3	1	22	APDARVLSNYLRQQCNYSSLVF	17410
1RYP	XL	MULTICATALYTIC PROTEINASE	L	1.3	1.3	1	19	VEDALYLGKRSILAAAHRD	17411
1RYP	XM	MULTICATALYTIC PROTEINASE	M	1.3	1.3	1	13	ASLIMPFLDNQVN	17412

1S0Y	AD	LYASE	A	1.3	1.3	1	20	DEQKRALSAGLLRVISEATG	17413
1S0Y	EB	LYASE	E	1.3	1.3	1	20	DEQKRALSAGLLRVISEATG	17414
1S1C	BY	SIGNALING PROTEIN	Y	1.3	1.3	1	21	NINTERTLKTQAVNKLAEIMN	17415
1S5E	BL	TRANSERASE,TOXIN	B	1.3	1.3	1	29	CDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	17416
1S5L	ad	PHOTOSYNTHESIS	a	1.3	1.3	1	14	SRSLHFFLAAWPVV	17417
1S5L	bd	PHOTOSYNTHESIS	d	1.3	1.3	1	16	VAAIFRFLLFFQGFHN	17418
1S78	CD	TRANSFERASE	C	1.3	1.3	1	5	DEQLK	17419
1SB3	DF	OXIDOREDUCTASE	F	1.3	1.3	1	16	VKIIKSVETAAAARLC	17420
1SB3	DF	OXIDOREDUCTASE	F	1.3	1.3	1	9	KLQAAFHEK	17421
1SBN	EI	COMPLEX (PROTEINASE/INHIBITOR)	E	1.3	1.3	1	13	YSWIINGIEWAIA	17422
1SBN	EI	COMPLEX (PROTEINASE/INHIBITOR)	E	1.3	1.3	1	10	HGTHVAGTVA	17423
1SCJ	AB	HYDROLASE	A	1.3	1.3	1	13	TALKTVVDKAVSS	17424
1SCT	EF	OXYGEN TRANSPORT	F	1.3	1.3	1	16	MEGTGLMLMANLFKTS	17425
1SFC	GH	TRANSPORT PROTEIN	G	1.3	1.3	1	19	DQLADESLESTRRMLQLVE	17426
1SHZ	DC	SIGNALING PROTEIN	C	1.3	1.3	1	18	QVAVGRQLEDFRSKRLMG	17427
1SP4	AB	HYDROLASE	B	1.3	1.3	1	9	AEDMLTCCG	17428
1SQB	AB	OXIDOREDUCTASE	A	1.3	1.3	1	21	DSQIEKERDVILQELQENDTS	17429
1SQB	CF	OXIDOREDUCTASE	C	1.3	1.3	1	22	PLSQCLFWALVADLLTLTWIGG	17430
1SQB	EK	OXIDOREDUCTASE	K	1.3	1.3	1	20	VPTAQLWGAVGAVGLVWATD	17431
1SQX	CF	OXIDOREDUCTASE	C	1.3	1.3	1	23	PLSQCLFWALVADLLTLTWIGGQ	17432
1SV0	AC	TRANSCRIPTION	A	1.3	1.3	1	17	GDVLHNVLQMLIIESHS	17433
1SV0	BD	TRANSCRIPTION	D	1.3	1.3	1	8	LDMYLCRV	17434
1SXJ	BC	REPLICATION	B	1.3	1.3	1	15	LEDSIQILRTDLWKK	17435
1SY9	AB	CALCIUM-BINDING PROTEIN	A	1.3	1.3	1	13	SEEEIREAFRVFD	17436
1T0Q	AC	OXIDOREDUCTASE	C	1.3	1.3	1	11	MDQVAEKCAYH	17437
1T34	BH	SIGNALING PROTEIN,MEMBRANE PROTEIN	B	1.3	1.3	1	13	SAAPVGRFTAHWR	17438
1T3L	AB	TRANSPORT PROTEIN	A	1.3	1.3	1	21	LEDACEHLADYLEAYWKATHP	17439
1T3Q	AB	OXIDOREDUCTASE	A	1.3	1.3	1	9	ALQDSFRRH	17440
1T3Q	BC	OXIDOREDUCTASE	B	1.3	1.3	1	9	RAIAEDAAQ	17441
1T3Q	DF	OXIDOREDUCTASE	F	1.3	1.3	1	7	QAVRNRG	17442
1TEC	EI	COMPLEX (SERINE PROTEINASE-INHIBITOR)	E	1.3	1.3	1	10	HGTHCAGIAA	17443
1TET	LH	IMMUNOGLOBULIN	L	1.3	1.3	1	6	SEQLTS	17444
1TFC	AC	TRANSCRIPTION	A	1.3	1.3	1	26	DIKALTTLCDLADRELVVIIGWAKHI	17445
1TII	EC	ENTEROTOXIN	C	1.3	1.3	1	32	CASLTNKLSQHDLADFKKYIKRKFTLMTLLSI	17446
1TII	GC	ENTEROTOXIN	C	1.3	1.3	1	32	CASLTNKLSQHDLADFKKYIKRKFTLMTLLSI	17447
1TII	HC	ENTEROTOXIN	H	1.3	1.3	1	19	DNVMTAEMRKIAMAAVLSG	17448
1TOC	HU	COMPLEX (HYDROLASE/INHIBITOR)	U	1.3	1.3	1	8	EVECQVAC	17449
1TYE	AB	CELL ADHESION	B	1.3	1.3	1	10	VNLYQNYSEL	17450

1TZN	Ff	TOXIN RECEPTOR/TOXIN	f	1.3	1.3	1	16	IHEGLKLANEQIQKAG	17451
1TZN	Oo	TOXIN RECEPTOR/TOXIN	o	1.3	1.3	1	16	IHEGLKLANEQIQKAG	17452
1U35	CD	STRUCTURAL PROTEIN/DNA	C	1.3	1.3	1	12	VGRMLRYIKKGH	17453
1U6G	AC	LIGASE	A	1.3	1.3	1	12	EIYSLALVTWRD	17454
1U6G	AC	LIGASE	A	1.3	1.3	1	14	TRLISGVVQSYVEL	17455
1UB4	BC	DNA BINDING PROTEIN	C	1.3	1.3	1	7	LAELVND	17456
1UF2	AE	VIRUS	E	1.3	1.3	1	7	DFITTYI	17457
1USV	AB	CHAPERONE	B	1.3	1.3	1	27	AKPLIRSELLPKLRQIFQQFGKDLLAT	17458
1UTB	AB	TRANSCRIPTION REGULATION	A	1.3	1.3	1	7	IGPILHS	17459
1UVQ	BC	IMMUNOLOGY	B	1.3	1.3	1	28	KEVLEGTRAELDTVCRHNYEVAFRGILQ	17460
1UW4	BC	RNA BINDING PROTEIN	B	1.3	1.3	1	20	LEESIRQVQDLEREFLIKLG	17461
1UW4	BC	RNA BINDING PROTEIN	C	1.3	1.3	1	12	QEDIILFRDRFD	17462
1UWX	KM	IMMUNE SYSTEM	K	1.3	1.3	1	6	SEQLTS	17463
1UWX	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEQLTS	17464
1UZH	EF	LYASE	E	1.3	1.3	1	12	GGDVIRSACKWS	17465
1UZH	KP	LYASE	K	1.3	1.3	1	12	GGDVIRSACKWS	17466
1V29	AB	LYASE	B	1.3	1.3	1	9	DEFRIGIEK	17467
1V4U	AB	OXYGEN STORAGE/TRANSPORT	A	1.3	1.3	1	16	ADAIGADALGRMLAVY	17468
1V4U	AD	OXYGEN STORAGE/TRANSPORT	A	1.3	1.3	1	19	PSNFKILSHCILVVVAKMF	17469
1V54	NW	OXIDOREDUCTASE	W	1.3	1.3	1	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	17470
1V54	PS	OXIDOREDUCTASE	S	1.3	1.3	1	11	LEREVMLAARK	17471
1V54	QV	OXIDOREDUCTASE	V	1.3	1.3	1	15	FAVAEKRKKAYADFY	17472
1V54	RV	OXIDOREDUCTASE	V	1.3	1.3	1	25	LLARRLRFHIVGAFMVSLGFATFYK	17473
1V9U	23	VIRUS/RECEPTOR	3	1.3	1.3	1	6	LVEICQ	17474
1VF5	CD	PHOTOSYNTHESIS	C	1.3	1.3	1	25	PNRVKWMIAFICLVMLAQLMLILKK	17475
1VF5	FH	PHOTOSYNTHESIS	H	1.3	1.3	1	21	WVALLVVFTWSIAMVVWGRNG	17476
1VF5	SU	PHOTOSYNTHESIS	U	1.3	1.3	1	24	VLGWVALLVVFTWSIAMVVWGRNG	17477
1VGE	LH	IMMUNOGLOBULIN	L	1.3	1.3	1	6	DEQLKS	17478
1VOQ	CN	RIBOSOME	C	1.3	1.3	1	21	KQYRHLLLEDQRIRGLLEKEL	17479
1VQP	FM	RIBOSOME	M	1.3	1.3	1	15	QLAELQWQRQQEWRN	17480
1VSP	CN	RIBOSOME	N	1.3	1.3	1	5	GALIK	17481
1W0Y	HL	HYDROLASE	H	1.3	1.3	1	10	RTFSERTLAF	17482
1W5C	IT	PHOTOSYNTHESIS	T	1.3	1.3	1	5	PKMRN	17483
1W63	BM	ENDOCYTOSIS	B	1.3	1.3	1	12	LKKLVYLYLMNY	17484
1W63	FO	ENDOCYTOSIS	F	1.3	1.3	1	12	LKKLVYLYLMNY	17485
1W63	HP	ENDOCYTOSIS	H	1.3	1.3	1	12	LKKLVYLYLMNY	17486
1W63	JR	ENDOCYTOSIS	J	1.3	1.3	1	17	YVVQEAIVVIKDIFRKY	17487
1W63	JR	ENDOCYTOSIS	J	1.3	1.3	1	12	LKKLVYLYLMNY	17488
1W63	LV	ENDOCYTOSIS	L	1.3	1.3	1	12	LKKLVYLYLMNY	17489
1W7P	AD	PROTEIN TRANSPORT	D	1.3	1.3	1	10	PMEMREACER	17490

1WCM	AB	TRANSCRIPTION	A	1.3	1.3	1	22	PQVCAKLFGNIQKVVNFWLLHN	17491
1WCM	BI	TRANSCRIPTION	B	1.3	1.3	1	14	WQMLEMLKPCVEDG	17492
1WCM	BJ	TRANSCRIPTION	J	1.3	1.3	1	7	LIEKFLR	17493
1WDC	AB	MUSCLE PROTEIN	B	1.3	1.3	1	11	IEYIKDLLENM	17494
1WDW	CD	LYASE	D	1.3	1.3	1	16	IEPLKELEKAYKRFKD	17495
1XCG	EF	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	E	1.3	1.3	1	6	LRDLII	17496
1XD2	BC	SIGNALING PROTEIN	B	1.3	1.3	1	10	KSALTIQLIQ	17497
1XFU	AO	LYASE/METAL BINDING PROTEIN	A	1.3	1.3	1	13	SAEFIKNLSSIRR	17498
1XFV	DR	LYASE/METAL BINDING PROTEIN	D	1.3	1.3	1	13	SAEFIKNLSSIRR	17499
1XFV	ES	LYASE/METAL BINDING PROTEIN	E	1.3	1.3	1	13	SAEFIKNLSSIRR	17500
1XFV	ES	LYASE/METAL BINDING PROTEIN	S	1.3	1.3	1	10	YEEFVQMMTA	17501
1XIU	AE	TRANSCRIPTION/TRANSFERASE	A	1.3	1.3	1	22	PVTNICQAADKQLFTLVEWAKR	17502
1XK4	EG	METAL BINDING PROTEIN	E	1.3	1.3	1	12	RDDLKKLLETES	17503
1XKM	CB	ANTIBIOTIC	B	1.3	1.3	1	23	LVSGLIEARKYLEQLHRKLKNCK	17504
1XLS	DL	TRANSCRIPTION	D	1.3	1.3	1	23	PVTNICQAADKQLFTLVEWAKRI	17505
1XQ5	AB	OXYGEN STORAGE/TRANSPORT	A	1.3	1.3	1	19	PANFKILSHCILVLLAVKF	17506
1XQS	AC	CHAPERONE	A	1.3	1.3	1	10	MDNAADFCQL	17507
1XQS	BD	CHAPERONE	B	1.3	1.3	1	13	QEELEFCEKLLQT	17508
1XV9	AB	DNA BINDING PROTEIN	A	1.3	1.3	1	22	AEVEALREKVYASLEAYCKHKY	17509
1XWJ	AB	CELL ADHESION/PROTEIN BINDING	A	1.3	1.3	1	45	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLT	17510
1XXH	DE	TRANSFERASE	D	1.3	1.3	1	15	RRMGVEMTLLRALAF	17511
1XXH	DE	TRANSFERASE	E	1.3	1.3	1	12	APARLHWLATLL	17512
1XXI	FG	TRANSFERASE	G	1.3	1.3	1	13	EHVLTALANGLSL	17513
1Y3A	BF	SIGNALING PROTEIN	B	1.3	1.3	1	14	RMHESMKLFDSICN	17514
1Y56	AB	OXIDOREDUCTASE	B	1.3	1.3	1	15	PFEATTAFAVKAKEY	17515
1Y76	AD	TRANSPORT PROTEIN	A	1.3	1.3	1	23	PAAEKMQVLQVLDRLRGKLQEKG	17516
1YA7	CI	HYDROLASE/HYDROLASE ACTIVATOR	I	1.3	1.3	1	23	VGDAQVLVRYMKAELELYRLQRR	17517
1YE9	BG	OXIDOREDUCTASE	G	1.3	1.3	1	7	FFAENEQ	17518
1YE9	JM	OXIDOREDUCTASE	J	1.3	1.3	1	12	AHKFPDFVHAVK	17519
1YHU	NO	OXYGEN STORAGE/TRANSPORT	O	1.3	1.3	1	15	DAAAAIVQAQWEDVW	17520
1YHU	OT	OXYGEN STORAGE/TRANSPORT	O	1.3	1.3	1	16	PDAWASCLAGIAAAIS	17521
1YHU	OT	OXYGEN STORAGE/TRANSPORT	T	1.3	1.3	1	16	PDAWSRCFNRITTGMT	17522
1YHU	WP	OXYGEN STORAGE/TRANSPORT	W	1.3	1.3	1	16	PDAWASCLAGIAAAIS	17523
1YKE	AB	GENE REGULATION	B	1.3	1.3	1	7	TLNYIDK	17524
1YKK	GH	OXIDOREDUCTASE	G	1.3	1.3	1	6	VHIGLA	17525
1YMM	BC	IMMUNE SYSTEM	B	1.3	1.3	1	13	ELGRPDAEYWNSQ	17526
1YNJ	CD	TRANSFERASE	D	1.3	1.3	1	8	PLYVMAQS	17527
1YNJ	CD	TRANSFERASE	D	1.3	1.3	1	15	VGVVAAESIGEPGTQ	17528
1YNJ	CD	TRANSFERASE	D	1.3	1.3	1	11	SFAQAEARIQM	17529

1YOV	AB	SIGNALING PROTEIN	B	1.3	1.3	1	13	KAEVAAEFLNDRV	17530
1YRT	AB	LAYSE, TOXIN	B	1.3	1.3	1	12	DEEVDEMIREAD	17531
1YTZ	IC	CONTRACTILE PROTEIN	C	1.3	1.3	1	11	IEELGEILRAT	17532
1YU6	BD	HYDROLASE	B	1.3	1.3	1	19	TSMASPHVAGAAALILSKH	17533
1Z0K	CD	PROTEIN TRANSPORT	C	1.3	1.3	1	9	RSVTRSYYR	17534
1Z2C	CD	SIGNALING PROTEIN	D	1.3	1.3	1	17	MHLLSCLESLRVSLNNN	17535
1Z2C	CD	SIGNALING PROTEIN	D	1.3	1.3	1	10	EEKQQPLREK	17536
1Z5X	UE	HORMONE/GROWTH FACTOR RECEPTOR	U	1.3	1.3	1	10	LPALRSIGLK	17537
1Z5Y	DE	OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN	E	1.3	1.3	1	6	PTSRAE	17538
1Z6O	AO	METAL BINDING PROTEIN	O	1.3	1.3	1	13	EALGEFIFDKKLL	17539
1Z6O	IS	METAL BINDING PROTEIN	S	1.3	1.3	1	13	EALGEFIFDKKLL	17540
1Z6O	KU	METAL BINDING PROTEIN	U	1.3	1.3	1	13	EALGEFIFDKKLL	17541
1Z7Q	AG	HYDROLASE/HYDROLASE ACTIVATOR	G	1.3	1.3	1	15	IPAFADRLGQYVQAH	17542
1Z7Q	DK	HYDROLASE/HYDROLASE ACTIVATOR	K	1.3	1.3	1	23	AGDTVQFAEYIQANIQLYSIRED	17543
1Z7Q	Ia	HYDROLASE/HYDROLASE ACTIVATOR	a	1.3	1.3	1	11	LIMPFLDNQVN	17544
1Z7Q	Ja	HYDROLASE/HYDROLASE ACTIVATOR	a	1.3	1.3	1	11	LIMPFLDNQVN	17545
1Z7Q	JK	HYDROLASE/HYDROLASE ACTIVATOR	K	1.3	1.3	1	17	PQAVSSFVRQELAKSIR	17546
1Z7Q	OV	HYDROLASE/HYDROLASE ACTIVATOR	V	1.3	1.3	1	22	AADTQAIADIVQYHLELYTSQY	17547
1ZA3	LH	IMMUNE SYSTEM/SIGNALING PROTEIN	L	1.3	1.3	1	7	DEQLKSG	17548
1ZAN	LH	IMMUNE SYSTEM	L	1.3	1.3	1	7	SEQLASG	17549
1ZBB	cd	STRUCTURAL PROTEIN/DNA	c	1.3	1.3	1	11	VGRVHRLLRKG	17550
1ZBB	CD	STRUCTURAL PROTEIN/DNA	C	1.3	1.3	1	11	VGRVHRLLRKG	17551
1ZBB	fh	STRUCTURAL PROTEIN/DNA	f	1.3	1.3	1	27	IYEETRGVLKVFLENVIRDAVTYTEHA	17552
1ZL8	AB	PROTEIN BINDING	A	1.3	1.3	1	14	EFFGAVREVYETVY	17553
1ZL8	AB	PROTEIN BINDING	B	1.3	1.3	1	17	HFMALLQTHDVVAHEVY	17554
1ZLA	AB	PROTEIN BINDING/VIRUS/DNA	A	1.3	1.3	1	14	KLPFQRLVREIAQD	17555
1ZLA	CD	PROTEIN BINDING/VIRUS/DNA	C	1.3	1.3	1	10	PRHLQLAVRN	17556
1ZNV	AB	HYDROLASE/PROTEIN BINDING	A	1.3	1.3	1	15	DVLDVLLEHFVKITE	17557
1ZOQ	AC	TRANSCRIPTION/TRANSFERASE	A	1.3	1.3	1	14	LGPFIVDLITFTEG	17558
1ZOY	AB	OXIDOREDUCTASE	A	1.3	1.3	1	5	HTVAA	17559
1ZOY	CD	OXIDOREDUCTASE	D	1.3	1.3	1	26	AASLHWTGERVVSVLLLGLLPAAYLN	17560
1ZTX	HL	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.3	1.3	1	6	SEQLTS	17561
1ZY8	GN	OXIDOREDUCTASE	G	1.3	1.3	1	6	CEDIAR	17562
1ZY8	HN	OXIDOREDUCTASE	N	1.3	1.3	1	9	PAARNILEK	17563
2A1J	AB	DNA BINDING PROTEIN	B	1.3	1.3	1	6	LEQLIA	17564
2A1T	DS	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.3	1.3	1	11	VPLIRRAWELG	17565

2A40	AC	STRUCTURAL PROTEIN	A	1.3	1.3	1	9	QAVLSLYAS	17566
2A45	JL	BLOOD CLOTTING	L	1.3	1.3	1	20	TCGIADFLSTYQTKVDKDLQ	17567
2A5Y	AB	APOPTOSIS	A	1.3	1.3	1	14	VRNLFVYTSLFIKT	17568
2A5Y	AB	APOPTOSIS	B	1.3	1.3	1	8	TDILLMLK	17569
2AAI	AB	GLYCOSIDASE	A	1.3	1.3	1	6	VSILIP	17570
2ACL	GH	TRANSCRIPTION	G	1.3	1.3	1	7	LFFFKLI	17571
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.3	1.3	1	29	FFVKFIMWGILTALAYHVVVGIRHMMMDF	17572
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.3	1.3	1	10	YEVWIGFFAS	17573
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.3	1.3	1	30	AFTKVFTLLALFSILIHAWIGMWQVLTDYV	17574
2AFH	AB	OXIDOREDUCTASE	A	1.3	1.3	1	29	ESIQKKCEEVIAKYKPEWEAVVAKYRPRL	17575
2AFH	AB	OXIDOREDUCTASE	A	1.3	1.3	1	12	GYEFEEFVKRIK	17576
2AFH	AD	OXIDOREDUCTASE	A	1.3	1.3	1	16	FDGFAIFARDMDMTLN	17577
2AFH	CD	OXIDOREDUCTASE	C	1.3	1.3	1	12	GYEFEEFVKRIK	17578
2AI0	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEQLTS	17579
2AK4	FR	IMMUNE SYSTEM	F	1.3	1.3	1	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	17580
2AK4	KM	IMMUNE SYSTEM	K	1.3	1.3	1	13	LCVEWLRRYLENG	17581
2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	A	1.3	1.3	1	16	KGLLDVTCKTVANMIK	17582
2AUH	AB	TRANSFERASE/SIGNALING PROTEIN	B	1.3	1.3	1	17	PTEALSVAVEEGLAWRK	17583
2AUS	AB	ISOMERASE/STRUCTURAL PROTEIN	A	1.3	1.3	1	8	EEYIRKAI	17584
2AXT	ad	ELECTRON TRANSPORT	d	1.3	1.3	1	5	NAIAF	17585
2AXT	ad	ELECTRON TRANSPORT	d	1.3	1.3	1	17	PFHMMGVAGVLGGALLC	17586
2AXT	bd	ELECTRON TRANSPORT	b	1.3	1.3	1	6	RYQWDS	17587
2AXT	bd	ELECTRON TRANSPORT	b	1.3	1.3	1	16	PRGWFTFAHAVFALLF	17588
2AXT	bd	ELECTRON TRANSPORT	d	1.3	1.3	1	21	FYTKNLLLNEGIRAWMAPQDQ	17589
2AXT	bh	ELECTRON TRANSPORT	h	1.3	1.3	1	20	TPLMAVFMGLFLVFLLIILE	17590
2AXT	bT	ELECTRON TRANSPORT	T	1.3	1.3	1	21	ETITYVFIFACIIALFFFAIF	17591
2AXT	DE	ELECTRON TRANSPORT	E	1.3	1.3	1	17	ITIPALFIAGWLFVSTG	17592
2AXT	de	ELECTRON TRANSPORT	e	1.3	1.3	1	17	ITIPALFIAGWLFVSTG	17593
2AXT	de	ELECTRON TRANSPORT	e	1.3	1.3	1	6	LAYDVF	17594
2B5T	AB	BLOOD CLOTTING	B	1.3	1.3	1	10	KKWIQKVIDQ	17595
2B8K	AB	TRANSFERASE	A	1.3	1.3	1	22	PQVCAKLFGNIQKVVNFWLLHN	17596
2B8K	AB	TRANSFERASE	A	1.3	1.3	1	10	FINIAQMSAC	17597
2B8K	AG	TRANSFERASE	G	1.3	1.3	1	12	MKQYLKTKLLEE	17598
2B8K	BJ	TRANSFERASE	J	1.3	1.3	1	7	LIEKFLR	17599
2BA0	EH	RNA BINDING PROTEIN	E	1.3	1.3	1	30	RDEVKQAIELAKKGALQIYEMQREAILRRY	17600
2BBV	CF	VIRUS/RNA	C	1.3	1.3	1	13	EVALQEYRTVARS	17601

2BCX	AB	CALCIUM BINDING PROTEIN	A	1.3	1.3	1	11	TKELGTVMRSL	17602
2BCX	AB	CALCIUM BINDING PROTEIN	A	1.3	1.3	1	13	EEQIAEFKEAFSL	17603
2BG9	DE	ION CHANNEL/RECEPTOR	E	1.3	1.3	1	25	GKYLIFVMFVSLVIVTNCVIVLNVS	17604
2BL0	AC	MUSCLE PROTEIN	C	1.3	1.3	1	13	DQVSEFKEAFELF	17605
2BP7	AD	OXIDOREDUCTASE	A	1.3	1.3	1	9	DHLRRQRQE	17606
2BR2	QB	HYDROLASE	B	1.3	1.3	1	28	PDEFRQAFDLAVKGINIIYNLEREALKS	17607
2BSK	EB	PROTEIN TRANSPORT	B	1.3	1.3	1	6	KKLTEL	17608
2BTQ	AB	STRUCTURAL PROTEIN	B	1.3	1.3	1	6	VEGEKV	17609
2BV8	ON	PHOTOSYNTHESIS	O	1.3	1.3	1	8	LSEINRSF	17610
2BYK	DA	DNA-BINDING PROTEIN	D	1.3	1.3	1	29	KEARAAIARAASVFAIFVTSSSTALAHKQ	17611
2BZW	AB	TRANSCRIPTION	A	1.3	1.3	1	8	WDTFVDLY	17612
2C1M	AB	PROTEIN TRANSPORT/MEMBRANE PROTEIN	A	1.3	1.3	1	11	TEKLSIMIEEC	17613
2C2V	SB	CHAPERONE	B	1.3	1.3	1	13	RRIIKETQRLLAE	17614
2C2V	VK	CHAPERONE	K	1.3	1.3	1	13	RRIIKETQRLLAE	17615
2C35	CD	POLYMERASE	C	1.3	1.3	1	17	NSEVHMLLEHRKQQNES	17616
2C4O	AD	LIGASE	A	1.3	1.3	1	8	KELNDLAR	17617
2C7J	AB	ELECTRON TRANSPORT	B	1.3	1.3	1	14	SNKRLDVVNRLTSN	17618
2CLY	AB	HYDROLASE	B	1.3	1.3	1	6	WVAFGE	17619
2CLY	DE	HYDROLASE	E	1.3	1.3	1	6	WVAFGE	17620
2CMY	AB	HYDROLASE	B	1.3	1.3	1	7	KVMCYAQ	17621
2CNW	AD	SIGNAL RECOGNITION	A	1.3	1.3	1	18	EEDLKATLREIRRALMDA	17622
2CZV	BD	HYDROLASE	B	1.3	1.3	1	11	PRDLISLGVVI	17623
2D03	LH	IMMUNE SYSTEM	L	1.3	1.3	1	7	SEQLTSG	17624
2D2M	BC	OXYGEN STORAGE/TRANSPORT	C	1.3	1.3	1	17	PAVLNEQLAHLSAQHQA	17625
2D3O	R1	RIBOSOME	R	1.3	1.3	1	7	YSAMERG	17626
2D9Q	AB	SIGNALING PROTEIN/CYTOKINE	A	1.3	1.3	1	15	PTLDTLQLDVADFAT	17627
2DD4	BC	HYDROLASE	B	1.3	1.3	1	9	AEERRRKQN	17628
2DD4	DF	HYDROLASE	F	1.3	1.3	1	10	PNYRRRLVRW	17629
2DD4	EF	HYDROLASE	E	1.3	1.3	1	7	QTVYLGM	17630
2DD4	HI	HYDROLASE	H	1.3	1.3	1	9	AEERRRKQN	17631
2DD8	HL	IMMUNE SYSTEM/VIRAL PROTEIN	L	1.3	1.3	1	6	SEEFQA	17632
2DE5	CF	OXIDOREDUCTASE	C	1.3	1.3	1	5	RKQQT	17633
2DF4	AC	LIGASE	A	1.3	1.3	1	8	PLTMYAND	17634
2DFS	AD	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	D	1.3	1.3	1	9	LGTVMRSLG	17635
2DFS	AF	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	F	1.3	1.3	1	6	LGTVMR	17636
2DFS	MR	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	R	1.3	1.3	1	10	EAELQDMINE	17637

2DOQ	AD	CELL CYCLE	A	1.3	1.3	1	6	AFQLFD	17638
2DWZ	CD	ONCOPROTEIN	C	1.3	1.3	1	8	PLHYAASK	17639
2DXB	BC	HYDROLASE	B	1.3	1.3	1	9	AEERRRKQN	17640
2DXB	EI	HYDROLASE	E	1.3	1.3	1	8	HTLFRAYT	17641
2DXB	JL	HYDROLASE	J	1.3	1.3	1	5	QKDLW	17642
2DXB	JL	HYDROLASE	L	1.3	1.3	1	10	PNYRRRLVRW	17643
2DXB	MO	HYDROLASE	M	1.3	1.3	1	6	AEDEAF	17644
2DXB	QR	HYDROLASE	Q	1.3	1.3	1	9	AEERRRKQN	17645
2DXB	SU	HYDROLASE	S	1.3	1.3	1	6	AEDEAF	17646
2DXB	SU	HYDROLASE	U	1.3	1.3	1	10	PNYRRRLVRW	17647
2E 30	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	A	1.3	1.3	1	5	MVGVN	17648
2E 32	AB	LIGASE	A	1.3	1.3	1	9	ATELVQACR	17649
2E 74	CD	PHOTOSYNTHESIS	D	1.3	1.3	1	31	MGRRQFMNLLAFGTVTGVALGALYPLVKYFI	17650
2E1M	BC	OXIDOREDUCTASE	C	1.3	1.3	1	5	QMTAF	17651
2E5L	CN	RIBOSOME	N	1.3	1.3	1	11	RICLRELAHKG	17652
2E9X	AD	REPLICATION	D	1.3	1.3	1	14	PEIVECVMEQLEHM	17653
2EC6	AB	CONTRACTILE PROTEIN	B	1.3	1.3	1	8	KDEMRMTF	17654
2EFC	CB	TRANSPORT PROTEIN	B	1.3	1.3	1	10	KSSLVLRFVK	17655
2EFC	CD	TRANSPORT PROTEIN	C	1.3	1.3	1	16	ADEFLPVLIYVTIKAN	17656
2EFC	CD	TRANSPORT PROTEIN	D	1.3	1.3	1	10	KSSLVLRFVK	17657
2EHB	AD	SIGNALLING PROTEIN/TRANSFERASE	A	1.3	1.3	1	9	KEEFQLALF	17658
2EHB	AD	SIGNALLING PROTEIN/TRANSFERASE	A	1.3	1.3	1	11	LFADRIFDVFD	17659
2EHO	AC	REPLICATION	C	1.3	1.3	1	9	AAEVEFLAE	17660
2EHO	BH	REPLICATION	B	1.3	1.3	1	5	ALRFH	17661
2EHO	GH	REPLICATION	G	1.3	1.3	1	5	LTKLL	17662
2EKV	AC	CONTRACTILE PROTEIN	C	1.3	1.3	1	18	KDEIEEVREVFDLFDFWD	17663
2EQB	AC	ENDOCYTOSIS/EXOCYTOSIS	A	1.3	1.3	1	11	RTITTAYYRGA	17664
2ES4	AD	HYDROLASE	D	1.3	1.3	1	18	GDEQRRQRHDLERIRIAN	17665
2ES4	BE	HYDROLASE	E	1.3	1.3	1	32	PEAAARAAQMQQDDEAWQTRYQAYAAERDRIA	17666
2ES4	BE	HYDROLASE	E	1.3	1.3	1	9	RAVREFFDY	17667
2ESV	AE	IMMUNE SYSTEM	A	1.3	1.3	1	10	QISEQKSNDA	17668
2F9I	AB	TRANSFERASE	A	1.3	1.3	1	6	GGALGI	17669
2FBW	NO	OXIDOREDUCTASE	N	1.3	1.3	1	26	TDLVETLELQNLMLCALQTIYGAEAR	17670
2FBW	OP	OXIDOREDUCTASE	O	1.3	1.3	1	6	NCTRTC	17671
2FHH	QZ	HYDROLASE	Z	1.3	1.3	1	23	AAVAVEFARLYAVELEHYEKLEG	17672
2FHJ	CD	TRANSFERASE	C	1.3	1.3	1	19	EDELKEQLLDRIGQCVMTA	17673
2FHZ	AB	IMMUNE SYSTEM, HYDROLASE	B	1.3	1.3	1	10	QKIRGQMPER	17674
2FJ7	AB	STRUCTURAL PROTEIN/DNA	B	1.3	1.3	1	11	AMDVVYALKRQ	17675
2FJ7	CD	STRUCTURAL PROTEIN/DNA	C	1.3	1.3	1	12	VGRVHRLLRKGN	17676

2FJ7	FD	STRUCTURAL PROTEIN/DNA	D	1.3	1.3	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	17677
2FKW	IJ	MEMBRANE PROTEIN, PHOTOSYNTHESIS	I	1.3	1.3	1	26	PAIGIPALLGSVTVIAILVHLAILSH	17678
2FKW	KL	MEMBRANE PROTEIN, PHOTOSYNTHESIS	K	1.3	1.3	1	26	PAIGIPALLGSVTVIAILVHLAILSH	17679
2FKW	OP	MEMBRANE PROTEIN, PHOTOSYNTHESIS	O	1.3	1.3	1	26	PAIGIPALLGSVTVIAILVHLAILSH	17680
2FOI	BC	OXIDOREDUCTASE	B	1.3	1.3	1	23	MSSAKAALESDTRVLAYHLGRNY	17681
2FSE	DF	IMMUNE SYSTEM, STRUCTURAL PROTEIN	D	1.3	1.3	1	13	KDLLEQRRAAVDT	17682
2FUG	12	OXIDOREDUCTASE	2	1.3	1.3	1	11	QDFLEETFAKY	17683
2FUG	27	OXIDOREDUCTASE	7	1.3	1.3	1	16	KERFFALADRAREALA	17684
2FUG	59	OXIDOREDUCTASE	5	1.3	1.3	1	5	PAEFR	17685
2FUG	69	OXIDOREDUCTASE	9	1.3	1.3	1	7	KPQRREA	17686
2FUG	CE	OXIDOREDUCTASE	C	1.3	1.3	1	11	RCVRYFEEVPG	17687
2FUG	ST	OXIDOREDUCTASE	T	1.3	1.3	1	13	AEELWDYLTETLG	17688
2FUG	VW	OXIDOREDUCTASE	V	1.3	1.3	1	13	PSFVNLQSLPYAC	17689
2FUG	WY	OXIDOREDUCTASE	W	1.3	1.3	1	5	PAEFR	17690
2FYM	AB	LYASE	A	1.3	1.3	1	19	ANAILAVSLANAKAAAAAK	17691
2FYM	AB	LYASE	A	1.3	1.3	1	18	SDRVAKYNQLIRIEEALG	17692
2FYM	CB	LYASE	C	1.3	1.3	1	19	ANAILAVSLANAKAAAAAK	17693
2FYM	FE	LYASE	F	1.3	1.3	1	18	SDRVAKYNQLIRIEEALG	17694
2FYN	EF	OXIDOREDUCTASE	E	1.3	1.3	1	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	17695
2FYN	GH	OXIDOREDUCTASE	H	1.3	1.3	1	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	17696
2FYN	MR	OXIDOREDUCTASE	M	1.3	1.3	1	17	QMSFWGATVITGLFGAI	17697
2FYN	MR	OXIDOREDUCTASE	M	1.3	1.3	1	31	NATLNRFFSLHYLLPFVIAALVAIHIWAFHS	17698
2G75	AB	IMMUNE SYSTEM	B	1.3	1.3	1	5	SEEFQ	17699
2G9H	AB	IMMUNE SYSTEM	B	1.3	1.3	1	10	RPDAEYWNSQ	17700
2GC4	MJ	OXIDOREDUCTASE, ELECTRON TRANSPORT	M	1.3	1.3	1	20	QAQETQGQAAARAAAADLAA	17701
2GFB	IJ	IMMUNOGLOBULIN	I	1.3	1.3	1	7	SEQLTSG	17702
2GFB	MN	IMMUNOGLOBULIN	M	1.3	1.3	1	6	SEQLTS	17703
2GGP	AB	CHAPERONE, METAL TRANSPORT	A	1.3	1.3	1	12	CSGAVNKVLTKL	17704
2GH0	DB	HORMONE/GROWTH FACTOR	B	1.3	1.3	1	14	DKCDRLRKAYGEAC	17705
2GHO	BD	TRANSFERASE	D	1.3	1.3	1	10	PDEALLAVAH	17706
2GHO	CD	TRANSFERASE	D	1.3	1.3	1	5	FRQNL	17707
2GID	HJ	TRANSLATION	J	1.3	1.3	1	12	HVDLAYLVGVCK	17708
2GID	PK	TRANSLATION	K	1.3	1.3	1	12	HVDLAYLVGVCK	17709
2GO5	12	TRANSLATION/RNA	2	1.3	1.3	1	11	KTLLFVRLLTG	17710
2GOL	AB	VIRAL PROTEIN	B	1.3	1.3	1	15	PRTLNAWVKVVEEKA	17711

2GUZ	AB	CHAPERONE, PROTEIN TRANSPORT	B	1.3	1.3	1	15	MDKINNRFNYLFEVN	17712
2GZD	AD	PROTEIN TRANSPORT	D	1.3	1.3	1	18	DTHIRELEDYIDNLLVRV	17713
2H1L	DP	VIRAL PROTEIN	D	1.3	1.3	1	14	LSVYQKMKFNVAMG	17714
2H1L	FR	VIRAL PROTEIN	F	1.3	1.3	1	15	QSRIVEWKERLDKEF	17715
2H1L	KW	VIRAL PROTEIN	W	1.3	1.3	1	11	PGRDRRTEEEN	17716
2H1O	AE	GENE REGULATION/DNA COMPLEX	A	1.3	1.3	1	9	ERVVAWLDS	17717
2H4M	AC	PROTEIN TRANSPORT	A	1.3	1.3	1	18	KTLLENTAITIGRLGYVC	17718
2H4M	BD	PROTEIN TRANSPORT	B	1.3	1.3	1	19	KRVQEAACSAFATLEEEAC	17719
2H7V	AD	SIGNALING PROTEIN	A	1.3	1.3	1	11	YPQGLAMAKEI	17720
2HDN	CD	TRANSLATION	D	1.3	1.3	1	13	PQTREHILLGRQV	17721
2HHH	CN	RIBOSOME	N	1.3	1.3	1	9	ICLRELAHK	17722
2HLD	BG	HYDROLASE	G	1.3	1.3	1	65	FEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGA	17723
2HLD	JP	HYDROLASE	P	1.3	1.3	1	46	SARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGASS	17724
2HLD	KO	HYDROLASE	O	1.3	1.3	1	6	RGISEL	17725
2HLD	OP	HYDROLASE	O	1.3	1.3	1	8	QDIIAILG	17726
2HLD	UV	HYDROLASE	V	1.3	1.3	1	15	TREGNDLYREMKETG	17727
2HOD	JK	BLOOD CLOTTING	K	1.3	1.3	1	15	KIQKLESDVSAQMEY	17728
2HOD	JL	BLOOD CLOTTING	L	1.3	1.3	1	33	THDSSIRYLQEIYNSNNQKIVNLKEKVAQLEAQ	17729
2HQW	AB	METAL BINDING PROTEIN	A	1.3	1.3	1	15	EEQIAEFKEAFSLFD	17730
2HSN	AB	LIGASE/RNA BINDING PROTEIN	B	1.3	1.3	1	16	KEQSAQAAQWESVLKS	17731
2HYB	EC	TRANSFERASE	C	1.3	1.3	1	5	GIYAA	17732
2HYI	GI	HYDROLASE/RNA BINDING PROTEIN/RNA	I	1.3	1.3	1	6	HEILEM	17733
2HZM	GH	TRANSCRIPTION	G	1.3	1.3	1	8	IDTILSSK	17734
2I2P	GK	RIBOSOME	K	1.3	1.3	1	13	PFAAQVAAERCAD	17735
2I2R	BE	TRANSPORT PROTEIN	B	1.3	1.3	1	11	ISAYDDELAFY	17736
2I2R	CG	TRANSPORT PROTEIN	G	1.3	1.3	1	13	VHEKLRWTFNLYD	17737
2I2R	DG	TRANSPORT PROTEIN	D	1.3	1.3	1	5	TEKEF	17738
2I2R	JN	TRANSPORT PROTEIN	N	1.3	1.3	1	12	EDTFKQIYAQFF	17739
2I2X	AB	TRANSFERASE	B	1.3	1.3	1	14	DIGKNIVTALLRAN	17740
2I2X	AB	TRANSFERASE	B	1.3	1.3	1	20	LPNVMMSADAMLEGIEYCKE	17741
2I2X	EF	TRANSFERASE	F	1.3	1.3	1	8	EASLKKVL	17742
2I2X	GF	TRANSFERASE	F	1.3	1.3	1	8	EASLKKVL	17743
2I2X	GF	TRANSFERASE	G	1.3	1.3	1	22	TVQCWSETLAYDCALMNTALET	17744
2I2X	IL	TRANSFERASE	I	1.3	1.3	1	22	TVQCWSETLAYDCALMNTALET	17745
2I2X	MN	TRANSFERASE	N	1.3	1.3	1	15	DIGKNIVTALLRANG	17746
2I2X	MN	TRANSFERASE	N	1.3	1.3	1	18	IDDALMVGMGVVIRLYDE	17747
2IAN	AC	IMMUNE SYSTEM	A	1.3	1.3	1	21	QGALANIAVDKANLEIMTKRS	17748

2IAN	GH	IMMUNE SYSTEM	G	1.3	1.3	1	13	ELGRPDAEYWNSQ	17749
2IAN	LJ	IMMUNE SYSTEM	L	1.3	1.3	1	9	RPDAEYWNS	17750
2IBZ	AE	OXIDOREDUCTASE	A	1.3	1.3	1	21	SNFEATKKSVLKQVQDFEDND	17751
2IBZ	AI	OXIDOREDUCTASE	I	1.3	1.3	1	27	VGTIFAGAFVFQTVFDTAITSWYENHN	17752
2IBZ	DH	OXIDOREDUCTASE	D	1.3	1.3	1	9	CDYIFSLLT	17753
2IBZ	DI	OXIDOREDUCTASE	D	1.3	1.3	1	30	HDERKRLGLKTVIILSSLYLLSIWVKKFKW	17754
2ICE	AB	IMMUNE SYSTEM	A	1.3	1.3	1	11	QSKIWDVVEKA	17755
2ICW	DE	IMMUNE SYSTEM	D	1.3	1.3	1	7	EEFGRFA	17756
2IDO	AB	TRANSFERASE	A	1.3	1.3	1	9	ADEFMDYIR	17757
2IE3	AC	SIGNALING PROTEIN,HYDROLASE	A	1.3	1.3	1	16	WRVRLAIIEYMPLLAG	17758
2INN	BD	OXIDOREDUCTASE	D	1.3	1.3	1	5	TTVSQ	17759
2INP	BD	OXIDOREDUCTASE	D	1.3	1.3	1	7	RYQEASY	17760
2IO1	CD	PROTEIN BINDING, HYDROLASE	C	1.3	1.3	1	8	FYPKLKSG	17761
2IO5	AB	CHAPERONE/STRUCTURAL PROTEIN	B	1.3	1.3	1	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	17762
2IO5	BC	CHAPERONE/STRUCTURAL PROTEIN	B	1.3	1.3	1	12	PKDIQLARRIRG	17763
2IX7	CA	CONTRACTILE PROTEIN/METAL BINDING	A	1.3	1.3	1	9	AAELRHVMT	17764
2IX7	CA	CONTRACTILE PROTEIN/METAL BINDING	A	1.3	1.3	1	8	LGTVMRSL	17765
2J0U	AB	HYDROLASE	B	1.3	1.3	1	11	EDLLRGIYAYG	17766
2J5G	ED	HYDROLASE	D	1.3	1.3	1	27	QRLKRLVNEGIGYGLALEGITATDLRN	17767
2J5G	FD	HYDROLASE	F	1.3	1.3	1	10	QRLKRLVNEG	17768
2J8X	AB	HYDROLASE/INHIBITOR	A	1.3	1.3	1	14	PSLRNIYAELHRSL	17769
2JF9	AP	TRANSCRIPTION	A	1.3	1.3	1	25	EASMMGLLTNLADRELVHMINWAKR	17770
2JF9	CR	TRANSCRIPTION	C	1.3	1.3	1	25	EASMMGLLTNLADRELVHMINWAKR	17771
2JFA	AB	TRANSCRIPTION	B	1.3	1.3	1	28	LKSLEEKDHIHRVLDKITDTLIHLMAKA	17772
2JGB	AB	TRANSLATION	A	1.3	1.3	1	15	LASRCWENLILAMLG	17773
2JIY	LH	PHOTOSYNTHESIS	H	1.3	1.3	1	17	LLEEDKICGYVAGGLMY	17774
2JIZ	BE	HYDROLASE	B	1.3	1.3	1	15	LSKQAVAYRQMSLLL	17775
2JIZ	DG	HYDROLASE	G	1.3	1.3	1	70	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAAL	17776
2JIZ	DG	HYDROLASE	G	1.3	1.3	1	38	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKP	17777
2JIZ	EG	HYDROLASE	G	1.3	1.3	1	70	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAAL	17778
2JIZ	JK	HYDROLASE	K	1.3	1.3	1	6	RAIAEL	17779
2JIZ	JK	HYDROLASE	K	1.3	1.3	1	5	EVFTG	17780
2JKR	BM	ENDOCYTOSIS	B	1.3	1.3	1	18	PMVVANAVAALSEISESH	17781
2JKR	BM	ENDOCYTOSIS	B	1.3	1.3	1	5	LASVY	17782
2JKR	EU	ENDOCYTOSIS	E	1.3	1.3	1	18	VDFVRKAVRAIGRCAIKV	17783
2JKR	LI	ENDOCYTOSIS	I	1.3	1.3	1	11	QTKVLKQLLML	17784

2JQK	AB	PROTEIN TRANSPORT	A	1.3	1.3	1	27	DKAKQSIRAKCTEYLDRAEKLKEYLKN	17785
2JSS	AB	CHAPERONE/NUCLEAR PROTEIN	A	1.3	1.3	1	21	ELAKHAVSEGTRAVTKYSSST	17786
2JTT	AD	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEIN	A	1.3	1.3	1	15	DAEIVKLMDDLDRNK	17787
2K7W	AB	APOPTOSIS	A	1.3	1.3	1	22	SEQIMKTGALLLQGFIQDRAGR	17788
2K91	AB	HORMONE	B	1.3	1.3	1	11	SDLVEALYLVC	17789
2NPT	AD	TRANSFERASE	A	1.3	1.3	1	21	DEEMKAMLSYYYSTVMEQQVN	17790
2NQB	AG	STRUCTURAL PROTEIN/DNA	A	1.3	1.3	1	13	TVALREIRRYQKS	17791
2NQB	FH	STRUCTURAL PROTEIN/DNA	H	1.3	1.3	1	12	SREIQTAVRLLL	17792
2NS8	CF	TRANSCRIPTION	C	1.3	1.3	1	18	EKQYETLENQLAFLTQQG	17793
2NTF	LH	IMMUNE SYSTEM	L	1.3	1.3	1	5	SEELE	17794
2NTI	DF	DNA BINDING PROTEIN	D	1.3	1.3	1	11	SSVKKILSKAS	17795
2NTY	AC	SIGNALING PROTEIN	C	1.3	1.3	1	19	KASYENVAKKWIPELRHYA	17796
2NTY	AD	SIGNALING PROTEIN	D	1.3	1.3	1	14	VKAVFDAAIKVVLQ	17797
2NU9	FB	LIGASE	F	1.3	1.3	1	12	CKDSILEAIDAG	17798
2NV2	CD	LYASE/TRANSFERASE	C	1.3	1.3	1	10	ERVKRGMAEM	17799
2NV2	OP	LYASE/TRANSFERASE	O	1.3	1.3	1	14	PAKFAKAIVEATTH	17800
2NV2	ST	LYASE/TRANSFERASE	T	1.3	1.3	1	11	VREHIHAIEAC	17801
2NVU	AB	PROTEIN TURNOVER, LIGASE	A	1.3	1.3	1	11	DDYVHEFCRYG	17802
2NVU	AB	PROTEIN TURNOVER, LIGASE	B	1.3	1.3	1	11	LGCELLKNLAL	17803
2NX5	FI	IMMUNE SYSTEM	F	1.3	1.3	1	14	GLCVEWLRRYLENG	17804
2NXX	AE	HORMONE/GROWTH FACTOR	E	1.3	1.3	1	22	GWKVEKIQEIYLEALRAYVDNR	17805
2NZD	CD	STRUCTURAL PROTEIN/DNA	C	1.3	1.3	1	11	VGRVHRLLRKG	17806
2O26	FW	CYTOKINE/SIGNALING PROTEIN	F	1.3	1.3	1	22	SHCWLRDMVIQLSLSLTTLLDK	17807
2O60	AB	METAL BINDING PROTEIN	A	1.3	1.3	1	9	YEEFVQMMT	17808
2O8A	AI	HYDROLASE/INHIBITOR	I	1.3	1.3	1	15	IKLARQLISKDLHDD	17809
2O8V	AB	OXIDOREDUCTASE	B	1.3	1.3	1	6	GPAKMI	17810
2O98	AQ	PROTEIN BINDING	Q	1.3	1.3	1	13	LKGHVESVVKLKG	17811
2O98	BQ	PROTEIN BINDING	B	1.3	1.3	1	20	SKVFYLKMKGDYHRYLAEFK	17812
2O9I	BD	TRANSCRIPTION	B	1.3	1.3	1	9	IEDQISLLK	17813
2ODE	AB	SIGNALING PROTEIN	B	1.3	1.3	1	13	FQTREATRKNLQE	17814
2ODY	BE	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	E	1.3	1.3	1	9	EEECELVCK	17815
2OF5	BH	APOPTOSIS	B	1.3	1.3	1	10	DRQINQLAQR	17816
2OF5	DJ	APOPTOSIS	D	1.3	1.3	1	16	VQSQVVEAFIRWRQRF	17817
2OGX	AB	METAL BINDING PROTEIN	B	1.3	1.3	1	9	FPVLDLLQS	17818
2OJZ	MI	IMMUNE SYSTEM	M	1.3	1.3	1	6	SEQLTS	17819
2OM0	AB	HORMONE	A	1.3	1.3	1	7	LYQLENY	17820
2OM0	AH	HORMONE	A	1.3	1.3	1	7	LYQLENY	17821
2OM0	IJ	HORMONE	I	1.3	1.3	1	5	IVEQC	17822

2OM0	il	HORMONE	l	1.3	1.3	1	19	VNQHLCGSHLVEALYLVCG	17823
2OM0	KF	HORMONE	K	1.3	1.3	1	7	LYQLENY	17824
2OV2	AI	PROTEIN BINDING/TRANSFERASE	A	1.3	1.3	1	10	KTCLLISYTT	17825
2OV2	BJ	PROTEIN BINDING/TRANSFERASE	B	1.3	1.3	1	10	KTCLLISYTT	17826
2OV2	CK	PROTEIN BINDING/TRANSFERASE	C	1.3	1.3	1	10	KTCLLISYTT	17827
2OV2	HP	PROTEIN BINDING/TRANSFERASE	H	1.3	1.3	1	10	KTCLLISYTT	17828
2OZA	AB	SIGNALING PROTEIN/TRANSFERASE	B	1.3	1.3	1	12	HIDQLKLILRLV	17829
2OZB	DE	RNA BINDING PROTEIN/RNA	D	1.3	1.3	1	9	HLPLLCEDK	17830
2P1N	AB	SIGNALING PROTEIN	A	1.3	1.3	1	5	PEEIR	17831
2P2C	BP	HYDROLASE	P	1.3	1.3	1	8	PLHLAAYD	17832
2P2C	DQ	HYDROLASE	Q	1.3	1.3	1	8	PLHLAAYD	17833
2P6A	AD	SIGNALING PROTEIN	A	1.3	1.3	1	9	SFHSTVINH	17834
2PBI	AB	SIGNALING PROTEIN	A	1.3	1.3	1	7	FSELIRD	17835
2PF4	DH	HYDROLASE REGULATOR/VIRAL PROTEIN	H	1.3	1.3	1	8	FDCFRMWF	17836
2PI2	AE	REPLICATION, DNA BINDING PROTEIN	E	1.3	1.3	1	14	LGLYNEAVKIIHDF	17837
2PI2	BF	REPLICATION, DNA BINDING PROTEIN	F	1.3	1.3	1	14	LGLYNEAVKIIHDF	17838
2PI2	CG	REPLICATION, DNA BINDING PROTEIN	G	1.3	1.3	1	14	LGLYNEAVKIIHDF	17839
2PJR	AB	HYDROLASE/DNA	B	1.3	1.3	1	5	LHAAK	17840
2PJX	BD	ENDOCYTOSIS/EXOCYTOSIS	B	1.3	1.3	1	9	SLFNKIKAS	17841
2PK9	CD	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	D	1.3	1.3	1	15	CHELNILENDFLKRV	17842
2PKG	BC	HYDROLASE REGULATOR/VIRAL PROTEIN	B	1.3	1.3	1	9	HMLPTVLRM	17843
2PMZ	AC	TRANSLATION, TRANSFERASE	C	1.3	1.3	1	11	IEAAREIIIRE	17844
2PQK	AB	APOPTOSIS	A	1.3	1.3	1	8	WDGFVEFF	17845
2PV2	BE	ISOMERASE	B	1.3	1.3	1	7	GIFAQAL	17846
2Q7N	CD	CYTOKINE RECEPTOR/CYTOKINE	D	1.3	1.3	1	24	VFQKKKLGCQLLGKYKQIIAVLAQ	17847
2QAC	AT	MEMBRANE PROTEIN	A	1.3	1.3	1	9	KSQMKNILT	17848
2QAC	AT	MEMBRANE PROTEIN	A	1.3	1.3	1	12	DQEAIDALNAFS	17849
2QAG	AB	CELL CYCLE, STRUCTURAL PROTEIN	B	1.3	1.3	1	16	KSELTKFKIKITSELV	17850
2QAR	AB	HYDROLASE REGULATOR	A	1.3	1.3	1	7	GKALLLL	17851
2QBY	AB	REPLICATION/DNA	A	1.3	1.3	1	9	PYRVLADLL	17852
2QE7	AD	HYDROLASE	A	1.3	1.3	1	14	QSTVAGVVETLRQH	17853
2QE7	BG	HYDROLASE	G	1.3	1.3	1	13	RSVKNTRQITKAM	17854
2QEX	AZ	RIBOSOME	Z	1.3	1.3	1	15	RVSRRRVAEIESEMN	17855
2QEX	NQ	RIBOSOME	N	1.3	1.3	1	11	YHQRLRLLKSG	17856
2QI9	AC	MEMBRANE PROTEIN	C	1.3	1.3	1	16	GGEWQRVRLAAVVLQI	17857
2QI9	AF	MEMBRANE PROTEIN	A	1.3	1.3	1	22	IRLPRTLAVLLVGAALAISGAV	17858
2QJK	MR	ELECTRON TRANSPORT	R	1.3	1.3	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	17859

2QJP	DC	ELECTRON TRANSPORT	D	1.3	1.3	1	15	QMSFWGATVITGLFG	17860
2QJP	JI	ELECTRON TRANSPORT	J	1.3	1.3	1	15	QMSFWGATVITGLFG	17861
2QJP	KL	ELECTRON TRANSPORT	L	1.3	1.3	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	17862
2QJY	PQ	OXIDOREDUCTASE	P	1.3	1.3	1	15	VDLAFASVEHIMRNV	17863
2QKI	DE	IMMUNE SYSTEM	D	1.3	1.3	1	11	QSKIWDVVEKA	17864
2QLV	AC	TRANSFERASE/PROTEIN BINDING	A	1.3	1.3	1	5	MSTFS	17865
2QME	AI	SIGNALING PROTEIN/TRANSFERASE	A	1.3	1.3	1	11	KTCLLISYTTN	17866
2QOG	DB	HYDROLASE	D	1.3	1.3	1	16	ATDRCCFVHDCCYGKL	17867
2QQP	GH	VIRUS	H	1.3	1.3	1	11	PSVIKGIAQQA	17868
2QR0	WU	IMMUNE SYSTEM	U	1.3	1.3	1	8	FMDVYQRS	17869
2QR1	AB	TRANSFERASE	A	1.3	1.3	1	16	APEILLAVYRALQRAG	17870
2R17	BD	PROTEIN TRANSPORT	D	1.3	1.3	1	15	KPDQGRAVSTCAHLF	17871
2R1H	AB	OXYGEN BINDING	B	1.3	1.3	1	20	PDNFRLLADCITVCVAAKLG	17872
2R1H	CD	OXYGEN BINDING	D	1.3	1.3	1	20	PDNFRLLADCITVCVAAKLG	17873
2R6C	EI	REPLICATION	E	1.3	1.3	1	11	LVTVTAELAAS	17874
2R9R	AB	MEMBRANE PROTEIN, TRANSPORT PROTEIN	B	1.3	1.3	1	7	PKKRMRY	17875
2RAO	AD	OXYGEN BINDING	A	1.3	1.3	1	19	PVNFKLLSHCLLVTLANHH	17876
2RAX	AB	CELL CYCLE	A	1.3	1.3	1	5	PAWQP	17877
2RAX	EF	CELL CYCLE	E	1.3	1.3	1	5	PAWQP	17878
2RGN	AB	SIGNALING PROTEIN COMPLEX	A	1.3	1.3	1	22	TENIRFVFAAVKDTILQLNLKE	17879
2RHS	AB	LIGASE	B	1.3	1.3	1	11	PVSIRHTSRRL	17880
2RI4	IJ	OXYGEN STORAGE, OXYGEN TRANSPORT	J	1.3	1.3	1	16	VDEVGAEALGRLLVVY	17881
2SNI	EI	COMPLEX (PROTEINASE/INHIBITOR)	E	1.3	1.3	1	13	AALKAAVDKAVAS	17882
2UUN	KH	ELECTRON TRANSPORT	K	1.3	1.3	1	8	IDEVNRTF	17883
2UUN	UX	ELECTRON TRANSPORT	U	1.3	1.3	1	8	IDEVNRTF	17884
2UY1	AB	RNA BINDING PROTEIN	A	1.3	1.3	1	19	SKELDLLRINHLNYVLKKR	17885
2UZ1	AB	LYASE	B	1.3	1.3	1	8	QVAMAAPI	17886
2V1Y	AB	TRANSFERASE	B	1.3	1.3	1	8	KEYIEKFK	17887
2V4J	AB	OXIDOREDUCTASE	B	1.3	1.3	1	6	PVIAKN	17888
2V4J	DE	OXIDOREDUCTASE	E	1.3	1.3	1	12	ASGPVKAIMDEV	17889
2V4J	DE	OXIDOREDUCTASE	E	1.3	1.3	1	6	PVIAKN	17890
2V51	BF	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	F	1.3	1.3	1	8	REELVSQG	17891
2V55	CD	TRANSFERASE	D	1.3	1.3	1	6	YDQGAN	17892
2V5H	BH	TRANSCRIPTION	H	1.3	1.3	1	11	LDEVKIALVNA	17893
2V7N	AB	IMMUNE SYSTEM	A	1.3	1.3	1	7	DEQLKSG	17894
2V7N	GH	IMMUNE SYSTEM	G	1.3	1.3	1	6	DEQLKS	17895
2V7Q	AD	HYDROLASE	A	1.3	1.3	1	15	LSKQAVAYRQMSLLL	17896

2V7Q	BF	HYDROLASE	B	1.3	1.3	1	7	LAQYREV	17897
2V7Q	BF	HYDROLASE	F	1.3	1.3	1	5	EVFTG	17898
2V7Q	CD	HYDROLASE	D	1.3	1.3	1	11	IFRFTQAGSEV	17899
2V7Q	DJ	HYDROLASE	D	1.3	1.3	1	28	SEHYDVARGVQKILQDYKSLQDIIAILG	17900
2V7Q	GJ	HYDROLASE	G	1.3	1.3	1	51	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYE	17901
2V8W	EF	TRANSLATION	E	1.3	1.3	1	15	DLDRFWLETLLCLIG	17902
2VAS	AB	MOTOR PROTEIN	B	1.3	1.3	1	11	AAELRHVMTNL	17903
2VBN	AB	HYDROLASE	A	1.3	1.3	1	12	RWFLDKLVDEIG	17904
2VDA	AB	PROTEIN TRANSPORT	A	1.3	1.3	1	10	MYKRVNKIIP	17905
2VDB	AB	PROTEIN BINDING	A	1.3	1.3	1	15	KDVFLGMFLYEYARR	17906
2VDC	CJ	OXIDOREDUCTASE	C	1.3	1.3	1	8	WAREVTKF	17907
2VDN	AB	CELL ADHESION/IMMUNE SYSTEM	B	1.3	1.3	1	10	VNLYQNYSEL	17908
2VDO	HL	CELL ADHESION/IMMUNE SYSTEM	L	1.3	1.3	1	6	SEQLTS	17909
2VGL	AM	PROTEIN TRANSPORT	A	1.3	1.3	1	15	VSVRQRAVDLLYAMC	17910
2VJM	AB	TRANSFERASE	A	1.3	1.3	1	8	ENVAQCSG	17911
2VLR	AD	IMMUNE SYSTEM	A	1.3	1.3	1	11	VAEQLRAYLEG	17912
2VLR	FI	IMMUNE SYSTEM	F	1.3	1.3	1	24	VAEQLRAYLEGTCVEWLRRYLENG	17913
2VML	AF	PHOTOSYNTHESIS	A	1.3	1.3	1	8	LREVNRTF	17914
2VOI	AB	APOPTOSIS	A	1.3	1.3	1	16	IDTARIIFNQVMEKEF	17915
2VPD	CD	GENE REGULATION	C	1.3	1.3	1	5	DTCMA	17916
2VSK	CB	HYDROLASE	B	1.3	1.3	1	7	KDQADRC	17917
2VSO	BF	HYDROLASE/TRANSLATION	F	1.3	1.3	1	14	KDEVERKMKSLLNK	17918
2VUS	BJ	TRANSCRIPTION	B	1.3	1.3	1	16	MEEYAREVFPIEEEAN	17919
2VWE	BL	IMMUNE SYSTEM	B	1.3	1.3	1	9	WIDVYTRAT	17920
2VZD	AC	CELL ADHESION	A	1.3	1.3	1	15	LKSTLRVLYNLFTKY	17921
2W19	AC	TRANSFERASE/ISOMERASE	A	1.3	1.3	1	16	TQQSLELAFLVAEMLR	17922
2W2M	PA	HYDROLASE/RECEPTOR	A	1.3	1.3	1	13	RVLNAACQRLARA	17923
2W80	AD	IMMUNE SYSTEM	A	1.3	1.3	1	6	ENMRRP	17924
2WAQ	AB	TRANSCRIPTION	B	1.3	1.3	1	13	YAFKLLIQELMSM	17925
2WAQ	DL	TRANSCRIPTION	L	1.3	1.3	1	5	IKGLT	17926
2WAQ	EF	TRANSCRIPTION	F	1.3	1.3	1	5	PDEVR	17927
2WB1	AB	TRANSCRIPTION	A	1.3	1.3	1	11	PTELFFHAAGG	17928
2WB1	AB	TRANSCRIPTION	B	1.3	1.3	1	5	VADKI	17929
2WB1	CB	TRANSCRIPTION	B	1.3	1.3	1	13	YAFKLLIQELMSM	17930
2WB1	RO	TRANSCRIPTION	O	1.3	1.3	1	6	RRMLLS	17931
2WB1	SO	TRANSCRIPTION	S	1.3	1.3	1	11	DEILAHRLALI	17932
2WB1	WY	TRANSCRIPTION	Y	1.3	1.3	1	8	LPRLIEIV	17933
2WH4	UV	RIBOSOME	U	1.3	1.3	1	5	DLAVR	17934
2WME	DC	OXIDOREDUCTASE	C	1.3	1.3	1	15	TSTGKKVMASASSSS	17935

2Z2L	DE	BIOSYNTHETIC PROTEIN	D	1.3	1.3	1	6	NSILAG	17936
2Z2L	EF	BIOSYNTHETIC PROTEIN	E	1.3	1.3	1	11	DATWLDYLNRF	17937
2Z2S	GH	TRANSCRIPTION	H	1.3	1.3	1	17	DECRARAGALDAVGGSL	17938
2ZAE	AB	HYDROLASE	A	1.3	1.3	1	5	YQEII	17939
2ZBK	AB	ISOMERASE	A	1.3	1.3	1	11	LNEAKRFMQTV	17940
2ZBK	EF	ISOMERASE	E	1.3	1.3	1	11	LNEAKRFMQTV	17941
2ZCY	DE	HYDROLASE	E	1.3	1.3	1	22	APDARVLSNYLRQQCNYSSLVF	17942
2ZCY	DK	HYDROLASE	D	1.3	1.3	1	22	TADARSMIEHARTAAVTHNLYY	17943
2ZCY	EM	HYDROLASE	M	1.3	1.3	1	20	ISDMQHIERLLKDLVTENAY	17944
2ZCY	FN	HYDROLASE	N	1.3	1.3	1	22	AADTQAIADIVQYHLELYTSQY	17945
2ZCY	IJ	HYDROLASE	J	1.3	1.3	1	17	PQAVSSFVRQELAKSIR	17946
2ZCY	OV	HYDROLASE	O	1.3	1.3	1	5	YKRIY	17947
2ZCY	S0	HYDROLASE	0	1.3	1.3	1	20	ISDMQHIERLLKDLVTENAY	17948
2ZCY	S0	HYDROLASE	0	1.3	1.3	1	18	PSYIFEYLATVMYQRRSK	17949
2ZCY	VL	HYDROLASE	V	1.3	1.3	1	19	KEEAIKLASDAIQAGIWND	17950
2ZCY	VM	HYDROLASE	M	1.3	1.3	1	14	FGAHMANPLLRKVV	17951
2ZCY	XK	HYDROLASE	K	1.3	1.3	1	19	VEDALYLGKRSILAAAHRD	17952
2ZJS	YE	PROTEIN TRANSPORT/IMMUNE SYSTEM	Y	1.3	1.3	1	24	IGLLIVVGVALDTLRQVESQLMLR	17953
2ZL1	AB	PROTEIN BINDING	B	1.3	1.3	1	17	FGMLKAKAQALVQYLEE	17954
2ZNE	AC	APOPTOSIS	A	1.3	1.3	1	12	KNELKQALSGFG	17955
2ZT9	BD	PHOTOSYNTHESIS	D	1.3	1.3	1	31	MGRRQFMNLLTFGTVTGVALGALYPVVNYFI	17956
2ZU0	AC	BIOSYNTHETIC PROTEIN/PROTEIN BINDING	A	1.3	1.3	1	13	QQDAQQMIIYAFA	17957
2ZU6	CB	HYDROLASE	C	1.3	1.3	1	14	RRKVDWLTEKMHAR	17958
2ZXE	AB	HYDROLASE/TRANSPORT PROTEIN	A	1.3	1.3	1	21	FPYSLIIFLYDEMRRFIIRRS	17959
3A0B	ad	ELECTRON TRANSPORT	a	1.3	1.3	1	12	IVAAHGYFGRLI	17960
3A0B	ad	ELECTRON TRANSPORT	a	1.3	1.3	1	8	NLGMEVMH	17961
3A0B	AD	ELECTRON TRANSPORT	D	1.3	1.3	1	18	MGVAGVLGGALLCAIHGA	17962
3A0B	CZ	ELECTRON TRANSPORT	Z	1.3	1.3	1	11	GLWIALVLVVG	17963
3A0B	DL	ELECTRON TRANSPORT	L	1.3	1.3	1	16	SLYLGLLLILVLALLF	17964
3A0B	JK	ELECTRON TRANSPORT	J	1.3	1.3	1	9	LWIVATVAG	17965
3B63	DE	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	E	1.3	1.3	1	12	KANREKMTQIMF	17966
3B63	KM	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	M	1.3	1.3	1	6	VDIRKD	17967
3B63	NL	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	N	1.3	1.3	1	10	IDIRKDLYAN	17968
3B63	NM	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	M	1.3	1.3	1	15	GRDLTDYLMKILTER	17969

3B8E	CD	HYDROLASE/TRANSPORT PROTEIN	C	1.3	1.3	1	9	GMIQALGGF	17970
3B9J	JK	OXIDOREDUCTASE	K	1.3	1.3	1	10	PEHAERAAHV	17971
3BBP	CF	PROTEIN TRANSPORT/SPLICING	F	1.3	1.3	1	28	LRETEATNAILMEQIKLLKSEIRRLERN	17972
3BC1	AF	SIGNALING PROTEIN/TRANSPORT PROTEIN	A	1.3	1.3	1	12	VRNWISQLQMHA	17973
3BIM	DK	TRANSCRIPTION REPRESSOR	D	1.3	1.3	1	15	HASDVLLNLNRLRSR	17974
3BIM	FN	TRANSCRIPTION REPRESSOR	F	1.3	1.3	1	7	GLFYSIF	17975
3BIM	GO	TRANSCRIPTION REPRESSOR	G	1.3	1.3	1	7	GLFYSIF	17976
3BKJ	LH	IMMUNE SYSTEM	L	1.3	1.3	1	7	SEQLTSG	17977
3BLW	CD	OXIDOREDUCTASE	C	1.3	1.3	1	14	KLGDGLFRNIITEI	17978
3BLW	KL	OXIDOREDUCTASE	K	1.3	1.3	1	15	SMYGTILGNIGAALI	17979
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.3	1.3	1	12	IDTCRSMVAVMD	17980
3BQO	AB	DNA BINDING PROTEIN	A	1.3	1.3	1	18	ACQLRTIYICQFLTRIAA	17981
3BRV	CB	TRANSFERASE/TRANSCRIPTION	B	1.3	1.3	1	60	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	17982
3BWN	DC	TRANSFERASE	C	1.3	1.3	1	15	KEVAKKMVEYIIVNS	17983
3BWN	DC	TRANSFERASE	D	1.3	1.3	1	15	STQLCQAAVHALSSL	17984
3BZ1	DE	ELECTRON TRANSPORT	E	1.3	1.3	1	6	LAYDVF	17985
3C1B	FD	STRUCTURAL PROTEIN/DNA	D	1.3	1.3	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	17986
3C66	AC	TRANSFERASE	A	1.3	1.3	1	11	HIPCTEFVNLC	17987
3C6L	AB	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	B	1.3	1.3	1	8	KAEIANKQ	17988
3C6L	EH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	H	1.3	1.3	1	21	PEILERTRAELDTVCRHNYEG	17989
3C6L	GH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	H	1.3	1.3	1	8	RPDAEYWN	17990
3C75	HM	OXIDOREDUCTASE	H	1.3	1.3	1	15	EGQRGAAEAAAALAA	17991
3C75	JL	OXIDOREDUCTASE	J	1.3	1.3	1	15	EGQRGAAEAAAALAA	17992
3C7B	DE	OXIDOREDUCTASE	D	1.3	1.3	1	10	LQPCFEDLGN	17993
3C7K	AB	SIGNALING PROTEIN	A	1.3	1.3	1	8	ERKKWIHC	17994
3C91	BI	HYDROLASE	B	1.3	1.3	1	23	VADARVLVDFARISAQQEKVTYG	17995
3C91	T1	HYDROLASE	T	1.3	1.3	1	23	VADARVLVDFARISAQQEKVTYG	17996
3CDK	AB	TRANSFERASE	B	1.3	1.3	1	8	AMDLVNGA	17997
3CF6	ER	SIGNALING PROTEIN/GTP-BINDING PROTEIN	E	1.3	1.3	1	15	MPLLIKDMTFTHEGN	17998
3CJC	AD	STRUCTURAL PROTEIN/HYDROLASE	D	1.3	1.3	1	11	VAVGKLLDYLN	17999
3CJH	ID	PROTEIN TRANSPORT	I	1.3	1.3	1	15	ELVNKISENCFEKCL	18000
3CJK	AB	METAL TRANSPORT/HYDROLASE	A	1.3	1.3	1	15	GGCAEAVSRVLNKLG	18001
3CM8	AB	RNA BINDING PROTEIN/TRANSFERASE	A	1.3	1.3	1	18	IGKVCRTLLAKSVFNSLY	18002
3CMA	FM	RIBOSOME	F	1.3	1.3	1	10	TNETTKSIER	18003

3CQG	AB	PROTEIN TRANSPORT	B	1.3	1.3	1	8	SWLHEINS	18004
3CSL	AC	MEMBRANE PROTEIN/HEME BINDING PROTEIN	A	1.3	1.3	1	5	AASND	18005
3CSL	BD	MEMBRANE PROTEIN/HEME BINDING PROTEIN	B	1.3	1.3	1	5	AASND	18006
3CSY	KJ	IMMUNE SYSTEM/VIRAL PROTEIN	J	1.3	1.3	1	13	ILNRKAIDFLLQR	18007
3CUE	BD	PROTEIN TRANSPORT	D	1.3	1.3	1	11	SLKAMGEEIWK	18008
3CUE	IL	PROTEIN TRANSPORT	I	1.3	1.3	1	23	QNEEDAKLLYGMIFSLRSITQKL	18009
3CUQ	AB	PROTEIN TRANSPORT	A	1.3	1.3	1	7	FWSEMLG	18010
3CWB	BS	OXIDOREDUCTASE	B	1.3	1.3	1	6	PWEVTD	18011
3CWB	CD	OXIDOREDUCTASE	C	1.3	1.3	1	12	AFSSVAHTCRNV	18012
3CWB	CR	OXIDOREDUCTASE	C	1.3	1.3	1	9	HTLVEWAWG	18013
3CWB	GH	OXIDOREDUCTASE	H	1.3	1.3	1	23	TEELFDFLHARDHCVAHKLFNKL	18014
3CWB	NO	OXIDOREDUCTASE	N	1.3	1.3	1	6	YAQTLQ	18015
3CWB	PE	OXIDOREDUCTASE	P	1.3	1.3	1	9	HTLVEWAWG	18016
3CWB	QR	OXIDOREDUCTASE	R	1.3	1.3	1	32	SEDRKGFSYLVTATACVATAYAAKNVVTQFIS	18017
3CXH	CH	OXIDOREDUCTASE	H	1.3	1.3	1	11	KAGREELERVN	18018
3CXH	CP	OXIDOREDUCTASE	C	1.3	1.3	1	14	QMSHWGATVITNLF	18019
3CXH	EH	OXIDOREDUCTASE	E	1.3	1.3	1	33	KGRSYAYFMVGAMGLLSSAGAKSTVETFISSMT	18020
3CXH	OQ	OXIDOREDUCTASE	Q	1.3	1.3	1	11	QLEDLREHFKN	18021
3D0L	AB	IMMUNE SYSTEM	A	1.3	1.3	1	7	DEQLKSG	18022
3D1M	BC	SIGNALING PROTEIN / CELL ADHESION	B	1.3	1.3	1	15	RSKYGMLARLAVEAG	18023
3D24	CD	TRANSCRIPTION	C	1.3	1.3	1	10	KLFLEMLEAM	18024
3D31	BD	TRANSPORT PROTEIN	B	1.3	1.3	1	12	VKKNLEFGMRMK	18025
3D54	AD	LIGASE	A	1.3	1.3	1	14	DGIIEGIADYGNSI	18026
3D5D	P8	RIBOSOME	8	1.3	1.3	1	8	KPEAERIK	18027
3D7U	AB	TRANSFERASE	A	1.3	1.3	1	9	LVDYLRSRG	18028
3D87	CD	CYTOKINE	C	1.3	1.3	1	34	PWQRLLLRFKILRSLQAFVAVAARVFAHGAATLS	18029
3DAC	AB	CELL CYCLE	A	1.3	1.3	1	15	VKEVMHYLGQYIMMK	18030
3DBH	EF	CELL CYCLE	F	1.3	1.3	1	12	LGCELLKNLALS	18031
3DGC	LR	CYTOKINE/SIGNALING PROTEIN	L	1.3	1.3	1	18	PYITNRTFMLAKEASLAD	18032
3DHH	AB	OXIDOREDUCTASE	A	1.3	1.3	1	15	WAAIAAKHFFDDIIT	18033
3DHH	AB	OXIDOREDUCTASE	A	1.3	1.3	1	8	LEGALKYM	18034
3DHH	AC	OXIDOREDUCTASE	A	1.3	1.3	1	14	WGRCWDVITENVLN	18035
3DHR	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	C	1.3	1.3	1	19	PVNFKLLGHCFLVVVAVHF	18036
3DHR	EH	OXYGEN STORAGE, OXYGEN TRANSPORT	E	1.3	1.3	1	19	PVNFKLLGHCFLVVVAVHF	18037
3DHW	BD	MEMBRANE PROTEIN/HYDROLASE	D	1.3	1.3	1	13	GGQKQRVAIARAL	18038

3DIN	AC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	A	1.3	1.3	1	17	VSLLYHLINALKALHLF	18039
3DL8	BH	PROTEIN TRANSPORT	B	1.3	1.3	1	28	REYQMEGFAMFEHMIESIEDEVAKFVMK	18040
3DNL	HI	VIRAL PROTEIN	I	1.3	1.3	1	9	MRDNWRSEL	18041
3DOM	CD	TRANSCRIPTION	D	1.3	1.3	1	13	PSIKALILQIDAK	18042
3DTP	AE	CONTRACTILE PROTEIN	E	1.3	1.3	1	11	FTMFLTIFGDR	18043
3DTP	AE	CONTRACTILE PROTEIN	E	1.3	1.3	1	5	FQLID	18044
3DTU	CB	OXIDOREDUCTASE	B	1.3	1.3	1	10	PEVEQQLIEA	18045
3DUF	AB	OXIDOREDUCTASE/TRANSFERASE	A	1.3	1.3	1	13	FNLKEQYEIYKEK	18046
3DUF	GH	OXIDOREDUCTASE/TRANSFERASE	G	1.3	1.3	1	13	FNLKEQYEIYKEK	18047
3DVE	AB	MEMBRANE PROTEIN	A	1.3	1.3	1	12	EEEIREAFRVFD	18048
3E 95	AC	LIGASE	A	1.3	1.3	1	10	SKVAEHFKQD	18049
3EA5	CD	TRANSPORT PROTEIN	D	1.3	1.3	1	16	EDDVFYAISALAASLG	18050
3EDX	CD	HYDROLASE	D	1.3	1.3	1	11	KRWIQKVIDQF	18051
3EH3	AC	OXIDOREDUCTASE	C	1.3	1.3	1	14	KGALAVILVLTLTI	18052
3EHU	BD	MEMBRANE PROTEIN	D	1.3	1.3	1	15	LAQQAHSNRKLMEII	18053
3EIQ	DC	HYDROLASE/ANTITUMOR PROTEIN	C	1.3	1.3	1	17	HLVKEIDMLLKEYLLSG	18054
3EPF	R3	VIRAL PROTEIN	3	1.3	1.3	1	5	PRLAH	18055
3ERC	BC	TRANSCRIPTION, TRANSFERASE/DNA, RNA	C	1.3	1.3	1	11	ENVLSSDILDL	18056
3ETR	LN	OXIDOREDUCTASE	N	1.3	1.3	1	22	PAIDIGQVEGAFVQGLGLFTLE	18057
3EUB	JL	OXIDOREDUCTASE	L	1.3	1.3	1	7	AAMQASG	18058
3EXG	Q2	OXIDOREDUCTASE	Q	1.3	1.3	1	25	VEELKEIDVEVRKEIEDAAQFATAD	18059
3EXG	WB	OXIDOREDUCTASE	B	1.3	1.3	1	6	LWKKYG	18060
3EXH	FG	OXIDOREDUCTASE	F	1.3	1.3	1	12	VKDIIFAIKKTL	18061
3EZQ	MN	APOPTOSIS	N	1.3	1.3	1	5	QNRSG	18062
3F1F	ET	RIBOSOME	T	1.3	1.3	1	9	GALIKLVES	18063
3F3P	FH	STRUCTURAL PROTEIN	H	1.3	1.3	1	9	NSFAFELCS	18064
3F7P	BD	STRUCTURAL PROTEIN/CELL ADHESION	B	1.3	1.3	1	18	RFHKLQNVQIALDYLRHR	18065
3F8U	AB	IMMUNE SYSTEM/ISOMERASE	A	1.3	1.3	1	16	GHAKRLAPEYEAAATR	18066
3F9K	AC	VIRAL PROTEIN, RECOMBINATION	A	1.3	1.3	1	15	IETIVLMAVHCMNFK	18067
3F9K	Re	VIRAL PROTEIN, RECOMBINATION	e	1.3	1.3	1	10	TEMITTLKKI	18068
3FAL	CB	SIGNALING PROTEIN	B	1.3	1.3	1	9	PLLSEIWDV	18069
3FCU	CD	CELL ADHESION/BLOOD CLOTTING	D	1.3	1.3	1	5	DGRLA	18070
3FH6	FB	TRANSPORT PROTEIN	F	1.3	1.3	1	11	PFQNFFKITLP	18071
3FH6	FG	TRANSPORT PROTEIN	G	1.3	1.3	1	16	SLVALYALFDRLGEYI	18072
3FH6	HI	TRANSPORT PROTEIN	I	1.3	1.3	1	16	SLVALYALFDRLGEYI	18073
3FIH	NC	RIBOSOME	C	1.3	1.3	1	21	TKEFADNLDSDFKVRQYLTKE	18074
3FIN	8:00:0	RIBOSOME	8	1.3	1.3	1	6	KGAKKR	18075

3FKS	CF	HYDROLASE	C	1.3	1.3	1	15	LSKQAVAYRQLSLLL	18076
3FKS	JN	HYDROLASE	N	1.3	1.3	1	16	IFRFTQAGSEVSALLG	18077
3FKS	KO	HYDROLASE	O	1.3	1.3	1	12	GNDLYREMKETG	18078
3FKS	LO	HYDROLASE	L	1.3	1.3	1	15	LSKQAVAYRQLSLLL	18079
3FKS	SW	HYDROLASE	W	1.3	1.3	1	5	PGARA	18080
3FKS	UX	HYDROLASE	X	1.3	1.3	1	10	PAPATTFAHL	18081
3FLO	GH	TRANSFERASE	G	1.3	1.3	1	15	LDELFLKLFTPILKT	18082
3FPN	AB	DNA BINDING PROTEIN	A	1.3	1.3	1	15	AARLADSLETALKLA	18083
3FS4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	1.3	1.3	1	19	PEVHASLDKFLCAVGAVLT	18084
3FWC	NO	CELL CYCLE, TRANSCRIPTION	O	1.3	1.3	1	13	QLKSQIQQYLVES	18085
3FWC	NP	CELL CYCLE, TRANSCRIPTION	P	1.3	1.3	1	15	TAQLKSQIQQYLVES	18086
3G43	CF	METAL BINDING PROTEIN	C	1.3	1.3	1	11	EAELQDMINEV	18087
3G43	DE	METAL BINDING PROTEIN	D	1.3	1.3	1	12	FPEFLTMMARKM	18088
3G4S	SV	RIBOSOME	V	1.3	1.3	1	16	AEREAELDDLKTELLN	18089
3G65	BC	CELL CYCLE	C	1.3	1.3	1	13	LKTMKSVVEKMKN	18090
3G9K	LS	HYDROLASE	S	1.3	1.3	1	15	RIPQILTPILDKYTH	18091
3GBM	CD	VIRAL PROTEIN / IMMUNE SYSTEM	D	1.3	1.3	1	22	KESTQKAIDGVTNKVNSIIDKM	18092
3GE8	DH	OXIDOREDUCTASE	D	1.3	1.3	1	16	FANMQFLGLAADAAEA	18093
3GHG	AB	BLOOD CLOTTING	B	1.3	1.3	1	14	QERPIRNSVDELNN	18094
3GHG	BC	BLOOD CLOTTING	C	1.3	1.3	1	19	TCGIADFLSTYQTKVDKDL	18095
3GHG	BC	BLOOD CLOTTING	C	1.3	1.3	1	8	ASILTHDS	18096
3GHG	GH	BLOOD CLOTTING	H	1.3	1.3	1	11	ERPIRNSVDEL	18097
3GHG	GI	BLOOD CLOTTING	I	1.3	1.3	1	44	MIDAATLKSRKMLEEIMKYEASILTHDSSIRYLQEIYNSNNQKI	18098
3GHG	HI	BLOOD CLOTTING	I	1.3	1.3	1	14	TCGIADFLSTYQTK	18099
3GHG	JK	BLOOD CLOTTING	K	1.3	1.3	1	21	VVNEYSSELEKHQLYIDETVN	18100
3GHG	KL	BLOOD CLOTTING	L	1.3	1.3	1	14	IMKYEASILTHDSS	18101
3GJF	KM	IMMUNE SYSTEM	K	1.3	1.3	1	6	SEELQA	18102
3GJX	FD	PROTEIN TRANSPORT	D	1.3	1.3	1	14	RNVSLKCLTEIAGV	18103
3GJX	FD	PROTEIN TRANSPORT	D	1.3	1.3	1	22	TEIFKICLEYWNHLAAELYRES	18104
3GLH	KL	TRANSFERASE	K	1.3	1.3	1	19	PLLLQESQDAVRQVAAAQG	18105
3GLH	KO	TRANSFERASE	K	1.3	1.3	1	15	TLQRELLLLVNLKRQ	18106
3GLI	AB	TRANSFERASE/DNA	A	1.3	1.3	1	14	SKRALHILQQLRLE	18107
3GLI	FJ	TRANSFERASE/DNA	F	1.3	1.3	1	25	PVILLRTLQRELLLLVNLKRQSAHT	18108
3GLI	GP	TRANSFERASE/DNA	G	1.3	1.3	1	15	RRMGVEMTLLRALAF	18109
3GMW	AB	PROTEIN BINDING	A	1.3	1.3	1	11	NTAANLLLTTI	18110
3GMW	CD	PROTEIN BINDING	C	1.3	1.3	1	11	NTAANLLLTTI	18111
3H0L	GE	LIGASE	E	1.3	1.3	1	10	KEWIEEIKKN	18112
3H0L	MN	LIGASE	M	1.3	1.3	1	11	IIAPSEASSNL	18113
3H0L	VW	LIGASE	V	1.3	1.3	1	11	IIAPSEASSNL	18114

3H32	EF	BLOOD CLOTTING	F	1.3	1.3	1	6	WIQYKE	18115
3H42	LH	HYDROLASE/IMMUNE SYSTEM	L	1.3	1.3	1	6	SEELQA	18116
3H4P	Ff	HYDROLASE	f	1.3	1.3	1	6	LYKMRT	18117
3H4P	Mm	HYDROLASE	m	1.3	1.3	1	6	LYKMRT	18118
3H4S	AE	MOTOR PROTEIN/CALCIUM BINDING PROTEIN	A	1.3	1.3	1	23	LKEAQSINKSLSALGDVIGALSS	18119
3HAE	LH	IMMUNE SYSTEM	L	1.3	1.3	1	6	SEELQA	18120
3HD7	GH	EXOCYTOSIS	G	1.3	1.3	1	11	ADQLADESLES	18121
3HD7	GH	EXOCYTOSIS	H	1.3	1.3	1	7	MARENEM	18122
3HG1	AE	IMMUNE SYSTEM	A	1.3	1.3	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	18123
3HGK	BE	TRANSFERASE	E	1.3	1.3	1	5	MPMHG	18124
3HH2	BC	SIGNALING PROTEIN/CYTOKINE	B	1.3	1.3	1	10	PHTHLVHQAN	18125
3HKZ	AB	TRANSFERASE	A	1.3	1.3	1	7	HVATYFD	18126
3HKZ	AC	TRANSFERASE	C	1.3	1.3	1	6	VLARAA	18127
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.3	1.3	1	9	NVKQMVMAG	18128
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.3	1.3	1	17	VAHLIECLLSKVAALSG	18129
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.3	1.3	1	10	FINIAQMSAC	18130
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.3	1.3	1	8	ASFLKERL	18131
3HRD	BD	OXIDOREDUCTASE	B	1.3	1.3	1	22	RSMVEGQIEGGVTMGQGFVLME	18132
3HRZ	CD	IMMUNE SYSTEM	C	1.3	1.3	1	21	EEFQKLCDDFAQFSYTLTEFG	18133
4RUB	AS	LYASE(CARBON-CARBON)	A	1.3	1.3	1	21	NAPGAVANRVALEACVKARNE	18134
5CSC	AB	OXO-ACID-LYASE	B	1.3	1.3	1	7	TDGLIAL	18135
9PAI	AB	HYDROLASE INHIBITOR	A	1.3	1.3	1	13	MAPALRHLYKELM	18136
15C8	LH	CATALYTIC ANTIBODY	L	1.2	1.2	1	6	SEQLTS	18137
1A4Y	DE	COMPLEX (INHIBITOR/NUCLEASE)	E	1.2	1.2	1	11	DRYCESIMRRR	18138
1AE6	LH	IMMUNOGLOBULIN	H	1.2	1.2	1	5	TTYYY	18139
1AGR	AE	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	E	1.2	1.2	1	11	SCTREETSRNM	18140
1AHJ	CD	LYASE	D	1.2	1.2	1	9	QDELESLAG	18141
1AHJ	GH	LYASE	H	1.2	1.2	1	9	QDELESLAG	18142
1ALL	AB	LIGHT HARVESTING PROTEIN	B	1.2	1.2	1	14	GELRVRAATTISAN	18143
1AOI	EC	DNA BINDING PROTEIN/DNA	E	1.2	1.2	1	13	TVALREIRRYQKS	18144
1AOI	EC	DNA BINDING PROTEIN/DNA	E	1.2	1.2	1	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	18145
1AOI	GH	DNA BINDING PROTEIN/DNA	G	1.2	1.2	1	6	RSSRAG	18146
1AON	DR	COMPLEX (GROEL/GROES)	D	1.2	1.2	1	11	LPVLEAVAKAG	18147

1AR1	AB	COMPLEX (OXIDOREDUCTASE/ANTIBODY)	A	1.2	1.2	1	25	TPMLWAFGFLFLFTVGGVTGVVLSQ	18148
1AVO	AB	PROTEASOME ACTIVATOR	A	1.2	1.2	1	23	PEAQAKVDVFREDLCTKTENLLG	18149
1AVO	ED	PROTEASOME ACTIVATOR	D	1.2	1.2	1	6	FEKLKK	18150
1AXT	LH	IMMUNOGLOBULIN	L	1.2	1.2	1	6	SEQLTS	18151
1AYY	CD	HYDROLASE	C	1.2	1.2	1	11	PISVARAVMEK	18152
1AZZ	AC	COMPLEX (SERINE PROTEASE/INHIBITOR)	A	1.2	1.2	1	9	NADCDAVYG	18153
1B33	AI	PHOTOSYNTHESIS	A	1.2	1.2	1	13	PGELDRIKSFVSS	18154
1B33	JI	PHOTOSYNTHESIS	I	1.2	1.2	1	25	TRRYAACIRDLDYYLRYATYAMLAG	18155
1B4U	AB	DIOXYGENASE	A	1.2	1.2	1	8	FQFAAGSM	18156
1B8D	AB	PHOTOSYNTHESIS	A	1.2	1.2	1	16	HEAVVKEAGDACFAKY	18157
1B8D	KL	PHOTOSYNTHESIS	K	1.2	1.2	1	16	HEAVVKEAGDACFAKY	18158
1BCC	AC	OXIDOREDUCTASE	A	1.2	1.2	1	6	YNRIRS	18159
1BCC	CE	OXIDOREDUCTASE	E	1.2	1.2	1	35	SRESDPSRKGFSYLVTAVTTLGVAYAAKNVVTQFV	18160
1BCC	DH	OXIDOREDUCTASE	H	1.2	1.2	1	10	PLTTVREQCE	18161
1BCP	BD	TOXIN	B	1.2	1.2	1	13	YSRLRKMLYLIYV	18162
1BCP	KL	TOXIN	K	1.2	1.2	1	13	PMEVMLRAVFMQQ	18163
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	A	1.2	1.2	1	8	SVAYGASE	18164
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.2	1.2	1	12	LTATRYSIGALG	18165
1BI4	AB	DNA INTEGRATION	A	1.2	1.2	1	13	AGERIVDIIATDI	18166
1BI8	AB	COMPLEX (KINASE/INHIBITOR)	B	1.2	1.2	1	10	TAIALELLKQ	18167
1BI8	AB	COMPLEX (KINASE/INHIBITOR)	B	1.2	1.2	1	10	LDTLKVLVEH	18168
1BI8	CD	COMPLEX (KINASE/INHIBITOR)	D	1.2	1.2	1	10	TAIALELLKQ	18169
1BI8	CD	COMPLEX (KINASE/INHIBITOR)	D	1.2	1.2	1	10	LDTLKVLVEH	18170
1BR1	EF	MUSCLE PROTEIN	F	1.2	1.2	1	9	EEEVEQLVA	18171
1BR1	GH	MUSCLE PROTEIN	H	1.2	1.2	1	9	EEEVEQLVA	18172
1BX2	DF	IMMUNE SYSTEM	D	1.2	1.2	1	23	AQGALANIAVDKANLEIMTKRSN	18173
1BXN	EK	LYASE	E	1.2	1.2	1	20	WRDRFLFVMDAVNKASAATG	18174
1C17	LM	MEMBRANE PROTEIN	L	1.2	1.2	1	34	IPLLRTQFFIVMGLVDAIPMIAVGLGLYVMFAVA	18175
1CAX	AD	SEED STORAGE PROTEIN	D	1.2	1.2	1	11	GEEVEELLENQ	18176
1CB7	AB	ISOMERASE	B	1.2	1.2	1	13	FQMVIDDIFAVGK	18177
1CB7	CD	ISOMERASE	D	1.2	1.2	1	13	FQMVIDDIFAVGK	18178
1CBW	BC	COMPLEX (SERINE PROTEASE/INHIBITOR)	C	1.2	1.2	1	13	VTALVNWVQQTLA	18179
1CDL	CG	CALCIUM-BINDING PROTEIN	C	1.2	1.2	1	10	FPEFLTMMAR	18180
1CE7	AB	RIBOSOME	A	1.2	1.2	1	13	NPILWRARQYINS	18181
1CN4	BC	HAEMATOPOIETIC CYTOKINE	C	1.2	1.2	1	14	FRKLFRVYSNFLRG	18182

1CP9	AB	HYDROLASE	B	1.2	1.2	1	12	TGAKLLYESLLE	18183
1CQ4	AB	HYDROLASE INHIBITOR	A	1.2	1.2	1	8	KKVILQDK	18184
1CQT	AI	GENE REGULATION/DNA	I	1.2	1.2	1	8	VKELLRRK	18185
1D3U	AB	GENE REGULATION/DNA	B	1.2	1.2	1	16	IESVMAACVYAACRLL	18186
1D4M	13	VIRUS	3	1.2	1.2	1	6	LMEIAE	18187
1DBA	LH	IMMUNOGLOBULIN	L	1.2	1.2	1	5	SEQLT	18188
1DFK	AZ	CONTRACTILE PROTEIN	Z	1.2	1.2	1	11	DEDVDEIIKLT	18189
1DFL	AZ	CONTRACTILE PROTEIN	Z	1.2	1.2	1	11	DEDVDEIIKLT	18190
1DFL	WX	CONTRACTILE PROTEIN	X	1.2	1.2	1	18	QDEIDDLKDVFELFDFWD	18191
1DIO	LE	LYASE	E	1.2	1.2	1	11	VAFVAVEGNRL	18192
1DML	EF	DNA BINDING PROTEIN/TRANSFERASE	F	1.2	1.2	1	9	DVAARLRAA	18193
1DML	GH	DNA BINDING PROTEIN/TRANSFERASE	H	1.2	1.2	1	9	DVAARLRAA	18194
1DOA	AB	CELL CYCLE	B	1.2	1.2	1	6	IQEIQE	18195
1DOW	AB	CELL ADHESION	A	1.2	1.2	1	21	DVYKLLVQLKVVEDGILKLRN	18196
1DY8	AC	SERINE PROTEASE	A	1.2	1.2	1	11	LLGCIITSLTG	18197
1E1H	CD	HYDROLASE	D	1.2	1.2	1	15	KLKFDKLYKMLTEIY	18198
1E6E	AB	OXIDOREDUCTASE	A	1.2	1.2	1	5	WVKRG	18199
1E6E	AB	OXIDOREDUCTASE	A	1.2	1.2	1	12	NVINTFTQTARS	18200
1E6V	BC	OXIDOREDUCTASE	B	1.2	1.2	1	24	MDLWNAYAAAGLVAAVMVNQGAAR	18201
1E6V	DB	OXIDOREDUCTASE	B	1.2	1.2	1	18	PYSGTLQAGMAVVHAIID	18202
1E6V	EF	OXIDOREDUCTASE	E	1.2	1.2	1	24	MDLWNAYAAAGLVAAVMVNQGAAR	18203
1E6Y	AE	OXIDOREDUCTASE	A	1.2	1.2	1	19	ANAGLSGWYLSMYLHKEAW	18204
1E6Y	DB	OXIDOREDUCTASE	B	1.2	1.2	1	19	MSATTVGAAAVTQTIMDMF	18205
1E6Y	DB	OXIDOREDUCTASE	D	1.2	1.2	1	19	ANAGLSGWYLSMYLHKEAW	18206
1E6Y	DE	OXIDOREDUCTASE	D	1.2	1.2	1	19	ANAGLSGWYLSMYLHKEAW	18207
1E6Y	DE	OXIDOREDUCTASE	E	1.2	1.2	1	20	AQNVSSTLLYFNDILEKETG	18208
1EFX	AD	IMMUNE SYSTEM	A	1.2	1.2	1	13	TAAQITQRKWEAA	18209
1EO8	AB	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.2	1.2	1	19	LKSTQAAIDQINGKLNRVI	18210
1ETZ	AH	IMMUNE SYSTEM	A	1.2	1.2	1	6	ARAWER	18211
1EXB	AE	METAL TRANSPORT	A	1.2	1.2	1	14	SMEIMEAYSVARQF	18212
1EYS	LH	ELECTRON TRANSPORT	H	1.2	1.2	1	17	LYEEDKVCAYYAGGKLY	18213
1EYS	LM	ELECTRON TRANSPORT	M	1.2	1.2	1	14	MESIHRWAWWCAVL	18214
1EYX	KL	PHOTOSYNTHESIS	K	1.2	1.2	1	9	GPLDEWGIA	18215
1EYX	KL	PHOTOSYNTHESIS	K	1.2	1.2	1	16	HEAVVKEAGDACFGKY	18216
1F11	AB	IMMUNE SYSTEM	A	1.2	1.2	1	6	SEQLTS	18217
1F2U	CD	REPLICATION	C	1.2	1.2	1	9	YNIFLNAIY	18218
1F34	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.2	1.2	1	22	AKDHAEVQTFREKIAAFEEQQE	18219
1F3V	AB	APOPTOSIS	A	1.2	1.2	1	14	EELAELEDALRNLK	18220
1F66	BD	STRUCTURAL PROTEIN/DNA	B	1.2	1.2	1	11	AMDVVYALKRQ	18221
1F66	CD	STRUCTURAL PROTEIN/DNA	C	1.2	1.2	1	7	EELDSLI	18222

1F66	EC	STRUCTURAL PROTEIN/DNA	E	1.2	1.2	1	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	18223
1F6M	BD	OXIDOREDUCTASE	D	1.2	1.2	1	12	KGQLKEFLDANL	18224
1F80	AE	TRANSFERASE	A	1.2	1.2	1	23	EARKNEFLAGRFAAKEAFSKAFG	18225
1F80	CF	TRANSFERASE	F	1.2	1.2	1	13	DVVELVMELEDEF	18226
1F93	CH	TRANSCRIPTION	C	1.2	1.2	1	10	RVALQAEKLD	18227
1F99	AL	PHOTOSYNTHESIS	A	1.2	1.2	1	8	LEEINRTF	18228
1F9E	AB	APOPTOSIS	A	1.2	1.2	1	15	THLDAGALTTTFEEL	18229
1F9E	KJ	APOPTOSIS	J	1.2	1.2	1	15	ILTILTEVNYEVSNK	18230
1FDH	AH	OXYGEN TRANSPORT	A	1.2	1.2	1	17	PVNFKLLSHCLLVTLAA	18231
1FDH	BG	OXYGEN TRANSPORT	B	1.2	1.2	1	17	PVNFKLLSHCLLVTLAA	18232
1FIQ	AB	OXIDOREDUCTASE	B	1.2	1.2	1	9	EIGIEMKFK	18233
1FMD	14	VIRUS	4	1.2	1.2	1	7	FSKLASS	18234
1FNT	Ia	HYDROLASE/HYDROLASE ACTIVATOR	a	1.2	1.2	1	18	VEEVIKLVRDSFTSATER	18235
1FNT	IJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.2	1.2	1	18	PEDLFETISQALLNAADR	18236
1FNT	Ja	HYDROLASE/HYDROLASE ACTIVATOR	J	1.2	1.2	1	18	PEDLFETISQALLNAADR	18237
1FNT	JZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.2	1.2	1	19	VEDALYLGKRSILAAAHRD	18238
1FNT	Tn	HYDROLASE/HYDROLASE ACTIVATOR	T	1.2	1.2	1	13	FQVEYALEAIKQG	18239
1FNT	TU	HYDROLASE/HYDROLASE ACTIVATOR	T	1.2	1.2	1	8	VERAGHLL	18240
1FNT	YZ	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.2	1.2	1	23	AGDTVQFAEYIQANIQLYSIRED	18241
1FNT	Za	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.2	1.2	1	13	VGELFWKVKEEEG	18242
1FOR	LH	IMMUNOGLOBULIN	L	1.2	1.2	1	7	SEQLTSG	18243
1FQV	CD	LIGASE	D	1.2	1.2	1	8	PEEIRKTF	18244
1FS1	CD	LIGASE	C	1.2	1.2	1	8	KRWYRLAS	18245
1FS1	CD	LIGASE	D	1.2	1.2	1	14	QGTLFELILAANYL	18246
1FSX	CB	OXYGEN STORAGE/TRANSPORT	B	1.2	1.2	1	20	PENFKLLGNVLVVVLARNFG	18247
1FSX	CD	OXYGEN STORAGE/TRANSPORT	D	1.2	1.2	1	21	PVLQADFQKVVAGVANALAHR	18248
1FYZ	DF	OXIDOREDUCTASE	F	1.2	1.2	1	12	DTRDAWVNKIAQ	18249
1G0U	FN	HYDROLASE	F	1.2	1.2	1	22	IPDGRHLVNRGREEAASFKKLY	18250
1G0U	HZ	HYDROLASE	Z	1.2	1.2	1	13	ASLIMPFLDNQVN	18251
1G0U	OV	HYDROLASE	O	1.2	1.2	1	18	GPDYRVLVDKSRKVAHTS	18252
1G0U	PX	HYDROLASE	P	1.2	1.2	1	23	TADAEILINTARIHAQNYLKTYN	18253
1G0U	QR	HYDROLASE	Q	1.2	1.2	1	15	VEYLTRYVAGVQQRY	18254
1G0U	RZ	HYDROLASE	Z	1.2	1.2	1	15	INSAARNIQHLLYGK	18255
1G0U	TU	HYDROLASE	T	1.2	1.2	1	15	IPAFADRLGQYVQAH	18256
1G0U	VL	HYDROLASE	L	1.2	1.2	1	13	ASLIMPFLDNQVN	18257
1G0U	VL	HYDROLASE	V	1.2	1.2	1	18	KEEAIKLASDAIQAGIWN	18258
1G1E	AB	TRANSCRIPTION	B	1.2	1.2	1	25	PDIYKAFLEILHTYQKEQRNAKEAG	18259
1G20	AB	OXIDOREDUCTASE	A	1.2	1.2	1	7	CPIGLIG	18260
1G20	CD	OXIDOREDUCTASE	C	1.2	1.2	1	7	CPIGLIG	18261
1G20	CD	OXIDOREDUCTASE	D	1.2	1.2	1	11	QDKIDEVFQWT	18262

1G20	CG	OXIDOREDUCTASE	C	1.2	1.2	1	7	CPIGLIG	18263
1GH0	CF	PHOTOSYNTHESIS	F	1.2	1.2	1	25	SRRMAACLRDMEIILRYVTYAVFAG	18264
1GH0	GJ	PHOTOSYNTHESIS	J	1.2	1.2	1	25	SRRMAACLRDMEIILRYVTYAVFAG	18265
1GH0	QR	PHOTOSYNTHESIS	R	1.2	1.2	1	13	TAQIDALSQMVAE	18266
1GH0	SV	PHOTOSYNTHESIS	V	1.2	1.2	1	25	SRRMAACLRDMEIILRYVTYAVFAG	18267
1GO4	GA	CELL CYCLE	G	1.2	1.2	1	28	PTSVARQRLREDHSQLQAECERLRGLLR	18268
1GPQ	BC	HYDROLASE/INHIBITOR	C	1.2	1.2	1	12	LGNWVCAAKFES	18269
1GXS	AD	LYASE	A	1.2	1.2	1	12	DETRDSGLKVCP	18270
1GXS	CD	LYASE	D	1.2	1.2	1	8	PEVQTALH	18271
1GXS	CD	LYASE	D	1.2	1.2	1	10	VSSTRRSLAA	18272
1H1L	AB	OXIDOREDUCTASE	A	1.2	1.2	1	12	SYELEAFVKALK	18273
1H1L	AB	OXIDOREDUCTASE	B	1.2	1.2	1	12	AQRVQEVFAWTT	18274
1H1L	CD	OXIDOREDUCTASE	D	1.2	1.2	1	7	EDAAVFG	18275
1H2R	SL	OXIDOREDUCTASE	L	1.2	1.2	1	16	AADLKAVQDKLKTFVE	18276
1H4L	AD	KINASE/KINASE ACTIVATOR	D	1.2	1.2	1	13	PHYFTQVFSDLKN	18277
1H5R	AB	TRANSFERASE	A	1.2	1.2	1	9	NYGQYLYKM	18278
1H5R	AB	TRANSFERASE	A	1.2	1.2	1	12	PQDTPRFQQLLG	18279
1H8B	AB	STRUCTURAL PROTEIN	A	1.2	1.2	1	11	PDQAQYCIKRM	18280
1HBH	AD	OXYGEN CARRIER	D	1.2	1.2	1	19	PDNFKLLSDCITIVLAAKM	18281
1HBM	AC	METHANOGENESIS	A	1.2	1.2	1	19	AQTGLSGWYLSMYLHKEQH	18282
1HBM	DB	METHANOGENESIS	D	1.2	1.2	1	8	FGYLADIC	18283
1HBR	CD	OXYGEN STORAGE/TRANSPORT	D	1.2	1.2	1	19	PENFRLLGDILIIVLAAHF	18284
1HQ4	CD	IMMUNE SYSTEM	C	1.2	1.2	1	6	SEQLTS	18285
1HQR	AB	IMMUNE SYSTEM	B	1.2	1.2	1	9	RPDAEYWNS	18286
1HR0	CN	RIBOSOME	N	1.2	1.2	1	11	RICLRELAHKG	18287
1HR8	EF	HYDROLASE	F	1.2	1.2	1	11	PEEVFEQVDKI	18288
1HR8	GH	HYDROLASE	H	1.2	1.2	1	11	PEEVFEQVDKI	18289
1HTL	DC	ENTEROTOXIN	C	1.2	1.2	1	30	DTCNEETQNLSTIYLREYQSKVKRQIFSDY	18290
1HTL	DC	ENTEROTOXIN	C	1.2	1.2	1	5	IYNRI	18291
1HVU	AB	TRANSFERASE/RNA	B	1.2	1.2	1	5	LVKLW	18292
1I3Q	AB	TRANSCRIPTION	B	1.2	1.2	1	6	AEEEES	18293
1I4D	BD	SIGNALING PROTEIN	B	1.2	1.2	1	50	ELELQIELLRETKRKYESVLQLGRALTAHLYSLLQTQHALGDAFADLSQK	18294
1I4O	AC	APOPTOSIS/HYDROLASE	A	1.2	1.2	1	13	WFVQALCSILEEH	18295
1I7W	AB	CELL ADHESION	A	1.2	1.2	1	18	DSVLFYAITTLHNLLLHQ	18296
1I84	ST	CONTRACTILE PROTEIN	T	1.2	1.2	1	11	YSQCGDVMRAL	18297
1I94	EH	RIBOSOME	E	1.2	1.2	1	14	PINIAYATMEALRQ	18298
1IAK	AB	HISTOCOMPATIBILITY ANTIGEN I-AK	B	1.2	1.2	1	14	ELGRPDAEYWNKQY	18299
1IBL	GK	RIBOSOME	K	1.2	1.2	1	18	PYAAQLAALDAAKKAMAY	18300
1IBL	LQ	RIBOSOME	L	1.2	1.2	1	8	INQLVRKG	18301

1IBR	AB	CELL CYCLE, TRANSLATION	A	1.2	1.2	1	14	FEKPFLWLARKLIG	18302
1IBR	CD	CELL CYCLE, TRANSLATION	D	1.2	1.2	1	18	EHMKESTLEAIGYICQDI	18303
1IBT	CD	LYASE	C	1.2	1.2	1	13	VLDGIVSYDRAET	18304
1ICF	CD	HYDROLASE	C	1.2	1.2	1	12	MDYAFQYVQDNG	18305
1II8	AB	REPLICATION	A	1.2	1.2	1	13	KSSLLDAILVGLY	18306
1II8	AB	REPLICATION	B	1.2	1.2	1	21	GGERIALGLAFRLAMSLYLAG	18307
1IQ5	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.2	1.2	1	12	EAELQDMINEVD	18308
1IR2	AI	LYASE	A	1.2	1.2	1	10	PELAAACEVW	18309
1IR2	T2	LYASE	T	1.2	1.2	1	21	NAPGAAANRVALEACTQARNE	18310
1IRU	AI	HYDROLASE	I	1.2	1.2	1	15	VVTANRMLKQMLFRY	18311
1IRU	FM	HYDROLASE	F	1.2	1.2	1	22	TADARLLCNFMRQECLDSRFVF	18312
1IRU	FN	HYDROLASE	N	1.2	1.2	1	18	PRAIHSWLTRAMYSRRSK	18313
1IRU	J1	HYDROLASE	J	1.2	1.2	1	9	AEQMYGMCE	18314
1IRU	OU	HYDROLASE	O	1.2	1.2	1	23	TADSRSQVQRARYEAANWKYKYG	18315
1IRU	T1	HYDROLASE	T	1.2	1.2	1	22	TADARLLCNFMRQECLDSRFVF	18316
1IW7	DF	TRANSFERASE	D	1.2	1.2	1	8	VKAARRML	18317
1IW7	LN	TRANSFERASE	N	1.2	1.2	1	11	PDEALLAVAHG	18318
1IWA	CH	LYASE	C	1.2	1.2	1	9	VILERERLD	18319
1IWA	EH	LYASE	E	1.2	1.2	1	15	GKNYGRVVYEALKGG	18320
1IWA	KL	LYASE	K	1.2	1.2	1	9	VILERERLD	18321
1IYJ	AB	GENE REGULATION/ANTITUMOR PROTEIN	B	1.2	1.2	1	22	SVWVSNHYRWIVWKLAAMEFAF	18322
1IZN	CD	PROTEIN BINDING	C	1.2	1.2	1	10	ALRAYVKDHY	18323
1J8H	BC	IMMUNE SYSTEM	B	1.2	1.2	1	9	YCRHNYGVG	18324
1J8H	DE	IMMUNE SYSTEM	E	1.2	1.2	1	8	EAEISHTQ	18325
1J9C	LH	BLOOD CLOTTING	H	1.2	1.2	1	10	RTFSERTLAF	18326
1JB0	AD	PHOTOSYNTHESIS	A	1.2	1.2	1	7	VLDRVLR	18327
1JB0	AD	PHOTOSYNTHESIS	D	1.2	1.2	1	15	KEQCLALAAQQLRPR	18328
1JD2	BJ	HYDROLASE	J	1.2	1.2	1	22	AGDTVQFAEYIQANIQLYSIRE	18329
1JD2	CD	HYDROLASE	D	1.2	1.2	1	22	TADARSMIEHARTAAVTHNLYY	18330
1JD2	DK	HYDROLASE	D	1.2	1.2	1	22	TADARSMIEHARTAAVTHNLYY	18331
1JD2	HT	HYDROLASE	T	1.2	1.2	1	19	VQVAEEAIVNAMRVLYYRD	18332
1JD2	LM	HYDROLASE	L	1.2	1.2	1	21	AADGDALVKRFKNSVKWYHFD	18333
1JD2	MU	HYDROLASE	U	1.2	1.2	1	6	PDEYEQ	18334
1JD2	OL	HYDROLASE	L	1.2	1.2	1	18	VEEVIKLVRDSFTSATER	18335
1JD2	OL	HYDROLASE	O	1.2	1.2	1	18	KEEAIKLASDAIQAGIWN	18336
1JD2	QR	HYDROLASE	Q	1.2	1.2	1	22	AGDTVQFAEYIQANIQLYSIRE	18337
1JD2	QR	HYDROLASE	R	1.2	1.2	1	15	VAAASKILSNLVYQY	18338
1JD2	ST	HYDROLASE	S	1.2	1.2	1	21	AADGDALVKRFKNSVKWYHFD	18339

1JD2	XR	HYDROLASE	R	1.2	1.2	1	15	VAAASKILSNLVYQY	18340
1JD2	YS	HYDROLASE	Y	1.2	1.2	1	22	TADARSMIEHARTAAVTHNLYY	18341
1JK9	CD	OXIDOREDUCTASE	C	1.2	1.2	1	5	CVSAG	18342
1JMT	AB	RNA BINDING PROTEIN	A	1.2	1.2	1	31	GLRSAVSDVEMQEHYDEFFEEVFTEMEEKYG	18343
1JMU	BH	VIRAL PROTEIN	H	1.2	1.2	1	19	LDTKLDQYWTALNLMIDSS	18344
1JMU	EF	VIRAL PROTEIN	F	1.2	1.2	1	17	EHAIANFTKAEMALEFN	18345
1JMX	AG	OXIDOREDUCTASE	A	1.2	1.2	1	15	AKEWEHLVNFHLGQW	18346
1JOW	AB	CELL CYCLE/TRANSFERASE	A	1.2	1.2	1	19	KKTLQKIGAACVLIGSKIR	18347
1JPW	AD	CELL ADHESION	A	1.2	1.2	1	16	QRLVQNCLWTLRNLSD	18348
1JPW	CF	CELL ADHESION	C	1.2	1.2	1	15	INVVTCAAGILSNLT	18349
1JR3	BE	TRANSFERASE	B	1.2	1.2	1	10	LRDALSLTDQ	18350
1JRO	GH	OXIDOREDUCTASE	G	1.2	1.2	1	5	YDDLL	18351
1JY7	AB	OXYGEN STORAGE/TRANSPORT	A	1.2	1.2	1	16	PVNFKLLSHCLLVTLA	18352
1JY7	PQ	OXYGEN STORAGE/TRANSPORT	Q	1.2	1.2	1	14	EVGGEALGRLLVVY	18353
1JY7	RS	OXYGEN STORAGE/TRANSPORT	S	1.2	1.2	1	14	EVGGEALGRLLVVY	18354
1JY7	UX	OXYGEN STORAGE/TRANSPORT	U	1.2	1.2	1	16	PVNFKLLSHCLLVTLA	18355
1JY7	WX	OXYGEN STORAGE/TRANSPORT	W	1.2	1.2	1	19	PAVHASLDKFLASVSTVLT	18356
1K3M	AB	HORMONE/GROWTH FACTOR	A	1.2	1.2	1	6	LYQLEN	18357
1K3Z	AD	TRANSCRIPTION	D	1.2	1.2	1	8	EPFLDFLL	18358
1K4C	AB	MEMBRANE PROTEIN	B	1.2	1.2	1	6	SEQLTS	18359
1K5D	JC	SIGNALING PROTEIN/SIGNALING ACTIVATOR	C	1.2	1.2	1	14	DVVDEIREVFSTRG	18360
1K6L	MH	PHOTOSYNTHESIS	M	1.2	1.2	1	8	WYVWGQNH	18361
1KEN	AD	VIRAL PROTEIN/IMMUNE SYSTEM	D	1.2	1.2	1	7	GKLNRVI	18362
1KEN	ED	VIRAL PROTEIN/IMMUNE SYSTEM	D	1.2	1.2	1	21	IQDLEKYVEDTKIDLWSYNAE	18363
1KF6	CD	OXIDOREDUCTASE	C	1.2	1.2	1	23	PEPIIKSLWAVTVVATIVILFVA	18364
1KF6	MN	OXIDOREDUCTASE	M	1.2	1.2	1	11	CPTEMTQLELW	18365
1KF6	NO	OXIDOREDUCTASE	N	1.2	1.2	1	7	PAQMAKY	18366
1KFY	ND	OXIDOREDUCTASE	D	1.2	1.2	1	21	GKWVFYGLAAILTVVTLIGVV	18367
1KKQ	BF	TRANSCRIPTION	F	1.2	1.2	1	8	AIIRKALM	18368
1KQF	AB	OXIDOREDUCTASE	A	1.2	1.2	1	5	PKGAG	18369
1KTD	CD	IMMUNE SYSTEM	C	1.2	1.2	1	5	EEFAK	18370
1KYO	MG	OXIDOREDUCTASE/ELECTRON TRANSPORT	M	1.2	1.2	1	21	PHELTESVLPAARYDYAVAEQ	18371
1KYO	PU	OXIDOREDUCTASE/ELECTRON TRANSPORT	P	1.2	1.2	1	8	PHEIQEAN	18372
1L0O	BC	PROTEIN BINDING	B	1.2	1.2	1	23	MDELTEIKTVVSEAVTNAIIHGY	18373
1L0X	CD	IMMUNE SYSTEM	D	1.2	1.2	1	5	QSKYL	18374
1L1O	DF	DNA BINDING PROTEIN	F	1.2	1.2	1	17	YREYGRRLVMSIRRSAL	18375
1L2W	DJ	CHAPERONE	D	1.2	1.2	1	16	YTQLEMLVQGAERLQT	18376

1L8C	AB	GENE REGULATION	A	1.2	1.2	1	14	CRTMKNVLNHMTHC	18377
1L9J	LM	PHOTOSYNTHESIS	L	1.2	1.2	1	18	TLGIHRLGLLLSLSAVFF	18378
1L9J	LM	PHOTOSYNTHESIS	M	1.2	1.2	1	14	MEGIHRWAIWMAVL	18379
1L9J	RS	PHOTOSYNTHESIS	S	1.2	1.2	1	17	HTAWAFLSAIWLWMVLG	18380
1L9J	ST	PHOTOSYNTHESIS	S	1.2	1.2	1	7	ELEQIAD	18381
1LB1	EF	SIGNALING PROTEIN	E	1.2	1.2	1	25	AEDLQEALSSILGILKAVNDSMHLI	18382
1LGH	AB	LIGHT HARVESTING COMPLEX	A	1.2	1.2	1	12	WIALGAAKSAAK	18383
1LGH	DE	LIGHT HARVESTING COMPLEX	D	1.2	1.2	1	12	WIALGAAKSAAK	18384
1LGH	GH	LIGHT HARVESTING COMPLEX	G	1.2	1.2	1	12	WIALGAAKSAAK	18385
1LGH	JK	LIGHT HARVESTING COMPLEX	J	1.2	1.2	1	12	WIALGAAKSAAK	18386
1LK3	AL	IMMUNE SYSTEM	A	1.2	1.2	1	10	EKGIYKAMSE	18387
1LK3	BL	IMMUNE SYSTEM	L	1.2	1.2	1	5	TEQLA	18388
1LKY	AB	TRANSCRIPTION	B	1.2	1.2	1	8	KEDFRYRS	18389
1LNU	EF	SUGAR BINDING PROTEIN	F	1.2	1.2	1	11	CRHNYEGPETH	18390
1LQ8	AB	BLOOD CLOTTING	A	1.2	1.2	1	11	EKTLRKWLKMF	18391
1LQ8	EH	BLOOD CLOTTING	E	1.2	1.2	1	11	DTFVSAMKTLY	18392
1LQ8	GH	BLOOD CLOTTING	G	1.2	1.2	1	11	EKTLRKWLKMF	18393
1LUJ	AB	STRUCTURAL PROTEIN	A	1.2	1.2	1	10	QESKLIILAS	18394
1LVC	BE	LYASE	B	1.2	1.2	1	9	GVTNLLIKY	18395
1LVC	BE	LYASE	B	1.2	1.2	1	5	QEKKR	18396
1LWU	AB	BLOOD CLOTTING	A	1.2	1.2	1	12	KNLQLEKAASYI	18397
1LWU	GI	BLOOD CLOTTING	I	1.2	1.2	1	31	AQIQELSEMWRVNQQFVTRLQQQLVDIRQTC	18398
1LYW	GF	ASPARTIC PROTEASE	F	1.2	1.2	1	11	VDEVRELQKAI	18399
1M1E	AB	STRUCTURAL PROTEIN	A	1.2	1.2	1	15	EDITEPAICALRHLT	18400
1M1J	AB	BLOOD CLOTTING	B	1.2	1.2	1	13	GCELQTTLLKQEK	18401
1M1J	EF	BLOOD CLOTTING	E	1.2	1.2	1	12	FSDTSTTMYQYV	18402
1M1J	EF	BLOOD CLOTTING	F	1.2	1.2	1	7	WVQYKEG	18403
1M2Z	DE	HORMONE/HORMONE ACTIVATOR	D	1.2	1.2	1	26	TWRIMTTLNMLGGRQVIAAVKWAKAI	18404
1M45	AB	CELL CYCLE PROTEIN	A	1.2	1.2	1	6	IFTLFD	18405
1M56	AB	OXIDOREDUCTASE	A	1.2	1.2	1	29	ATWNFVSSLGAFLSFASFLFFLGVIFYTL	18406
1M56	IJ	OXIDOREDUCTASE	J	1.2	1.2	1	33	TQQEKTFAGFVRMVTWAAVVIVAALIFLALANA	18407
1M63	AC	HYDROLASE/ISOMERASE	A	1.2	1.2	1	15	VFTWSLPFVGEKVTE	18408
1M93	AB	VIRAL PROTEIN	B	1.2	1.2	1	8	DSFLRKIG	18409
1MDU	DE	STRUCTURAL PROTEIN	E	1.2	1.2	1	9	QAVLSLYAS	18410
1MHY	BG	OXIDOREDUCTASE	B	1.2	1.2	1	30	WNEILWAGHAVYDATFGQFARREFFQRLAT	18411
1MJG	AM	OXIDOREDUCTASE	A	1.2	1.2	1	36	AWTIVARNVGLMILTGAAAHCEHGNHIAHALVEMAE	18412
1MJG	BM	OXIDOREDUCTASE	M	1.2	1.2	1	30	VALFREVYHGAITATSYAEILLNQAIRTYG	18413
1MJG	BN	OXIDOREDUCTASE	B	1.2	1.2	1	36	AWTIVARNVGLMILTGAAAHCEHGNHIAHALVEMAE	18414
1MK9	EF	STRUCTURAL PROTEIN	F	1.2	1.2	1	15	EIEAKVRYVKLARSL	18415
1MTY	BG	MONOOXYGENASE	G	1.2	1.2	1	6	EVDFRH	18416

1MU2	AB	TRANSFERASE	B	1.2	1.2	1	20	GIRLLAQVVQKIGKEALVIW	18417
1MVW	JK	CONTRACTILE PROTEIN	K	1.2	1.2	1	11	KDDLRETFAAM	18418
1MXE	AE	METAL BINDING PROTEIN	A	1.2	1.2	1	11	AAELRHVMTNL	18419
1MXE	BF	METAL BINDING PROTEIN	B	1.2	1.2	1	11	AAELRHVMTNL	18420
1MZN	CD	TRANSCRIPTION	C	1.2	1.2	1	11	LDDQVILLRAG	18421
1MZN	EF	TRANSCRIPTION	E	1.2	1.2	1	11	LDDQVILLRAG	18422
1N34	EH	RIBOSOME	E	1.2	1.2	1	9	KADVERLRK	18423
1N4M	BD	CELL CYCLE	B	1.2	1.2	1	13	AFDFYKVIESFIK	18424
1N4Q	KD	TRANSFERASE	K	1.2	1.2	1	13	KEYWRYIGRSLQS	18425
1N5W	AB	OXIDOREDUCTASE	B	1.2	1.2	1	7	VEDIRFT	18426
1N73	BC	BLOOD CLOTTING	B	1.2	1.2	1	14	QKEIENRYKEVKIR	18427
1N86	DF	BLOOD CLOTTING	D	1.2	1.2	1	9	LLQKNVRAQ	18428
1N8Z	AB	TRANSFERASE	A	1.2	1.2	1	5	DEQLK	18429
1NBF	BC	HYDROLASE	B	1.2	1.2	1	9	IFESFVDYV	18430
1NBW	CD	HYDROLASE	D	1.2	1.2	1	16	DDQLRTLGANAGQLVK	18431
1NDO	EF	NON-HEME IRON DIOXYGENASE	E	1.2	1.2	1	8	ASSLRSGE	18432
1NEK	BC	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.2	1.2	1	16	PTRAIGHIKSMLLQRN	18433
1NI4	AD	OXIDOREDUCTASE	D	1.2	1.2	1	13	VKDIIFAIKKTLN	18434
1NIK	AB	TRANSCRIPTION	A	1.2	1.2	1	9	FINIAQMSA	18435
1NIW	CD	SIGNALING PROTEIN/OXIDOREDUCTASE	C	1.2	1.2	1	6	YEEFVQ	18436
1NSN	LH	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)	L	1.2	1.2	1	6	SEQLTS	18437
1NT2	AB	RNA BINDING PROTEIN	B	1.2	1.2	1	6	MERLVR	18438
1NTK	AG	OXIDOREDUCTASE	A	1.2	1.2	1	7	YNRIRSG	18439
1NVP	BD	TRANSCRIPTION/DNA	D	1.2	1.2	1	23	PQLALQVLLQFDKAINAALAQRV	18440
1O18	DF	CONTRACTILE PROTEIN	F	1.2	1.2	1	9	EDFVEGLRV	18441
1O18	JK	CONTRACTILE PROTEIN	K	1.2	1.2	1	12	FTVFLTMFGEKL	18442
1O96	QZ	ELECTRON TRANSFER	Q	1.2	1.2	1	17	EWDDFSLEEAMKIKESS	18443
1OAO	AD	OXIDOREDUCTASE	A	1.2	1.2	1	36	AWTIVARNVGLMILTGAAAHCEHGNHIAHALVEMAE	18444
1OCC	AL	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.2	1.2	1	36	QIYNVVVTAHAFVMIFFMVMPIMIGGFGNWLVPLMI	18445
1OCC	CG	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	C	1.2	1.2	1	23	PWPLTGALSALLMTSGLTMWFHF	18446
1OCC	DE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	E	1.2	1.2	1	14	PKIIDAALRACRRL	18447
1OCC	DI	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	I	1.2	1.2	1	11	SMKDFEEMRKA	18448

1OCC	DK	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	1.2	1.2	1	7	PIQGFSA	18449
1OCC	EF	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	E	1.2	1.2	1	14	AWELRKGMNTLVGY	18450
1OCC	NQ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.2	1.2	1	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	18451
1OCC	OU	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	U	1.2	1.2	1	11	EWYRRVYKSLC	18452
1OCC	PT	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	P	1.2	1.2	1	23	PWPLTGALSALLMTSGLTMWFHF	18453
1OCC	QR	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	R	1.2	1.2	1	14	PKIIDAALRACRRL	18454
1OCC	QV	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	V	1.2	1.2	1	11	SMKDFEEMRKA	18455
1OCC	RS	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	R	1.2	1.2	1	14	AWELRKGMNTLVGY	18456
1OEY	CL	IMMUNE SYSTEM	L	1.2	1.2	1	6	DEDVAL	18457
1ONV	AB	TRANSCRIPTION	A	1.2	1.2	1	16	SEQTVNVLAQILKRLN	18458
1OQP	AB	PROTEIN BINDING	A	1.2	1.2	1	12	IKDLRRVAKELG	18459
1OR0	AB	HYDROLASE	B	1.2	1.2	1	7	QIERVSR	18460
1OR7	AC	TRANSCRIPTION	A	1.2	1.2	1	14	SEELRQIVFRTIES	18461
1ORQ	AB	MEMBRANE PROTEIN	A	1.2	1.2	1	6	SEQLTS	18462
1OSV	AC	DNA BINDING PROTEIN	A	1.2	1.2	1	7	PLLCEIW	18463
1OSV	BD	DNA BINDING PROTEIN	B	1.2	1.2	1	8	PLLCEIWD	18464
1OUU	AB	OXYGEN TRANSPORT	B	1.2	1.2	1	19	DNFRVLADVLTIVIAAKFG	18465
1OW7	BE	TRANSFERASE	B	1.2	1.2	1	24	PEEYVPMVKEVGLALRTLLATVDE	18466
1OXK	AD	SIGNALING PROTEIN	A	1.2	1.2	1	5	KSIIN	18467
1OXK	CF	SIGNALING PROTEIN	F	1.2	1.2	1	12	GLLSTKMIRRDL	18468
1OXK	EB	SIGNALING PROTEIN	B	1.2	1.2	1	12	GLLSTKMIRRDL	18469
1OXK	IJ	SIGNALING PROTEIN	I	1.2	1.2	1	18	LTELDNLGHFLKGSSAAL	18470
1OXK	KL	SIGNALING PROTEIN	K	1.2	1.2	1	26	FSKGLIIQFIDQAQTTFAQMQRQLDG	18471
1PK1	AB	TRANSCRIPTION REPRESSION	A	1.2	1.2	1	7	GQALLLL	18472
1PK1	CD	TRANSCRIPTION REPRESSION	C	1.2	1.2	1	7	GQALLLL	18473
1PMX	AB	HORMONE/GROWTH FACTOR	B	1.2	1.2	1	9	VAALRRCMY	18474
1PNS	DE	RIBOSOME	E	1.2	1.2	1	11	AVPRAILELAG	18475
1PNS	EH	RIBOSOME	E	1.2	1.2	1	8	KADVERLR	18476
1PRC	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.2	1.2	1	15	ILSHLDWVNNFGYQY	18477
1PSB	BD	METAL BINDING PROTEIN	B	1.2	1.2	1	12	QEVVDKVMETLD	18478
1PTO	AD	TOXIN	D	1.2	1.2	1	12	PMEVMLRAVFMQ	18479
1PVH	AB	SIGNALING PROTEIN/CYTOKINE	B	1.2	1.2	1	29	LSLHSKLNATADILRGLLSNVLCRLCSKY	18480

1Q16	AB	OXIDOREDUCTASE	B	1.2	1.2	1	6	IERAAS	18481
1Q5R	AH	HYDROLASE	H	1.2	1.2	1	7	FTDYLRG	18482
1Q5R	DL	HYDROLASE	D	1.2	1.2	1	19	GRSLANAYAQTLGTIFTEQ	18483
1Q5R	FN	HYDROLASE	F	1.2	1.2	1	19	GRSLANAYAQTLGTIFTEQ	18484
1Q90	BD	PHOTOSYNTHESIS	B	1.2	1.2	1	25	ELTWVTGVIMAVCTVSFGVTGYSLP	18485
1QGW	AC	PHOTOSYNTHESIS	C	1.2	1.2	1	16	ASCIVSDAVSGMICEN	18486
1QLE	AC	OXIDOREDUCTASE/IMMUNE SYSTEM	C	1.2	1.2	1	8	WPFFGAIG	18487
1QO0	AD	BINDING PROTEIN	A	1.2	1.2	1	14	PDRYRLCAEDFIRN	18488
1QO0	BE	BINDING PROTEIN	E	1.2	1.2	1	11	PAVLSQIIELE	18489
1QPW	AD	OXYGEN TRANSPORT	A	1.2	1.2	1	19	PVNFKLLSHCLLVTLAAHH	18490
1QRJ	AB	VIRAL PROTEIN	B	1.2	1.2	1	14	MKDLQAIKQEVSQA	18491
1QVF	R1	RIBOSOME	1	1.2	1.2	1	14	KATKKRLAKLDNQN	18492
1QVI	AY	CONTRACTILE PROTEIN	Y	1.2	1.2	1	15	QKQIQEMKEAFSMID	18493
1R4M	AB	CELL CYCLE	B	1.2	1.2	1	9	YRLTQGVVK	18494
1R4M	CD	CELL CYCLE	C	1.2	1.2	1	5	DRQLR	18495
1R4M	EB	CELL CYCLE	E	1.2	1.2	1	22	NYQVEEDIGKLKSCLTGFLQEY	18496
1R4M	EF	CELL CYCLE	E	1.2	1.2	1	5	DRQLR	18497
1R4M	GH	CELL CYCLE	G	1.2	1.2	1	5	DRQLR	18498
1R4M	GL	CELL CYCLE	G	1.2	1.2	1	13	YKEKEDFRDLIRQ	18499
1R4Q	AD	TOXIN	A	1.2	1.2	1	10	WGRLSSVLPD	18500
1R4Q	AD	TOXIN	D	1.2	1.2	1	13	WNLQSLLLSAQIT	18501
1R4Q	AE	TOXIN	E	1.2	1.2	1	13	WNLQSLLLSAQIT	18502
1RCO	BC	LYASE	C	1.2	1.2	1	14	TDQLARQVDYLLNN	18503
1RCO	EF	LYASE	F	1.2	1.2	1	14	TDQLARQVDYLLNN	18504
1RCO	HI	LYASE	I	1.2	1.2	1	14	TDQLARQVDYLLNN	18505
1RCO	LS	LYASE	S	1.2	1.2	1	14	TDQLARQVDYLLNN	18506
1RCO	VW	LYASE	W	1.2	1.2	1	14	TDQLARQVDYLLNN	18507
1RF8	AB	BIOSYNTHETIC PROTEIN, TRANSLATION	B	1.2	1.2	1	10	VSHILNVLKD	18508
1RI8	AB	IMMUNE SYSTEM/HYDROLASE	B	1.2	1.2	1	12	LGNWVCAAKFES	18509
1RM6	AB	OXIDOREDUCTASE	A	1.2	1.2	1	8	REETFIAH	18510
1RM6	BC	OXIDOREDUCTASE	C	1.2	1.2	1	15	TPGMIMASEALLRKN	18511
1RP3	EF	TRANSCRIPTION	E	1.2	1.2	1	8	AKEVAKIL	18512
1RP3	EF	TRANSCRIPTION	E	1.2	1.2	1	15	PYSNQIEREELILKY	18513
1RSO	AD	NEUROPEPTIDE/MEMBRANE PROTEIN	D	1.2	1.2	1	17	QHLHTLLDLYDKINTKS	18514
1RTD	CD	TRANSFERASE/DNA	C	1.2	1.2	1	20	DVKQLTEAVQKITTESIVIW	18515
1RTD	CD	TRANSFERASE/DNA	D	1.2	1.2	1	18	VNDIQKLVGKLNWASQIY	18516
1RU7	ED	VIRAL PROTEIN	E	1.2	1.2	1	10	YEELREQLSS	18517
1RU7	KJ	VIRAL PROTEIN	K	1.2	1.2	1	10	YEELREQLSS	18518
1RUZ	JI	VIRAL PROTEIN	J	1.2	1.2	1	10	YEELREQLSS	18519

1RYP	AB	MULTICATALYTIC PROTEINASE	A	1.2	1.2	1	18	CDVLAKRMANLSQIYTQR	18520
1RYP	EF	MULTICATALYTIC PROTEINASE	F	1.2	1.2	1	22	APDARVLSNYLRQQCNYSSLVF	18521
1RYP	EM	MULTICATALYTIC PROTEINASE	M	1.2	1.2	1	22	AADGDALVKRFKNSVKWYHFDH	18522
1RYP	JK	MULTICATALYTIC PROTEINASE	K	1.2	1.2	1	17	PQAVSSFVRQELAKSIR	18523
1RYP	OU	MULTICATALYTIC PROTEINASE	U	1.2	1.2	1	15	IPAFADRLGQYVQAH	18524
1RYP	TU	MULTICATALYTIC PROTEINASE	T	1.2	1.2	1	6	LDTFIK	18525
1RYP	WM	MULTICATALYTIC PROTEINASE	W	1.2	1.2	1	18	KEEAIKLASDAIQAGIWN	18526
1RYP	WN	MULTICATALYTIC PROTEINASE	N	1.2	1.2	1	18	VQVAEEAIVNAMRVLYYR	18527
1RZG	AB	IMMUNE SYSTEM	B	1.2	1.2	1	6	DEQLKS	18528
1S1C	BX	SIGNALING PROTEIN	B	1.2	1.2	1	9	DRLRPLSYP	18529
1S5L	AD	PHOTOSYNTHESIS	D	1.2	1.2	1	9	ISQEIRAAE	18530
1S5L	BO	PHOTOSYNTHESIS	B	1.2	1.2	1	10	PPTVKSYARK	18531
1S5L	FJ	PHOTOSYNTHESIS	J	1.2	1.2	1	21	IVATVAGMGVIVIVGLFFYGA	18532
1SA0	DE	CELL CYCLE	E	1.2	1.2	1	19	ESNKENREAHLAAMLERLQ	18533
1SB3	AC	OXIDOREDUCTASE	C	1.2	1.2	1	9	KLQAAFHEK	18534
1SBS	HL	MONOCLONAL ANTIBODY	L	1.2	1.2	1	6	SEQLTS	18535
1SCT	EH	OXYGEN TRANSPORT	E	1.2	1.2	1	16	IEATGLMLMSNLFTLR	18536
1SHZ	AC	SIGNALING PROTEIN	C	1.2	1.2	1	15	PAHLMALLQHVALQF	18537
1SQB	AB	OXIDOREDUCTASE	B	1.2	1.2	1	16	SEGFLDEVGSQALAAG	18538
1SQB	EK	OXIDOREDUCTASE	E	1.2	1.2	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	18539
1SQX	AB	OXIDOREDUCTASE	B	1.2	1.2	1	11	SFKITRGIEAV	18540
1SQX	AC	OXIDOREDUCTASE	A	1.2	1.2	1	18	IDDMMFVLQGQWMRLCTS	18541
1SQX	CF	OXIDOREDUCTASE	C	1.2	1.2	1	33	HPYITIGQLASVLYFLLILVLMPTAGTIENKLL	18542
1SQX	DH	OXIDOREDUCTASE	H	1.2	1.2	1	20	EKCVKARERLELCDERVSSR	18543
1SQX	EK	OXIDOREDUCTASE	E	1.2	1.2	1	35	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMS	18544
1SQX	GF	OXIDOREDUCTASE	F	1.2	1.2	1	20	ENLYDDRVFRIKRALDLSMR	18545
1SV0	BD	TRANSCRIPTION	B	1.2	1.2	1	17	GDVLHNVLQMLIIESHS	18546
1SXJ	BC	REPLICATION	B	1.2	1.2	1	20	ESVRLEMIKEIGLTHMRILE	18547
1T03	AB	TRANSFERASE/ANTIBODY/DNA	A	1.2	1.2	1	20	DVKQLTEAVQKITTESIVIW	18548
1T03	AB	TRANSFERASE/ANTIBODY/DNA	B	1.2	1.2	1	7	KETWETW	18549
1T3Q	DF	OXIDOREDUCTASE	D	1.2	1.2	1	10	LADALREVVG	18550
1T3Q	EF	OXIDOREDUCTASE	E	1.2	1.2	1	9	RAIAEDAAQ	18551
1T66	CD	IMMUNE SYSTEM	C	1.2	1.2	1	6	SEQLTS	18552
1T6V	LN	HYDROLASE/IMMUNE SYSTEM	L	1.2	1.2	1	8	VAWRNRCK	18553
1T6V	MN	HYDROLASE/IMMUNE SYSTEM	M	1.2	1.2	1	12	TASVNCAKKIVS	18554
1T9G	DS	OXIDOREDUCTASE, ELECTRON TRANSPORT	D	1.2	1.2	1	11	VPLIRRAWELG	18555
1T9G	DS	OXIDOREDUCTASE, ELECTRON TRANSPORT	S	1.2	1.2	1	10	LPNIMKAKKK	18556

1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	1.2	1.2	1	15	VETARCTAGTLHNLS	18557
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	D	1.2	1.2	1	5	VELRI	18558
1TI2	CD	OXIDOREDUCTASE	C	1.2	1.2	1	6	HTARLV	18559
1TME	34	VIRUS	4	1.2	1.2	1	5	NQYQN	18560
1TN6	AB	TRANSFERASE	B	1.2	1.2	1	20	VTSIEQAKVEEKIQEVFSSY	18561
1TOC	DT	COMPLEX (HYDROLASE/INHIBITOR)	D	1.2	1.2	1	8	KQTAAKLL	18562
1TU3	BH	PROTEIN TRANSPORT	H	1.2	1.2	1	31	LQTELDVSEQVQRDFVKLSQTLQVQLERIRQ	18563
1TU3	DH	PROTEIN TRANSPORT	D	1.2	1.2	1	5	ERYHS	18564
1TZN	Aa	TOXIN RECEPTOR/TOXIN	a	1.2	1.2	1	14	LVPSYAEKEAKISR	18565
1TZN	Cc	TOXIN RECEPTOR/TOXIN	c	1.2	1.2	1	14	LVPSYAEKEAKISR	18566
1TZN	Ee	TOXIN RECEPTOR/TOXIN	e	1.2	1.2	1	14	LVPSYAEKEAKISR	18567
1TZN	Ff	TOXIN RECEPTOR/TOXIN	f	1.2	1.2	1	14	LVPSYAEKEAKISR	18568
1TZN	Gg	TOXIN RECEPTOR/TOXIN	g	1.2	1.2	1	14	LVPSYAEKEAKISR	18569
1TZN	Kk	TOXIN RECEPTOR/TOXIN	k	1.2	1.2	1	14	LVPSYAEKEAKISR	18570
1TZN	Ll	TOXIN RECEPTOR/TOXIN	l	1.2	1.2	1	14	LVPSYAEKEAKISR	18571
1U5T	AC	TRANSPORT PROTEIN	C	1.2	1.2	1	20	SLTRRQQISTWIDIISQYCK	18572
1U6G	AC	LIGASE	A	1.2	1.2	1	33	KTEQKQEQETTHKNIEEDRKLLIQAAIVRIMKM	18573
1U6G	AC	LIGASE	C	1.2	1.2	1	18	EQLRDISSIGLKTVIGEL	18574
1UGH	EI	GLYCOSYLASE	E	1.2	1.2	1	12	PSLENIYKELST	18575
1UGH	EI	GLYCOSYLASE	I	1.2	1.2	1	9	PEEVEEVIG	18576
1UKL	BF	PROTEIN TRANSPORT/DNA BINDING PROTEIN	F	1.2	1.2	1	6	KSGVLR	18577
1UWE	LH	ANTIBODY	L	1.2	1.2	1	6	AEQLAS	18578
1UZD	EI	LYASE	E	1.2	1.2	1	5	LDRYK	18579
1UZH	BC	LYASE	B	1.2	1.2	1	12	GGDVIRSACKWS	18580
1UZH	KI	LYASE	K	1.2	1.2	1	20	WRDRFLFVAEAIYKAQAETG	18581
1UZH	RM	LYASE	R	1.2	1.2	1	12	GGDVIRSACKWS	18582
1UZH	VW	LYASE	V	1.2	1.2	1	12	GGDVIRSACKWS	18583
1V4U	AB	OXYGEN STORAGE/TRANSPORT	B	1.2	1.2	1	19	VETQCAFQKFLAVVVFALG	18584
1V4U	CD	OXYGEN STORAGE/TRANSPORT	D	1.2	1.2	1	6	PDAIKG	18585
1V54	AF	OXIDOREDUCTASE	A	1.2	1.2	1	16	YMGMVWAMMSIGFLGF	18586
1V54	GH	OXIDOREDUCTASE	H	1.2	1.2	1	14	ISWVSTWDDRRAEG	18587
1V54	OU	OXIDOREDUCTASE	U	1.2	1.2	1	11	EWYRRVYKSLC	18588
1V54	WY	OXIDOREDUCTASE	Y	1.2	1.2	1	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	18589
1V54	YZ	OXIDOREDUCTASE	Z	1.2	1.2	1	6	LDNYKK	18590
1V75	AB	OXYGEN STORAGE/TRANSPORT	B	1.2	1.2	1	19	PENFKLLGNILIIVLATHF	18591
1VCB	GH	TRANSCRIPTION	G	1.2	1.2	1	12	VFELKRIVEGIL	18592
1VF5	AB	PHOTOSYNTHESIS	A	1.2	1.2	1	10	AYASVQYIMN	18593

1VF5	NO	PHOTOSYNTHESIS	N	1.2	1.2	1	25	ELTWISGVILAVITVSFGVTGYSLP	18594
1VF5	OP	PHOTOSYNTHESIS	P	1.2	1.2	1	25	PNRVKWMIAFICLVMLAQLMLILKK	18595
1VF5	PU	PHOTOSYNTHESIS	U	1.2	1.2	1	24	VLGWVALLVVFTWSIAMVVWGRNG	18596
1VF5	TU	PHOTOSYNTHESIS	T	1.2	1.2	1	7	VLGLVFA	18597
1VF5	TU	PHOTOSYNTHESIS	U	1.2	1.2	1	24	VLGWVALLVVFTWSIAMVVWGRNG	18598
1VQN	FM	RIBOSOME	F	1.2	1.2	1	11	TNETTKSIERG	18599
1VQN	NQ	RIBOSOME	N	1.2	1.2	1	9	YHQRLRLLK	18600
1VQN	SV	RIBOSOME	V	1.2	1.2	1	24	PAEREAELDDLKTELLNARAVQAA	18601
1VQP	AZ	RIBOSOME	Z	1.2	1.2	1	8	PGGKTVRR	18602
1VRQ	AB	OXIDOREDUCTASE	A	1.2	1.2	1	10	VADVLRATGA	18603
1VYW	AD	TRANSFERASE	D	1.2	1.2	1	15	KKQVLRMEHLVLKVL	18604
1W2W	EF	ISOMERASE	F	1.2	1.2	1	11	TLQLAVICKQF	18605
1W2W	IJ	ISOMERASE	J	1.2	1.2	1	11	TLQLAVICKQF	18606
1W5C	AD	PHOTOSYNTHESIS	A	1.2	1.2	1	7	ISGTFNF	18607
1W5C	GJ	PHOTOSYNTHESIS	J	1.2	1.2	1	7	SQEIRAA	18608
1W5C	HJ	PHOTOSYNTHESIS	H	1.2	1.2	1	6	RYQWDS	18609
1W63	BM	ENDOCYTOSIS	B	1.2	1.2	1	6	AKLHDI	18610
1W63	BM	ENDOCYTOSIS	B	1.2	1.2	1	18	KEKKKEAVKKVIASMTVG	18611
1W63	BM	ENDOCYTOSIS	B	1.2	1.2	1	17	YVVQEAIVVIKDIFRKY	18612
1W63	DN	ENDOCYTOSIS	D	1.2	1.2	1	6	AKLHDI	18613
1W63	DN	ENDOCYTOSIS	D	1.2	1.2	1	18	KEKKKEAVKKVIASMTVG	18614
1W63	FO	ENDOCYTOSIS	F	1.2	1.2	1	6	AKLHDI	18615
1W63	FO	ENDOCYTOSIS	F	1.2	1.2	1	18	KEKKKEAVKKVIASMTVG	18616
1W63	HP	ENDOCYTOSIS	H	1.2	1.2	1	6	AKLHDI	18617
1W63	HP	ENDOCYTOSIS	H	1.2	1.2	1	18	KEKKKEAVKKVIASMTVG	18618
1W63	JR	ENDOCYTOSIS	J	1.2	1.2	1	6	AKLHDI	18619
1W63	JR	ENDOCYTOSIS	J	1.2	1.2	1	18	KEKKKEAVKKVIASMTVG	18620
1W63	JR	ENDOCYTOSIS	R	1.2	1.2	1	12	FVIIYELLDELM	18621
1W63	LV	ENDOCYTOSIS	L	1.2	1.2	1	6	AKLHDI	18622
1WA8	AB	TUBERCULOSIS	B	1.2	1.2	1	32	EAYQGVQQKWDATATELNNALQNLARTISEAG	18623
1WCM	AB	TRANSCRIPTION	A	1.2	1.2	1	10	FINIAQMSAC	18624
1WDK	AC	LYASE,OXIDOREDUCTASE/TRANSFERASE	C	1.2	1.2	1	12	MGLTAEMLGKMH	18625
1WR6	AE	PROTEIN TRANSPORT/SIGNALING PROTEIN	A	1.2	1.2	1	19	ELFDQCENKRRTLFKLASE	18626
1WYU	AB	OXIDOREDUCTASE	B	1.2	1.2	1	11	ALDLAKGLLEL	18627
1WYU	EB	OXIDOREDUCTASE	B	1.2	1.2	1	25	LEGLKKAAALAVLNARYLKELLKEK	18628
1X75	AD	ISOMERASE/SIGNALING PROTEIN	D	1.2	1.2	1	14	ENDIKNAINLMFWG	18629
1X86	GH	SIGNALING PROTEIN/MEMBRANE PROTEIN	G	1.2	1.2	1	8	TQMQRLTK	18630

1XD3	AB	HYDROLASE	A	1.2	1.2	1	16	LLEDAIEVCKKFMERD	18631
1XD3	CD	HYDROLASE	C	1.2	1.2	1	15	LLEDAIEVCKKFMER	18632
1XFU	DR	LYASE/METAL BINDING PROTEIN	D	1.2	1.2	1	9	QKEWDKVVN	18633
1XFU	ES	LYASE/METAL BINDING PROTEIN	S	1.2	1.2	1	10	YEEFVQMMTA	18634
1XFU	FT	LYASE/METAL BINDING PROTEIN	F	1.2	1.2	1	13	SAEFIKNLSSIRR	18635
1XFV	BP	LYASE/METAL BINDING PROTEIN	P	1.2	1.2	1	13	SEEEIREAFRVFD	18636
1XFV	CQ	LYASE/METAL BINDING PROTEIN	C	1.2	1.2	1	7	GYLSDYY	18637
1XGP	BC	IMMUNE SYSTEM	C	1.2	1.2	1	12	TASVNCAKKIVS	18638
1XK4	BD	METAL BINDING PROTEIN	B	1.2	1.2	1	12	RDDLKKLLETES	18639
1XKP	AC	MEMBRANE PROTEIN/CHAPERON	C	1.2	1.2	1	14	VTLLRSLMQQALAW	18640
1XLS	CG	TRANSCRIPTION	G	1.2	1.2	1	25	LYAKLMGLLADLRSINNAYSYELQR	18641
1XLT	BC	OXIDOREDUCTASE	C	1.2	1.2	1	9	HMNVLLAEA	18642
1XM4	AB	HYDROLASE	A	1.2	1.2	1	16	VLENHHLAVGFKLLQE	18643
1XMQ	LQ	RIBOSOME	L	1.2	1.2	1	8	INQLVRKG	18644
1XQ5	AB	OXYGEN STORAGE/TRANSPORT	A	1.2	1.2	1	19	PEVHISYDKFFSALARALA	18645
1XXH	AE	TRANSFERASE	E	1.2	1.2	1	11	DLLLRIEHYLQ	18646
1XXI	IJ	TRANSFERASE	J	1.2	1.2	1	21	PSRLQAILGDVCHIREQLMSV	18647
1Y3A	DH	SIGNALING PROTEIN	D	1.2	1.2	1	14	RMHESMKLFDSICN	18648
1Y8H	AD	OXYGEN STORAGE/TRANSPORT	A	1.2	1.2	1	19	PVNFKLLSHCLLSTLAVHL	18649
1Y8H	CD	OXYGEN STORAGE/TRANSPORT	D	1.2	1.2	1	15	EEVGGEALGRLLVVY	18650
1YA7	EK	HYDROLASE/HYDROLASE ACTIVATOR	K	1.2	1.2	1	23	VGDAQVLVRYMKAELELYRLQRR	18651
1YA7	GQ	HYDROLASE/HYDROLASE ACTIVATOR	G	1.2	1.2	1	13	FQVEYAREAVKKG	18652
1YAG	AG	CONTRACTILE PROTEIN	A	1.2	1.2	1	5	TTFQQ	18653
1YE9	CH	OXIDOREDUCTASE	C	1.2	1.2	1	9	FPDFVHAVK	18654
1YED	AB	CATALYTIC ANTIBODY	A	1.2	1.2	1	6	SEQLTS	18655
1YEW	IJ	OXIDOREDUCTASE, MEMBRANE PROTEIN	J	1.2	1.2	1	26	YLFTAIVGAMGWGLIFYPGNWPIIAP	18656
1YHU	CH	OXYGEN STORAGE/TRANSPORT	C	1.2	1.2	1	16	PDAWASCLAGIAAAIS	18657
1YHU	FG	OXYGEN STORAGE/TRANSPORT	G	1.2	1.2	1	15	DAAAAIVQAQWEDVW	18658
1YHU	GL	OXYGEN STORAGE/TRANSPORT	G	1.2	1.2	1	16	PDAWASCLAGIAAAIS	18659
1YHU	GL	OXYGEN STORAGE/TRANSPORT	L	1.2	1.2	1	16	PDAWSRCFNRITTGMT	18660
1YHU	MO	OXYGEN STORAGE/TRANSPORT	O	1.2	1.2	1	19	AASRVSAGEEVFAALFKMV	18661
1YHU	NO	OXYGEN STORAGE/TRANSPORT	N	1.2	1.2	1	15	PLQRLKVKRQWAEAY	18662
1YHU	OT	OXYGEN STORAGE/TRANSPORT	T	1.2	1.2	1	17	PATLNEQLSHLATQHKA	18663
1YJD	LH	IMMUNE SYSTEM/SIGNALING PROTEIN	L	1.2	1.2	1	6	SEQLTS	18664
1YL3	M1	RIBOSOME	1	1.2	1.2	1	20	KRDFRRLWIQRINAGARLHG	18665
1YL4	HK	RIBOSOME	H	1.2	1.2	1	9	KADVERLRK	18666
1YL4	JL	RIBOSOME	L	1.2	1.2	1	6	VRAVAA	18667
1YNJ	CJ	TRANSFERASE	C	1.2	1.2	1	13	ESFRVLVKELQAL	18668

1YNJ	JK	TRANSFERASE	J	1.2	1.2	1	8	RTLKAIEE	18669
1YOV	CD	SIGNALING PROTEIN	C	1.2	1.2	1	34	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQSIG	18670
1YQ3	BD	OXIDOREDUCTASE	B	1.2	1.2	1	6	PSYWWN	18671
1YR5	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.2	1.2	1	12	DEEVDEMIREAD	18672
1YSL	AB	LYASE	A	1.2	1.2	1	16	GATAGLQLAKNHVALH	18673
1YSL	AB	LYASE	B	1.2	1.2	1	24	GPLSNETYIQSFAQVWDEHKKRTG	18674
1YTZ	IC	CONTRACTILE PROTEIN	C	1.2	1.2	1	12	EEDIEDLMKDSD	18675
1YTZ	TC	CONTRACTILE PROTEIN	C	1.2	1.2	1	8	FDEFLKMM	18676
1YU6	AC	HYDROLASE	A	1.2	1.2	1	10	HGTHVAGTVA	18677
1YUH	AB	IMMUNOGLOBULIN	A	1.2	1.2	1	6	SEELET	18678
1YYF	BC	CHAPERONE/HYDROLASE	C	1.2	1.2	1	7	LKRAAVE	18679
1Z3G	MI	IMMUNE SYSTEM/CELL ADHESION	M	1.2	1.2	1	6	SEQLTS	18680
1Z6O	AM	METAL BINDING PROTEIN	A	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18681
1Z6O	BN	METAL BINDING PROTEIN	B	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18682
1Z6O	CO	METAL BINDING PROTEIN	C	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18683
1Z6O	DP	METAL BINDING PROTEIN	D	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18684
1Z6O	EQ	METAL BINDING PROTEIN	E	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18685
1Z6O	FR	METAL BINDING PROTEIN	F	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18686
1Z6O	GS	METAL BINDING PROTEIN	G	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18687
1Z6O	HT	METAL BINDING PROTEIN	H	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18688
1Z6O	HX	METAL BINDING PROTEIN	X	1.2	1.2	1	13	EALGEFIFDKKLL	18689
1Z6O	IU	METAL BINDING PROTEIN	I	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18690
1Z6O	JV	METAL BINDING PROTEIN	J	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18691
1Z6O	JV	METAL BINDING PROTEIN	J	1.2	1.2	1	16	LSLALYVFDEYLQKTV	18692
1Z6O	KW	METAL BINDING PROTEIN	K	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18693
1Z6O	KW	METAL BINDING PROTEIN	K	1.2	1.2	1	16	LSLALYVFDEYLQKTV	18694
1Z6O	LX	METAL BINDING PROTEIN	L	1.2	1.2	1	35	PEIAQYLEEEFIEDHAEKIRTLAGHTSDLKKFITA	18695
1Z7Q	Hb	HYDROLASE/HYDROLASE ACTIVATOR	H	1.2	1.2	1	22	AADTQAIADIVQYHLELYTSQY	18696
1Z7Q	HN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.2	1.2	1	20	ISDMQHIERLLKDLVTENAY	18697
1Z7Q	Ia	HYDROLASE/HYDROLASE ACTIVATOR	a	1.2	1.2	1	18	VEEVIKLVRDSFTSATER	18698
1Z7Q	Ja	HYDROLASE/HYDROLASE ACTIVATOR	a	1.2	1.2	1	18	VEEVIKLVRDSFTSATER	18699
1Z7Q	KL	HYDROLASE/HYDROLASE ACTIVATOR	K	1.2	1.2	1	23	AGDTVQFAEYIQANIQLYSIRED	18700
1Z7Q	OU	HYDROLASE/HYDROLASE ACTIVATOR	U	1.2	1.2	1	15	IPAFADRLGQYVQAH	18701
1Z7Q	Sm	HYDROLASE/HYDROLASE ACTIVATOR	S	1.2	1.2	1	13	FQVEYSLEAIKLG	18702
1Z7X	ZY	HYDROLASE/HYDROLASE INHIBITOR	Z	1.2	1.2	1	10	RAKKFQRQHM	18703
1ZBB	CD	STRUCTURAL PROTEIN/DNA	C	1.2	1.2	1	10	PRHLQLAVRN	18704
1ZBD	AB	G PROTEIN	B	1.2	1.2	1	10	KICLEQREVW	18705
1ZDT	AP	TRANSCRIPTION	A	1.2	1.2	1	22	FGLLCRMADQTFISIVDWARRC	18706
1ZGL	GH	IMMUNE SYSTEM	G	1.2	1.2	1	20	GALANIAVDKANLEIMTKRS	18707

1ZLA	BD	PROTEIN BINDING/VIRUS/DNA	B	1.2	1.2	1	12	AMDVVYALKRQG	18708
1ZLA	HK	PROTEIN BINDING/VIRUS/DNA	H	1.2	1.2	1	12	AIYVYKVLKQVH	18709
1ZNV	AD	HYDROLASE/PROTEIN BINDING	A	1.2	1.2	1	16	EAEFVQLLKEIEKENV	18710
1ZNV	CB	HYDROLASE/PROTEIN BINDING	C	1.2	1.2	1	16	EAEFVQLLKEIEKENV	18711
1ZRT	DE	OXIDOREDUCTASE/METAL TRANSPORT	E	1.2	1.2	1	27	RDFLYHATAATGVVVTGAAVWPLINQM	18712
1ZUN	AB	TRANSFERASE	A	1.2	1.2	1	7	HLARKAF	18713
2A78	AB	PROTEIN BINDING/TRANSFERASE	A	1.2	1.2	1	19	MESFAATADFREQILRVKE	18714
2A79	AB	MEMBRANE PROTEIN	A	1.2	1.2	1	15	REKVEVQLPELFHKI	18715
2ACL	EF	TRANSCRIPTION	E	1.2	1.2	1	5	LFFFK	18716
2ACZ	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.2	1.2	1	5	HTVSA	18717
2AHM	CG	VIRAL PROTEIN, REPLICATION	C	1.2	1.2	1	5	INRLC	18718
2AJZ	LH	IMMUNE SYSTEM	L	1.2	1.2	1	5	SEQLT	18719
2AQ1	GH	IMMUNE SYSTEM	H	1.2	1.2	1	8	QSKYLMMY	18720
2ASQ	AB	PROTEIN BINDING	A	1.2	1.2	1	13	LKKLKESYCQRQG	18721
2AVU	DF	TRANSCRIPTION ACTIVATOR	F	1.2	1.2	1	17	NGVDAVIKAYRLYLEQC	18722
2AXT	ad	ELECTRON TRANSPORT	d	1.2	1.2	1	28	GLWTFIALHGAFGLIGFMLRQFEIARLV	18723
2AXT	bd	ELECTRON TRANSPORT	b	1.2	1.2	1	12	FFGHIWHGARTL	18724
2AXT	BH	ELECTRON TRANSPORT	B	1.2	1.2	1	7	QRLYKAL	18725
2AXT	bh	ELECTRON TRANSPORT	b	1.2	1.2	1	7	QRLYKAL	18726
2AXT	Bt	ELECTRON TRANSPORT	t	1.2	1.2	1	21	ETITYVFIFACIIALFFFAIF	18727
2AXT	CO	ELECTRON TRANSPORT	C	1.2	1.2	1	6	LNKIKN	18728
2AXT	dm	ELECTRON TRANSPORT	d	1.2	1.2	1	10	ISQEIRAAED	18729
2AXT	DO	ELECTRON TRANSPORT	D	1.2	1.2	1	21	FYTKNLLLNEGIRAWMAPQDQ	18730
2AXT	do	ELECTRON TRANSPORT	d	1.2	1.2	1	21	FYTKNLLLNEGIRAWMAPQDQ	18731
2AZE	AB	CELL CYCLE, TRANSCRIPTION	A	1.2	1.2	1	9	DIEVLKRMG	18732
2AZE	BC	CELL CYCLE, TRANSCRIPTION	C	1.2	1.2	1	12	TSEKFQKINQMV	18733
2B8K	AB	TRANSFERASE	A	1.2	1.2	1	9	NVKQMVMAG	18734
2B9M	DE	RIBOSOME	D	1.2	1.2	1	17	DYAVRLREKQKLRRIYG	18735
2B9S	AB	ISOMERASE/DNA	B	1.2	1.2	1	7	ATIQKKF	18736
2BA0	FI	RNA BINDING PROTEIN	F	1.2	1.2	1	30	RDEVKQAIELAKKGALQIYEMQREAILRRY	18737
2BCX	AB	CALCIUM BINDING PROTEIN	A	1.2	1.2	1	12	EAELQDMINEVD	18738
2BCX	AB	CALCIUM BINDING PROTEIN	A	1.2	1.2	1	10	EIREAFRVFD	18739
2BE7	CF	TRANSFERASE	C	1.2	1.2	1	7	AARLASE	18740
2BFZ	AB	HYDROLASE	B	1.2	1.2	1	12	KGLLLHTLDLLK	18741
2BMO	AB	OXIDOREDUCTASE	A	1.2	1.2	1	22	ADMIPDLMAFGAAKQEKLAKEI	18742
2BNQ	AD	IMMUNE SYSTEM/RECEPTOR	A	1.2	1.2	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	18743
2BR2	MX	HYDROLASE	M	1.2	1.2	1	13	IIKKESIVSLFEK	18744
2BR2	QB	HYDROLASE	Q	1.2	1.2	1	13	IIKKESIVSLFEK	18745

2BTQ	AB	STRUCTURAL PROTEIN	A	1.2	1.2	1	9	LRELLTNLV	18746
2BTV	BH	VIRUS	B	1.2	1.2	1	17	EPIYRIYNRLQGYIEAV	18747
2BV8	ED	PHOTOSYNTHESIS	E	1.2	1.2	1	9	GPMDEYLIA	18748
2BYK	BC	DNA-BINDING PROTEIN	C	1.2	1.2	1	27	NEVLFLMTKCTELFVRHLAGAAYTEEF	18749
2BYK	DC	DNA-BINDING PROTEIN	D	1.2	1.2	1	11	AKDILQTLTEL	18750
2BYP	DJ	RECEPTOR	J	1.2	1.2	1	6	PRCAWR	18751
2C2V	HI	CHAPERONE	I	1.2	1.2	1	15	RNFRLLEELEEGQKG	18752
2C35	GH	POLYMERASE	G	1.2	1.2	1	17	NSEVHMLLEHRKQQNES	18753
2C7J	AB	ELECTRON TRANSPORT	A	1.2	1.2	1	10	TGPLDDYVVA	18754
2CCI	AB	CELL CYCLE	B	1.2	1.2	1	15	KKQVLRMEHLVLKVL	18755
2CDF	AB	CELL RECEPTOR	B	1.2	1.2	1	8	EAEISHTQ	18756
2CLY	DF	HYDROLASE	F	1.2	1.2	1	18	PEYQQDLDRELFKLKQMY	18757
2CNW	BD	SIGNAL RECOGNITION	D	1.2	1.2	1	9	ERRATLRKL	18758
2CZV	AC	HYDROLASE	A	1.2	1.2	1	11	KEAYELAKEWF	18759
2D1P	HI	TRANSLATION	H	1.2	1.2	1	7	AASLRER	18760
2DBU	CB	TRANSFERASE	B	1.2	1.2	1	11	PDTLKLLEAKG	18761
2DD4	GI	HYDROLASE	I	1.2	1.2	1	10	PNYRRRLVRW	18762
2DD4	JL	HYDROLASE	J	1.2	1.2	1	6	AEDEAF	18763
2DD4	JL	HYDROLASE	L	1.2	1.2	1	8	PRQVLAEF	18764
2DD4	KI	HYDROLASE	I	1.2	1.2	1	10	PNYRRRLVRW	18765
2DFK	CB	CELL CYCLE	C	1.2	1.2	1	25	LEEKIRWLRAFREERKMVQEDEKIG	18766
2DFK	CD	CELL CYCLE	C	1.2	1.2	1	27	QDGFWIYSEYCNNHLDACMELSKLMKD	18767
2DFS	MN	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	N	1.2	1.2	1	10	EAELQDMINE	18768
2DFS	MO	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	O	1.2	1.2	1	10	YEEFVQMMTA	18769
2DOQ	BD	CELL CYCLE	B	1.2	1.2	1	15	EEQKQEIYEAFSLFD	18770
2DOQ	CD	CELL CYCLE	C	1.2	1.2	1	7	YHELKVA	18771
2DS2	CD	PLANT PROTEIN	D	1.2	1.2	1	13	PALRQCCNQLRQV	18772
2DXB	AC	HYDROLASE	C	1.2	1.2	1	8	PRQVLAEF	18773
2DXB	EF	HYDROLASE	E	1.2	1.2	1	9	AEERRRKQN	18774
2DXB	HI	HYDROLASE	H	1.2	1.2	1	9	AEERRRKQN	18775
2DXB	MO	HYDROLASE	O	1.2	1.2	1	8	PRQVLAEF	18776
2DXB	PR	HYDROLASE	P	1.2	1.2	1	6	AEDEAF	18777
2DXB	VN	HYDROLASE	N	1.2	1.2	1	16	YYGRWLLTAARILVDK	18778
2DXB	WX	HYDROLASE	W	1.2	1.2	1	9	AEERRRKQN	18779
2DZN	AB	PROTEIN BINDING	A	1.2	1.2	1	8	PLHRAASV	18780
2DZN	AB	PROTEIN BINDING	B	1.2	1.2	1	10	QSDLEEAYAT	18781
2E 30	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	A	1.2	1.2	1	5	VEQKM	18782

2E 32	CD	LIGASE	C	1.2	1.2	1	9	ATELVQACR	18783
2E 74	AB	PHOTOSYNTHESIS	A	1.2	1.2	1	22	CLGGITLTCFLIQFATGFAMTF	18784
2E1M	AC	OXIDOREDUCTASE	A	1.2	1.2	1	12	SRMLPETLAKDL	18785
2E1M	BC	OXIDOREDUCTASE	B	1.2	1.2	1	6	FSSLRF	18786
2E3K	CQ	TRANSCRIPTION	C	1.2	1.2	1	19	AQEFAADVRLMFSNCYKYN	18787
2E9X	FG	REPLICATION	F	1.2	1.2	1	11	YMELTKLLLNH	18788
2EHO	IK	REPLICATION	K	1.2	1.2	1	10	GTFLTQALNH	18789
2EKV	AB	CONTRACTILE PROTEIN	B	1.2	1.2	1	5	MLKEC	18790
2EMT	BD	CELL ADHESION	B	1.2	1.2	1	22	LRINKRILALCMGNHELYMRRR	18791
2EQ7	AC	OXIDOREDUCTASE	C	1.2	1.2	1	10	PAAERLMQEK	18792
2EQ9	HI	OXIDOREDUCTASE	H	1.2	1.2	1	6	LTDLAL	18793
2ES4	BE	HYDROLASE	B	1.2	1.2	1	17	RGEQLLAYVKQVLAATG	18794
2F5Z	BK	OXIDOREDUCTASE/PROTEIN BINDING	K	1.2	1.2	1	10	KEDALKLVQL	18795
2F5Z	CL	OXIDOREDUCTASE/PROTEIN BINDING	L	1.2	1.2	1	7	ARNILEK	18796
2F5Z	DL	OXIDOREDUCTASE/PROTEIN BINDING	D	1.2	1.2	1	7	CEDIARV	18797
2F5Z	HN	OXIDOREDUCTASE/PROTEIN BINDING	N	1.2	1.2	1	7	KEDALKL	18798
2F5Z	IO	OXIDOREDUCTASE/PROTEIN BINDING	O	1.2	1.2	1	6	ARNILE	18799
2F9I	CD	TRANSFERASE	C	1.2	1.2	1	7	AHDIKQL	18800
2FBW	AB	OXIDOREDUCTASE	A	1.2	1.2	1	26	TDLVETLELQNLMLCALQTIYGAEAR	18801
2FBW	BC	OXIDOREDUCTASE	B	1.2	1.2	1	6	NCTRTC	18802
2FFD	BC	BLOOD CLOTTING	C	1.2	1.2	1	7	WIQYKEG	18803
2FFD	DF	BLOOD CLOTTING	D	1.2	1.2	1	7	QLLQKNV	18804
2FK0	KJ	VIRAL PROTEIN	J	1.2	1.2	1	23	KESTQKAIDGVTNKVNSIIDKMN	18805
2FK0	MN	VIRAL PROTEIN	N	1.2	1.2	1	22	ESTQKAIDGVTNKVNSIIDKMN	18806
2FKW	AB	MEMBRANE PROTEIN, PHOTOSYNTHESIS	A	1.2	1.2	1	26	PAIGIPALLGSVTVIAILVHLAILSH	18807
2FKW	EF	MEMBRANE PROTEIN, PHOTOSYNTHESIS	E	1.2	1.2	1	26	PAIGIPALLGSVTVIAILVHLAILSH	18808
2FKW	GH	MEMBRANE PROTEIN, PHOTOSYNTHESIS	G	1.2	1.2	1	25	PAIGIPALLGSVTVIAILVHLAILS	18809
2FKW	KL	MEMBRANE PROTEIN, PHOTOSYNTHESIS	K	1.2	1.2	1	9	TWFPAYWQG	18810
2FKW	OP	MEMBRANE PROTEIN, PHOTOSYNTHESIS	O	1.2	1.2	1	9	TWFPAYWQG	18811
2FKW	RS	MEMBRANE PROTEIN, PHOTOSYNTHESIS	R	1.2	1.2	1	26	PAIGIPALLGSVTVIAILVHLAILSH	18812
2FTK	DH	TRANSFERASE	D	1.2	1.2	1	31	TALTNELIHLLGHSRHDWMNKLQLIKGNLSL	18813
2FUG	AB	OXIDOREDUCTASE	A	1.2	1.2	1	9	ETALMNSLE	18814
2FUG	DF	OXIDOREDUCTASE	D	1.2	1.2	1	6	FEKTME	18815
2FUG	DG	OXIDOREDUCTASE	G	1.2	1.2	1	6	LCAAAC	18816

2FUG	JK	OXIDOREDUCTASE	K	1.2	1.2	1	16	RRAAIMPLLRRVQQEE	18817
2FUG	MP	OXIDOREDUCTASE	M	1.2	1.2	1	9	YLQNITYTP	18818
2FUG	VW	OXIDOREDUCTASE	W	1.2	1.2	1	11	EREVYDLFGIV	18819
2FUG	XY	OXIDOREDUCTASE	Y	1.2	1.2	1	7	KPQRREA	18820
2FYN	AC	OXIDOREDUCTASE	C	1.2	1.2	1	23	YATAGAGAVATGAAVWPLINQMN	18821
2FYN	DE	OXIDOREDUCTASE	E	1.2	1.2	1	6	ISQLFN	18822
2FYN	DF	OXIDOREDUCTASE	F	1.2	1.2	1	23	YATAGAGAVATGAAVWPLINQMN	18823
2FYN	HI	OXIDOREDUCTASE	H	1.2	1.2	1	28	LMARKQAGFTAVMFLTVLSVLLYLTNKR	18824
2FYN	JI	OXIDOREDUCTASE	J	1.2	1.2	1	17	QMSFWGATVITGLFGAI	18825
2FYN	JL	OXIDOREDUCTASE	L	1.2	1.2	1	23	YATAGAGAVATGAAVWPLINQMN	18826
2FYN	MN	OXIDOREDUCTASE	M	1.2	1.2	1	7	IEEDFNA	18827
2G38	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.2	1.2	1	6	APMTTA	18828
2GFB	OP	IMMUNOGLOBULIN	O	1.2	1.2	1	7	SEQLTSG	18829
2GGP	AB	CHAPERONE, METAL TRANSPORT	B	1.2	1.2	1	10	ADSIKEIIED	18830
2GOX	AB	CELL ADHESION/TOXIN	B	1.2	1.2	1	24	DATIKKEQKLIQAQNLVREFEKTH	18831
2GOX	CD	CELL ADHESION/TOXIN	D	1.2	1.2	1	18	KVKKMVLQERIDNVLKQG	18832
2GTL	GH	OXYGEN STORAGE/TRANSPORT	H	1.2	1.2	1	16	VTESLKVKLQWASAFG	18833
2GYK	EF	ANTIBIOTIC/ANTIBIOTIC INHIBITOR	F	1.2	1.2	1	15	FDDFRKAVWEEVSKD	18834
2H0D	AB	METAL BINDING PROTEIN/LIGASE	A	1.2	1.2	1	8	KTCIVRYL	18835
2H1L	AM	VIRAL PROTEIN	M	1.2	1.2	1	5	PHHER	18836
2H1L	DP	VIRAL PROTEIN	D	1.2	1.2	1	12	GIALLLMLIWYR	18837
2H1L	DP	VIRAL PROTEIN	D	1.2	1.2	1	8	KERLDKEF	18838
2H1L	EQ	VIRAL PROTEIN	E	1.2	1.2	1	7	WKERLDK	18839
2H1L	IU	VIRAL PROTEIN	I	1.2	1.2	1	14	LSVYQKMKFNVAMG	18840
2H1L	JV	VIRAL PROTEIN	V	1.2	1.2	1	11	PGRDRRTEEEN	18841
2H1O	AE	GENE REGULATION/DNA COMPLEX	A	1.2	1.2	1	9	TNVISEPLR	18842
2H1O	DH	GENE REGULATION/DNA COMPLEX	D	1.2	1.2	1	9	ERVVAWLDS	18843
2H4M	BD	PROTEIN TRANSPORT	B	1.2	1.2	1	19	HKNLLILYDAIGTLADSVG	18844
2H4P	AB	HYDROLASE INHIBITOR	A	1.2	1.2	1	9	YERLSEWAD	18845
2H61	AC	METAL BINDING PROTEIN, SIGNALING PROTEIN	C	1.2	1.2	1	18	ELEKAMVALIDVFHQYSG	18846
2H7D	AB	STRUCTURAL PROTEIN	A	1.2	1.2	1	19	GEQIAQLIAGYIDIILKKK	18847
2H9G	AB	IMMUNE SYSTEM/APOTOSIS	A	1.2	1.2	1	6	DEQLKS	18848
2HDN	KL	TRANSLATION	L	1.2	1.2	1	13	PQTREHILLGRQV	18849
2HFG	LH	IMMUNE SYSTEM	L	1.2	1.2	1	7	DEQLKSG	18850
2HGJ	W1	RIBOSOME	1	1.2	1.2	1	21	VELEKLVREKKRELMELRFQA	18851
2HGR	IU	RIBOSOME	U	1.2	1.2	1	18	GKEQRILAKTIKRARILG	18852
2HIO	AB	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	B	1.2	1.2	1	13	YSIYVYKVLKQVH	18853

2HLD	AD	HYDROLASE	A	1.2	1.2	1	7	AELFYKG	18854
2HLD	AE	HYDROLASE	E	1.2	1.2	1	15	IFRFTQAGSEVSALL	18855
2HLD	JN	HYDROLASE	N	1.2	1.2	1	15	IFRFTQAGSEVSALL	18856
2HLD	KO	HYDROLASE	O	1.2	1.2	1	5	EVFTG	18857
2HLD	LM	HYDROLASE	M	1.2	1.2	1	18	EQDKLTVERARKIQRFLS	18858
2HLD	LM	HYDROLASE	M	1.2	1.2	1	5	EVFTG	18859
2HLD	TX	HYDROLASE	X	1.2	1.2	1	5	RGISE	18860
2HLD	UX	HYDROLASE	U	1.2	1.2	1	14	RSTVAQLVQTLEQH	18861
2HLD	VY	HYDROLASE	Y	1.2	1.2	1	38	LKEVEMRLKSIKNIEKITKTMKIVASTRLSKAEKAKIS	18862
2HLF	EF	PROTON TRANSPORT, MEMBRANE PROTEIN	F	1.2	1.2	1	5	SEQLT	18863
2HQW	AB	METAL BINDING PROTEIN	A	1.2	1.2	1	11	AAELRHVMTNL	18864
2HUE	AC	DNA BINDING PROTEIN	C	1.2	1.2	1	27	IYEETRGVLKVFLENVIRDAVTYTEHA	18865
2HV8	AD	PROTEIN TRANSPORT	A	1.2	1.2	1	8	AITSAYYR	18866
2HYB	AB	TRANSFERASE	B	1.2	1.2	1	16	IYAWEALEVVLIGAAF	18867
2HYB	BC	TRANSFERASE	B	1.2	1.2	1	11	SARVSELMNES	18868
2HYB	JK	TRANSFERASE	J	1.2	1.2	1	8	VAAAQRRG	18869
2HZE	AB	ELECTRON TRANSPORT, OXIDOREDUCTASE	A	1.2	1.2	1	8	AEEFVQQR	18870
2HZS	AB	TRANSCRIPTION	B	1.2	1.2	1	9	VSSLMNGLG	18871
2I2P	DE	RIBOSOME	D	1.2	1.2	1	6	LIVELY	18872
2I2R	BF	TRANSPORT PROTEIN	F	1.2	1.2	1	9	STYAHYLFN	18873
2I2R	IM	TRANSPORT PROTEIN	M	1.2	1.2	1	12	EDTFKQIYAQFF	18874
2I2T	S0	RIBOSOME	S	1.2	1.2	1	5	LDILT	18875
2I2X	MN	TRANSFERASE	N	1.2	1.2	1	8	EASLKKVL	18876
2I2X	MP	TRANSFERASE	P	1.2	1.2	1	8	EASLKKVL	18877
2I3S	AB	CELL CYCLE	B	1.2	1.2	1	5	FNLIY	18878
2I94	AB	PROTEIN BINDING	B	1.2	1.2	1	12	SLETVVANSAFI	18879
2IAE	AC	HYDROLASE	A	1.2	1.2	1	14	YAIREAATSNLKKL	18880
2IAE	BC	HYDROLASE	C	1.2	1.2	1	9	GFYDECLRK	18881
2IAE	EF	HYDROLASE	E	1.2	1.2	1	16	SPKEVMFLNELEEILD	18882
2IAM	CD	IMMUNE SYSTEM	D	1.2	1.2	1	8	EAEISHTQ	18883
2IAN	FH	IMMUNE SYSTEM	F	1.2	1.2	1	21	QGALANIAVDKANLEIMTKRS	18884
2IBF	AD	CELL ADHESION, STRUCTURAL PROTEIN	D	1.2	1.2	1	17	KAKEVSSALSKVLSKID	18885
2IBX	CB	VIRAL PROTEIN	B	1.2	1.2	1	22	KESTQKAIDGVTNKVNSIIDKM	18886
2IBX	CD	VIRAL PROTEIN	C	1.2	1.2	1	10	YEELKHLLSR	18887
2IBZ	CD	OXIDOREDUCTASE	D	1.2	1.2	1	5	AGIKT	18888
2IBZ	DF	OXIDOREDUCTASE	F	1.2	1.2	1	20	EDESYARAYRIIRAHQTELT	18889
2ICW	AB	IMMUNE SYSTEM	A	1.2	1.2	1	7	EEFGRFA	18890

2IDO	AB	TRANSFERASE	B	1.2	1.2	1	17	RTYFMERLRHYRQLSLQ	18891
2IDO	CD	TRANSFERASE	C	1.2	1.2	1	9	ADEFMDYIR	18892
2IDO	CD	TRANSFERASE	D	1.2	1.2	1	18	RTYFMERLRHYRQLSLQL	18893
2INN	AC	OXIDOREDUCTASE	A	1.2	1.2	1	5	KKDIF	18894
2INN	AC	OXIDOREDUCTASE	C	1.2	1.2	1	5	TTVSQ	18895
2INN	AC	OXIDOREDUCTASE	C	1.2	1.2	1	8	KLVEDTLV	18896
2INN	AF	OXIDOREDUCTASE	A	1.2	1.2	1	19	TFDKYYRPRYEYLAKEAAA	18897
2INN	BD	OXIDOREDUCTASE	B	1.2	1.2	1	5	KKDIF	18898
2INP	AC	OXIDOREDUCTASE	A	1.2	1.2	1	8	GPHMHDRV	18899
2INP	BD	OXIDOREDUCTASE	D	1.2	1.2	1	11	QPMRKLVEDTL	18900
2J0S	CD	HYDROLASE	C	1.2	1.2	1	15	KSVMEELKRIIDDSE	18901
2J3R	AB	TRANSPORT	B	1.2	1.2	1	16	NCAAFTGGIVEAILTH	18902
2J59	AM	HYDROLASE	A	1.2	1.2	1	7	RPLWRHY	18903
2J59	BN	HYDROLASE	N	1.2	1.2	1	15	RDDMLAWIKTIQESS	18904
2J59	CO	HYDROLASE	C	1.2	1.2	1	6	RPLWRH	18905
2J7A	DF	OXIDOREDUCTASE	D	1.2	1.2	1	5	RNEMR	18906
2J7A	DF	OXIDOREDUCTASE	D	1.2	1.2	1	6	CADCHM	18907
2J7A	JI	OXIDOREDUCTASE	I	1.2	1.2	1	13	VALATVAFGMKYT	18908
2J7A	PR	OXIDOREDUCTASE	P	1.2	1.2	1	5	RNEMR	18909
2J8X	CD	HYDROLASE/INHIBITOR	C	1.2	1.2	1	14	PSLRNIYAELHRSL	18910
2JBL	CL	ELECTRON TRANSPORT	C	1.2	1.2	1	9	YVVRLAKYT	18911
2JDQ	BD	PROTEIN TRANSPORT	B	1.2	1.2	1	16	CTLQFESAWVLTNIAS	18912
2JET	BC	HYDROLASE	C	1.2	1.2	1	9	MPWVQQILE	18913
2JIZ	AE	HYDROLASE	A	1.2	1.2	1	12	VFYLHSRLLERA	18914
2JIZ	BF	HYDROLASE	F	1.2	1.2	1	21	PGARARVALTGLTVAEYFRDQ	18915
2JIZ	CF	HYDROLASE	F	1.2	1.2	1	12	LATDMGTMQERI	18916
2JIZ	DG	HYDROLASE	D	1.2	1.2	1	27	SEHYDVARGVQKILQDYKSLQDIIAIL	18917
2JIZ	LN	HYDROLASE	L	1.2	1.2	1	28	SEHYDVARGVQKILQDYKSLQDIIAILG	18918
2JJ0	LH	PHOTOSYNTHESIS	H	1.2	1.2	1	19	LLEEDKICGYVAGGLMYAA	18919
2JJ0	LM	PHOTOSYNTHESIS	L	1.2	1.2	1	15	IWTHLDWVSNTGYTY	18920
2JJZ	AB	METAL BINDING PROTEIN	B	1.2	1.2	1	15	LPEKLTAFKEKYMEF	18921
2JKR	BM	ENDOCYTOSIS	B	1.2	1.2	1	14	IYVKLEKLDIMIRL	18922
2JKR	EU	ENDOCYTOSIS	E	1.2	1.2	1	13	PLIRALAVRTMGC	18923
2JKR	LE	ENDOCYTOSIS	L	1.2	1.2	1	14	ENLVKVGGYILGEF	18924
2JND	AB	LIGAND BINDING PROTEIN	B	1.2	1.2	1	8	EAHKNRKL	18925
2JXM	AB	ELECTRON TRANSPORT	B	1.2	1.2	1	8	PFYAQYNY	18926
2KIN	AB	MOTOR PROTEIN	B	1.2	1.2	1	13	AEEWKKKYEKEKE	18927
2NGR	AB	HYDROLASE	B	1.2	1.2	1	7	AAITLKA	18928
2NN6	EF	HYDROLASE/TRANSFERASE	E	1.2	1.2	1	18	PESIFEMMETGKRVGKVL	18929
2NNW	CD	TRANSFERASE	D	1.2	1.2	1	11	PRVLRELVPIV	18930

2NOJ	AB	IMMUNE SYSTEM	A	1.2	1.2	1	5 WEKFG	18931
2NOJ	EF	IMMUNE SYSTEM	E	1.2	1.2	1	19 KRQGALELIKKGYTQQLAF	18932
2NOJ	EF	IMMUNE SYSTEM	F	1.2	1.2	1	16 YEKKKLQRQIDLVLKY	18933
2NPP	DF	SIGNALING PROTEIN,HYDROLASE	D	1.2	1.2	1	14 ANVRFNVAKSLQKI	18934
2NPP	EF	SIGNALING PROTEIN,HYDROLASE	F	1.2	1.2	1	8 FYDECLRK	18935
2NQB	CD	STRUCTURAL PROTEIN/DNA	C	1.2	1.2	1	6 RSNRAG	18936
2NTI	DF	DNA BINDING PROTEIN	F	1.2	1.2	1	14 SDGFKSAISEVSTV	18937
2NTY	BC	SIGNALING PROTEIN	C	1.2	1.2	1	11 KTCMLISYTSN	18938
2NUU	DL	TRANSPORT PROTEIN/SIGNALING PROTEIN	D	1.2	1.2	1	6 EEQERE	18939
2NV2	CD	LYASE/TRANSFERASE	C	1.2	1.2	1	11 PTIVEEVMNAV	18940
2NVU	AB	PROTEIN TURNOVER, LIGASE	B	1.2	1.2	1	10 YRLTQGVVKR	18941
2NX5	KN	IMMUNE SYSTEM	K	1.2	1.2	1	13 LCVEWLRRYLENG	18942
2NYL	AB	HYDROLASE	B	1.2	1.2	1	11 QKFVLQLLELF	18943
2NYL	AC	HYDROLASE	A	1.2	1.2	1	10 WRVRLAIIEY	18944
2NYL	BC	HYDROLASE	B	1.2	1.2	1	5 SPKEV	18945
2NYL	DF	HYDROLASE	D	1.2	1.2	1	14 ANVRFNVAKSLQKI	18946
2NZ0	CD	MEMBRANE PROTEIN	C	1.2	1.2	1	8 HVDVFFQK	18947
2NZD	AB	STRUCTURAL PROTEIN/DNA	B	1.2	1.2	1	11 AMDVVYALKRQ	18948
2O01	AD	PHOTOSYNTHESIS	A	1.2	1.2	1	8 LLDRVLRH	18949
2O60	AB	METAL BINDING PROTEIN	A	1.2	1.2	1	11 AAELRHVMTNL	18950
2O8F	AB	DNA BINDING PROTEIN/DNA	A	1.2	1.2	1	8 GIHVAELA	18951
2O8F	AB	DNA BINDING PROTEIN/DNA	B	1.2	1.2	1	14 EIAFGRYSDSLVQK	18952
2O98	AP	PROTEIN BINDING	A	1.2	1.2	1	22 GDSKVFYLKMKGDYHRYLAEFK	18953
2O98	AP	PROTEIN BINDING	A	1.2	1.2	1	19 PIRLGLALNFSVFYYEILN	18954
2OBH	AC	CELL CYCLE	A	1.2	1.2	1	12 DEELQEMIDEAD	18955
2ODB	AB	PROTEIN BINDING	A	1.2	1.2	1	10 KTCLLISYTT	18956
2OF5	EH	APOPTOSIS	E	1.2	1.2	1	11 QTDIYRCKANH	18957
2OJZ	LH	IMMUNE SYSTEM	L	1.2	1.2	1	6 SEQLTS	18958
2OM0	cd	HORMONE	c	1.2	1.2	1	5 IVEQC	18959
2OM0	ef	HORMONE	e	1.2	1.2	1	5 IVEQC	18960
2OM0	gj	HORMONE	j	1.2	1.2	1	19 VNQHLCGSHLVEALYLVCG	18961
2OM0	UV	HORMONE	U	1.2	1.2	1	7 LYQLENY	18962
2ONK	HJ	MEMBRANE PROTEIN	H	1.2	1.2	1	12 APTLIYERYLSE	18963
2OQJ	AE	IMMUNE SYSTEM	A	1.2	1.2	1	6 DEQLKS	18964
2OS8	AB	CONTRACTILE PROTEIN	B	1.2	1.2	1	11 IEYIKDLLENM	18965
2OSL	LH	IMMUNE SYSTEM	L	1.2	1.2	1	5 DEQLK	18966
2OTK	CF	DE NOVO PROTEIN, PEPTIDE BINDING PROTEIN	F	1.2	1.2	1	18 PSQSANLLAEAKKLNDAQ	18967
2OV2	DL	PROTEIN BINDING/TRANSFERASE	D	1.2	1.2	1	10 KTCLLISYTT	18968

2OV2	FN	PROTEIN BINDING/TRANSFERASE	F	1.2	1.2	1	10	KTCLLISYTT	18969
2P22	AC	TRANSPORT PROTEIN	A	1.2	1.2	1	5	AQIDV	18970
2P28	AB	CELL ADHESION	A	1.2	1.2	1	5	DSIRC	18971
2P2C	EF	HYDROLASE	F	1.2	1.2	1	13	WYIEALAQVFSER	18972
2P4N	KA	TRANSPORT PROTEIN	A	1.2	1.2	1	6	EGEFSE	18973
2P58	BC	TRANSPORT PROTEIN/CHAPERONE	B	1.2	1.2	1	6	STIVRS	18974
2P5T	GH	TRANSCRIPTION REGULATOR	G	1.2	1.2	1	19	PWILMSDDLSDLIHTNIYL	18975
2P9V	AB	HYDROLASE	B	1.2	1.2	1	11	KTLQQGIQLAQ	18976
2PBI	AB	SIGNALING PROTEIN	B	1.2	1.2	1	5	LHQVA	18977
2PF4	AE	HYDROLASE REGULATOR/VIRAL PROTEIN	A	1.2	1.2	1	9	PMVRRAAAS	18978
2PF4	CG	HYDROLASE REGULATOR/VIRAL PROTEIN	C	1.2	1.2	1	10	PMVRRAAASK	18979
2PK9	AB	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	B	1.2	1.2	1	15	CHELNILENDFLKRV	18980
2PKG	AC	HYDROLASE REGULATOR/VIRAL PROTEIN	A	1.2	1.2	1	9	PMVRRAAAS	18981
2PKG	AD	HYDROLASE REGULATOR/VIRAL PROTEIN	D	1.2	1.2	1	6	WPECAK	18982
2PKG	BD	HYDROLASE REGULATOR/VIRAL PROTEIN	B	1.2	1.2	1	18	PMVRRAAASKLGEFAKVL	18983
2PKQ	OR	OXIDOREDUCTASE	O	1.2	1.2	1	10	VKSATHLLKY	18984
2PMZ	QR	TRANSLATION, TRANSFERASE	R	1.2	1.2	1	6	MERDCL	18985
2PMZ	SX	TRANSLATION, TRANSFERASE	X	1.2	1.2	1	22	PKDALLKAIENIRGMTSHYIDE	18986
2PQA	AB	REPLICATION	A	1.2	1.2	1	7	ISQLLSA	18987
2PV2	AE	ISOMERASE	A	1.2	1.2	1	9	GIFAQALST	18988
2PV2	DF	ISOMERASE	D	1.2	1.2	1	7	GIFAQAL	18989
2PXY	CD	IMMUNE SYSTEM	D	1.2	1.2	1	11	RPDAEYYNKQY	18990
2Q26	AB	VIRUS/RNA	A	1.2	1.2	1	14	EVALQEYRTVARSL	18991
2Q26	EF	VIRUS/RNA	E	1.2	1.2	1	13	VALQEYRTVARSL	18992
2Q97	AT	STRUCTURAL PROTEIN/CELL INVASION	A	1.2	1.2	1	13	EREIVRDIKEKLC	18993
2Q9Q	CD	REPLICATION	D	1.2	1.2	1	8	LWLAKGLF	18994
2Q9Q	EF	REPLICATION	E	1.2	1.2	1	22	LMEINTSGTFLTQALNHMYKLR	18995
2Q9Q	EH	REPLICATION	E	1.2	1.2	1	12	YMELTKLLLNHA	18996
2QAC	AT	MEMBRANE PROTEIN	A	1.2	1.2	1	11	VEELIKMFAHF	18997
2QAC	AT	MEMBRANE PROTEIN	A	1.2	1.2	1	10	YKLFCEDILQ	18998
2QB0	AD	HYDROLASE REGULATOR	D	1.2	1.2	1	8	KEDFRYRS	18999
2QBE	XT	RIBOSOME	X	1.2	1.2	1	11	EQFNLRMQAAS	19000
2QE7	CD	HYDROLASE	D	1.2	1.2	1	15	IFRFTQAGSEVSALL	19001

2QJK	DC	ELECTRON TRANSPORT	C	1.2	1.2	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	19002
2QJK	HI	ELECTRON TRANSPORT	H	1.2	1.2	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	19003
2QJK	JI	ELECTRON TRANSPORT	J	1.2	1.2	1	17	QMSFWGATVITGLFGAI	19004
2QJK	MR	ELECTRON TRANSPORT	M	1.2	1.2	1	17	QMSFWGATVITGLFGAI	19005
2QJK	MR	ELECTRON TRANSPORT	M	1.2	1.2	1	9	HSIQTWLLG	19006
2QJK	PO	ELECTRON TRANSPORT	P	1.2	1.2	1	9	HSIQTWLLG	19007
2QJP	DF	ELECTRON TRANSPORT	F	1.2	1.2	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	19008
2QJP	EF	ELECTRON TRANSPORT	E	1.2	1.2	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	19009
2QJP	KL	ELECTRON TRANSPORT	K	1.2	1.2	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	19010
2QJY	AF	OXIDOREDUCTASE	A	1.2	1.2	1	18	AKFFGVLAMFGAILVMAL	19011
2QJY	JI	OXIDOREDUCTASE	J	1.2	1.2	1	17	QMSFWGATVITGLFGAI	19012
2QJY	MO	OXIDOREDUCTASE	M	1.2	1.2	1	23	IWGVVLAFCLVLQIVTGIVLAMH	19013
2QJY	NO	OXIDOREDUCTASE	N	1.2	1.2	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	19014
2QJY	QR	OXIDOREDUCTASE	Q	1.2	1.2	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	19015
2QLV	AB	TRANSFERASE/PROTEIN BINDING	B	1.2	1.2	1	12	PSVMERYYYTLD	19016
2QLV	DE	TRANSFERASE/PROTEIN BINDING	D	1.2	1.2	1	14	LDVMGEIYIALKNL	19017
2QM6	CD	TRANSFERASE	C	1.2	1.2	1	16	AIDAAVAIGFALAVVH	19018
2QOY	KU	RIBOSOME	U	1.2	1.2	1	7	VLAEVRR	19019
2QP0	KG	RIBOSOME	K	1.2	1.2	1	14	PFAAQVAAERCADA	19020
2QQD	BF	LYASE	B	1.2	1.2	1	20	KKEAEKTVREMAKIGFEMRG	19021
2QQK	HL	SIGNALING PROTEIN	L	1.2	1.2	1	6	DEQLKS	19022
2QQP	AB	VIRUS	A	1.2	1.2	1	8	DEVVQLAN	19023
2QR0	AB	IMMUNE SYSTEM	A	1.2	1.2	1	7	DEQLKSG	19024
2QR0	GH	IMMUNE SYSTEM	G	1.2	1.2	1	7	DEQLKSG	19025
2QR0	ST	IMMUNE SYSTEM	S	1.2	1.2	1	7	DEQLKSG	19026
2QR1	DG	TRANSFERASE	G	1.2	1.2	1	8	AIAEIDKF	19027
2R6C	EI	REPLICATION	I	1.2	1.2	1	10	FLTAARIAKE	19028
2R9R	GH	MEMBRANE PROTEIN, TRANSPORT PROTEIN	H	1.2	1.2	1	7	PKKRMRY	19029
2RAO	AB	OXYGEN BINDING	B	1.2	1.2	1	19	PQVQAAYQKVVAGVANALA	19030
2RAO	CB	OXYGEN BINDING	B	1.2	1.2	1	20	PENFRLLGNVLVIVLSHHFG	19031
2RAX	EB	CELL CYCLE	E	1.2	1.2	1	22	LGEFLKLDRERAKNKIAKETNN	19032
2REX	AB	SIGNALING PROTEIN/LIPOPROTEIN	B	1.2	1.2	1	12	LKKWRTEILDYC	19033
2REX	CD	SIGNALING PROTEIN/LIPOPROTEIN	D	1.2	1.2	1	12	LKKWRTEILDYC	19034
2RF9	BD	TRANSFERASE	B	1.2	1.2	1	9	SEISSILEK	19035
2RGN	EF	SIGNALING PROTEIN COMPLEX	E	1.2	1.2	1	8	IKPVQRIM	19036
2RGN	EF	SIGNALING PROTEIN COMPLEX	E	1.2	1.2	1	16	YQLLLKDFLKYYNRAG	19037
2RHK	BD	VIRAL PROTEIN/NUCLEAR PROTEIN	D	1.2	1.2	1	5	KHWLR	19038
2RI4	KL	OXYGEN STORAGE, OXYGEN TRANSPORT	K	1.2	1.2	1	18	VNFKLLSHSLLVTLACHL	19039

2RIV	AB	SIGNALING PROTEIN	A	1.2	1.2	1	16	MVEIQHGFQHLICSLN	19040
2RMK	AB	MEMBRANE PROTEIN/TRANSFERASE	A	1.2	1.2	1	6	LSYPQT	19041
2RNR	AB	TRANSCRIPTION	A	1.2	1.2	1	16	PEEKEAYIAMGQRMFE	19042
2ROD	AB	APOPTOSIS	A	1.2	1.2	1	15	EGDVKSFSRVMVHVF	19043
2SNI	EI	COMPLEX (PROTEINASE/INHIBITOR)	E	1.2	1.2	1	14	YSWIINGIEWAIAN	19044
2UUN	CF	ELECTRON TRANSPORT	C	1.2	1.2	1	8	IDEVNRTF	19045
2UUN	SV	ELECTRON TRANSPORT	S	1.2	1.2	1	8	IDEVNRTF	19046
2UUN	WT	ELECTRON TRANSPORT	T	1.2	1.2	1	25	SDRMAACLRDMEIILRYVTYAVFAG	19047
2UZ1	AB	LYASE	B	1.2	1.2	1	10	VTPIANAWLD	19048
2V1Y	AB	TRANSFERASE	B	1.2	1.2	1	36	NYDKLKSRISEIIDSRRRLEEDLKKQAAEYREIDKR	19049
2V3B	AB	OXIDOREDUCTASE	A	1.2	1.2	1	16	VMPLMACARALAQTLA	19050
2V4J	AC	OXIDOREDUCTASE	C	1.2	1.2	1	10	PGKGACKMAG	19051
2V4J	DF	OXIDOREDUCTASE	F	1.2	1.2	1	10	PGKGACKMAG	19052
2V5H	EK	TRANSCRIPTION	E	1.2	1.2	1	10	IPQSRELIAQ	19053
2V6Q	AB	APOPTOSIS	A	1.2	1.2	1	13	SETFTETWNRFIT	19054
2V7N	EF	IMMUNE SYSTEM	E	1.2	1.2	1	6	DEQLKS	19055
2V7Q	CF	HYDROLASE	F	1.2	1.2	1	28	SEHYDVARGVQKILQDYKSLQDIIAILG	19056
2VAS	AB	MOTOR PROTEIN	B	1.2	1.2	1	10	TKELGTVMRS	19057
2VDN	HL	CELL ADHESION/IMMUNE SYSTEM	L	1.2	1.2	1	6	SEQLTS	19058
2VDW	CD	TRANSFERASE	C	1.2	1.2	1	15	PSTRNFFELNRGAIK	19059
2VDW	EF	TRANSFERASE	E	1.2	1.2	1	16	PSTRNFFELNRGAIKC	19060
2VE7	AC	CELL CYCLE	C	1.2	1.2	1	6	TADILC	19061
2VE7	BD	CELL CYCLE	B	1.2	1.2	1	17	KAFIQQCIRQLCEFLTE	19062
2VGL	AM	PROTEIN TRANSPORT	M	1.2	1.2	1	7	EENIKNN	19063
2VGX	AB	CHAPERONE	B	1.2	1.2	1	8	FQALCVLD	19064
2VHM	QR	RIBOSOME	Q	1.2	1.2	1	15	KVAFTALVEKAKAAL	19065
2VJT	AB	PHOTOSYNTHESIS	B	1.2	1.2	1	14	GAVRVRAAAVISSN	19066
2VLH	AB	LYASE	A	1.2	1.2	1	16	DEMFSSAKELVVVYEG	19067
2VLJ	AD	IMMUNE SYSTEM	A	1.2	1.2	1	11	VAEQLRAYLEG	19068
2VML	IL	PHOTOSYNTHESIS	I	1.2	1.2	1	8	LREVNRTF	19069
2VML	IL	PHOTOSYNTHESIS	L	1.2	1.2	1	25	NRRMAACLRDMEIILRYVSYALLAG	19070
2VOY	BD	HYDROLASE	D	1.2	1.2	1	22	LFFRYMAIGGYVGAATVGAAAW	19071
2VOY	HI	HYDROLASE	H	1.2	1.2	1	17	AVITTCLALGTRRMAKK	19072
2VPE	AB	GENE REGULATION	A	1.2	1.2	1	6	DTCMAD	19073
2VPG	AB	GENE REGULATION	A	1.2	1.2	1	6	DTCMAD	19074
2VUS	CK	TRANSCRIPTION	C	1.2	1.2	1	14	RQAASLIRVAAAVG	19075
2VVL	FG	OXIDOREDUCTASE	G	1.2	1.2	1	9	YQGCMDCLM	19076
2VWE	AC	IMMUNE SYSTEM	A	1.2	1.2	1	9	WIDVYTRAT	19077
2VZD	AC	CELL ADHESION	A	1.2	1.2	1	9	AFDTLFDHA	19078
2W2H	AC	RNA BINDING PROTEIN	A	1.2	1.2	1	13	AANLLQDMGQRLN	19079

2W72	AB	OXYGEN TRANSPORT	A	1.2	1.2	1	18	PVNFKLLSHCLLVTLAAH	19080
2W83	BC	PROTEIN TRANSPORT	C	1.2	1.2	1	64	PEFMGREVENLILENTQLLETKNALNIVKNDLIAKVDELTCEKDVLQGE LEAVKQAKLKLEEKN	19081
2WAQ	AB	TRANSCRIPTION	A	1.2	1.2	1	8	YHVATYFD	19082
2WAQ	BC	TRANSCRIPTION	C	1.2	1.2	1	8	VVENIIIG	19083
2WB1	FE	TRANSCRIPTION	F	1.2	1.2	1	12	LQRTYDYLNSVE	19084
2WB1	YT	TRANSCRIPTION	T	1.2	1.2	1	8	LNEIALNE	19085
2WBE	AC	STRUCTURAL PROTEIN	C	1.2	1.2	1	16	QSLLTLGRVITALVDR	19086
2WBJ	CD	IMMUNE SYSTEM	D	1.2	1.2	1	8	EAEISHTQ	19087
2WH2	UV	RIBOSOME	U	1.2	1.2	1	5	DLAVR	19088
2WIU	CB	TRANSFERASE/TRANSCRIPTION	C	1.2	1.2	1	10	IARIMAFLMG	19089
2Z2S	AH	TRANSCRIPTION	H	1.2	1.2	1	12	EAFSLVVATHLS	19090
2Z2S	CF	TRANSCRIPTION	C	1.2	1.2	1	18	LGTIKSRIRLALDRLRQH	19091
2Z2S	GH	TRANSCRIPTION	H	1.2	1.2	1	10	DALLTAYAAG	19092
2Z3R	KJ	CYTOKINE/CYTOKINE RECEPTOR	K	1.2	1.2	1	20	KVTAMKCFLLELQVISLESG	19093
2ZAE	CD	HYDROLASE	C	1.2	1.2	1	6	PEMRLK	19094
2ZCY	AB	HYDROLASE	A	1.2	1.2	1	15	TKLLVSEVAKIMQEA	19095
2ZCY	BI	HYDROLASE	B	1.2	1.2	1	22	TADAEILINTARIHAQNYLKTY	19096
2ZCY	EM	HYDROLASE	M	1.2	1.2	1	18	PSYIFEYLATVMYQRRSK	19097
2ZCY	OP	HYDROLASE	O	1.2	1.2	1	15	TKLLVSEVAKIMQEA	19098
2ZCY	OV	HYDROLASE	O	1.2	1.2	1	18	GPDYRVLVDKSRKVAHTS	19099
2ZCY	T1	HYDROLASE	1	1.2	1.2	1	22	AADTQAIADIVQYHLELYTSQY	19100
2ZCY	V1	HYDROLASE	1	1.2	1.2	1	22	AADTQAIADIVQYHLELYTSQY	19101
2ZCY	WL	HYDROLASE	W	1.2	1.2	1	18	PEDLFETISQALLNAADR	19102
2ZCY	WX	HYDROLASE	X	1.2	1.2	1	17	PQAVSSFVRQELAKSIR	19103
2ZCY	XK	HYDROLASE	X	1.2	1.2	1	13	YSGFYTFSLLDHH	19104
2ZET	AC	SIGNALING PROTEIN	A	1.2	1.2	1	10	ERFRSLTTAF	19105
2ZET	AC	SIGNALING PROTEIN	C	1.2	1.2	1	9	EWYYQHVRA	19106
2ZIV	AB	HYDROLASE	A	1.2	1.2	1	19	AKESAAYLTIMTRYLQKLY	19107
2ZIV	AB	HYDROLASE	B	1.2	1.2	1	17	WKELADFTCAFTKAVAE	19108
2ZJQ	QV	RIBOSOME	V	1.2	1.2	1	11	KELMELRFQAA	19109
2ZT9	BD	PHOTOSYNTHESIS	B	1.2	1.2	1	26	PNDLLYVFPIVIMGSFACIVALAVLD	19110
2ZU6	DE	HYDROLASE	D	1.2	1.2	1	14	RELAQQIQKVVMAL	19111
2ZU6	DE	HYDROLASE	E	1.2	1.2	1	16	FEKTLTPIIQEYFEHG	19112
2ZVN	EB	SIGNALING PROTEIN/TRANSCRIPTION	B	1.2	1.2	1	31	QLQQAEEALVAKQELIDKLKEEAEQHKIVME	19113
2ZXE	AB	HYDROLASE/TRANSPORT PROTEIN	A	1.2	1.2	1	30	YEQRKIVEFTCHTSFFISIVVVQWADLIIC	19114
3A0B	ad	ELECTRON TRANSPORT	a	1.2	1.2	1	5	ICVAY	19115
3A0B	BO	ELECTRON TRANSPORT	B	1.2	1.2	1	10	PPTVKSYARK	19116
3A0B	ci	ELECTRON TRANSPORT	i	1.2	1.2	1	7	FVFGFLS	19117
3A0B	CK	ELECTRON TRANSPORT	C	1.2	1.2	1	9	FPFFVVGVV	19118

3A0B	ck	ELECTRON TRANSPORT	c	1.2	1.2	1	20	FPFFVVGVVHLISSAVLGFG	19119
3A0B	CU	ELECTRON TRANSPORT	C	1.2	1.2	1	19	GPEASQAQAMTFLIRDQKL	19120
3A0B	cu	ELECTRON TRANSPORT	c	1.2	1.2	1	19	GPEASQAQAMTFLIRDQKL	19121
3A0B	CV	ELECTRON TRANSPORT	C	1.2	1.2	1	19	GPEASQAQAMTFLIRDQKL	19122
3A0B	DE	ELECTRON TRANSPORT	D	1.2	1.2	1	7	FTRWCQL	19123
3A0B	DX	ELECTRON TRANSPORT	X	1.2	1.2	1	29	PSLKGFFIGLLSGAVVLGLTFAVLIAISQ	19124
3A0B	ky	ELECTRON TRANSPORT	y	1.2	1.2	1	9	IIFLLAVRR	19125
3A0B	YZ	ELECTRON TRANSPORT	Z	1.2	1.2	1	11	VILSFVMVIGV	19126
3A1Q	EF	GENE REGULATION/SIGNALING PROTEIN	F	1.2	1.2	1	38	EEEQFALALKMSEQEAREVNNQEEKEEELLRKAIAESL	19127
3B2U	UT	IMMUNE SYSTEM/TRANSFERASE	U	1.2	1.2	1	7	DEQLKSG	19128
3B5N	BD	MEMBRANE PROTEIN	D	1.2	1.2	1	61	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLD INLHMNTNRLAG	19129
3B63	AC	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	A	1.2	1.2	1	12	TAEREIVRDIKE	19130
3B63	AC	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	C	1.2	1.2	1	9	VDVRKELYG	19131
3B63	BC	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	C	1.2	1.2	1	16	KSNREKMTQIMFETFN	19132
3B71	BE	PROTEIN BINDING	B	1.2	1.2	1	28	HREIEMAQKLLNSDLGELINKMKLAQQY	19133
3B9J	IJ	OXIDOREDUCTASE	J	1.2	1.2	1	10	TEIGIEMKFK	19134
3BBN	DE	RIBOSOME	D	1.2	1.2	1	17	QYRIRLEEKQKLRFHYG	19135
3BH6	AB	SIGNALING PROTEIN	A	1.2	1.2	1	9	KTTLLKQLA	19136
3BKY	HL	IMMUNE SYSTEM	L	1.2	1.2	1	7	DEQLKSG	19137
3BLW	EF	OXIDOREDUCTASE	E	1.2	1.2	1	14	KLGDGLFRNIITEI	19138
3BLW	EF	OXIDOREDUCTASE	F	1.2	1.2	1	16	NLYGDILSDLNSGLSA	19139
3BLW	IJ	OXIDOREDUCTASE	I	1.2	1.2	1	11	VDNASMQAVAK	19140
3BLW	MN	OXIDOREDUCTASE	N	1.2	1.2	1	16	NLYGDILSDLNSGLSA	19141
3BLW	OP	OXIDOREDUCTASE	P	1.2	1.2	1	16	NLYGDILSDLNSGLSA	19142
3BU8	AC	DNA BINDING PROTEIN	A	1.2	1.2	1	18	HTVSRLLRVMQCLSRIEE	19143
3BZ1	CU	ELECTRON TRANSPORT	U	1.2	1.2	1	10	PTLAKLIVKN	19144
3BZ1	CV	ELECTRON TRANSPORT	C	1.2	1.2	1	19	GPEASQAQAMTFLIRDQKL	19145
3BZ1	DO	ELECTRON TRANSPORT	D	1.2	1.2	1	19	FYTKNLLLNEGIRAWMAPQ	19146
3C03	AC	MEMBRANE PROTEIN, PROTEIN TRANSPORT	A	1.2	1.2	1	13	AKALQIIKLAELY	19147
3C0R	AB	CELL CYCLE, HYDROLASE	A	1.2	1.2	1	5	DAILD	19148
3C0R	AB	CELL CYCLE, HYDROLASE	A	1.2	1.2	1	10	NKDYAQWILK	19149
3C1B	EC	STRUCTURAL PROTEIN/DNA	E	1.2	1.2	1	13	TVALREIRRYQKS	19150
3C3Q	AB	TRANSPORT PROTEIN	B	1.2	1.2	1	8	EEDDDMKE	19151
3C5J	AC	MEMBRANE PROTEIN	A	1.2	1.2	1	22	AQGALANIAVDKANLEIMTKRS	19152

3C5W	AC	HYDROLASE	C	1.2	1.2	1	12	FHDLMELFRIGG	19153
3C5W	CP	HYDROLASE	P	1.2	1.2	1	6	WDGWFR	19154
3C5Z	FH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	H	1.2	1.2	1	21	PEILERTRAELDTVCRHNYEG	19155
3C7K	CD	SIGNALING PROTEIN	C	1.2	1.2	1	25	QYKPVVYSNTIQSLAAIVRAMDTLG	19156
3C7K	CD	SIGNALING PROTEIN	D	1.2	1.2	1	13	HETRELTKTNLQA	19157
3C8K	AD	IMMUNE SYSTEM	D	1.2	1.2	1	9	LDMKIKKMN	19158
3CDG	AK	IMMUNE SYSTEM	A	1.2	1.2	1	24	EAEHQRAYLEDTCVEWLHKYLEKG	19159
3CDG	EF	IMMUNE SYSTEM	F	1.2	1.2	1	10	EEMKFLSIIS	19160
3CF4	AG	OXIDOREDUCTASE	G	1.2	1.2	1	14	KADHYAALDELINA	19161
3CFV	BE	HISTONE/CHAPERONE	B	1.2	1.2	1	5	ENIYN	19162
3CHX	AB	MEMBRANE PROTEIN	A	1.2	1.2	1	15	DRRVGAIVLAVTILA	19163
3CHX	EF	MEMBRANE PROTEIN	E	1.2	1.2	1	15	DRRVGAIVLAVTILA	19164
3CHX	IJ	MEMBRANE PROTEIN	I	1.2	1.2	1	15	DRRVGAIVLAVTILA	19165
3CJB	AG	STRUCTURAL PROTEIN	A	1.2	1.2	1	9	QAVLSLYAS	19166
3CJC	AG	STRUCTURAL PROTEIN/HYDROLASE	A	1.2	1.2	1	9	QAVLSLYAS	19167
3CJI	BD	VIRUS	B	1.2	1.2	1	7	LLQLARI	19168
3CJT	KL	TRANSFERASE/RIBOSOMAL PROTEIN	K	1.2	1.2	1	6	AWRRDL	19169
3CJT	KL	TRANSFERASE/RIBOSOMAL PROTEIN	L	1.2	1.2	1	12	IMEFVKAFNAAT	19170
3CJT	MN	TRANSFERASE/RIBOSOMAL PROTEIN	N	1.2	1.2	1	12	IMEFVKAFNAAT	19171
3CMA	FM	RIBOSOME	M	1.2	1.2	1	7	LDKARSQ	19172
3CPJ	GB	PROTEIN TRANSPORT	G	1.2	1.2	1	15	LGELPQGFARLSAIY	19173
3CQX	AD	CHAPERONE	A	1.2	1.2	1	6	DAAKNQ	19174
3CSY	CN	IMMUNE SYSTEM/VIRAL PROTEIN	N	1.2	1.2	1	23	LICGLRQLANETTQALQLFLRAT	19175
3CUE	AD	PROTEIN TRANSPORT	A	1.2	1.2	1	24	NLAIQIADNFLRKVYCLYSDYVMK	19176
3CUE	CF	PROTEIN TRANSPORT	C	1.2	1.2	1	23	QNEEDAKLLYGMIFSLRSITQKL	19177
3CUE	GL	PROTEIN TRANSPORT	G	1.2	1.2	1	21	SNEYLILASTLHGVFAIASQL	19178
3CUE	HJ	PROTEIN TRANSPORT	J	1.2	1.2	1	11	SLKAMGEEIWK	19179
3CUE	MR	PROTEIN TRANSPORT	M	1.2	1.2	1	21	SNEYLILASTLHGVFAIASQL	19180
3CUE	NP	PROTEIN TRANSPORT	P	1.2	1.2	1	11	SLKAMGEEIWK	19181
3CUE	OQ	PROTEIN TRANSPORT	O	1.2	1.2	1	17	TQVLQYIYSHIYVKYVS	19182
3CUE	TV	PROTEIN TRANSPORT	V	1.2	1.2	1	11	SLKAMGEEIWK	19183
3CUE	UW	PROTEIN TRANSPORT	U	1.2	1.2	1	17	TQVLQYIYSHIYVKYVS	19184
3CUQ	AC	PROTEIN TRANSPORT	A	1.2	1.2	1	23	VGDFYYELGVQIIEVCLALKHRN	19185
3CWB	AE	OXIDOREDUCTASE	A	1.2	1.2	1	6	LKEMDN	19186
3CWB	AE	OXIDOREDUCTASE	A	1.2	1.2	1	14	MTNVTFDYLHATAF	19187
3CWB	CF	OXIDOREDUCTASE	C	1.2	1.2	1	23	PLSQTLFWLLVANLLILTWIGSQ	19188
3CWB	CF	OXIDOREDUCTASE	F	1.2	1.2	1	20	DLYNERMFRIKRALDLSLKH	19189
3CWB	CG	OXIDOREDUCTASE	C	1.2	1.2	1	29	IIIGQMASLSYFTILLILFPTIGTLENKM	19190
3CWB	QT	OXIDOREDUCTASE	Q	1.2	1.2	1	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	19191

3CXH	DI	OXIDOREDUCTASE	D	1.2	1.2	1	19	HASIRRGYQVYREVCAACH	19192
3CXH	LS	OXIDOREDUCTASE	L	1.2	1.2	1	7	YMRIRSD	19193
3CXH	PU	OXIDOREDUCTASE	P	1.2	1.2	1	8	PHEIQEAN	19194
3D2E	CD	CHAPERONE	D	1.2	1.2	1	8	RARFEELC	19195
3D4X	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	1.2	1.2	1	19	PQVQAAFQKVVAGVANALA	19196
3D54	AC	LIGASE	C	1.2	1.2	1	15	PRGETIERVLREEKG	19197
3D5B	P8	RIBOSOME	8	1.2	1.2	1	8	KPEAERIK	19198
3D5D	G4	RIBOSOME	G	1.2	1.2	1	16	ARILEKAAQELALITG	19199
3D85	AC	IMMUNE SYSTEM/CYTOKINE	C	1.2	1.2	1	32	PWQRLLLRFKILRSLQAFVAVAARVFAHGAAT	19200
3DAB	EF	CELL CYCLE	E	1.2	1.2	1	15	VKEVMHYLGQYIMVK	19201
3DBH	CD	CELL CYCLE	C	1.2	1.2	1	34	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQSIG	19202
3DBH	CD	CELL CYCLE	C	1.2	1.2	1	5	GEDAG	19203
3DBH	CH	CELL CYCLE	H	1.2	1.2	1	15	PEHCIEYVRMLQWPK	19204
3DBH	EK	CELL CYCLE	K	1.2	1.2	1	13	VERIKERVEEKEG	19205
3DBH	GH	CELL CYCLE	G	1.2	1.2	1	14	ATGTEILKNLVLPG	19206
3DGE	BD	TRANSFERASE/SIGNALING PROTEIN	B	1.2	1.2	1	32	LSTLKEFLEVIIDQSNHLENLLNELLDFSRLE	19207
3DGP	AB	TRANSCRIPTION	B	1.2	1.2	1	15	PSIKALILQIDAKMS	19208
3DHH	AE	OXIDOREDUCTASE	A	1.2	1.2	1	19	YTFANLISSIQTDESRHAQ	19209
3DHH	AE	OXIDOREDUCTASE	E	1.2	1.2	1	8	TLADQALH	19210
3DHR	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.2	1.2	1	19	PVNFKLLGHCFLVVVAVHF	19211
3DHR	GF	OXYGEN STORAGE, OXYGEN TRANSPORT	G	1.2	1.2	1	19	PVNFKLLGHCFLVVVAVHF	19212
3DHW	EG	MEMBRANE PROTEIN/HYDROLASE	E	1.2	1.2	1	9	LIEASRAMG	19213
3DIF	AB	IMMUNE SYSTEM	A	1.2	1.2	1	6	SEQLTS	19214
3DIN	BF	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	1.2	1.2	1	22	GTSALIAVGVALDIIQQMETHM	19215
3DIN	FG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	1.2	1.2	1	33	RSTEQYLHRVLNRVTFIGAVFLVVIALLPYLVQ	19216
3DRA	AB	TRANSFERASE	A	1.2	1.2	1	12	NSAWSHRFFLLF	19217
3DTP	AC	CONTRACTILE PROTEIN	C	1.2	1.2	1	12	YSQCGDVMRALG	19218
3DTP	BD	CONTRACTILE PROTEIN	B	1.2	1.2	1	5	DVIIA	19219
3DTP	BD	CONTRACTILE PROTEIN	D	1.2	1.2	1	14	EEQTAEFKEAFQLF	19220
3DTV	CD	LYASE	D	1.2	1.2	1	16	AAFNAALTVAMREATG	19221
3DVG	AB	IMMUNE SYSTEM	A	1.2	1.2	1	6	DEQLKS	19222
3DW8	DE	HYDROLASE	D	1.2	1.2	1	13	DEVLLALAEQLGT	19223
3DXR	AB	PROTEIN TRANSPORT	A	1.2	1.2	1	28	QKVVEQKQMKDFMRLYSNLVERCFTDCV	19224
3E 20	AB	TRANSLATION	B	1.2	1.2	1	16	VKYVQEKKLIQRFFDE	19225
3E 20	EH	TRANSLATION	H	1.2	1.2	1	16	VKYVQEKKLIQRFFDE	19226

3E0J	EF	TRANSFERASE	E	1.2	1.2	1	27	LTKKTQAASVEAVKMLDEILLQLSASV	19227
3E1K	GH	TRANSCRIPTION	H	1.2	1.2	1	8	MDDVYNYI	19228
3EA5	AB	TRANSPORT PROTEIN	B	1.2	1.2	1	15	SVKTQQFAQRWITQV	19229
3EA5	CD	TRANSPORT PROTEIN	D	1.2	1.2	1	14	KAVRLAALNALADS	19230
3EA5	CD	TRANSPORT PROTEIN	D	1.2	1.2	1	16	VSMSAGACLQLFAQNC	19231
3ECH	AC	TRANSCRIPTION, TRANSCRIPTION REGULATION	A	1.2	1.2	1	13	PPDVHVLKLIDEQ	19232
3EG5	AB	SIGNALING PROTEIN	B	1.2	1.2	1	15	IVIKREMVSQYLHTS	19233
3EG5	CD	SIGNALING PROTEIN	D	1.2	1.2	1	15	IVIKREMVSQYLHTS	19234
3EJB	AB	OXIDOREDUCTASE/LIPID TRANSPORT	A	1.2	1.2	1	7	DEEAEKI	19235
3ENO	AC	HYDROLASE/UNKNOWN FUNCTION	A	1.2	1.2	1	19	APSLRVTATAARTISVLTG	19236
3EOA	BJ	IMMUNE SYSTEM/CELL ADHESION	J	1.2	1.2	1	18	PDEFQKILDFMKDVMKKL	19237
3ET6	AB	LYASE	B	1.2	1.2	1	15	LLDELYQRFDAAIEE	19238
3ETR	MN	OXIDOREDUCTASE	N	1.2	1.2	1	8	PEKIRNAC	19239
3EUH	AD	CELL CYCLE	D	1.2	1.2	1	16	ELDMMVGKILCYLYLS	19240
3EX7	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.2	1.2	1	11	VGEDIRKLDYG	19241
3EXG	EF	OXIDOREDUCTASE	E	1.2	1.2	1	13	GQIFEAYNMAALW	19242
3EXG	MN	OXIDOREDUCTASE	N	1.2	1.2	1	14	EMGFAGIAVGAAMA	19243
3EXG	MP	OXIDOREDUCTASE	P	1.2	1.2	1	6	KILEDN	19244
3EXG	Q2	OXIDOREDUCTASE	Q	1.2	1.2	1	27	REDGLKYYRMMQTVRRMELKADQLYKQ	19245
3EXH	BC	OXIDOREDUCTASE	B	1.2	1.2	1	5	VAQYD	19246
3EYM	CD	VIRAL PROTEIN	D	1.2	1.2	1	19	LKSTQAAIDQINGKLNRVI	19247
3EZQ	EF	APOPTOSIS	F	1.2	1.2	1	16	LTERVRESLRIWKNTE	19248
3EZQ	OP	APOPTOSIS	O	1.2	1.2	1	15	SDVDLSKYITTIAGV	19249
3F1F	OT	RIBOSOME	O	1.2	1.2	1	7	RELREKG	19250
3F1F	OT	RIBOSOME	T	1.2	1.2	1	5	YFIRN	19251
3F3P	EG	STRUCTURAL PROTEIN	G	1.2	1.2	1	9	NSFAFELCS	19252
3F3P	EH	STRUCTURAL PROTEIN	H	1.2	1.2	1	6	SAEYLQ	19253
3F5C	AB	TRANSCRIPTION	B	1.2	1.2	1	23	VKYIEGLQWRTQQILTEHIRMMQ	19254
3F6Z	CD	HYDROLASE	C	1.2	1.2	1	13	LGNWVCAAKFESN	19255
3F9K	BC	VIRAL PROTEIN, RECOMBINATION	B	1.2	1.2	1	13	GRQTALFLLKLAS	19256
3F9K	ce	VIRAL PROTEIN, RECOMBINATION	e	1.2	1.2	1	10	TEMITTLKKI	19257
3F9K	de	VIRAL PROTEIN, RECOMBINATION	d	1.2	1.2	1	13	GRQTALFLLKLAS	19258
3F9K	Ja	VIRAL PROTEIN, RECOMBINATION	J	1.2	1.2	1	10	NLVARQIVNS	19259
3F9K	NO	VIRAL PROTEIN, RECOMBINATION	N	1.2	1.2	1	13	GRQTALFLLKLAS	19260
3F9K	RC	VIRAL PROTEIN, RECOMBINATION	C	1.2	1.2	1	21	QVIMEKSTMLYNKFKNMFLVG	19261
3F9K	UW	VIRAL PROTEIN, RECOMBINATION	U	1.2	1.2	1	12	IEPAQEEHEKYH	19262
3F9K	VW	VIRAL PROTEIN, RECOMBINATION	V	1.2	1.2	1	13	GRQTALFLLKLAS	19263
3FCS	AB	CELL ADHESION/BLOOD CLOTTING	B	1.2	1.2	1	11	VNLYQNYSELI	19264

3FFC	FB	IMMUNE SYSTEM	F	1.2	1.2	1	29	PEYWDRNTQIFKTNTQTDRESLRNLRGYY	19265
3FH6	FG	TRANSPORT PROTEIN	G	1.2	1.2	1	9	MFPLLMVVA	19266
3FH6	HI	TRANSPORT PROTEIN	I	1.2	1.2	1	9	MFPLLMVVA	19267
3FHI	AB	TRANSFERASE	B	1.2	1.2	1	14	RDSYRRILMGSTLR	19268
3FIK	QR	RIBOSOME	Q	1.2	1.2	1	6	QYAYRD	19269
3FKS	BE	HYDROLASE	B	1.2	1.2	1	15	LSKQAVAYRQLSLLL	19270
3FKS	EG	HYDROLASE	E	1.2	1.2	1	28	QEHYDVASKVQETLQTYKSLQDIIAILG	19271
3FKS	FG	HYDROLASE	G	1.2	1.2	1	10	LKEVEMRLKS	19272
3FKS	JM	HYDROLASE	J	1.2	1.2	1	15	LSKQAVAYRQLSLLL	19273
3FKS	JM	HYDROLASE	J	1.2	1.2	1	7	AELFYKG	19274
3FKS	KO	HYDROLASE	O	1.2	1.2	1	23	PGARARVALTGLTIAEYFRDEEG	19275
3FKS	KO	HYDROLASE	O	1.2	1.2	1	16	IFRFTQAGSEVSALLG	19276
3FKS	LM	HYDROLASE	M	1.2	1.2	1	5	EVFTG	19277
3FKS	TX	HYDROLASE	X	1.2	1.2	1	7	RGISELG	19278
3FKU	AD	VIRAL PROTEIN/IMMUNE SYSTEM	A	1.2	1.2	1	10	YEELKHLLSR	19279
3FS4	CB	OXYGEN STORAGE, OXYGEN TRANSPORT	C	1.2	1.2	1	19	PVNFKLLGQCFLVVVAIHH	19280
3FSG	BD	HYDROLASE	D	1.2	1.2	1	10	YQEQLKLINH	19281
3FUB	AB	HORMONE	A	1.2	1.2	1	11	NCLDAAKACNL	19282
3FWC	AB	CELL CYCLE, TRANSCRIPTION	A	1.2	1.2	1	11	YHELKVAMKAL	19283
3FWC	FG	CELL CYCLE, TRANSCRIPTION	G	1.2	1.2	1	8	NYELISNE	19284
3G43	CF	METAL BINDING PROTEIN	C	1.2	1.2	1	15	EEQIAEFKEAFSLFD	19285
3G4S	S2	RIBOSOME	2	1.2	1.2	1	14	KATKKRLAKLDNQN	19286
3G6J	GH	IMMUNE SYSTEM	G	1.2	1.2	1	6	DEQLKS	19287
3GBM	CD	VIRAL PROTEIN / IMMUNE SYSTEM	C	1.2	1.2	1	9	YEELKHLLS	19288
3GE8	AB	OXIDOREDUCTASE	A	1.2	1.2	1	7	LFFPHEY	19289
3GE8	AB	OXIDOREDUCTASE	A	1.2	1.2	1	7	IVDRFLA	19290
3GE8	AE	OXIDOREDUCTASE	E	1.2	1.2	1	5	MQELE	19291
3GE8	DF	OXIDOREDUCTASE	F	1.2	1.2	1	8	ERELWEKE	19292
3GHG	AB	BLOOD CLOTTING	A	1.2	1.2	1	29	GCRMKGLIDEVNQDFTNRINKLKNSLFEY	19293
3GHG	AB	BLOOD CLOTTING	B	1.2	1.2	1	10	YMYLLKDLWQ	19294
3GHG	DE	BLOOD CLOTTING	D	1.2	1.2	1	17	GCRMKGLIDEVNQDFTN	19295
3GHG	DE	BLOOD CLOTTING	E	1.2	1.2	1	8	LYIDETVN	19296
3GHG	EF	BLOOD CLOTTING	F	1.2	1.2	1	7	TCGIADF	19297
3GLH	FG	TRANSFERASE	G	1.2	1.2	1	21	PTDIQLYYQTLLIGRKELPYA	19298
3GLH	IJ	TRANSFERASE	J	1.2	1.2	1	12	VDAVREVTEKLN	19299
3GLH	NO	TRANSFERASE	N	1.2	1.2	1	17	PTDIQLYYQTLLIGRKE	19300
3GLI	BO	TRANSFERASE/DNA	B	1.2	1.2	1	15	RRMGVEMTLLRALAF	19301
3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	A	1.2	1.2	1	12	ALNCGIMLRECI	19302

3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	B	1.2	1.2	1	5	HMENL	19303
3GTM	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.2	1.2	1	6	LIEKFL	19304
3GTU	AB	TRANSFERASE	A	1.2	1.2	1	27	EKEQIREDILENQFMDSRMQLAKLCYD	19305
3H0L	AE	LIGASE	E	1.2	1.2	1	15	TKIGKEVIKEMVETG	19306
3H0L	GH	LIGASE	G	1.2	1.2	1	11	IIAPSEASSNL	19307
3H0L	JK	LIGASE	J	1.2	1.2	1	19	YLKAQKVRRLITNDFLKAF	19308
3H0L	PQ	LIGASE	P	1.2	1.2	1	19	YLKAQKVRRLITNDFLKAF	19309
3H0L	ST	LIGASE	S	1.2	1.2	1	11	IIAPSEASSNL	19310
3H0L	VW	LIGASE	V	1.2	1.2	1	19	YLKAQKVRRLITNDFLKAF	19311
3H2V	AE	CELL ADHESION	A	1.2	1.2	1	30	TKRALIQCAKDIAKASDEVTRLAKEVAKQC	19312
3H32	AB	BLOOD CLOTTING	A	1.2	1.2	1	14	LKDYEDQQKQLEQV	19313
3H4P	Hi	HYDROLASE	i	1.2	1.2	1	6	LYKMRT	19314
3H4P	Mn	HYDROLASE	n	1.2	1.2	1	11	ACATLLSNILH	19315
3H4P	Nn	HYDROLASE	n	1.2	1.2	1	6	LYKMRT	19316
3HAX	AC	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	A	1.2	1.2	1	8	EEYFRKAI	19317
3HC0	AB	IMMUNE SYSTEM	B	1.2	1.2	1	6	DEQLKS	19318
3HD7	FH	EXOCYTOSIS	F	1.2	1.2	1	96	KQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVE HAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG	19319
3HJY	AB	ISOMERASE/RNA	A	1.2	1.2	1	15	LHDLVDYYYFWKEDG	19320
3HJY	AB	ISOMERASE/RNA	B	1.2	1.2	1	11	GEYRRRWKREV	19321
3HKZ	AB	TRANSFERASE	B	1.2	1.2	1	5	RLLDN	19322
3HKZ	AC	TRANSFERASE	A	1.2	1.2	1	9	YMQRRLINA	19323
3HKZ	AC	TRANSFERASE	C	1.2	1.2	1	8	VVENIIIG	19324
3HKZ	CH	TRANSFERASE	C	1.2	1.2	1	11	IEAAREIIIRE	19325
3HKZ	IM	TRANSFERASE	I	1.2	1.2	1	10	VKHIYEFLKA	19326
3HKZ	IM	TRANSFERASE	M	1.2	1.2	1	8	TVKHLLDA	19327
3HKZ	JV	TRANSFERASE	V	1.2	1.2	1	11	HTLGNLIAGTL	19328
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.2	1.2	1	10	FINIAQMSAC	19329
3HOU	NV	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	V	1.2	1.2	1	7	LIEKFLR	19330
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.2	1.2	1	11	ASFLKERLMEA	19331
3HOY	BK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	K	1.2	1.2	1	12	HTLGNLIRAELL	19332
3HPG	CJ	TRANSFERASE	J	1.2	1.2	1	10	VNRCIEALDE	19333

3HPG	EL	TRANSFERASE	E	1.2	1.2	1	15	GQEFRVQTMKWYAMF	19334
3HRD	AD	OXIDOREDUCTASE	D	1.2	1.2	1	9	LLQQCFLEA	19335
3HRD	FH	OXIDOREDUCTASE	F	1.2	1.2	1	22	RSMVEGQIEGGVTMGQGFVLME	19336
3HRW	AB	OXYGEN TRANSPORT	B	1.2	1.2	1	18	PENFRLLGNMIVIVLGHH	19337
3I2C	LH	IMMUNE SYSTEM	L	1.2	1.2	1	6	SEQLTS	19338
3I3T	ED	HYDROLASE	E	1.2	1.2	1	10	TRFRAVFQKY	19339
4RUB	AT	LYASE(CARBON-CARBON)	A	1.2	1.2	1	15	CEEMIKRAVFARELG	19340
4SGB	EI	COMPLEX (SERINE PROTEINASE-INHIBITOR)	E	1.2	1.2	1	5	GHCTD	19341
6RLX	AD	HORMONE (MUSCLE RELAXANT)	D	1.2	1.2	1	14	RELVRAQIAICGMS	19342
7INS	CD	HORMONE	C	1.2	1.2	1	7	LYQLENY	19343
9PAI	AB	HYDROLASE INHIBITOR	A	1.2	1.2	1	10	AQLISHWKGN	19344
1A0O	EF	CHEMOTAXIS	E	1.1	1.1	1	15	AATLEEKLNKIFEKL	19345
1A3L	LH	IMMUNOGLOBULIN	L	1.1	1.1	1	6	SEQLTS	19346
1A9W	CF	OXYGEN TRANSPORT	F	1.1	1.1	1	20	PENFKLLGNVMVIILATHFG	19347
1AD9	LH	IMMUNOGLOBULIN	L	1.1	1.1	1	5	DEQLK	19348
1AE6	LH	IMMUNOGLOBULIN	L	1.1	1.1	1	6	SEQLTS	19349
1AHJ	AB	LYASE	B	1.1	1.1	1	9	QDELESLAG	19350
1AHJ	EF	LYASE	E	1.1	1.1	1	6	KDCLIG	19351
1AOI	AG	DNA BINDING PROTEIN/DNA	A	1.1	1.1	1	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	19352
1AON	CQ	COMPLEX (GROEL/GROES)	C	1.1	1.1	1	11	LPVLEAVAKAG	19353
1AVO	KJ	PROTEASOME ACTIVATOR	J	1.1	1.1	1	6	FEKLKK	19354
1B33	AB	PHOTOSYNTHESIS	B	1.1	1.1	1	14	GELRVRAATTIAAN	19355
1B33	AI	PHOTOSYNTHESIS	I	1.1	1.1	1	14	AAAIVKEAVAKSLL	19356
1B33	LM	PHOTOSYNTHESIS	L	1.1	1.1	1	13	PGELDRIKSFVSS	19357
1B4U	CD	DIOXYGENASE	C	1.1	1.1	1	8	FQFAAGSM	19358
1B6C	CH	COMPLEX (ISOMERASE/PROTEIN KINASE)	H	1.1	1.1	1	8	LFDYLNRY	19359
1BBT	14	VIRUS	1	1.1	1.1	1	5	VSFIM	19360
1BCC	CE	OXIDOREDUCTASE	C	1.1	1.1	1	21	FGSLLAVCLMTQILTGLLLAM	19361
1BCP	GJ	TOXIN	G	1.1	1.1	1	6	YESIAY	19362
1BCR	AB	COMPLEX (SERINE PROTEASE/INHIBITOR)	B	1.1	1.1	1	5	VPLHR	19363
1BEV	23	VIRUS	3	1.1	1.1	1	8	LLGTLAKH	19364
1BFO	GH	ANTIBODY	G	1.1	1.1	1	5	TEQLA	19365
1BGY	OP	ELECTRON TRANSPORT	O	1.1	1.1	1	26	GWIIRYMHANGASMFFICLYMHVGRG	19366
1BGY	PQ	ELECTRON TRANSPORT	Q	1.1	1.1	1	35	EARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSA	19367
1BI7	AB	COMPLEX (KINASE/ANTI-ONCOGENE)	B	1.1	1.1	1	9	DWLATAAAR	19368
1BJO	AB	AMINOTRANSFERASE	A	1.1	1.1	1	13	YWAASAIKEAKKY	19369
1BJO	AB	AMINOTRANSFERASE	B	1.1	1.1	1	12	GRGQFAAVPLNI	19370

1BP3	AB	HORMONE/GROWTH FACTOR	A	1.1	1.1	1	5	REETQ	19371
1BR1	CD	MUSCLE PROTEIN	D	1.1	1.1	1	9	EEEVEQLVA	19372
1BR1	EF	MUSCLE PROTEIN	F	1.1	1.1	1	9	FEDYVEGLR	19373
1BR1	GH	MUSCLE PROTEIN	H	1.1	1.1	1	9	FEDYVEGLR	19374
1BTH	LH	COMPLEX (SERINE PROTEASE/INHIBITOR)	L	1.1	1.1	1	9	ERELLESYI	19375
1BXN	AI	LYASE	A	1.1	1.1	1	20	WRDRFLFVMDAVNKASAATG	19376
1BXN	CI	LYASE	C	1.1	1.1	1	14	GRNYGRVVYEGLKG	19377
1BXN	GL	LYASE	G	1.1	1.1	1	20	WRDRFLFVMDAVNKASAATG	19378
1C08	BC	IMMUNE SYSTEM/HYDROLASE	C	1.1	1.1	1	5	SRWWC	19379
1C12	AB	IMMUNE SYSTEM	A	1.1	1.1	1	7	SEQLTSG	19380
1C4Z	AD	LIGASE	D	1.1	1.1	1	5	MKELE	19381
1C5D	AB	IMMUNE SYSTEM	A	1.1	1.1	1	6	TEQLAT	19382
1C9B	IJ	TRANSCRIPTION/DNA	I	1.1	1.1	1	7	FKEICAV	19383
1C9B	MN	TRANSCRIPTION/DNA	M	1.1	1.1	1	7	FKEICAV	19384
1CAX	CF	SEED STORAGE PROTEIN	C	1.1	1.1	1	7	YDEIEQT	19385
1CB7	AB	ISOMERASE	A	1.1	1.1	1	12	WPDVEKRFKDMG	19386
1CBV	LH	IMMUNE SYSTEM/DNA	L	1.1	1.1	1	5	SEQLT	19387
1CDL	CG	CALCIUM-BINDING PROTEIN	C	1.1	1.1	1	12	AAELRHVMTNLG	19388
1CDL	CG	CALCIUM-BINDING PROTEIN	C	1.1	1.1	1	8	YEEFVQMM	19389
1CDL	DH	CALCIUM-BINDING PROTEIN	D	1.1	1.1	1	7	YEEFVQM	19390
1CG5	AB	OXYGEN TRANSPORT	A	1.1	1.1	1	19	PHNFHLFADCIVVTLAVNL	19391
1CN4	AC	HAEMATOPOIETIC CYTOKINE	C	1.1	1.1	1	25	EPLQLHVDKAVSGLRSLTTLLRALG	19392
1CPC	AB	LIGHT HARVESTING PROTEIN	B	1.1	1.1	1	13	GSQIDALSALVAD	19393
1CPC	KL	LIGHT HARVESTING PROTEIN	L	1.1	1.1	1	19	SVLDDRCLNGLKETYLALG	19394
1D2Z	CD	APOPTOSIS	D	1.1	1.1	1	13	FSAADFVALDFLN	19395
1DCE	CD	TRANSFERASE	C	1.1	1.1	1	20	EQKLKLYQSATQAVFQKRQA	19396
1DD4	BC	RIBOSOME	C	1.1	1.1	1	11	TIDEIIEAIEK	19397
1DE4	DF	METAL TRANSPORT INHIBITOR/RECEPTOR	D	1.1	1.1	1	26	IRARQNRAYLERDCPAQLQQLLELGR	19398
1DE4	GI	METAL TRANSPORT INHIBITOR/RECEPTOR	I	1.1	1.1	1	17	ERYNSQLLSFVRDLNQY	19399
1DEE	AB	IMMUNE SYSTEM	A	1.1	1.1	1	6	DEQLKS	19400
1DFK	AY	CONTRACTILE PROTEIN	Y	1.1	1.1	1	9	EETIRNAFA	19401
1DFK	YZ	CONTRACTILE PROTEIN	Z	1.1	1.1	1	18	QDEIDDLKDVFELFDFWD	19402
1DGH	AD	OXIDOREDUCTASE	D	1.1	1.1	1	15	IFIQKKAVKNFTEVH	19403
1DGH	CB	OXIDOREDUCTASE	B	1.1	1.1	1	9	FPSFIHSQK	19404
1DGH	CB	OXIDOREDUCTASE	B	1.1	1.1	1	19	KMLQGRLFAYPDTHRHRLG	19405
1DGH	CB	OXIDOREDUCTASE	C	1.1	1.1	1	9	FPSFIHSQK	19406
1DGR	BV	PLANT PROTEIN	V	1.1	1.1	1	6	SQLRDL	19407

1DN0	CD	IMMUNE SYSTEM	C	1.1	1.1	1	6	DEQLKS	19408
1DX5	AO	SERINE PROTEINASE	O	1.1	1.1	1	11	KKWIQKVIDQF	19409
1DX5	BM	SERINE PROTEINASE	M	1.1	1.1	1	11	KKWIQKVIDQF	19410
1DX5	BN	SERINE PROTEINASE	N	1.1	1.1	1	11	KKWIQKVIDQF	19411
1DX5	CN	SERINE PROTEINASE	N	1.1	1.1	1	8	RETAASLL	19412
1E0A	AB	SIGNALLING PROTEIN	B	1.1	1.1	1	8	EQWARLLQ	19413
1E1C	AB	ISOMERASE	A	1.1	1.1	1	13	AARRFEELAAKAG	19414
1E3D	AB	HYDROGENASE	B	1.1	1.1	1	10	PRDAQHFTQR	19415
1E6Y	BC	OXIDOREDUCTASE	B	1.1	1.1	1	15	IGTVIESVVRRAIEA	19416
1EAY	BD	SIGNAL TRANSDUCTION COMPLEX	D	1.1	1.1	1	13	EVDLLEEELGHLT	19417
1EF1	BD	MEMBRANE PROTEIN	B	1.1	1.1	1	7	QRVLEQH	19418
1EFP	AB	ELECTRON TRANSPORT	B	1.1	1.1	1	11	ATGQMLAAILG	19419
1EFP	CD	ELECTRON TRANSPORT	D	1.1	1.1	1	15	PLAVAKILAAVARAE	19420
1EFU	AB	COMPLEX (TWO ELONGATION FACTORS)	A	1.1	1.1	1	16	KTTLTAAITTVLAKTY	19421
1EFU	AB	COMPLEX (TWO ELONGATION FACTORS)	A	1.1	1.1	1	10	HADYVKNMIT	19422
1EJR	CA	HYDROLASE	A	1.1	1.1	1	5	VPEMI	19423
1EV1	13	VIRUS	3	1.1	1.1	1	6	LMEIAE	19424
1EV1	24	VIRUS	4	1.1	1.1	1	6	PGKFTE	19425
1EYS	CM	ELECTRON TRANSPORT	C	1.1	1.1	1	18	LKQAEWTFGLMMNISDSL	19426
1EYS	LH	ELECTRON TRANSPORT	L	1.1	1.1	1	12	SEHENTFFRDIV	19427
1EYX	AB	PHOTOSYNTHESIS	A	1.1	1.1	1	9	GPLDEWGIA	19428
1EZX	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	19	TPNLAEFAFSLYRQLAHQS	19429
1F45	AB	CYTOKINE/CYTPKINE	B	1.1	1.1	1	16	NLLRAVSNMLQKARQT	19430
1F4W	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6	SEELET	19431
1F66	EF	STRUCTURAL PROTEIN/DNA	F	1.1	1.1	1	11	AMDVVYALKRQ	19432
1F66	GH	STRUCTURAL PROTEIN/DNA	G	1.1	1.1	1	5	RSQRA	19433
1F6M	FH	OXIDOREDUCTASE	F	1.1	1.1	1	7	ATCDGFF	19434
1F93	AE	TRANSCRIPTION	A	1.1	1.1	1	10	RVALQAEKLD	19435
1F96	BC	INHIBITOR/OXIDOREDUCTASE	B	1.1	1.1	1	17	EKDIAAHIKKEFDKKYN	19436
1F99	AL	PHOTOSYNTHESIS	L	1.1	1.1	1	25	SRRMAACLRDMEIVLRYVSYAMIAG	19437
1F99	KN	PHOTOSYNTHESIS	N	1.1	1.1	1	25	SRRMAACLRDMEIVLRYVSYAMIAG	19438
1FBI	PQ	COMPLEX (ANTIBODY/ANTIGEN)	P	1.1	1.1	1	7	SEQLTSG	19439
1FDL	LH	COMPLEX (ANTIBODY-ANTIGEN)	L	1.1	1.1	1	7	SEQLTSG	19440
1FDL	LY	COMPLEX (ANTIBODY-ANTIGEN)	Y	1.1	1.1	1	5	VQAWI	19441
1FFT	AB	OXIDOREDUCTASE	B	1.1	1.1	1	11	SLILTAFGLML	19442
1FFT	AC	OXIDOREDUCTASE	A	1.1	1.1	1	27	VDYWIWSLQLSGIGTTLTGINFFVTIL	19443
1FIQ	AC	OXIDOREDUCTASE	A	1.1	1.1	1	7	RPILQGF	19444
1FMD	14	VIRUS	1	1.1	1.1	1	6	VAFVLD	19445

1FMD	23	VIRUS	3	1.1	1.1	1	6	PEEAAH	19446
1FNT	CJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.1	1.1	1	22	ATDVTTLNEMFRYKTNLYKLKE	19447
1FNT	Fg	HYDROLASE/HYDROLASE ACTIVATOR	F	1.1	1.1	1	13	FQVEYALEAIKQG	19448
1FNT	Ia	HYDROLASE/HYDROLASE ACTIVATOR	a	1.1	1.1	1	11	LIMPFLDNQVN	19449
1FNT	PW	HYDROLASE/HYDROLASE ACTIVATOR	P	1.1	1.1	1	18	GPDYRVLVDKSRKVAHTS	19450
1FNT	Sa	HYDROLASE/HYDROLASE ACTIVATOR	a	1.1	1.1	1	21	AADGDALVKRFKNSVKWYHFD	19451
1FNT	Ta	HYDROLASE/HYDROLASE ACTIVATOR	T	1.1	1.1	1	23	APDARVLSNYLRQQCNYSSLVFN	19452
1FNT	VW	HYDROLASE/HYDROLASE ACTIVATOR	V	1.1	1.1	1	20	AADTQAIADIVQYHLELYTS	19453
1FNT	WN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.1	1.1	1	11	FGAHMANPLLR	19454
1FNT	XL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.1	1.1	1	13	VGELFWKVKEEEG	19455
1FQV	EF	LIGASE	F	1.1	1.1	1	14	QGTLFELILAANYL	19456
1FQV	GH	LIGASE	H	1.1	1.1	1	10	EEEEAQVRKE	19457
1FQV	IJ	LIGASE	J	1.1	1.1	1	11	EEEEAQVRKEN	19458
1FQV	MN	LIGASE	N	1.1	1.1	1	11	EEEEAQVRKEN	19459
1FRG	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.1	1.1	1	6	SEQLTS	19460
1FS0	EG	HYDROLASE	E	1.1	1.1	1	20	YAQASAELAKAIAQLRVIEL	19461
1FSK	HI	IMMUNE SYSTEM	H	1.1	1.1	1	5	SEQLT	19462
1FX0	AB	HYDROLASE	A	1.1	1.1	1	10	ASSVAQVVTN	19463
1FX0	AB	HYDROLASE	A	1.1	1.1	1	11	QVRKYLVELRT	19464
1FXK	AC	CHAPERONE	C	1.1	1.1	1	48	FEDAMESIKSQKNELESTLQKMGENLRAITDIMMKLSPQAEELLAAVA	19465
1FXW	AF	HYDROLASE	A	1.1	1.1	1	18	RLGYTPVCRALHSLLLRL	19466
1FYH	AB	IMMUNE SYSTEM	A	1.1	1.1	1	7	LIQVMAE	19467
1FYZ	AC	OXIDOREDUCTASE	C	1.1	1.1	1	9	AVPKAEWTN	19468
1FYZ	BC	OXIDOREDUCTASE	C	1.1	1.1	1	23	KEEITASLYRVVDDWIEDYASRI	19469
1FYZ	BD	OXIDOREDUCTASE	D	1.1	1.1	1	9	AVPKAEWTN	19470
1G0U	AG	HYDROLASE	G	1.1	1.1	1	16	QQEITTNLENHFKKSK	19471
1G0U	CJ	HYDROLASE	C	1.1	1.1	1	22	NADSRILIEKARVEAQSHRLTL	19472
1G0U	FG	HYDROLASE	G	1.1	1.1	1	23	IPDARNAALRAKAEAAEFRYKYG	19473
1G0U	JK	HYDROLASE	J	1.1	1.1	1	23	AGDTVQFAEYIQANIQLYSIRED	19474
1G0U	M2	HYDROLASE	2	1.1	1.1	1	6	SGSTFI	19475
1G0U	Z1	HYDROLASE	1	1.1	1.1	1	17	PSYIFEYLATVMYQRRS	19476
1G20	DH	OXIDOREDUCTASE	D	1.1	1.1	1	12	EKTKKFVEGTWK	19477
1G3I	WQ	CHAPERONE/HYDROLASE	Q	1.1	1.1	1	13	LLKSAVELAKDWR	19478
1G3I	XR	CHAPERONE/HYDROLASE	R	1.1	1.1	1	13	LLKSAVELAKDWR	19479
1G3N	AC	CELL CYCLE, SIGNALING PROTEIN	C	1.1	1.1	1	15	RQELIDQEKELLEKL	19480
1GH0	EB	PHOTOSYNTHESIS	E	1.1	1.1	1	9	GPMDEYLIA	19481
1GH0	GH	PHOTOSYNTHESIS	H	1.1	1.1	1	14	SNKRLDVVNRITSN	19482
1GH0	OV	PHOTOSYNTHESIS	V	1.1	1.1	1	16	ASTIVSNAARSLFAEQ	19483
1GH0	QN	PHOTOSYNTHESIS	N	1.1	1.1	1	25	SRRMAACLRDMEIILRYVTYAVFAG	19484

1GO3	EF	TRANSFERASE	E	1.1	1.1	1	12	LEWIEEEKAKKQ	19485
1GPQ	BD	HYDROLASE/INHIBITOR	B	1.1	1.1	1	14	SIDGKTVLFAALTG	19486
1GPW	AD	LYASE/TRANSFERASE	A	1.1	1.1	1	7	NTAAVEN	19487
1GXS	AB	LYASE	B	1.1	1.1	1	8	PEVQTALH	19488
1GXS	CB	LYASE	C	1.1	1.1	1	15	PECTEVWNKALAEQG	19489
1H1L	AB	OXIDOREDUCTASE	B	1.1	1.1	1	11	KFIQRDTLAKG	19490
1H1L	AD	OXIDOREDUCTASE	D	1.1	1.1	1	16	LAATDELLMTVSQLSG	19491
1H1L	CD	OXIDOREDUCTASE	C	1.1	1.1	1	6	CPVGLI	19492
1H2A	SL	OXIDOREDUCTASE	S	1.1	1.1	1	7	GCSESVL	19493
1H3O	CB	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	B	1.1	1.1	1	5	EDVEE	19494
1HBM	AE	METHANOGENESIS	A	1.1	1.1	1	8	FGYLADIC	19495
1HBM	DB	METHANOGENESIS	B	1.1	1.1	1	19	SAAPLVTATAFVQAIINEF	19496
1HBR	CD	OXYGEN STORAGE/TRANSPORT	C	1.1	1.1	1	20	PVNFKLLSQCIQVVLAVHMG	19497
1HC9	BD	TOXIN/PEPTIDE	B	1.1	1.1	1	5	CSSRG	19498
1HR8	AB	HYDROLASE	B	1.1	1.1	1	11	PEEVFEQVDKI	19499
1HT1	ZG	CHAPERONE	Z	1.1	1.1	1	17	TADAFTLFELFERKLEM	19500
1HTL	GC	ENTEROTOXIN	G	1.1	1.1	1	21	DSQKKAIERMKDTLRITYLTE	19501
1HV4	AF	OXYGEN STORAGE/TRANSPORT	F	1.1	1.1	1	14	AEEKQLITGLWGKV	19502
1HXY	AB	IMMUNE SYSTEM/TOXIN	B	1.1	1.1	1	12	ELGRPDAEYWNS	19503
1I1Q	AB	LYASE	B	1.1	1.1	1	11	TWNLADQLRTN	19504
1I3O	DF	APOPTOSIS	F	1.1	1.1	1	5	FFVLG	19505
1I3Q	AE	TRANSCRIPTION	A	1.1	1.1	1	25	LKLQVLLDEEYKQLVKDRKFLREVF	19506
1I3R	CF	IMMUNE SYSTEM	C	1.1	1.1	1	22	AQGALANIAVNKANLDVMKERS	19507
1I51	CF	HYDROLASE/HYDROLASE INHIBITOR	F	1.1	1.1	1	8	HADYLLRT	19508
1IA0	AK	TRANSPORT PROTEIN	A	1.1	1.1	1	19	FSEAREDMAALEKDYEEVG	19509
1IBL	DE	RIBOSOME	E	1.1	1.1	1	9	AVPRAILEL	19510
1IGF	LH	IMMUNOGLOBULIN	L	1.1	1.1	1	5	SEQLT	19511
1II8	AB	REPLICATION	B	1.1	1.1	1	38	KDFTEELIEKVKKYKALAREAALSKIGELASEIFAEFT	19512
1IL1	AB	IMMUNE SYSTEM	B	1.1	1.1	1	5	SEQLT	19513
1IR2	FN	LYASE	F	1.1	1.1	1	14	AKNYGRAVYECLRG	19514
1IR2	X6	LYASE	6	1.1	1.1	1	14	DEQIAAQVDYIVAN	19515
1IRE	AB	LYASE	B	1.1	1.1	1	16	YYWHWIRTYIHHGVRT	19516
1IRU	DE	HYDROLASE	E	1.1	1.1	1	22	IADAKTLIDKARVETQNHWFTY	19517
1IRU	I1	HYDROLASE	I	1.1	1.1	1	18	EEEAKNLVSEAIAAGIFN	19518
1IRU	OW	HYDROLASE	W	1.1	1.1	1	15	VVTANRMLKQMLFRY	19519
1IRU	PW	HYDROLASE	P	1.1	1.1	1	23	GPDYRVLVHRARKLAQQYYLVYQ	19520
1IRU	TU	HYDROLASE	U	1.1	1.1	1	23	LADARSLADIAREEASNFRSNFG	19521
1IRU	VN	HYDROLASE	N	1.1	1.1	1	15	YGAYLAQPLLREVLE	19522
1IRU	XM	HYDROLASE	X	1.1	1.1	1	9	AEQMYGMCE	19523

1IW7	BC	TRANSFERASE	C	1.1	1.1	1	6	EELLKR	19524
1IW7	BD	TRANSFERASE	D	1.1	1.1	1	10	PDEALLAVAH	19525
1IW7	CD	TRANSFERASE	D	1.1	1.1	1	6	RKLVDV	19526
1IW7	DF	TRANSFERASE	D	1.1	1.1	1	20	EIIIRNEKRMLQEAVDALLD	19527
1IW7	MN	TRANSFERASE	M	1.1	1.1	1	10	EMEVWALEAY	19528
1IW7	MN	TRANSFERASE	N	1.1	1.1	1	23	VLEYFISSHGARKGGADTALRTA	19529
1IW7	MN	TRANSFERASE	N	1.1	1.1	1	6	SIVRRY	19530
1IW7	NP	TRANSFERASE	N	1.1	1.1	1	6	DEEYRE	19531
1IWA	CF	LYASE	C	1.1	1.1	1	15	GKNYGRVVYEALKGG	19532
1IWA	ED	LYASE	E	1.1	1.1	1	9	VILERERLD	19533
1IWA	ED	LYASE	E	1.1	1.1	1	18	WRERYLFTMEAVNKASAA	19534
1IWA	OF	LYASE	F	1.1	1.1	1	15	PAAVLFEINACRKAR	19535
1IWA	ON	LYASE	O	1.1	1.1	1	9	VILERERLD	19536
1IWP	LE	LYASE	E	1.1	1.1	1	10	VSFMAWDAAN	19537
1IWP	LM	LYASE	L	1.1	1.1	1	7	EAVFTDG	19538
1IWQ	AB	METAL BINDING PROTEIN/PROTEIN BINDING	A	1.1	1.1	1	12	EEEIREAFRVFD	19539
1J1D	DF	CONTRACTILE PROTEIN	D	1.1	1.1	1	10	LEELKIMLQA	19540
1J1D	DF	CONTRACTILE PROTEIN	D	1.1	1.1	1	9	FDEFLVMMV	19541
1JB0	BC	PHOTOSYNTHESIS	B	1.1	1.1	1	10	TRRIWYAIAM	19542
1JD2	2O	HYDROLASE	O	1.1	1.1	1	22	AADTEAVTQLIGSNIELHSLYT	19543
1JD2	DE	HYDROLASE	E	1.1	1.1	1	22	APDARVLSNYLRQQCNYSSLVF	19544
1JD2	DL	HYDROLASE	L	1.1	1.1	1	21	AADGDALVKRFKNSVKWYHFD	19545
1JD2	HI	HYDROLASE	I	1.1	1.1	1	12	SDQLFGMCESLY	19546
1JD2	IS	HYDROLASE	I	1.1	1.1	1	18	PEDLFETISQALLNAADR	19547
1JD2	JK	HYDROLASE	J	1.1	1.1	1	22	AGDTVQFAEYIQANIQLYSIRE	19548
1JD2	OU	HYDROLASE	O	1.1	1.1	1	11	SLAAMAVLESH	19549
1JD2	QK	HYDROLASE	Q	1.1	1.1	1	13	YSGFYTFSLLDHH	19550
1JD2	VW	HYDROLASE	V	1.1	1.1	1	15	TKLLVSEVAKIMQEA	19551
1JD2	WQ	HYDROLASE	Q	1.1	1.1	1	17	PQAVSSFVRQELAKSIR	19552
1JD2	ZT	HYDROLASE	T	1.1	1.1	1	20	ISDMQHIERLLKDLVTENAY	19553
1JEY	AB	DNA BINDING PROTEIN/DNA	B	1.1	1.1	1	16	PRFQRLFQCLLHRALH	19554
1JJ2	MP	RIBOSOME	M	1.1	1.1	1	11	YHQRLRLLKSG	19555
1JK0	AB	OXIDOREDUCTASE	A	1.1	1.1	1	26	PEAKSFYGFQIMIENIHSETYSLLID	19556
1JMU	AB	VIRAL PROTEIN	B	1.1	1.1	1	12	MQSVVKLLDDQL	19557
1JMU	CD	VIRAL PROTEIN	D	1.1	1.1	1	17	EHAIANFTKAEMALEFN	19558
1JMU	DH	VIRAL PROTEIN	H	1.1	1.1	1	5	APIVL	19559
1JPW	AD	CELL ADHESION	A	1.1	1.1	1	15	INVVTCAAGILSNLT	19560
1JPW	BE	CELL ADHESION	B	1.1	1.1	1	17	EKLLWTTSRVLKVLSVC	19561
1JR3	BE	TRANSFERASE	B	1.1	1.1	1	17	PTDIQLYYQTLLIGRKE	19562

1JRO	AB	OXIDOREDUCTASE	B	1.1	1.1	1	8	HRAARIAA	19563
1JSU	AB	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	B	1.1	1.1	1	15	KKQVLRMEHLVLKVL	19564
1JTG	AB	HYDROLASE	A	1.1	1.1	1	6	PVTEKH	19565
1JTG	CD	HYDROLASE	C	1.1	1.1	1	18	MDERNRQIAEIGASLIKH	19566
1JY7	CB	OXYGEN STORAGE/TRANSPORT	B	1.1	1.1	1	19	PENFRLLGNVLVCVLAHHF	19567
1JY7	CD	OXYGEN STORAGE/TRANSPORT	D	1.1	1.1	1	14	EVGGEALGRLLVVY	19568
1JY7	UV	OXYGEN STORAGE/TRANSPORT	V	1.1	1.1	1	14	EVGGEALGRLLVVY	19569
1JYO	AF	CHAPERONE	F	1.1	1.1	1	14	ETAVNDALLMSRIN	19570
1K6L	LM	PHOTOSYNTHESIS	M	1.1	1.1	1	27	GLWLIASFFMFVAVWSWWGRTYLRAQA	19571
1K74	DE	TRANSCRIPTION	D	1.1	1.1	1	23	LNDQVTLLKYGVHEIIYTMLASL	19572
1KA9	HF	TRANSFERASE	H	1.1	1.1	1	14	KAGLAFLALARRYF	19573
1KEL	LH	CATALYTIC ANTIBODY	L	1.1	1.1	1	6	SEQLTS	19574
1KF6	MN	OXIDOREDUCTASE	M	1.1	1.1	1	5	HTVAA	19575
1KF6	NO	OXIDOREDUCTASE	N	1.1	1.1	1	6	PQFGLN	19576
1KFY	AB	OXIDOREDUCTASE	B	1.1	1.1	1	10	THFIESLEAI	19577
1KFY	AB	OXIDOREDUCTASE	B	1.1	1.1	1	10	PAQMAKYHQF	19578
1KFY	MN	OXIDOREDUCTASE	N	1.1	1.1	1	10	THFIESLEAI	19579
1KJ2	IE	IMMUNE SYSTEM	I	1.1	1.1	1	11	EAERLRAYLEG	19580
1KJ2	IE	IMMUNE SYSTEM	I	1.1	1.1	1	29	PEYWERETQKAKGNEQSFRVDLRTLLGYY	19581
1KN2	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6	SEQLTS	19582
1KPS	AD	LIGASE/PROTEIN TRANSPORT	D	1.1	1.1	1	13	FARHNLLQTLYNI	19583
1KV6	AC	GENE REGULATION	A	1.1	1.1	1	24	LADQMSLLQSAWMEILILGVVYRS	19584
1KX4	AG	STRUCTURAL PROTEIN/DNA	A	1.1	1.1	1	13	TVALREIRRYQKS	19585
1KYO	AR	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.1	1.1	1	9	KLLDNIQEY	19586
1KYO	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.1	1.1	1	6	AGIKTR	19587
1KYO	DF	OXIDOREDUCTASE/ELECTRON TRANSPORT	F	1.1	1.1	1	23	EEGKALVHHYEECAERVKIQQQQ	19588
1KYO	LN	OXIDOREDUCTASE/ELECTRON TRANSPORT	L	1.1	1.1	1	18	IDDLIHFTLKQWNRLTIS	19589
1KYO	NE	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	1.1	1.1	1	10	LLPFYAILRS	19590
1KYO	NO	OXIDOREDUCTASE/ELECTRON TRANSPORT	N	1.1	1.1	1	15	IELAFSSVEHIMRDV	19591
1KYO	OT	OXIDOREDUCTASE/ELECTRON TRANSPORT	O	1.1	1.1	1	16	HASIRRGYQVYREVCA	19592
1KYO	PT	OXIDOREDUCTASE/ELECTRON TRANSPORT	T	1.1	1.1	1	27	VGTIFAGAFVFQTVFDTAITSWYENHN	19593

1L0O	AC	PROTEIN BINDING	C	1.1	1.1	1	13	PEDVVLAQEAVRL	19594
1L4A	BC	ENDOCYTOSIS/EXOCYTOSIS	C	1.1	1.1	1	7	DRIEEGL	19595
1L5G	AB	CELL ADHESION	B	1.1	1.1	1	11	LGLMTEKLSQK	19596
1L8C	AB	GENE REGULATION	B	1.1	1.1	1	8	SYDCEVNA	19597
1L9B	LH	PHOTOSYNTHESIS	H	1.1	1.1	1	18	LLEEDKICGYVAGGLMYA	19598
1L9B	LM	PHOTOSYNTHESIS	L	1.1	1.1	1	26	TLGIHRLGLLLSLSAVFFSALCMIIT	19599
1L9J	MH	PHOTOSYNTHESIS	H	1.1	1.1	1	18	LLEEDKICGYVAGGLMYA	19600
1LB1	GH	SIGNALING PROTEIN	G	1.1	1.1	1	25	AEDLQEALSSILGILKAVNDSMHLI	19601
1LB1	GH	SIGNALING PROTEIN	H	1.1	1.1	1	19	PDSLENIPEKWTPEVKHFC	19602
1LDK	AD	LIGASE	A	1.1	1.1	1	5	AYLNR	19603
1LGH	AB	LIGHT HARVESTING COMPLEX	A	1.1	1.1	1	26	PSTWLPVIWIVATVVAIAVHAAVLAA	19604
1LGH	DE	LIGHT HARVESTING COMPLEX	D	1.1	1.1	1	26	PSTWLPVIWIVATVVAIAVHAAVLAA	19605
1LGH	GH	LIGHT HARVESTING COMPLEX	G	1.1	1.1	1	26	PSTWLPVIWIVATVVAIAVHAAVLAA	19606
1LGH	JK	LIGHT HARVESTING COMPLEX	J	1.1	1.1	1	26	PSTWLPVIWIVATVVAIAVHAAVLAA	19607
1LQM	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	14	PSLLNMYKELENTI	19608
1LQM	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.1	1.1	1	9	PEEVEEVIG	19609
1LUJ	AB	STRUCTURAL PROTEIN	A	1.1	1.1	1	10	YKNKMMVCQV	19610
1LVC	CF	LYASE	C	1.1	1.1	1	6	KEWDKV	19611
1LVC	CF	LYASE	C	1.1	1.1	1	12	VKKIAGYLSDYY	19612
1LVC	CF	LYASE	C	1.1	1.1	1	24	PEYKNYFQYLKERITNQVQLLLTH	19613
1LWU	DE	BLOOD CLOTTING	D	1.1	1.1	1	12	KNLQLEKAASYI	19614
1M1Y	AB	OXIDOREDUCTASE	A	1.1	1.1	1	10	EKARKDRNKH	19615
1M1Y	IJ	OXIDOREDUCTASE	J	1.1	1.1	1	11	LWHLRSLVFTD	19616
1M2Z	AB	HORMONE/HORMONE ACTIVATOR	A	1.1	1.1	1	13	EMLAEIITNQIPK	19617
1MEX	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6	SEQLTG	19618
1MIO	AB	MOLYBDENUM-IRON PROTEIN	A	1.1	1.1	1	12	HHDMEVVLEKLK	19619
1MIO	CD	MOLYBDENUM-IRON PROTEIN	D	1.1	1.1	1	11	FFDVHQWIKNE	19620
1MIO	CD	MOLYBDENUM-IRON PROTEIN	D	1.1	1.1	1	15	GSNIKTAVKNIFSLY	19621
1MJG	BM	OXIDOREDUCTASE	M	1.1	1.1	1	14	LGDLPPILNRKRAQ	19622
1MK2	AB	TRANSCRIPTION	B	1.1	1.1	1	7	PLQQAQA	19623
1MMO	CH	OXIDOREDUCTASE (MONOOXYGENASE)	H	1.1	1.1	1	9	KWEAEKIHI	19624
1MNM	BC	TRANSCRIPTION/DNA	B	1.1	1.1	1	26	KTRRHVTFSKRKHGIMKKAFELSVLT	19625
1MTY	CH	MONOOXYGENASE	H	1.1	1.1	1	15	KWEAEKIHIGFRQAY	19626
1MVW	GH	CONTRACTILE PROTEIN	H	1.1	1.1	1	12	FTVFLTMFGEKL	19627
1MVW	MO	CONTRACTILE PROTEIN	O	1.1	1.1	1	10	DFKEAFLLFD	19628
1N4Q	EF	TRANSFERASE	E	1.1	1.1	1	5	LQDRG	19629
1N95	AB	TRANSFERASE	B	1.1	1.1	1	14	IVATDVCQFLELCQ	19630
1NBF	AD	HYDROLASE	A	1.1	1.1	1	9	IFESFVDYV	19631
1NBU	AC	LYASE	C	1.1	1.1	1	15	IETVGAEIADHVMDD	19632

1ND0	AB	IMMUNE SYSTEM	A	1.1	1.1	1	6	SEQLTS	19633
1NEK	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.1	1.1	1	12	PAGLLAAYRFLI	19634
1NEK	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.1	1.1	1	30	AFTKVFTLLALFSILIHAWIGMWQVLTDYV	19635
1NGM	AB	TRANSCRIPTION/DNA	A	1.1	1.1	1	12	EDDSKLASRKYA	19636
1NIK	BK	TRANSCRIPTION	K	1.1	1.1	1	12	HTLGNLIRAELL	19637
1NIW	AB	SIGNALING PROTEIN/OXIDOREDUCTASE	A	1.1	1.1	1	15	EEQIAEFKEAFSLFD	19638
1NRL	AC	TRANSCRIPTION	A	1.1	1.1	1	22	LPHMADMSTYMFKGIISFAKVI	19639
1NTK	AC	OXIDOREDUCTASE	A	1.1	1.1	1	7	YNRIRSG	19640
1NU9	DF	HYDROLASE/PROTEIN BINDING	F	1.1	1.1	1	23	DWYLKGRLTSLESQFINALGILE	19641
1NVM	CD	LYASE/OXIDOREDUCTASE	C	1.1	1.1	1	11	KQHIEYARNLG	19642
1NX0	BD	HYDROLASE	B	1.1	1.1	1	14	EVRQFRRLFAQLAG	19643
1NY7	12	VIRUS	1	1.1	1.1	1	7	PIMNVLR	19644
1O18	GH	CONTRACTILE PROTEIN	H	1.1	1.1	1	12	FTVFLTMFGEKL	19645
1O96	CD	ELECTRON TRANSFER	C	1.1	1.1	1	16	AIVVGRILTEVIKKEA	19646
1O96	EF	ELECTRON TRANSFER	F	1.1	1.1	1	7	FDIEEEL	19647
1OAO	BC	OXIDOREDUCTASE	B	1.1	1.1	1	36	AWTIVARNVGLMILTGAAAHCEHGNHIAHALVEMAE	19648
1OCC	AJ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	J	1.1	1.1	1	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	19649
1OCC	NW	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	W	1.1	1.1	1	30	ATDNILYRVTMTLCLGGTLYSLYCLGWASF	19650
1OE9	AB	ATPASE/MYOSIN	B	1.1	1.1	1	9	EEEVETVLA	19651
1OED	AE	ION CHANNEL/RECEPTOR	A	1.1	1.1	1	29	MTLSISVLLSLTVFLLVIVELIPSTSSAV	19652
1OED	DC	ION CHANNEL/RECEPTOR	C	1.1	1.1	1	29	MSTAISVLLAQAVFLLLTSQRLPETALAV	19653
1OED	DC	ION CHANNEL/RECEPTOR	D	1.1	1.1	1	29	MTLSISVLLSLTVFLLVIVELIPSTSSAV	19654
1ONV	AB	TRANSCRIPTION	A	1.1	1.1	1	8	TKDLLKKF	19655
1OO0	AB	SIGNALING PROTEIN	A	1.1	1.1	1	15	QSVMEELKRIIIDSE	19656
1OOP	AB	VIRUS	B	1.1	1.1	1	5	PKSLS	19657
1OQO	AC	IMMUNE SYSTEM	C	1.1	1.1	1	14	EEQRNAKIKSIRDD	19658
1OQS	CD	HYDROLASE	C	1.1	1.1	1	16	ATDRCCFVHDCCYGTV	19659
1OR0	CD	HYDROLASE	D	1.1	1.1	1	5	EQYFD	19660
1OR7	AC	TRANSCRIPTION	A	1.1	1.1	1	15	VPDVVQEAFIKAYRA	19661
1OR7	BF	TRANSCRIPTION	B	1.1	1.1	1	14	SEELRQIVFRTIES	19662
1ORS	BC	MEMBRANE PROTEIN	C	1.1	1.1	1	14	AGLLALIEGHLAGL	19663
1OUU	CD	OXYGEN TRANSPORT	D	1.1	1.1	1	16	IDEIGPLALARVLIVY	19664
1OVA	AB	SERPIN	A	1.1	1.1	1	16	ADQARELINSWVESQT	19665
1OVL	AB	TRANSCRIPTION	A	1.1	1.1	1	20	PKRVEELQNKIVNCLKDHVT	19666

1OW3	AB	GENE REGULATION/SIGNALING PROTEIN	A	1.1	1.1	1	14	INPINTFTKFLLDH	19667
1OXK	CD	SIGNALING PROTEIN	C	1.1	1.1	1	26	FSKGLIIQFIDQAQTTFAQMQRQLDG	19668
1OXK	CD	SIGNALING PROTEIN	C	1.1	1.1	1	18	LTELDNLGHFLKGSSAAL	19669
1OXK	EF	SIGNALING PROTEIN	E	1.1	1.1	1	26	FSKGLIIQFIDQAQTTFAQMQRQLDG	19670
1OXK	KL	SIGNALING PROTEIN	K	1.1	1.1	1	18	LTELDNLGHFLKGSSAAL	19671
1P22	AB	SIGNALING PROTEIN	B	1.1	1.1	1	7	TLFELIL	19672
1P4E	AD	DNA BINDING PROTEIN/RECOMBINATION/DNA	D	1.1	1.1	1	9	DHYFALVSR	19673
1P4E	BC	DNA BINDING PROTEIN/RECOMBINATION/DNA	B	1.1	1.1	1	8	TELTNVVG	19674
1P4E	BC	DNA BINDING PROTEIN/RECOMBINATION/DNA	C	1.1	1.1	1	9	DHYFALVSR	19675
1P4Q	AB	TRANSCRIPTION/TRANSFERASE	A	1.1	1.1	1	12	EEVLMSLVIEMG	19676
1PC8	AB	HYDROLASE	A	1.1	1.1	1	9	VYMLELETS	19677
1PCQ	AO	CHAPERONE	A	1.1	1.1	1	13	IREMLPVLEAVAK	19678
1PCQ	BP	CHAPERONE	B	1.1	1.1	1	13	IREMLPVLEAVAK	19679
1PG7	IM	IMMUNE SYSTEM	M	1.1	1.1	1	6	DEQLKS	19680
1PHN	AB	ELECTRON TRANSPORT	B	1.1	1.1	1	13	NTQLDALSKMVSE	19681
1PMA	AB	PROTEASE	B	1.1	1.1	1	22	VGDAQVLVRYMKAELELYRLQR	19682
1PMA	M1	PROTEASE	M	1.1	1.1	1	18	IENLVKRVADQMQQYTQY	19683
1PON	AB	CALCIUM-BINDING PROTEIN	B	1.1	1.1	1	11	EDIEDLMKDSD	19684
1PRC	CL	PHOTOSYNTHETIC REACTION CENTER	L	1.1	1.1	1	5	WPEWW	19685
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	M	1.1	1.1	1	7	PAVFLRD	19686
1PTO	GK	TOXIN	K	1.1	1.1	1	12	PMEVMLRAVFMQ	19687
1PVH	CD	SIGNALING PROTEIN/CYTOKINE	D	1.1	1.1	1	14	LMNQIRSQLAQLNG	19688
1Q5R	CK	HYDROLASE	C	1.1	1.1	1	19	GRSLANAYAQTLGTIFTEQ	19689
1Q5R	GH	HYDROLASE	G	1.1	1.1	1	19	GRSLANAYAQTLGTIFTEQ	19690
1Q7L	CB	HYDROLASE	B	1.1	1.1	1	8	DNRYIRAV	19691
1Q7L	CD	HYDROLASE	C	1.1	1.1	1	7	PEFHALR	19692
1Q86	OR	RIBOSOME	O	1.1	1.1	1	11	YHQRLRLLKSG	19693
1Q90	AB	PHOTOSYNTHESIS	B	1.1	1.1	1	28	GWLIRSIHRWSASMMVLMMVLHVFRVYL	19694
1Q95	FL	TRANSFERASE	F	1.1	1.1	1	8	AARLATEF	19695
1QFN	AB	ELECTRON TRANSPORT/OXIDOREDUCTASE	A	1.1	1.1	1	13	YTDFAAWVKENLD	19696
1QGC	23	VIRUS/IMMUNE SYSTEM	3	1.1	1.1	1	6	PEEAAH	19697
1QGW	AD	PHOTOSYNTHESIS	D	1.1	1.1	1	20	ANSNARAVSIMKACAVAFVN	19698
1QHH	AC	HYDROLASE	A	1.1	1.1	1	14	PRTILGTISAAKNE	19699
1QHH	BC	HYDROLASE	C	1.1	1.1	1	12	VTELVEEVLDKS	19700
1QLE	AB	OXIDOREDUCTASE/IMMUNE SYSTEM	A	1.1	1.1	1	27	WAGQLHFWMMFIGSNLIFFPQHFLGRQ	19701

1QVI	AY	CONTRACTILE PROTEIN	Y	1.1	1.1	1	10 IEYIKDLLEN	19702
1R1R	AD	OXIDOREDUCTASE	A	1.1	1.1	1	9 KLMYTRLLK	19703
1R1R	BE	OXIDOREDUCTASE	B	1.1	1.1	1	9 KLMYTRLLK	19704
1R20	AD	HORMONE/GROWTH FACTOR RECEPTOR	D	1.1	1.1	1	17 AYVIEDLLHFCRCMYSM	19705
1R2B	BD	TRANSCRIPTION	B	1.1	1.1	1	7 GLFYSIF	19706
1R4M	AI	CELL CYCLE	A	1.1	1.1	1	13 YKEKEDFRDLIRQ	19707
1R4M	EF	CELL CYCLE	E	1.1	1.1	1	9 ATGTEILKN	19708
1R4P	AB	TOXIN	B	1.1	1.1	1	13 WNLQPLLQSAQLT	19709
1R4Q	LG	TOXIN	G	1.1	1.1	1	13 WNLQSLLLSAQIT	19710
1R4Q	LJ	TOXIN	J	1.1	1.1	1	12 LQSLLLSAQITG	19711
1R8Q	BF	PROTEIN TRANSPORT/EXCHANGE FACTOR	F	1.1	1.1	1	8 LERFVAMN	19712
1RCO	OP	LYASE	P	1.1	1.1	1	14 TDQLARQVDYLLNN	19713
1RDT	AD	HORMONE/GROWTH FACTOR	A	1.1	1.1	1	21 RLPALRSIGLKCLEHLFFFKL	19714
1RHI	23	VIRUS	3	1.1	1.1	1	7 LLGEIAQ	19715
1RIH	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6 SEQLTS	19716
1RJ9	AB	PROTEIN TRANSPORT	A	1.1	1.1	1	14 QNGLEQAKKFHEAV	19717
1RJ9	AB	PROTEIN TRANSPORT	A	1.1	1.1	1	15 LSATEEILQEVRASG	19718
1RLD	BT	LYASE(CARBON-CARBON)	T	1.1	1.1	1	13 QEQLLSEVEYLLK	19719
1RM6	DE	OXIDOREDUCTASE	D	1.1	1.1	1	8 REETFIAH	19720
1RP3	GD	TRANSCRIPTION	G	1.1	1.1	1	21 VSRVSQLKAKALERLREMLSN	19721
1RSO	AB	NEUROPEPTIDE/MEMBRANE PROTEIN	A	1.1	1.1	1	12 NLFQALIDIQEF	19722
1RSO	AB	NEUROPEPTIDE/MEMBRANE PROTEIN	A	1.1	1.1	1	17 KQDTQRALHLLEEYRSK	19723
1RTD	AB	TRANSFERASE/DNA	A	1.1	1.1	1	5 SIVIW	19724
1RU7	AB	VIRAL PROTEIN	A	1.1	1.1	1	10 YEELREQLSS	19725
1RU7	AB	VIRAL PROTEIN	B	1.1	1.1	1	22 QKSTQNAINGITNKVNSVIEKM	19726
1RU7	CD	VIRAL PROTEIN	D	1.1	1.1	1	22 QKSTQNAINGITNKVNSVIEKM	19727
1RU7	EF	VIRAL PROTEIN	F	1.1	1.1	1	22 QKSTQNAINGITNKVNSVIEKM	19728
1RU7	IJ	VIRAL PROTEIN	J	1.1	1.1	1	22 QKSTQNAINGITNKVNSVIEKM	19729
1RU7	KH	VIRAL PROTEIN	H	1.1	1.1	1	53 KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEK VKSQLK	19730
1RUZ	HI	VIRAL PROTEIN	H	1.1	1.1	1	10 YEELREQLSS	19731
1RYP	12	MULTICATALYTIC PROTEINASE	2	1.1	1.1	1	14 FGAHMANPLLRKVV	19732
1RYP	DL	MULTICATALYTIC PROTEINASE	L	1.1	1.1	1	15 VAAASKILSNLVYQY	19733
1RYP	H2	MULTICATALYTIC PROTEINASE	H	1.1	1.1	1	19 KEETVDFIKHSLSQAIKWD	19734
1RYP	I1	MULTICATALYTIC PROTEINASE	I	1.1	1.1	1	18 KEEAIKLASDAIQAGIWN	19735
1RYP	IJ	MULTICATALYTIC PROTEINASE	J	1.1	1.1	1	12 SDQLFGMCESLY	19736
1RYP	SZ	MULTICATALYTIC PROTEINASE	S	1.1	1.1	1	22 TADARSMIEHARTAAVTHNLYY	19737
1RYP	UV	MULTICATALYTIC PROTEINASE	V	1.1	1.1	1	15 TETAASVFKELCYEN	19738

1RYP	YZ	MULTICATALYTIC PROTEINASE	Y	1.1	1.1	1	22	GDTVQFAEYIQANIQLYSIRED	19739
1RZI	OP	IMMUNE SYSTEM	O	1.1	1.1	1	7	DEQLKSG	19740
1RZR	AD	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	A	1.1	1.1	1	8	AVARGLAS	19741
1RZR	GL	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	G	1.1	1.1	1	15	IFYAELARGIEDIAT	19742
1S0Y	KH	LYASE	K	1.1	1.1	1	20	DEQKRALSAGLLRVISEATG	19743
1S4Z	BC	GENE REGULATION	B	1.1	1.1	1	11	PQVVISFYEER	19744
1S5L	ac	PHOTOSYNTHESIS	c	1.1	1.1	1	19	GPEASQAQAMTFLIRDQKL	19745
1S5L	ai	PHOTOSYNTHESIS	a	1.1	1.1	1	11	LWERFCNWVTS	19746
1S5L	BD	PHOTOSYNTHESIS	B	1.1	1.1	1	24	TVLSSSIAAVFFAAFVVAGTMWYG	19747
1S5L	BL	PHOTOSYNTHESIS	L	1.1	1.1	1	24	RTSLYLGLLLILVLALLFSSYFFN	19748
1S5L	co	PHOTOSYNTHESIS	c	1.1	1.1	1	7	LNKIKND	19749
1S5L	CO	PHOTOSYNTHESIS	C	1.1	1.1	1	7	LNKIKND	19750
1S5L	CO	PHOTOSYNTHESIS	O	1.1	1.1	1	5	YDDIV	19751
1S5L	dx	PHOTOSYNTHESIS	x	1.1	1.1	1	30	SLKGFFIGLLSGAVVLGLTFAVLIAISQID	19752
1S70	AB	HYDROLASE	B	1.1	1.1	1	8	ALHVAAAK	19753
1SB3	AC	OXIDOREDUCTASE	C	1.1	1.1	1	8	RDEIKAAL	19754
1SB3	DF	OXIDOREDUCTASE	F	1.1	1.1	1	8	RDEIKAAL	19755
1SCT	GF	OXYGEN TRANSPORT	F	1.1	1.1	1	15	ADQKDLLRMSWGVLS	19756
1SKY	BE	ATP SYNTHASE	B	1.1	1.1	1	15	LSKQAAAYRQLSLLL	19757
1SQB	BI	OXIDOREDUCTASE	B	1.1	1.1	1	14	PQAHVIENLHAAAY	19758
1SQX	AE	OXIDOREDUCTASE	A	1.1	1.1	1	21	DSQIEKERDVILQELQENDTS	19759
1SQX	AI	OXIDOREDUCTASE	A	1.1	1.1	1	11	LAEWESRIAEV	19760
1SQX	AK	OXIDOREDUCTASE	K	1.1	1.1	1	19	VPTASLWGAVGAVGLVWAT	19761
1SQX	ED	OXIDOREDUCTASE	D	1.1	1.1	1	37	PEHDHRKRMGLKMLLMMGLLLPLVYAMKRHKWSVLKS	19762
1SUV	CE	METAL TRANSPORT	C	1.1	1.1	1	6	AKMYLG	19763
1SUV	DF	METAL TRANSPORT	D	1.1	1.1	1	6	AKMYLG	19764
1SVD	AM	LYASE	A	1.1	1.1	1	15	AKNYGRAVYECLRGG	19765
1SXJ	BC	REPLICATION	C	1.1	1.1	1	14	NAAQNALRRVIERY	19766
1SXJ	CD	REPLICATION	D	1.1	1.1	1	12	DHAVTVLKKTLK	19767
1SY9	AB	CALCIUM-BINDING PROTEIN	A	1.1	1.1	1	11	EAELQDMINEV	19768
1T2V	BG	ANTITUMOR PROTEIN	B	1.1	1.1	1	14	PEEFMLVYKFARKH	19769
1T3Q	DE	OXIDOREDUCTASE	D	1.1	1.1	1	9	ALQDSFRRH	19770
1T66	LH	IMMUNE SYSTEM	L	1.1	1.1	1	7	SEQLTSG	19771
1TBG	CG	COMPLEX (GTP-BINDING/TRANSDUCER)	C	1.1	1.1	1	5	LSQIT	19772
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.1	1.1	1	15	VETARCTAGTLHNLS	19773

1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	B	1.1	1.1	1	17	EKLLWTTSRVLKVLSVC	19774
1TI2	AB	OXIDOREDUCTASE	A	1.1	1.1	1	13	ACEIRALARQWAK	19775
1TN6	AB	TRANSFERASE	A	1.1	1.1	1	17	PYLIAFLVDIYEDMLEN	19776
1TN6	AB	TRANSFERASE	A	1.1	1.1	1	17	DKFRDVYDYFRAVLQRD	19777
1TX4	AB	COMPLEX (GTPASE ACTIVATN/PROTO-ONCOGENE)	A	1.1	1.1	1	14	INPINTFTKFLLDH	19778
1TYE	CD	CELL ADHESION	D	1.1	1.1	1	9	VNLYQNYSE	19779
1U35	EC	STRUCTURAL PROTEIN/DNA	E	1.1	1.1	1	29	SSAVMALQEACEAYLVGLFEDTNLCAIHA	19780
1U5T	AB	TRANSPORT PROTEIN	A	1.1	1.1	1	14	LDDLEKSIDMLKSL	19781
1U6G	AC	LIGASE	C	1.1	1.1	1	17	LAVRKRTIIALGHLVMS	19782
1U7F	CB	SIGNALING PROTEIN	B	1.1	1.1	1	8	VDDLRRLC	19783
1U9I	ED	CIRCADIAN CLOCK PROTEIN	E	1.1	1.1	1	6	VEEFVS	19784
1UDI	EI	HYDROLASE/INHIBITOR	E	1.1	1.1	1	14	PSLRNVLAAVKNCY	19785
1UEA	AB	COMPLEX (METALLOPROTEASE/INHIBITOR)	A	1.1	1.1	1	14	LFLVAAHEIGHSLG	19786
1UF2	AJ	VIRUS	J	1.1	1.1	1	14	GDFNALSNMFTQLS	19787
1UM9	CD	OXIDOREDUCTASE	C	1.1	1.1	1	14	VPPAAGAAISMKLL	19788
1URQ	BD	TRANSPORT PROTEIN	D	1.1	1.1	1	60	SRENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT	19789
1UTB	AB	TRANSCRIPTION REGULATION	B	1.1	1.1	1	7	IGPILHS	19790
1UVQ	AB	IMMUNOLOGY	B	1.1	1.1	1	9	RPDAEYWNS	19791
1UW4	DC	RNA BINDING PROTEIN	D	1.1	1.1	1	17	NQRRISSAKFLGELYNY	19792
1UWE	XY	ANTIBODY	X	1.1	1.1	1	6	AEQLAS	19793
1UZH	EF	LYASE	E	1.1	1.1	1	10	PELAAACEVW	19794
1UZH	OT	LYASE	O	1.1	1.1	1	12	GGDVIRSACKWS	19795
1UZH	OT	LYASE	O	1.1	1.1	1	10	PELAAACEVW	19796
1UZH	VW	LYASE	V	1.1	1.1	1	10	PELAAACEVW	19797
1V29	AB	LYASE	B	1.1	1.1	1	14	PKLVKVVEKALLEG	19798
1V54	CF	OXIDOREDUCTASE	F	1.1	1.1	1	11	LEREVMLAARK	19799
1V54	CF	OXIDOREDUCTASE	F	1.1	1.1	1	5	DEEQA	19800
1V54	CJ	OXIDOREDUCTASE	C	1.1	1.1	1	33	VYGSTFFVATGFHGLHVIIGSTFLIVCFFRQLK	19801
1V54	DI	OXIDOREDUCTASE	I	1.1	1.1	1	12	SMKDFEEMRKAG	19802
1V54	JL	OXIDOREDUCTASE	L	1.1	1.1	1	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	19803
1V54	LM	OXIDOREDUCTASE	M	1.1	1.1	1	6	LDNYKK	19804
1V54	NX	OXIDOREDUCTASE	N	1.1	1.1	1	32	TMWNTISSMGSFISLTAVMLMVFIIWEAFASK	19805
1V54	NZ	OXIDOREDUCTASE	N	1.1	1.1	1	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	19806
1V54	QR	OXIDOREDUCTASE	R	1.1	1.1	1	14	PKIIDAALRACRRL	19807
1V54	QV	OXIDOREDUCTASE	V	1.1	1.1	1	12	SMKDFEEMRKAG	19808
1V7N	KZ	IMMUNE SYSTEM/CYTOKINE	Z	1.1	1.1	1	14	GQVRLLLGALQSLL	19809

1V7N	OK	IMMUNE SYSTEM/CYTOKINE	O	1.1	1.1	1	6	SEQLTS	19810
1V9U	14	VIRUS/RECEPTOR	1	1.1	1.1	1	5	LESFL	19811
1V9U	23	VIRUS/RECEPTOR	3	1.1	1.1	1	5	ENMYS	19812
1VCB	HF	TRANSCRIPTION	H	1.1	1.1	1	15	PEIALELLMAANFLD	19813
1VF5	AB	PHOTOSYNTHESIS	B	1.1	1.1	1	17	LGVLLMASVPLGLILVP	19814
1VF5	CH	PHOTOSYNTHESIS	C	1.1	1.1	1	25	PNRVKWMIAFICLVMLAQLMLILKK	19815
1VF5	GH	PHOTOSYNTHESIS	G	1.1	1.1	1	7	VLGLVFA	19816
1VF5	GH	PHOTOSYNTHESIS	H	1.1	1.1	1	21	WVALLVVFTWSIAMVVWGRNG	19817
1VOQ	GK	RIBOSOME	K	1.1	1.1	1	5	YAAQL	19818
1VSA	GV	RIBOSOME	V	1.1	1.1	1	5	YELVE	19819
1VSP	GV	RIBOSOME	V	1.1	1.1	1	9	IPKVYELVE	19820
1VSP	OP	RIBOSOME	O	1.1	1.1	1	6	GNYAYA	19821
1VYT	AE	TRANSPORT PROTEIN	A	1.1	1.1	1	19	LDDACEHLAEYLEVYWRAT	19822
1W2B	AY	RIBOSOME	Y	1.1	1.1	1	6	KAVMKA	19823
1W2B	MP	RIBOSOME	M	1.1	1.1	1	11	YHQRLRLLKSG	19824
1W2W	AB	ISOMERASE	B	1.1	1.1	1	11	TLQLAVICKQF	19825
1W5C	BD	PHOTOSYNTHESIS	B	1.1	1.1	1	13	FFGHIWHGARTLF	19826
1W5C	DF	PHOTOSYNTHESIS	F	1.1	1.1	1	25	VRWVAVHTLAVPTIFFLGAIAAMQF	19827
1W5C	HJ	PHOTOSYNTHESIS	H	1.1	1.1	1	13	FFGHIWHGARTLF	19828
1W5C	JL	PHOTOSYNTHESIS	L	1.1	1.1	1	25	VRWVAVHTLAVPTIFFLGAIAAMQF	19829
1W63	GP	ENDOCYTOSIS	P	1.1	1.1	1	7	EESIRDN	19830
1WCM	AB	TRANSCRIPTION	A	1.1	1.1	1	7	KSIAKTL	19831
1WCM	AB	TRANSCRIPTION	B	1.1	1.1	1	11	EMERDCMIAHG	19832
1WDC	AB	MUSCLE PROTEIN	B	1.1	1.1	1	11	KDEMRMTFKEA	19833
1WDW	AB	LYASE	B	1.1	1.1	1	15	LKDAINEALRDWVAT	19834
1WDW	IJ	LYASE	J	1.1	1.1	1	16	IEPLKELEKAYKRFKD	19835
1WE3	DR	CHAPERONE	D	1.1	1.1	1	15	VRELLPILEQVAQTG	19836
1WKW	AB	TRANSLATION/PROTEIN BINDING	B	1.1	1.1	1	7	RKFLMEC	19837
1WMI	CD	HYDROLASE/HYDROLASE INHIBITOR	D	1.1	1.1	1	13	EEEIAELLELARD	19838
1WQL	AB	OXIDOREDUCTASE	A	1.1	1.1	1	8	LSGVLSSL	19839
1WR1	AB	SIGNALING PROTEIN	B	1.1	1.1	1	11	EHQLRQLNDMG	19840
1WR6	CG	PROTEIN TRANSPORT/SIGNALING PROTEIN	C	1.1	1.1	1	6	DGDREL	19841
1WR6	CG	PROTEIN TRANSPORT/SIGNALING PROTEIN	C	1.1	1.1	1	19	ELFDQCENKRRTLFKLASE	19842
1WWW	VY	NERVE GROWTH FACTOR/TRKA COMPLEX	V	1.1	1.1	1	5	PIFHR	19843
1WYU	CD	OXIDOREDUCTASE	D	1.1	1.1	1	11	ALDLAKGLLEL	19844
1XCT	AB	IMMUNE SYSTEM	A	1.1	1.1	1	6	SEQLTS	19845
1XCT	CM	IMMUNE SYSTEM	M	1.1	1.1	1	14	FEEATAEAYRYAAL	19846

1XD2	BC	SIGNALING PROTEIN	C	1.1	1.1	1	5	KEINS	19847
1XDK	AB	HORMONE/GROWTH FACTOR RECEPTOR	B	1.1	1.1	1	15	EPLLEALKIYIRKRR	19848
1XDK	EF	HORMONE/GROWTH FACTOR RECEPTOR	E	1.1	1.1	1	21	RLPALRSIGLKCLEHLFFFKL	19849
1XEW	XY	CELL CYCLE	Y	1.1	1.1	1	16	LEKAMKILEEIRKKQG	19850
1XFU	BP	LYASE/METAL BINDING PROTEIN	B	1.1	1.1	1	8	LTEIKKQI	19851
1XFU	BP	LYASE/METAL BINDING PROTEIN	B	1.1	1.1	1	13	SAEFIKNLSSIRR	19852
1XFU	CQ	LYASE/METAL BINDING PROTEIN	C	1.1	1.1	1	8	LTEIKKQI	19853
1XFU	DR	LYASE/METAL BINDING PROTEIN	D	1.1	1.1	1	8	LTEIKKQI	19854
1XFU	DR	LYASE/METAL BINDING PROTEIN	D	1.1	1.1	1	13	SAEFIKNLSSIRR	19855
1XFU	ES	LYASE/METAL BINDING PROTEIN	E	1.1	1.1	1	8	LTEIKKQI	19856
1XFU	ES	LYASE/METAL BINDING PROTEIN	E	1.1	1.1	1	13	DEFAKKESVKKIA	19857
1XFV	ES	LYASE/METAL BINDING PROTEIN	E	1.1	1.1	1	24	QEKKRKISIFRGIQAYNEIENVLK	19858
1XK4	JL	METAL BINDING PROTEIN	J	1.1	1.1	1	12	RDDLKKLLETES	19859
1XKP	BC	MEMBRANE PROTEIN/CHAPERON	B	1.1	1.1	1	6	CEDAMV	19860
1XMQ	DE	RIBOSOME	D	1.1	1.1	1	17	DYAVRLREKQKLRRIYG	19861
1XPK	DC	TRANSFERASE	C	1.1	1.1	1	24	GALSKDAYIRSFQQSWNEYAKRQG	19862
1XQ5	CB	OXYGEN STORAGE/TRANSPORT	C	1.1	1.1	1	19	PANFKILSHCILVLLAVKF	19863
1XV9	CD	DNA BINDING PROTEIN	D	1.1	1.1	1	21	RDEIDQLQEEMALTLQSYIKG	19864
1XWD	AC	HORMONE/GROWTH FACTOR	A	1.1	1.1	1	6	LRSKKT	19865
1XXH	FG	TRANSFERASE	G	1.1	1.1	1	19	WEALLVEMLGLLHRIAMVQ	19866
1XXI	AB	TRANSFERASE	A	1.1	1.1	1	15	LLALAQALERLSLLW	19867
1XXI	AB	TRANSFERASE	B	1.1	1.1	1	13	EHVLTALANGLSL	19868
1Y3A	CG	SIGNALING PROTEIN	C	1.1	1.1	1	14	RMHESMKLFDSICN	19869
1Y74	CB	TRANSPORT PROTEIN	B	1.1	1.1	1	16	PHFMALLQTHDVVAHE	19870
1Y74	CB	TRANSPORT PROTEIN	C	1.1	1.1	1	13	PQKLQALQRVLQS	19871
1Y76	CB	TRANSPORT PROTEIN	B	1.1	1.1	1	20	KDFQNAFKIHNAITVHMNKA	19872
1Y76	CD	TRANSPORT PROTEIN	C	1.1	1.1	1	20	PLFNQILTLQQSIKQLKGQL	19873
1Y76	CD	TRANSPORT PROTEIN	D	1.1	1.1	1	20	KDFQNAFKIHNAITVHMNKA	19874
1Y8H	AB	OXYGEN STORAGE/TRANSPORT	B	1.1	1.1	1	19	PENFRLLGNVLVVVLARHF	19875
1Y8R	AB	LIGASE	B	1.1	1.1	1	9	RFDIKSMAG	19876
1Y8R	DE	LIGASE	D	1.1	1.1	1	9	LEAQKRLRA	19877
1Y8X	AB	LIGASE	A	1.1	1.1	1	12	AAQLRIQKDINE	19878
1YA7	AH	HYDROLASE/HYDROLASE ACTIVATOR	A	1.1	1.1	1	15	IENLVKRVADQMQQY	19879
1YA7	AH	HYDROLASE/HYDROLASE ACTIVATOR	H	1.1	1.1	1	23	VGDAQVLVRYMKAELELYRLQRR	19880
1YA7	EL	HYDROLASE/HYDROLASE ACTIVATOR	L	1.1	1.1	1	23	VGDAQVLVRYMKAELELYRLQRR	19881
1YA7	GM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.1	1.1	1	23	VGDAQVLVRYMKAELELYRLQRR	19882
1YE9	AH	OXIDOREDUCTASE	H	1.1	1.1	1	8	TDTQISRL	19883
1YE9	IN	OXIDOREDUCTASE	I	1.1	1.1	1	9	FPDFVHAVK	19884

1YE9	JO	OXIDOREDUCTASE	O	1.1	1.1	1	13	FHRRELWEAIEAG	19885
1YE9	LO	OXIDOREDUCTASE	L	1.1	1.1	1	9	FPDFVHAVK	19886
1YHU	EG	OXYGEN STORAGE/TRANSPORT	G	1.1	1.1	1	19	AASRVSAGEEVFAALFKMV	19887
1YHU	EG	OXYGEN STORAGE/TRANSPORT	G	1.1	1.1	1	18	IPTLESMLDHLAGQHAVR	19888
1YHU	IK	OXYGEN STORAGE/TRANSPORT	K	1.1	1.1	1	19	AASRVSAGEEVFAALFKMV	19889
1YHU	JK	OXYGEN STORAGE/TRANSPORT	J	1.1	1.1	1	15	PLQRLKVKRQWAEAY	19890
1YHU	JK	OXYGEN STORAGE/TRANSPORT	K	1.1	1.1	1	15	DAAAAIVQAQWEDVW	19891
1YHU	SX	OXYGEN STORAGE/TRANSPORT	X	1.1	1.1	1	16	PDAWSRCFNRITTGMT	19892
1YHU	UW	OXYGEN STORAGE/TRANSPORT	W	1.1	1.1	1	19	AASRVSAGEEVFAALFKMV	19893
1YKK	KL	OXIDOREDUCTASE	K	1.1	1.1	1	5	VHIGL	19894
1YL3	M1	RIBOSOME	M	1.1	1.1	1	14	GRVASQVAEQALDG	19895
1YNJ	BD	TRANSFERASE	D	1.1	1.1	1	10	PDEALLAVAH	19896
1YNJ	CD	TRANSFERASE	D	1.1	1.1	1	9	PQQIRQLCG	19897
1YNJ	CD	TRANSFERASE	D	1.1	1.1	1	9	IILGLYYIT	19898
1YNJ	CK	TRANSFERASE	K	1.1	1.1	1	16	YRLTVVVAKRAQQLLR	19899
1YOV	AB	SIGNALING PROTEIN	A	1.1	1.1	1	5	DRQLR	19900
1YOV	AB	SIGNALING PROTEIN	B	1.1	1.1	1	5	VSNLN	19901
1YRT	AB	LAYSE, TOXIN	A	1.1	1.1	1	9	RDSARSSVT	19902
1YSL	AB	LYASE	B	1.1	1.1	1	17	YGATAGLQLAKNHVALH	19903
1YUC	BD	TRANSCRIPTION REGULATION	B	1.1	1.1	1	7	LLIEMLH	19904
1YUH	LH	IMMUNOGLOBULIN	L	1.1	1.1	1	6	SEELET	19905
1Z00	AB	HYDROLASE	B	1.1	1.1	1	7	IAELAAL	19906
1Z2C	AB	SIGNALING PROTEIN	A	1.1	1.1	1	5	LSYPD	19907
1Z2C	CD	SIGNALING PROTEIN	D	1.1	1.1	1	14	IVIKREMVSQYLHT	19908
1Z5S	BD	LIGASE	B	1.1	1.1	1	11	LKKLKESYCQR	19909
1Z6O	AM	METAL BINDING PROTEIN	A	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19910
1Z6O	BM	METAL BINDING PROTEIN	M	1.1	1.1	1	13	EALGEFIFDKKLL	19911
1Z6O	BN	METAL BINDING PROTEIN	B	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19912
1Z6O	CO	METAL BINDING PROTEIN	C	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19913
1Z6O	DP	METAL BINDING PROTEIN	D	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19914
1Z6O	EQ	METAL BINDING PROTEIN	E	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19915
1Z6O	FR	METAL BINDING PROTEIN	F	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19916
1Z6O	GS	METAL BINDING PROTEIN	G	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19917
1Z6O	GW	METAL BINDING PROTEIN	W	1.1	1.1	1	13	EALGEFIFDKKLL	19918
1Z6O	HT	METAL BINDING PROTEIN	H	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19919
1Z6O	IU	METAL BINDING PROTEIN	I	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19920
1Z6O	LX	METAL BINDING PROTEIN	L	1.1	1.1	1	16	LSLALYVFDEYLQKTV	19921
1Z7M	AE	TRANSFERASE	A	1.1	1.1	1	9	LSGLNAFIE	19922
1Z7Q	CD	HYDROLASE/HYDROLASE ACTIVATOR	D	1.1	1.1	1	21	NADSRILIEKARVEAQSHRLT	19923
1Z7Q	CJ	HYDROLASE/HYDROLASE ACTIVATOR	C	1.1	1.1	1	22	TADAEILINTARIHAQNYLKTY	19924

1Z7Q	FN	HYDROLASE/HYDROLASE ACTIVATOR	F	1.1	1.1	1	5	SLVFN	19925
1Z7Q	GH	HYDROLASE/HYDROLASE ACTIVATOR	H	1.1	1.1	1	22	AADTQAIADIVQYHLELYTSQY	19926
1Z7Q	Ja	HYDROLASE/HYDROLASE ACTIVATOR	J	1.1	1.1	1	18	PEDLFETISQALLNAADR	19927
1Z7Q	QR	HYDROLASE/HYDROLASE ACTIVATOR	R	1.1	1.1	1	21	NADSRILIEKARVEAQSHRLT	19928
1Z7Q	RZ	HYDROLASE/HYDROLASE ACTIVATOR	Z	1.1	1.1	1	15	VAAASKILSNLVYQY	19929
1Z7Q	Sa	HYDROLASE/HYDROLASE ACTIVATOR	a	1.1	1.1	1	22	AADGDALVKRFKNSVKWYHFDH	19930
1Z7Q	WN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.1	1.1	1	7	FGAHMAN	19931
1Z7X	ZY	HYDROLASE/HYDROLASE INHIBITOR	Y	1.1	1.1	1	14	EEMEDRLQALEKDK	19932
1Z8U	AB	ELECTRON TRANSPORT	A	1.1	1.1	1	20	KANKDLISAGLKEFSVLLNQ	19933
1ZBA	12	VIRUS	2	1.1	1.1	1	6	TREKYQ	19934
1ZBB	ec	STRUCTURAL PROTEIN/DNA	c	1.1	1.1	1	10	PRHLQLAVRN	19935
1ZBB	fd	STRUCTURAL PROTEIN/DNA	d	1.1	1.1	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	19936
1ZBB	FD	STRUCTURAL PROTEIN/DNA	D	1.1	1.1	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	19937
1ZBB	gh	STRUCTURAL PROTEIN/DNA	g	1.1	1.1	1	5	RSSRA	19938
1ZBB	GH	STRUCTURAL PROTEIN/DNA	G	1.1	1.1	1	5	RSSRA	19939
1ZLA	EC	PROTEIN BINDING/VIRUS/DNA	E	1.1	1.1	1	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	19940
1ZLA	FD	PROTEIN BINDING/VIRUS/DNA	D	1.1	1.1	1	29	SKAMSIMNSFVNDVFERIAGEASRLAHYN	19941
1ZLA	GH	PROTEIN BINDING/VIRUS/DNA	G	1.1	1.1	1	10	PRHLQLAVRN	19942
1ZLH	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.1	1.1	1	5	ECVSK	19943
1ZQ1	AC	LYASE	C	1.1	1.1	1	10	DDLKKKIKEN	19944
1ZT2	AB	REPLICATION, TRANSFERASE	A	1.1	1.1	1	6	WVGRKN	19945
1ZVV	AW	TRANSCRIPTION/DNA	A	1.1	1.1	1	17	IFYAELARGIEDIASMY	19946
2A1T	CR	OXIDOREDUCTASE/ELECTRON TRANSPORT	R	1.1	1.1	1	6	RAAVDA	19947
2A1T	DS	OXIDOREDUCTASE/ELECTRON TRANSPORT	S	1.1	1.1	1	13	QCQETIRTALAMG	19948
2A40	DF	STRUCTURAL PROTEIN	D	1.1	1.1	1	9	QAVLSLYAS	19949
2A45	DE	BLOOD CLOTTING	D	1.1	1.1	1	6	ERELLE	19950
2A45	GI	BLOOD CLOTTING	I	1.1	1.1	1	24	TCGIADFLSTYQTKVDKDLQSLED	19951
2A6Q	BE	TOXIN INHIBITOR/TOXIN	B	1.1	1.1	1	11	LEEYNSLEETA	19952
2ACL	AF	TRANSCRIPTION	F	1.1	1.1	1	28	MFPRMLMKLVSLRTLSSVHSEQVFALRL	19953
2ACZ	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	A	1.1	1.1	1	16	TGHALLHTLYQQNLKN	19954
2AFH	CB	OXIDOREDUCTASE	B	1.1	1.1	1	16	LDWTDEFLMKVSEISG	19955
2AFH	CD	OXIDOREDUCTASE	D	1.1	1.1	1	14	SYGKFIQRDTLHKG	19956
2AI0	OK	IMMUNE SYSTEM	O	1.1	1.1	1	5	SEQLT	19957
2AJF	BF	HYDROLASE/VIRAL PROTEIN	B	1.1	1.1	1	33	IEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTN	19958
2AXT	AC	ELECTRON TRANSPORT	A	1.1	1.1	1	5	ICVAY	19959
2AXT	ac	ELECTRON TRANSPORT	a	1.1	1.1	1	5	ICVAY	19960
2AXT	AI	ELECTRON TRANSPORT	A	1.1	1.1	1	23	WFGVIMIPTLLAATICFVIAFIA	19961

2AXT	ai	ELECTRON TRANSPORT	a	1.1	1.1	1	23	WFGVIMIPTLLAATICFVIAFIA	19962
2AXT	BH	ELECTRON TRANSPORT	B	1.1	1.1	1	26	LPKMFGIHLFLAGLLCFGFGAFHLTG	19963
2AXT	bm	ELECTRON TRANSPORT	m	1.1	1.1	1	25	GLIATALFVLVPSVFLIILYVQTES	19964
2AXT	CK	ELECTRON TRANSPORT	K	1.1	1.1	1	25	DPLVDVLPVIPVLFLALAFVWQAAV	19965
2AXT	co	ELECTRON TRANSPORT	c	1.1	1.1	1	6	LNKIKN	19966
2B4J	BD	VIRAL PROTEIN, RECOMBINATION	D	1.1	1.1	1	17	SMDSRLQRIHAEIKNSL	19967
2B5T	AI	BLOOD CLOTTING	A	1.1	1.1	1	5	PRTFG	19968
2B8K	AB	TRANSFERASE	A	1.1	1.1	1	6	VEILFE	19969
2B8K	AB	TRANSFERASE	A	1.1	1.1	1	7	KSIAKTL	19970
2B8K	AE	TRANSFERASE	A	1.1	1.1	1	10	QLVKDRKFLR	19971
2B9M	CE	RIBOSOME	C	1.1	1.1	1	15	VRRAIKQAVQRVMES	19972
2BA0	AD	RNA BINDING PROTEIN	D	1.1	1.1	1	16	SRTACLNAASVALVDA	19973
2BA0	BE	RNA BINDING PROTEIN	B	1.1	1.1	1	5	VPRVI	19974
2BA0	CF	RNA BINDING PROTEIN	F	1.1	1.1	1	16	SRTACLNAASVALVDA	19975
2BAP	BD	SIGNALING PROTEIN	D	1.1	1.1	1	6	DSLLEA	19976
2BBM	AB	CALCIUM-BINDING PROTEIN	A	1.1	1.1	1	12	AAELRHVMTNLG	19977
2BBM	AB	CALCIUM-BINDING PROTEIN	A	1.1	1.1	1	10	TKELGTVMRS	19978
2BBM	AB	CALCIUM-BINDING PROTEIN	A	1.1	1.1	1	10	FPEFLTMMAR	19979
2BE6	CF	MEMBRANE PROTEIN	C	1.1	1.1	1	11	FPEFLTMMARK	19980
2BEQ	CE	VIRAL PROTEIN	E	1.1	1.1	1	5	LNESL	19981
2BH1	BY	TRANSPORT PROTEIN	B	1.1	1.1	1	6	LSLLAA	19982
2BL0	AC	MUSCLE PROTEIN	C	1.1	1.1	1	11	KEGLQTVLKQF	19983
2BP7	AD	OXIDOREDUCTASE	D	1.1	1.1	1	5	EWAYF	19984
2BR2	SH	HYDROLASE	S	1.1	1.1	1	13	IIKKESIVSLFEK	19985
2BR2	UP	HYDROLASE	U	1.1	1.1	1	13	IIKKESIVSLFEK	19986
2BWE	LS	SIGNALING PROTEIN	L	1.1	1.1	1	9	VQGALDSLL	19987
2BYK	DC	DNA-BINDING PROTEIN	C	1.1	1.1	1	11	YEHLSQVVNKN	19988
2C7J	AB	ELECTRON TRANSPORT	B	1.1	1.1	1	10	SVMDDRCLNG	19989
2C7J	AB	ELECTRON TRANSPORT	B	1.1	1.1	1	13	NDEINALQAIVAD	19990
2CDG	AB	CELL RECEPTOR	B	1.1	1.1	1	8	EAEISHTQ	19991
2CMR	LA	IMMUNE SYSTEM	A	1.1	1.1	1	34	MEWDREINNYTSLIHSLIEESQNQQEKNEQELLE	19992
2CZV	BD	HYDROLASE	B	1.1	1.1	1	6	LRPLLY	19993
2D1P	EF	TRANSLATION	E	1.1	1.1	1	9	ADALRRELA	19994
2D5R	AB	TRANSCRIPTION	A	1.1	1.1	1	7	VKYLMKS	19995
2DBU	AB	TRANSFERASE	A	1.1	1.1	1	12	TVAGFSLALDKY	19996
2DBU	AB	TRANSFERASE	A	1.1	1.1	1	16	AVDAAVAVGYALAVTH	19997
2DBU	AD	TRANSFERASE	D	1.1	1.1	1	11	PDTLKLLEAKG	19998
2DBU	CD	TRANSFERASE	C	1.1	1.1	1	16	AVDAAVAVGYALAVTH	19999
2DD4	GI	HYDROLASE	G	1.1	1.1	1	5	AEDEA	20000
2DD4	HF	HYDROLASE	F	1.1	1.1	1	10	PNYRRRLVRW	20001

2DE5	CF	OXIDOREDUCTASE	C	1.1	1.1	1	7	EAILKRV	20002
2DF4	AB	LIGASE	A	1.1	1.1	1	15	KEVKRRIFLGTFALS	20003
2DF4	AC	LIGASE	A	1.1	1.1	1	13	LEELYKMSRSEGF	20004
2DFS	AD	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	D	1.1	1.1	1	9	AAELRHVMT	20005
2DFS	AE	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	E	1.1	1.1	1	9	AAELRHVMT	20006
2DFS	MP	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	P	1.1	1.1	1	9	AAELRHVMT	20007
2DFX	EI	HYDROLASE	I	1.1	1.1	1	18	IPENNRLAIENIKDDIEN	20008
2DOQ	CD	CELL CYCLE	C	1.1	1.1	1	12	LDEIKRAFQLFD	20009
2DS2	CD	PLANT PROTEIN	D	1.1	1.1	1	13	PQQLRRLFDAARN	20010
2DSQ	IG	PROTEIN BINDING/HORMONE/GROWTH FACTOR	G	1.1	1.1	1	8	PCRIELYR	20011
2DSQ	IG	PROTEIN BINDING/HORMONE/GROWTH FACTOR	G	1.1	1.1	1	7	VVESLAK	20012
2DSR	GI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	I	1.1	1.1	1	12	AELVDALQFVCG	20013
2DWZ	AB	ONCOPROTEIN	B	1.1	1.1	1	6	LEDYVA	20014
2DXB	KL	HYDROLASE	K	1.1	1.1	1	9	AEERRRKQN	20015
2DXB	MO	HYDROLASE	M	1.1	1.1	1	5	QKDLW	20016
2DXB	PR	HYDROLASE	R	1.1	1.1	1	8	PRQVLAEF	20017
2DXB	SU	HYDROLASE	S	1.1	1.1	1	5	QKDLW	20018
2DXB	TU	HYDROLASE	T	1.1	1.1	1	9	AEERRRKQN	20019
2DXB	WO	HYDROLASE	O	1.1	1.1	1	10	PNYRRRLVRW	20020
2DZN	CD	PROTEIN BINDING	D	1.1	1.1	1	6	LDSLII	20021
2E 74	AB	PHOTOSYNTHESIS	B	1.1	1.1	1	10	KLLGVLLMAS	20022
2E 74	FH	PHOTOSYNTHESIS	F	1.1	1.1	1	29	EEMLYAALLSFGLIFVGWGLGVLLLKIQG	20023
2E 74	FH	PHOTOSYNTHESIS	H	1.1	1.1	1	24	IDVLGWVALLVVFTWSIAMVVWGR	20024
2E1M	AC	OXIDOREDUCTASE	C	1.1	1.1	1	5	QMTAF	20025
2E1M	BC	OXIDOREDUCTASE	C	1.1	1.1	1	17	DAERYGYALENLQSVHG	20026
2E3X	AB	HYDROLASE, BLOOD CLOTTING, TOXIN	A	1.1	1.1	1	7	DSCFQEN	20027
2E9W	AC	TRANSFERASE/HORMONE	C	1.1	1.1	1	20	NYSIIDKLVNIVDDLVECVK	20028
2EFC	CB	TRANSPORT PROTEIN	C	1.1	1.1	1	26	PRDKLVCILNCCKVINNLLLNASIAS	20029
2EFC	CD	TRANSPORT PROTEIN	C	1.1	1.1	1	26	PRDKLVCILNCCKVINNLLLNASIAS	20030
2EHO	IK	REPLICATION	I	1.1	1.1	1	8	DLKVSIHQ	20031

2EHO	KL	REPLICATION	K	1.1	1.1	1	8	LTKLLLNH	20032
2EHO	KL	REPLICATION	L	1.1	1.1	1	15	NADISQSLLQTFIGR	20033
2EQ9	EF	OXIDOREDUCTASE	E	1.1	1.1	1	7	LTDLALT	20034
2EXW	CD	MEMBRANE PROTEIN	D	1.1	1.1	1	5	SEQLT	20035
2F43	AG	HYDROLASE	G	1.1	1.1	1	12	KELIEIISGAAA	20036
2F5Z	CL	OXIDOREDUCTASE/PROTEIN BINDING	C	1.1	1.1	1	6	CEDIAR	20037
2F5Z	GN	OXIDOREDUCTASE/PROTEIN BINDING	N	1.1	1.1	1	10	PAARNILEKH	20038
2F66	AC	TRANSPORT PROTEIN	A	1.1	1.1	1	26	LDTFVKQGRELARQQFLVRWHIQRIT	20039
2F8N	AB	STRUCTURAL PROTEIN/DNA	A	1.1	1.1	1	11	TVALREIRRYQ	20040
2F8N	AG	STRUCTURAL PROTEIN/DNA	A	1.1	1.1	1	11	TVALREIRRYQ	20041
2F9I	AB	TRANSFERASE	A	1.1	1.1	1	7	AHDIKQL	20042
2F9I	CB	TRANSFERASE	B	1.1	1.1	1	7	AEFLLEH	20043
2F9Y	AB	LIGASE	B	1.1	1.1	1	6	PRVIEQ	20044
2FBW	BC	OXIDOREDUCTASE	C	1.1	1.1	1	30	PALIYSAKFALVFPLSYHTWNGIRHLVWDM	20045
2FDB	MP	HORMONE/GROWTH FACTOR/TRANSFERASE	P	1.1	1.1	1	5	EKMEK	20046
2FJF	MN	IMMUNE SYSTEM	M	1.1	1.1	1	7	DEQLKSG	20047
2FJF	QR	IMMUNE SYSTEM	Q	1.1	1.1	1	7	DEQLKSG	20048
2FJH	AB	HORMONE/GROWTH FACTOR/IMMUNE SYSTEM	A	1.1	1.1	1	6	DEQLKS	20049
2FJH	WB	HORMONE/GROWTH FACTOR/IMMUNE SYSTEM	W	1.1	1.1	1	8	FMDVYQRS	20050
2FKW	KJ	MEMBRANE PROTEIN, PHOTOSYNTHESIS	K	1.1	1.1	1	9	TWFPAYWQG	20051
2FL5	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6	SEELQA	20052
2FMM	ED	TRANSCRIPTION	E	1.1	1.1	1	14	TERHRAEVRRAVND	20053
2FRV	AB	OXIDOREDUCTASE	A	1.1	1.1	1	11	HAVEEALHEAI	20054
2FRV	CD	OXIDOREDUCTASE	C	1.1	1.1	1	11	HAVEEALHEAI	20055
2FRV	EF	OXIDOREDUCTASE	E	1.1	1.1	1	11	HAVEEALHEAI	20056
2FRV	GH	OXIDOREDUCTASE	G	1.1	1.1	1	11	HAVEEALHEAI	20057
2FRV	GJ	OXIDOREDUCTASE	J	1.1	1.1	1	32	TLGRTAARGIQCLTAAQEVEVWLDKLEANVKA	20058
2FRV	IJ	OXIDOREDUCTASE	I	1.1	1.1	1	11	HAVEEALHEAI	20059
2FRV	SL	OXIDOREDUCTASE	S	1.1	1.1	1	11	HAVEEALHEAI	20060
2FUG	49	OXIDOREDUCTASE	4	1.1	1.1	1	10	YLQNITYTPR	20061
2FUG	LN	OXIDOREDUCTASE	N	1.1	1.1	1	5	PAEFR	20062
2FUG	MO	OXIDOREDUCTASE	O	1.1	1.1	1	13	PEALIYAVMQLQK	20063
2FUG	SU	OXIDOREDUCTASE	S	1.1	1.1	1	16	EKDVENLEALLPLIEG	20064
2FUG	VY	OXIDOREDUCTASE	Y	1.1	1.1	1	6	LCAAAC	20065
2FYN	GH	OXIDOREDUCTASE	G	1.1	1.1	1	22	PMFKIYFWLLAADFVILTWVGA	20066
2FYN	JK	OXIDOREDUCTASE	J	1.1	1.1	1	22	PMFKIYFWLLAADFVILTWVGA	20067

2FYN	JK	OXIDOREDUCTASE	J	1.1	1.1	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	20068
2FYN	MN	OXIDOREDUCTASE	M	1.1	1.1	1	22	PMFKIYFWLLAADFVILTWVGA	20069
2FYN	MN	OXIDOREDUCTASE	M	1.1	1.1	1	29	GFMLRYLHANGASLFFIAVYLHIFRGLYY	20070
2FYN	PQ	OXIDOREDUCTASE	Q	1.1	1.1	1	5	ISQLF	20071
2FYN	QR	OXIDOREDUCTASE	R	1.1	1.1	1	23	YATAGAGAVATGAAVWPLINQMN	20072
2G2U	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	18	MAERNQQIAGIGAALIEH	20073
2G77	AB	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	A	1.1	1.1	1	12	IPTWHQIEIDIP	20074
2G9J	CB	STRUCTURAL PROTEIN	C	1.1	1.1	1	29	IDDLEDELYAQKLKYKAISEELDHALKDM	20075
2GBW	AB	OXIDOREDUCTASE	A	1.1	1.1	1	8	AAALSQIG	20076
2GFB	GH	IMMUNOGLOBULIN	G	1.1	1.1	1	7	SEQLTSG	20077
2GH0	DB	HORMONE/GROWTH FACTOR	B	1.1	1.1	1	12	LCLKFAMLCTLN	20078
2GHO	AC	TRANSFERASE	C	1.1	1.1	1	13	KREKEVLARAEKL	20079
2GHO	CD	TRANSFERASE	D	1.1	1.1	1	9	LKYYGFTLS	20080
2GJ7	AF	IMMUNE SYSTEM/VIRUS/VIRAL PROTEIN	A	1.1	1.1	1	6	PKDTLM	20081
2GJX	AC	HYDROLASE	A	1.1	1.1	1	15	SVLDEAFQRYRDLLF	20082
2GL7	AB	TRANSCRIPTION	A	1.1	1.1	1	10	QESKLIILAS	20083
2GL7	DE	TRANSCRIPTION	D	1.1	1.1	1	17	EKLLWTTSRVLKVLSVC	20084
2GL7	DF	TRANSCRIPTION	D	1.1	1.1	1	17	QVVVNKAAVMVHQLSKK	20085
2GTL	AB	OXYGEN STORAGE/TRANSPORT	B	1.1	1.1	1	16	VLEGLKVKSEWGRAYG	20086
2GTL	AG	OXYGEN STORAGE/TRANSPORT	A	1.1	1.1	1	16	LVLQSHLGHLADQHIQ	20087
2GTL	JK	OXYGEN STORAGE/TRANSPORT	J	1.1	1.1	1	16	PATLKEELDHLQVQHE	20088
2GTL	KN	OXYGEN STORAGE/TRANSPORT	K	1.1	1.1	1	15	EEDHRIVQKQWDILW	20089
2GUZ	EF	CHAPERONE, PROTEIN TRANSPORT	E	1.1	1.1	1	15	KKKLKEVHRKIMLAN	20090
2GUZ	GB	CHAPERONE, PROTEIN TRANSPORT	G	1.1	1.1	1	15	KKKLKEVHRKIMLAN	20091
2GUZ	IJ	CHAPERONE, PROTEIN TRANSPORT	I	1.1	1.1	1	15	KKKLKEVHRKIMLAN	20092
2GV5	AC	CELL CYCLE	A	1.1	1.1	1	8	ENEFIAIC	20093
2GWF	AF	HYDROLASE/LIGASE	A	1.1	1.1	1	7	MQDYQDS	20094
2GY9	CE	RIBOSOME	C	1.1	1.1	1	15	FRRAMKRAVQNAMRL	20095
2GYA	MU	RIBOSOME	M	1.1	1.1	1	7	RKLQELG	20096
2H1L	GS	VIRAL PROTEIN	G	1.1	1.1	1	14	LSVYQKMKFNVAMG	20097
2H1O	CG	GENE REGULATION/DNA COMPLEX	C	1.1	1.1	1	9	TNVISEPLR	20098
2H4P	AB	HYDROLASE INHIBITOR	A	1.1	1.1	1	6	EQLERE	20099
2H7V	AC	SIGNALING PROTEIN	C	1.1	1.1	1	26	FSDIGSLVRAHKHLETLLEVLVTLSQ	20100
2HGI	MQ	RIBOSOME	Q	1.1	1.1	1	7	RELAHKG	20101
2HGR	JN	RIBOSOME	N	1.1	1.1	1	18	PYAAQLAALDAAKKAMAY	20102
2HHH	LQ	RIBOSOME	L	1.1	1.1	1	8	INQLVRKG	20103
2HHH	MS	RIBOSOME	M	1.1	1.1	1	9	YRGLRHRRG	20104
2HII	XZ	REPLICATION	Z	1.1	1.1	1	14	SDGFKSAISEVSTV	20105

2HIK	LM	REPLICATION	L	1.1	1.1	1	10	ESVLNVIAAD	20106
2HLD	AD	HYDROLASE	D	1.1	1.1	1	12	LATDMGLLQERI	20107
2HLD	AD	HYDROLASE	D	1.1	1.1	1	20	QEHYDVASKVQETLQTYKSL	20108
2HLD	BE	HYDROLASE	E	1.1	1.1	1	12	LATDMGLLQERI	20109
2HLD	DG	HYDROLASE	D	1.1	1.1	1	7	QDIIAIL	20110
2HLD	JM	HYDROLASE	J	1.1	1.1	1	7	AELFYKG	20111
2HLD	KO	HYDROLASE	K	1.1	1.1	1	8	YIPTNVIS	20112
2HLD	SV	HYDROLASE	V	1.1	1.1	1	20	QEHYDVASKVQETLQTYKSL	20113
2HLD	SW	HYDROLASE	W	1.1	1.1	1	16	IFRFTQAGSEVSALLG	20114
2HLD	VY	HYDROLASE	V	1.1	1.1	1	8	QDIIAILG	20115
2HNT	LF	SERINE PROTEASE	L	1.1	1.1	1	8	ERELLESY	20116
2HOD	AB	BLOOD CLOTTING	A	1.1	1.1	1	16	QKNVRAQLVDMKRLEV	20117
2HOD	DF	BLOOD CLOTTING	F	1.1	1.1	1	30	SSIRYLQEIYNSNNQKIVNLKEKVAQLEAQ	20118
2HOD	GI	BLOOD CLOTTING	G	1.1	1.1	1	12	RLEVDIDIKIRS	20119
2HOD	KL	BLOOD CLOTTING	K	1.1	1.1	1	13	LRVLRSILENLRS	20120
2HSN	AB	LIGASE/RNA BINDING PROTEIN	A	1.1	1.1	1	15	DKYQFALASLQNLLY	20121
2HSN	AB	LIGASE/RNA BINDING PROTEIN	B	1.1	1.1	1	11	LDQLNLVLRDN	20122
2HV8	CE	PROTEIN TRANSPORT	E	1.1	1.1	1	33	RDELMEAIQKQEEINFRLQDYIDRIIVAIMETN	20123
2HY5	BC	TRANSFERASE	B	1.1	1.1	1	7	RDSLEAR	20124
2HYB	KI	TRANSFERASE	I	1.1	1.1	1	6	DGIYAA	20125
2HYB	NO	TRANSFERASE	N	1.1	1.1	1	11	SARVSELMNES	20126
2HYB	QR	TRANSFERASE	Q	1.1	1.1	1	11	SARVSELMNES	20127
2HYI	CD	HYDROLASE/RNA BINDING PROTEIN/RNA	C	1.1	1.1	1	10	PGRVFDMIRR	20128
2HZS	CD	TRANSCRIPTION	D	1.1	1.1	1	8	VSSLMNGL	20129
2HZS	EF	TRANSCRIPTION	F	1.1	1.1	1	8	VSSLMNGL	20130
2I2R	CG	TRANSPORT PROTEIN	G	1.1	1.1	1	9	STYAHYLFN	20131
2I2R	KO	TRANSPORT PROTEIN	O	1.1	1.1	1	9	STYAHYLFN	20132
2I2R	LO	TRANSPORT PROTEIN	L	1.1	1.1	1	11	ISAYDDELAFY	20133
2I2X	AB	TRANSFERASE	A	1.1	1.1	1	12	CAQANTAMFIGG	20134
2I2X	EF	TRANSFERASE	F	1.1	1.1	1	14	DIGKNIVTALLRAN	20135
2I2X	EF	TRANSFERASE	F	1.1	1.1	1	21	LPNVMMSADAMLEGIEYCKEN	20136
2I2X	GH	TRANSFERASE	H	1.1	1.1	1	23	PIDLIDDALMVGMGVVIRLYDEG	20137
2I2X	IL	TRANSFERASE	I	1.1	1.1	1	22	KEKLIKEYERITTDVMERMVQV	20138
2I2X	ON	TRANSFERASE	N	1.1	1.1	1	8	EASLKKVL	20139
2IAN	AB	IMMUNE SYSTEM	B	1.1	1.1	1	10	RPDAEYWNSQ	20140
2IAN	FJ	IMMUNE SYSTEM	F	1.1	1.1	1	21	QGALANIAVDKANLEIMTKRS	20141
2IAN	LI	IMMUNE SYSTEM	L	1.1	1.1	1	9	KDLLEQRRA	20142
2IBZ	AC	OXIDOREDUCTASE	C	1.1	1.1	1	5	FRKSN	20143
2IBZ	CE	OXIDOREDUCTASE	C	1.1	1.1	1	15	IELAFSSVEHIMRDV	20144

2IBZ	EI	OXIDOREDUCTASE	I	1.1	1.1	1	27	VGTIFAGAFVFQTVFDTAITSWYENHN	20145
2ICE	AB	IMMUNE SYSTEM	A	1.1	1.1	1	7	KGVFVLN	20146
2ICE	AC	IMMUNE SYSTEM	C	1.1	1.1	1	5	KYELD	20147
2ICE	DE	IMMUNE SYSTEM	D	1.1	1.1	1	11	QSKIWDVVEKA	20148
2ICW	HL	IMMUNE SYSTEM	H	1.1	1.1	1	28	EETKEVLKLFKLKVNQFYRHAFGIVNDY	20149
2IFG	AE	TRANSFERASE	E	1.1	1.1	1	5	PIFHR	20150
2IFQ	AB	OXIDOREDUCTASE	B	1.1	1.1	1	7	QDVASEC	20151
2IJ0	AE	PROTEIN BINDING	A	1.1	1.1	1	16	ISTLDFEIRHQLTQIH	20152
2INN	BE	OXIDOREDUCTASE	B	1.1	1.1	1	22	PDTFDKYYRPRYEYLAKEAAAG	20153
2INN	BE	OXIDOREDUCTASE	B	1.1	1.1	1	7	PEKYIQA	20154
2INP	AF	OXIDOREDUCTASE	A	1.1	1.1	1	6	PEKYIQ	20155
2INP	BD	OXIDOREDUCTASE	D	1.1	1.1	1	8	GHIARRFG	20156
2IO1	EF	PROTEIN BINDING, HYDROLASE	E	1.1	1.1	1	9	FYPKLKSGG	20157
2IPK	AD	IMMUNE SYSTEM	D	1.1	1.1	1	8	QSKYLMMY	20158
2ISS	CF	LYASE, TRANSFERASE	C	1.1	1.1	1	11	AEQAKIAEEAG	20159
2IX7	CB	CONTRACTILE PROTEIN/METAL BINDING	B	1.1	1.1	1	14	EEQIAEFKEAFSLF	20160
2IY1	AB	HYDROLASE/NUCLEAR PROTEIN	A	1.1	1.1	1	8	RKDIQTLN	20161
2IZO	BC	HYDROLASE	C	1.1	1.1	1	15	ESVLNVIAADVTLVG	20162
2J0Q	CD	HYDROLASE	C	1.1	1.1	1	15	KSVMEELKRIIDDSE	20163
2J0Q	FG	HYDROLASE	F	1.1	1.1	1	15	KSVMEELKRIIDDSE	20164
2J0S	AT	HYDROLASE	A	1.1	1.1	1	16	EEWKFDTLCDLYDTLT	20165
2J0T	AD	HYDROLASE	A	1.1	1.1	1	14	LHRVAAHELGHSLG	20166
2J28	QR	RIBOSOME	Q	1.1	1.1	1	10	GQYAYRDRRQ	20167
2J3W	CF	TRANSPORT	F	1.1	1.1	1	27	VSELQARLADMGQGVGASLLDVLVMRE	20168
2J59	BN	HYDROLASE	B	1.1	1.1	1	7	RPLWRHY	20169
2J59	EQ	HYDROLASE	E	1.1	1.1	1	7	RPLWRHY	20170
2J5G	ED	HYDROLASE	E	1.1	1.1	1	10	QRLKRLVNEG	20171
2J5G	FD	HYDROLASE	F	1.1	1.1	1	15	LMERAWEIARTLAKQ	20172
2J7A	AF	OXIDOREDUCTASE	F	1.1	1.1	1	9	NPVGVTHKL	20173
2J7A	GI	OXIDOREDUCTASE	I	1.1	1.1	1	15	METKEVVNANCKACH	20174
2J7A	GL	OXIDOREDUCTASE	L	1.1	1.1	1	5	RPFCT	20175
2J7A	GL	OXIDOREDUCTASE	L	1.1	1.1	1	9	NPVGVTHKL	20176
2J7A	KL	OXIDOREDUCTASE	L	1.1	1.1	1	5	RPFCT	20177
2J98	AB	RNA BINDING PROTEIN	A	1.1	1.1	1	15	NLRRGAVLGYIGATV	20178
2JBL	CL	ELECTRON TRANSPORT	L	1.1	1.1	1	5	WPEWW	20179
2JBL	CM	ELECTRON TRANSPORT	M	1.1	1.1	1	15	IWPHIDWLTAFSIRY	20180
2JBL	HL	ELECTRON TRANSPORT	H	1.1	1.1	1	17	LREEDKVSAYYAGGLLY	20181
2JDQ	AE	PROTEIN TRANSPORT	A	1.1	1.1	1	15	TDVLADACWALSYLS	20182
2JE6	AI	HYDROLASE	A	1.1	1.1	1	8	IIKKESIV	20183

2JFA	BQ	TRANSCRIPTION	B	1.1	1.1	1	24	LHDQVHLLECAWLEILMIGLVWRS	20184
2JGZ	AB	TRANSFERASE	B	1.1	1.1	1	17	LQLVGVTAMFIASKYEE	20185
2JIY	LM	PHOTOSYNTHESIS	L	1.1	1.1	1	15	IWTHLDWVSNTGYTY	20186
2JIZ	CD	HYDROLASE	D	1.1	1.1	1	5	EVFTG	20187
2JIZ	HL	HYDROLASE	L	1.1	1.1	1	15	IFRFTQAGSEVSALL	20188
2JIZ	JM	HYDROLASE	M	1.1	1.1	1	12	LATDMGTMQERI	20189
2JIZ	KN	HYDROLASE	N	1.1	1.1	1	38	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKP	20190
2JJZ	AB	METAL BINDING PROTEIN	B	1.1	1.1	1	18	LKARQERRLAEINREFLC	20191
2JKR	AB	ENDOCYTOSIS	B	1.1	1.1	1	9	PVTAKEVVL	20192
2JKR	AS	ENDOCYTOSIS	A	1.1	1.1	1	16	TNLRYLALESMCTLAS	20193
2JKR	AS	ENDOCYTOSIS	A	1.1	1.1	1	16	GYSKKKYVCKLLFIFL	20194
2JKR	AS	ENDOCYTOSIS	S	1.1	1.1	1	11	QTKVLKQLLML	20195
2JKR	LB	ENDOCYTOSIS	B	1.1	1.1	1	16	PDLRDRGYIYWRLLST	20196
2JKR	LE	ENDOCYTOSIS	E	1.1	1.1	1	9	PVTAKEVVL	20197
2JKR	LE	ENDOCYTOSIS	L	1.1	1.1	1	17	VELQQRAVEYLRLSTVA	20198
2JKR	LI	ENDOCYTOSIS	L	1.1	1.1	1	15	PTFMGLALHCIANVG	20199
2JKR	LI	ENDOCYTOSIS	L	1.1	1.1	1	16	GYSKKKYVCKLLFIFL	20200
2JMF	AB	LIGASE/SIGNALING PROTEIN	B	1.1	1.1	1	5	YEDCI	20201
2K03	AB	CYTOKINE	A	1.1	1.1	1	12	KWIQEYLEKCLN	20202
2K3W	AB	PROTEIN TRANSPORT	A	1.1	1.1	1	26	DKAKESIRAKCVQYLDRAEKLKDYLR	20203
2K5B	AB	CHAPERONE	A	1.1	1.1	1	13	SGTKAFMEALQAG	20204
2K5B	AB	CHAPERONE	B	1.1	1.1	1	9	CALMEQVAH	20205
2K7L	BA	TRANSCRIPTION	A	1.1	1.1	1	9	TKDLLKKFQ	20206
2K7W	AB	APOPTOSIS	A	1.1	1.1	1	26	PELIRTIMGWTLDFLRERLLGWIQDQ	20207
2KBR	AB	STRUCTURAL PROTEIN/CELL ADHESION	A	1.1	1.1	1	18	DAEKDYLYDVLRMYHQTM	20208
2NGR	AB	HYDROLASE	B	1.1	1.1	1	13	NTNLAVVFGPNLL	20209
2NN6	BH	HYDROLASE/TRANSFERASE	B	1.1	1.1	1	32	LERVLEAAAQAARDVHTLLDRVVRQHVREASI	20210
2NOJ	GH	IMMUNE SYSTEM	H	1.1	1.1	1	16	YEKKKLQRQIDLVLKY	20211
2NQB	AB	STRUCTURAL PROTEIN/DNA	B	1.1	1.1	1	11	AMDVVYALKRQ	20212
2NQB	CD	STRUCTURAL PROTEIN/DNA	C	1.1	1.1	1	7	EELNKLL	20213
2NTY	BD	SIGNALING PROTEIN	B	1.1	1.1	1	38	VGQAVLESYSRILESLAYTVMSRIEDVLYTDTLALKQT	20214
2NU9	AB	LIGASE	A	1.1	1.1	1	14	GTLTYEAVKQTTDY	20215
2NV2	GH	LYASE/TRANSFERASE	H	1.1	1.1	1	11	STTMRRLIDTY	20216
2NV2	IJ	LYASE/TRANSFERASE	I	1.1	1.1	1	11	AEQAKIAEEAG	20217
2NV2	IJ	LYASE/TRANSFERASE	J	1.1	1.1	1	11	STTMRRLIDTY	20218
2NV2	WX	LYASE/TRANSFERASE	W	1.1	1.1	1	8	YKLIAELS	20219
2NX5	QT	IMMUNE SYSTEM	Q	1.1	1.1	1	13	LCVEWLRRYLENG	20220
2NZ0	AD	MEMBRANE PROTEIN	A	1.1	1.1	1	7	LEQLEAQ	20221
2O25	AD	LIGASE	A	1.1	1.1	1	6	NLCAMG	20222

2O26	AX	CYTOKINE/SIGNALING PROTEIN	A	1.1	1.1	1	22	SHCWLRDMVIQLSLSLTTLLDK	20223
2O9I	BD	TRANSCRIPTION	B	1.1	1.1	1	21	LPHMADMSTYMFKGIISFAKV	20224
2OBH	BD	CELL CYCLE	B	1.1	1.1	1	9	EQEFLRIMK	20225
2ODG	AC	MEMBRANE PROTEIN, PROTEIN BINDING	C	1.1	1.1	1	17	RRLYEKKIFEYETQRRR	20226
2ODY	CD	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	C	1.1	1.1	1	5	EKTFG	20227
2OF5	DK	APOPTOSIS	D	1.1	1.1	1	16	VQSQVVEAFIRWRQRF	20228
2OM0	AB	HORMONE	A	1.1	1.1	1	5	IVEQC	20229
2OM0	QT	HORMONE	T	1.1	1.1	1	18	NQHLCGSHLVEALYLVCG	20230
2OM0	S4	HORMONE	S	1.1	1.1	1	7	LYQLENY	20231
2OM0	ST	HORMONE	S	1.1	1.1	1	7	LYQLENY	20232
2OS8	AB	CONTRACTILE PROTEIN	B	1.1	1.1	1	5	FSSLG	20233
2OT8	AC	TRANSPORT PROTEIN	A	1.1	1.1	1	18	PEVRQSSFALLGDLTKAC	20234
2OT8	BD	TRANSPORT PROTEIN	B	1.1	1.1	1	19	HKNLLILYDAIGTLADSVG	20235
2OTJ	NQ	RIBOSOME	N	1.1	1.1	1	11	YHQRLRLLKSG	20236
2OTJ	NQ	RIBOSOME	Q	1.1	1.1	1	5	PQRAV	20237
2OUL	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	5	DDFAF	20238
2OVQ	AB	TRANSCRIPTION/CELL CYCLE	B	1.1	1.1	1	18	PWKSAYIRQHRIDTNWRR	20239
2OXQ	AC	LIGASE	C	1.1	1.1	1	12	RKDIEEHLQRVG	20240
2OZB	DE	RNA BINDING PROTEIN/RNA	D	1.1	1.1	1	10	ANEATKTLNR	20241
2P22	AC	TRANSPORT PROTEIN	C	1.1	1.1	1	18	RILESKYVASWQDYHSEF	20242
2P2C	AB	HYDROLASE	A	1.1	1.1	1	15	GDVDHSTLVTLFKLL	20243
2P2C	FR	HYDROLASE	R	1.1	1.1	1	8	PLHLAAYD	20244
2P2C	LU	HYDROLASE	U	1.1	1.1	1	8	PLHLAAYD	20245
2P2C	LU	HYDROLASE	U	1.1	1.1	1	9	PLHLAAKTG	20246
2P2C	LU	HYDROLASE	U	1.1	1.1	1	8	PLHLAADN	20247
2P58	AC	TRANSPORT PROTEIN/CHAPERONE	A	1.1	1.1	1	8	VETVRSIT	20248
2P5T	CD	TRANSCRIPTION REGULATOR	C	1.1	1.1	1	32	PVEDYELTLKIEIVKERGANLLSRLYRYQDSQ	20249
2PBI	AB	SIGNALING PROTEIN	A	1.1	1.1	1	12	GGDVLQWITQRL	20250
2PBI	CD	SIGNALING PROTEIN	D	1.1	1.1	1	5	LHQVA	20251
2PCP	AB	IMMUNOGLOBULIN	A	1.1	1.1	1	7	SEQLTSG	20252
2PCP	CD	IMMUNOGLOBULIN	C	1.1	1.1	1	6	SEQLTS	20253
2PF4	AE	HYDROLASE REGULATOR/VIRAL PROTEIN	A	1.1	1.1	1	10	WRVRYMVADK	20254
2PF4	AE	HYDROLASE REGULATOR/VIRAL PROTEIN	E	1.1	1.1	1	10	REESLQLMDL	20255
2PI2	DH	REPLICATION, DNA BINDING PROTEIN	D	1.1	1.1	1	7	ISQLLSA	20256
2PI2	DH	REPLICATION, DNA BINDING PROTEIN	H	1.1	1.1	1	14	LGLYNEAVKIIHDF	20257
2PJW	HV	ENDOCYTOSIS/EXOCYTOSIS	V	1.1	1.1	1	6	ASLVEK	20258

2PK9	AD	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	D	1.1	1.1	1	9	NAHYAKVGG	20259
2PMZ	AC	TRANSLATION, TRANSFERASE	C	1.1	1.1	1	13	IRHILLIADVMTR	20260
2PMZ	QG	TRANSLATION, TRANSFERASE	Q	1.1	1.1	1	9	VKHIYEFLK	20261
2PMZ	QR	TRANSLATION, TRANSFERASE	R	1.1	1.1	1	5	RLLDN	20262
2PQR	BD	APOPTOSIS	B	1.1	1.1	1	15	YSMAKRYVDTLFEHE	20263
2PRG	AC	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	A	1.1	1.1	1	23	LNDQVTLLKYGVHEIIYTMLASL	20264
2Q0O	BD	TRANSCRIPTION	B	1.1	1.1	1	12	PREMLCLVWASK	20265
2Q0O	BD	TRANSCRIPTION	D	1.1	1.1	1	33	GPVLQTLQDEYVARQKRSEAQQEELSDILDALG	20266
2Q6W	EF	IMMUNE SYSTEM	E	1.1	1.1	1	9	YCRHNYGVG	20267
2Q8A	AH	IMMUNE SYSTEM	A	1.1	1.1	1	10	ELTLCSRHAG	20268
2Q8A	LH	IMMUNE SYSTEM	L	1.1	1.1	1	5	SEQLT	20269
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	B	1.1	1.1	1	25	RDSYRRILMGSTLRKRKMYEEFLSK	20270
2QFA	AB	CELL CYCLE/CELL CYCLE/CELL CYCLE	A	1.1	1.1	1	5	PAWQP	20271
2QHO	CB	PROTEIN BINDING/LIGASE	B	1.1	1.1	1	11	EELISQAQVVL	20272
2QI9	BD	MEMBRANE PROTEIN	B	1.1	1.1	1	20	TLARQQQRQNIRWLLSLSVL	20273
2QI9	BF	MEMBRANE PROTEIN	F	1.1	1.1	1	5	EQVLA	20274
2QIY	AC	SIGNALING PROTEIN/HYDROLASE	A	1.1	1.1	1	19	VQDICFAFLQNYYERMRTD	20275
2QJK	MR	ELECTRON TRANSPORT	M	1.1	1.1	1	9	FLPFYAILR	20276
2QJK	PO	ELECTRON TRANSPORT	O	1.1	1.1	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	20277
2QJP	AB	ELECTRON TRANSPORT	A	1.1	1.1	1	22	PMFKIYFWLLAADFVILTWVGA	20278
2QJP	GI	ELECTRON TRANSPORT	I	1.1	1.1	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	20279
2QJP	HI	ELECTRON TRANSPORT	H	1.1	1.1	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	20280
2QJP	JI	ELECTRON TRANSPORT	J	1.1	1.1	1	18	AKFFGVLAMFGAILVMAL	20281
2QJP	JL	ELECTRON TRANSPORT	L	1.1	1.1	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	20282
2QJY	GL	OXIDOREDUCTASE	G	1.1	1.1	1	18	AKFFGVLAMFGAILVMAL	20283
2QKI	AB	IMMUNE SYSTEM	A	1.1	1.1	1	11	QSKIWDVVEKA	20284
2QNA	AB	TRANSPORT PROTEIN	A	1.1	1.1	1	18	NDLQSLLCATLQNVLRKV	20285
2QNA	AB	TRANSPORT PROTEIN	A	1.1	1.1	1	19	RSVKPQILSVFGDIALAIG	20286
2QOY	MS	RIBOSOME	M	1.1	1.1	1	18	GDLRREISMSIKRLMDLG	20287
2QP0	EH	RIBOSOME	E	1.1	1.1	1	8	PEMVAAKR	20288
2QP0	MS	RIBOSOME	M	1.1	1.1	1	16	LRREISMSIKRLMDLG	20289
2QQP	CD	VIRUS	D	1.1	1.1	1	5	TVSAL	20290
2R17	AC	PROTEIN TRANSPORT	C	1.1	1.1	1	15	KPDQGRAVSTCAHLF	20291
2R1H	AB	OXYGEN BINDING	A	1.1	1.1	1	19	PTNFKILAHNLIVVIAAYF	20292
2R1H	CD	OXYGEN BINDING	C	1.1	1.1	1	19	PTNFKILAHNLIVVIAAYF	20293
2R5C	AB	TRANSFERASE	B	1.1	1.1	1	13	EALLKNLQMVHQN	20294
2R6C	BG	REPLICATION	G	1.1	1.1	1	13	EQELEDYIRHVLN	20295

2R6C	CH	REPLICATION	C	1.1	1.1	1	11 VSYLSELADAV	20296
2R6G	EF	HYDROLASE/TRANSPORT PROTEIN	E	1.1	1.1	1	10 KELAKEFLEN	20297
2R6G	EF	HYDROLASE/TRANSPORT PROTEIN	F	1.1	1.1	1	7 RQALSDI	20298
2R6G	FG	HYDROLASE/TRANSPORT PROTEIN	G	1.1	1.1	1	13 PWQAFRLVLLPLS	20299
2RAO	AB	OXYGEN BINDING	A	1.1	1.1	1	16 GGEYGAEAVERMFLGF	20300
2RD0	AB	TRANSFERASE/ONCOPROTEIN	B	1.1	1.1	1	9 SIKPDLIQL	20301
2RD7	AC	IMMUNE SYSTEM	C	1.1	1.1	1	6 RFLQER	20302
2RET	AB	PROTEIN TRANSPORT	B	1.1	1.1	1	17 LSQERTARLNELQRALV	20303
2RET	GH	PROTEIN TRANSPORT	H	1.1	1.1	1	16 SQERTARLNELQRALV	20304
2RHS	AB	LIGASE	B	1.1	1.1	1	16 DRQHKTRTLKETLEGA	20305
2RHS	AD	LIGASE	A	1.1	1.1	1	6 QQLAEE	20306
2RHS	CB	LIGASE	C	1.1	1.1	1	16 MSDLKGTLELVAKKLF	20307
2RI4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.1	1.1	1	19 PAVHASLDKFLANVSTVLT	20308
2RI4	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	1.1	1.1	1	19 PENFKLLGNVLVVVLARHH	20309
2RII	AX	OXIDOREDUCTASE COMPLEX	X	1.1	1.1	1	9 LSDLRVYLG	20310
2RMS	AB	TRANSCRIPTION	A	1.1	1.1	1	12 TPGVISRVSQLF	20311
2UUN	CF	ELECTRON TRANSPORT	F	1.1	1.1	1	25 SDRMAACLRDMEIILRYVTYAVFAG	20312
2UUN	KL	ELECTRON TRANSPORT	L	1.1	1.1	1	13 ANKRLDAVNRITA	20313
2UUN	MP	ELECTRON TRANSPORT	P	1.1	1.1	1	25 SDRMAACLRDMEIILRYVTYAVFAG	20314
2UUN	QN	ELECTRON TRANSPORT	N	1.1	1.1	1	25 SDRMAACLRDMEIILRYVTYAVFAG	20315
2UZ1	DC	LYASE	C	1.1	1.1	1	15 EAAAGHAAEGYARAG	20316
2UZ1	DC	LYASE	C	1.1	1.1	1	10 VTPIANAWLD	20317
2V1C	AC	RECOMBINATION	C	1.1	1.1	1	5 PERYA	20318
2V1D	AC	OXIDOREDUCTASE/REPRESSOR	A	1.1	1.1	1	26 KEKDEMVEQEFNRLLEATSYLSHQLD	20319
2V1S	CL	OXIDOREDUCTASE	C	1.1	1.1	1	24 LKDAEAVQKFFLEEIQLGEELLAQ	20320
2V36	CD	TRANSFERASE	C	1.1	1.1	1	13 PLASEIGADVLKK	20321
2V4I	CB	TRANSFERASE	B	1.1	1.1	1	11 WGRVAMAIGKC	20322
2V4Z	AB	CELL CYCLE	B	1.1	1.1	1	14 EENIEFWLACEDFK	20323
2V51	DE	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	E	1.1	1.1	1	7 REELVSQ	20324
2V6X	AB	PROTEIN TRANSPORT	A	1.1	1.1	1	15 YEEAYTAYYNGLDYL	20325
2V7N	CD	IMMUNE SYSTEM	C	1.1	1.1	1	7 DEQLKSG	20326
2V7Q	BF	HYDROLASE	F	1.1	1.1	1	15 TREGNDLYHEMIESG	20327
2V7Q	EG	HYDROLASE	E	1.1	1.1	1	6 IIAILG	20328
2VAS	AB	MOTOR PROTEIN	A	1.1	1.1	1	6 DKLARL	20329
2VDW	CD	TRANSFERASE	C	1.1	1.1	1	17 PLGILSNYVKTLLISMY	20330
2VDW	GH	TRANSFERASE	G	1.1	1.1	1	16 PSTRNFFELNRGAIKC	20331
2VGL	BM	PROTEIN TRANSPORT	B	1.1	1.1	1	17 KEKRKEAVKKVIAAMTV	20332

2VHN	EL	RIBOSOME	E	1.1	1.1	1	11	VHQVVVAYAAG	20333
2VJH	AB	PHOTOSYNTHESIS	A	1.1	1.1	1	16	HAAVVKEAGDVVFKKY	20334
2VJM	AB	TRANSFERASE	A	1.1	1.1	1	6	PSLQKV	20335
2VJT	AB	PHOTOSYNTHESIS	A	1.1	1.1	1	13	PGELDRIKSFVAS	20336
2VLH	AB	LYASE	B	1.1	1.1	1	8	DKQWAGMM	20337
2VLR	AE	IMMUNE SYSTEM	A	1.1	1.1	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	20338
2VOG	AB	APOPTOSIS	A	1.1	1.1	1	7	GFIKKFE	20339
2VOY	DE	HYDROLASE	E	1.1	1.1	1	10	FVILLILIAN	20340
2VR0	BC	OXIDOREDUCTASE	C	1.1	1.1	1	10	NPVGVTHKLS	20341
2VRC	BD	OXIDOREDUCTASE	B	1.1	1.1	1	10	EGLRASTESG	20342
2VUS	AI	TRANSCRIPTION	I	1.1	1.1	1	11	NACGLFLKLHG	20343
2VUS	BJ	TRANSCRIPTION	B	1.1	1.1	1	14	RQAASLIRVAAAVG	20344
2VUS	BJ	TRANSCRIPTION	J	1.1	1.1	1	10	NACGLFLKLH	20345
2VVL	FG	OXIDOREDUCTASE	G	1.1	1.1	1	10	SHVWREITRY	20346
2VWE	BJ	IMMUNE SYSTEM	B	1.1	1.1	1	9	WIDVYTRAT	20347
2VXS	KO	CYTOKINE	O	1.1	1.1	1	6	SEELQA	20348
2VYN	DA	OXIDOREDUCTASE	D	1.1	1.1	1	19	NEYGYSHRVVDLLRYMFSR	20349
2W19	BD	TRANSFERASE/ISOMERASE	B	1.1	1.1	1	16	TQQSLELAFLVAEMLR	20350
2W2H	BD	RNA BINDING PROTEIN	B	1.1	1.1	1	13	AANLLQDMGQRLN	20351
2W73	AK	METAL BINDING PROTEIN	A	1.1	1.1	1	29	FPEFLTMMARKMKDTDSEEEIREAFRVFD	20352
2W73	FM	METAL BINDING PROTEIN	F	1.1	1.1	1	29	FPEFLTMMARKMKDTDSEEEIREAFRVFD	20353
2WAQ	AC	TRANSCRIPTION	C	1.1	1.1	1	8	VVENIIIG	20354
2WB1	AB	TRANSCRIPTION	A	1.1	1.1	1	7	EIIARTL	20355
2WB1	CB	TRANSCRIPTION	B	1.1	1.1	1	6	AMLLKD	20356
2WB1	WI	TRANSCRIPTION	I	1.1	1.1	1	6	SIAEEE	20357
2WB1	WY	TRANSCRIPTION	Y	1.1	1.1	1	8	VVENIIIG	20358
2WB1	ZJ	TRANSCRIPTION	J	1.1	1.1	1	11	EAKRLFEDNYK	20359
2WC0	EF	HYDROLASE/HORMONE	F	1.1	1.1	1	11	HLVEALYLVCG	20360
2WH4	NU	RIBOSOME	U	1.1	1.1	1	5	DLAVR	20361
2WII	AB	IMMUNE SYSTEM	A	1.1	1.1	1	12	QSKIWDVVEKAD	20362
2WIN	IM	IMMUNE SYSTEM	M	1.1	1.1	1	8	LNVNELAT	20363
2WME	BC	OXIDOREDUCTASE	B	1.1	1.1	1	11	LARAHRAIHRL	20364
2WME	HE	OXIDOREDUCTASE	E	1.1	1.1	1	18	AMQRSRILRRAVDILRER	20365
2WME	HE	OXIDOREDUCTASE	H	1.1	1.1	1	11	LARAHRAIHRL	20366
2Z2L	AB	BIOSYNTHETIC PROTEIN	A	1.1	1.1	1	5	NSILA	20367
2Z2S	AB	TRANSCRIPTION	A	1.1	1.1	1	5	TVWQK	20368
2ZCY	CK	HYDROLASE	K	1.1	1.1	1	15	VAAASKILSNLVYQY	20369
2ZCY	HN	HYDROLASE	N	1.1	1.1	1	22	AADTQAIADIVQYHLELYTSQY	20370
2ZCY	JK	HYDROLASE	J	1.1	1.1	1	22	AGDTVQFAEYIQANIQLYSIRE	20371
2ZCY	QY	HYDROLASE	Y	1.1	1.1	1	15	VAAASKILSNLVYQY	20372

2ZCY	VM	HYDROLASE	M	1.1	1.1	1	18	VQVAEEAIVNAMRVLYYR	20373
2ZCY	XY	HYDROLASE	X	1.1	1.1	1	22	AGDTVQFAEYIQANIQLYSIRE	20374
2ZCY	Z0	HYDROLASE	0	1.1	1.1	1	14	FGAHMANPLLRKVV	20375
2ZHX	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	14	RSLANIFDEYTADL	20376
2ZHX	AL	HYDROLASE/HYDROLASE INHIBITOR	L	1.1	1.1	1	9	PEEVEEVIG	20377
2ZIV	AB	HYDROLASE	A	1.1	1.1	1	11	GDKAAAVLEHY	20378
2ZIV	AB	HYDROLASE	B	1.1	1.1	1	11	PELSRRIYLQM	20379
2ZIX	AB	HYDROLASE	B	1.1	1.1	1	5	PQLLV	20380
2ZNW	AZ	IMMUNE SYSTEM/HYDROLASE	Z	1.1	1.1	1	12	LGNWVCAAKFES	20381
2ZSH	AB	HORMONE RECEPTOR	B	1.1	1.1	1	11	LYTWLDSMLTD	20382
2ZT9	AD	PHOTOSYNTHESIS	A	1.1	1.1	1	28	GWLIRSIHRWSASMMVLMMILHVFRVYL	20383
2ZU6	AB	HYDROLASE	B	1.1	1.1	1	19	TTDVEKSFDKLLKDLPELA	20384
2ZU6	AB	HYDROLASE	B	1.1	1.1	1	9	RGYERIYNE	20385
2ZVN	CF	SIGNALING PROTEIN/TRANSCRIPTION	F	1.1	1.1	1	84	EDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLK	20386
2ZVN	EH	SIGNALING PROTEIN/TRANSCRIPTION	H	1.1	1.1	1	51	IVMETVPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKL	20387
2ZVN	GB	SIGNALING PROTEIN/TRANSCRIPTION	B	1.1	1.1	1	35	TVPVLKAQADIYKADFQAERHAREKLVEKKEYLQE	20388
2ZYZ	AB	SPLICING	A	1.1	1.1	1	14	IQTLLSVINMGETL	20389
3A0B	ac	ELECTRON TRANSPORT	a	1.1	1.1	1	5	ICVAY	20390
3A0B	ad	ELECTRON TRANSPORT	d	1.1	1.1	1	12	FYTKNLLLNEGI	20391
3A0B	bd	ELECTRON TRANSPORT	d	1.1	1.1	1	5	NAIAF	20392
3A0B	bd	ELECTRON TRANSPORT	d	1.1	1.1	1	9	ISQEIRAAE	20393
3A0B	CO	ELECTRON TRANSPORT	O	1.1	1.1	1	5	YDDIV	20394
3A0B	DH	ELECTRON TRANSPORT	D	1.1	1.1	1	9	WFDILDDWL	20395
3A0B	dl	ELECTRON TRANSPORT	l	1.1	1.1	1	18	RTSLYLGLLLILVLALLF	20396
3A0B	jk	ELECTRON TRANSPORT	j	1.1	1.1	1	9	LWIVATVAG	20397
3B2U	TS	IMMUNE SYSTEM/TRANSFERASE	S	1.1	1.1	1	6	PVAFRG	20398
3B63	IJ	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	I	1.1	1.1	1	11	GRDLTDYLMKI	20399
3B63	NM	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	N	1.1	1.1	1	6	PSFIGM	20400
3B8E	AB	HYDROLASE/TRANSPORT PROTEIN	A	1.1	1.1	1	20	QIGMIQALGGFFTYFVILAE	20401
3B9J	AB	OXIDOREDUCTASE	B	1.1	1.1	1	10	TEIGIEMKFK	20402
3B9J	IJ	OXIDOREDUCTASE	I	1.1	1.1	1	8	VEEIEDAF	20403
3BCQ	CD	TRANSPORT PROTEIN/OXYGEN BINDING	C	1.1	1.1	1	19	PEVHVSMDKFLSLLSWSLS	20404
3BCQ	CD	TRANSPORT PROTEIN/OXYGEN BINDING	D	1.1	1.1	1	20	PDNFRLLADCITVCVAMKFG	20405
3BG0	DC	PROTEIN TRANSPORT, HYDROLASE	C	1.1	1.1	1	11	TFAFAAQLEFA	20406

3BGF	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.1	1.1	1	6	SEQLTS	20407
3BIM	AJ	TRANSCRIPTION REPRESSOR	A	1.1	1.1	1	15	HASDVLLNLNRLRSR	20408
3BIM	HO	TRANSCRIPTION REPRESSOR	H	1.1	1.1	1	15	HASDVLLNLNRLRSR	20409
3BLW	AB	OXIDOREDUCTASE	A	1.1	1.1	1	14	KLGDGLFRNIITEI	20410
3BLW	CD	OXIDOREDUCTASE	C	1.1	1.1	1	11	VDNASMQAVAK	20411
3BLW	CD	OXIDOREDUCTASE	C	1.1	1.1	1	15	SMYGTILGNIGAALI	20412
3BLW	KL	OXIDOREDUCTASE	K	1.1	1.1	1	14	KLGDGLFRNIITEI	20413
3BLW	MN	OXIDOREDUCTASE	M	1.1	1.1	1	14	KLGDGLFRNIITEI	20414
3BLW	OP	OXIDOREDUCTASE	O	1.1	1.1	1	11	VDNASMQAVAK	20415
3BO0	AB	RIBOSOME	B	1.1	1.1	1	25	DEYLAVAKVTALGISLLGIIGYIIH	20416
3BOW	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	11	IETCKIMVDML	20417
3BOW	AC	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	6	KNFFLT	20418
3BPL	AB	CYTOKINE/CYTOKINE RECEPTOR	A	1.1	1.1	1	19	EKETFCRAATVLRQFYSHH	20419
3BPL	AC	CYTOKINE/CYTOKINE RECEPTOR	A	1.1	1.1	1	16	ITLQEIIKTLNSLTEQ	20420
3BTP	AB	DNA BINDING PROTEIN, CHAPERONE	A	1.1	1.1	1	8	VDYLLQNL	20421
3BU8	BC	DNA BINDING PROTEIN	B	1.1	1.1	1	22	EAVVESSRKLVKEAAVIICIKN	20422
3BUA	DH	DNA BINDING PROTEIN	D	1.1	1.1	1	15	SRLLRVMQCLSRIEE	20423
3BVH	AB	BLOOD CLOTTING	A	1.1	1.1	1	16	LKDYEDQQKQLEQVIA	20424
3BVH	EF	BLOOD CLOTTING	F	1.1	1.1	1	7	WIQYKEG	20425
3BX4	CD	TOXIN	C	1.1	1.1	1	10	WDEAEKFCRA	20426
3BXK	CD	MEMBRANE PROTEIN, SIGNALING PROTEIN	C	1.1	1.1	1	12	EAELQDMINEVD	20427
3BYH	AB	STRUCTURAL PROTEIN	B	1.1	1.1	1	16	QKMILILTASIMYWSL	20428
3BZ1	AI	ELECTRON TRANSPORT	A	1.1	1.1	1	10	LWERFCNWVT	20429
3BZ1	AV	ELECTRON TRANSPORT	V	1.1	1.1	1	19	EKDLVAIAGHILVEPKILG	20430
3BZ1	BD	ELECTRON TRANSPORT	D	1.1	1.1	1	19	FYTKNLLLNEGIRAWMAPQ	20431
3BZ1	BU	ELECTRON TRANSPORT	U	1.1	1.1	1	6	VVDEKL	20432
3BZ1	CZ	ELECTRON TRANSPORT	Z	1.1	1.1	1	26	DRSKQLIFLGSGLWIALVLVVGVLNF	20433
3BZ1	DO	ELECTRON TRANSPORT	O	1.1	1.1	1	7	EEELARA	20434
3BZ1	JK	ELECTRON TRANSPORT	J	1.1	1.1	1	24	LWIVATVAGMGVIVIVGLFFYGAY	20435
3BZ1	Jy	ELECTRON TRANSPORT	J	1.1	1.1	1	24	LWIVATVAGMGVIVIVGLFFYGAY	20436
3BZ1	Ky	ELECTRON TRANSPORT	y	1.1	1.1	1	9	LTMIAMIGI	20437
3BZ1	Ky	ELECTRON TRANSPORT	y	1.1	1.1	1	7	IFLLAVR	20438
3BZ4	AH	IMMUNE SYSTEM	A	1.1	1.1	1	5	KDEYE	20439
3C01	AE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	E	1.1	1.1	1	18	IDEVLRLLVWLEEVENAG	20440
3C01	BE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	B	1.1	1.1	1	9	EQVKSDIEN	20441
3C01	CG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	G	1.1	1.1	1	20	IDEVLRLLVWLEEVENAGKD	20442

3C14	BC	LYASE/LYASE INHIBITOR	B	1.1	1.1	1	19	LECLRLLNEIIADFDDLLS	20443
3C72	AB	TRANSFERASE	A	1.1	1.1	1	14	FHCWDYRRFVAAQA	20444
3C7B	DB	OXIDOREDUCTASE	D	1.1	1.1	1	8	MREFLKVI	20445
3C7K	CD	SIGNALING PROTEIN	D	1.1	1.1	1	6	KDSYPR	20446
3C91	U2	HYDROLASE	U	1.1	1.1	1	23	VADARVLVDFARISAQQEKVTYG	20447
3CBJ	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.1	1.1	1	5	SDFLL	20448
3CF4	AG	OXIDOREDUCTASE	A	1.1	1.1	1	10	IPEAMGFAKK	20449
3CFA	LA	FLUORESCENT PROTEIN	A	1.1	1.1	1	6	YFKQSF	20450
3CFD	LH	IMMUNE SYSTEM	L	1.1	1.1	1	7	SEQLTSG	20451
3CFK	ED	IMMUNE SYSTEM	E	1.1	1.1	1	7	DEQLKSG	20452
3CFK	LH	IMMUNE SYSTEM	L	1.1	1.1	1	7	DEQLKSG	20453
3CHX	EF	MEMBRANE PROTEIN	F	1.1	1.1	1	18	GATFAVSGLLIGEWINRY	20454
3CJH	AB	PROTEIN TRANSPORT	B	1.1	1.1	1	28	SQEEQCLSNCVNRFLDTNIRIVNGLQNT	20455
3CJH	EB	PROTEIN TRANSPORT	B	1.1	1.1	1	20	KQKVQMSIHQFTNICFKKCV	20456
3CJH	GJ	PROTEIN TRANSPORT	J	1.1	1.1	1	20	KQKVQMSIHQFTNICFKKCV	20457
3CJT	EF	TRANSFERASE/RIBOSOMAL PROTEIN	F	1.1	1.1	1	12	IMEFVKAFNAAT	20458
3CJT	IJ	TRANSFERASE/RIBOSOMAL PROTEIN	J	1.1	1.1	1	12	IMEFVKAFNAAT	20459
3CL3	AE	VIRAL PROTEIN/SIGNALING PROTEIN	E	1.1	1.1	1	52	VQVDQLRMQGQSVEAALRMERQAASEEKRKLAQLQVAYHQLFQEYDNHIKSS	20460
3CMA	AZ	RIBOSOME	Z	1.1	1.1	1	8	PGGKTVRR	20461
3CMA	KU	RIBOSOME	U	1.1	1.1	1	9	SKCENNADL	20462
3CMA	SV	RIBOSOME	V	1.1	1.1	1	24	PAEREAELDDLKTELLNARAVQAA	20463
3CMO	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6	SEQLTS	20464
3CPJ	GB	PROTEIN TRANSPORT	B	1.1	1.1	1	5	SAYYR	20465
3CSY	IN	IMMUNE SYSTEM/VIRAL PROTEIN	N	1.1	1.1	1	13	ILNRKAIDFLLQR	20466
3CUE	QR	PROTEIN TRANSPORT	R	1.1	1.1	1	9	KSCLLLRFS	20467
3CUE	UQ	PROTEIN TRANSPORT	U	1.1	1.1	1	17	TQVLQYIYSHIYVKYVS	20468
3CUQ	AB	PROTEIN TRANSPORT	B	1.1	1.1	1	10	PEDLVNACKM	20469
3CUQ	AC	PROTEIN TRANSPORT	C	1.1	1.1	1	22	VDTRQKQLAAWCSLVLSFCRLH	20470
3CWB	DG	OXIDOREDUCTASE	D	1.1	1.1	1	35	DQRKRMGLKMLLISALLTSLLYYMKRHKWSVLKSR	20471
3CWB	NR	OXIDOREDUCTASE	N	1.1	1.1	1	14	MTNVTFDYLHATAF	20472
3CWB	PS	OXIDOREDUCTASE	P	1.1	1.1	1	23	PLSQTLFWLLVANLLILTWIGSQ	20473
3CXH	DF	OXIDOREDUCTASE	F	1.1	1.1	1	23	EEGKALVHHYEECAERVKIQQQQ	20474
3CXH	EI	OXIDOREDUCTASE	I	1.1	1.1	1	27	VGTIFAGAFVFQTVFDTAITSWYENHN	20475
3CXH	FH	OXIDOREDUCTASE	F	1.1	1.1	1	17	VEEFFHLQHYLDTATAP	20476
3CXH	LG	OXIDOREDUCTASE	L	1.1	1.1	1	9	KLLDNIQEY	20477
3CXH	LM	OXIDOREDUCTASE	M	1.1	1.1	1	12	ALKLVRESELLG	20478
3CXH	MG	OXIDOREDUCTASE	M	1.1	1.1	1	22	PHELTESVLPAARYDYAVAEQC	20479
3CXH	NO	OXIDOREDUCTASE	O	1.1	1.1	1	5	AGIKT	20480
3D31	BD	TRANSPORT PROTEIN	D	1.1	1.1	1	10	PRLENAARSL	20481

3D3C	AK	TRANSCRIPTION	K	1.1	1.1	1	18	HRLIDQATAEIVETAKRT	20482
3D3C	BK	TRANSCRIPTION	K	1.1	1.1	1	18	HRLIDQATAEIVETAKRT	20483
3D3C	CL	TRANSCRIPTION	L	1.1	1.1	1	18	HRLIDQATAEIVETAKRT	20484
3D4X	AD	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.1	1.1	1	19	PVNFKFLSHCLLVTLACHH	20485
3D5A	EH	RIBOSOME	E	1.1	1.1	1	10	KADVERLRKG	20486
3D5B	ET	RIBOSOME	T	1.1	1.1	1	9	GALIKLVES	20487
3D5B	G4	RIBOSOME	G	1.1	1.1	1	16	ARILEKAAQELALITG	20488
3D5D	ET	RIBOSOME	T	1.1	1.1	1	9	GALIKLVES	20489
3D87	CD	CYTOKINE	C	1.1	1.1	1	18	WTQCQQLSQKLCTLAWSA	20490
3D9A	LH	HYDROLASE/IMMUNE SYSTEM	L	1.1	1.1	1	6	SEQLTS	20491
3DBH	AB	CELL CYCLE	B	1.1	1.1	1	5	NHVKK	20492
3DBH	AB	CELL CYCLE	B	1.1	1.1	1	9	YRLTQGVVK	20493
3DBH	GH	CELL CYCLE	G	1.1	1.1	1	11	DDYVHEFCRYG	20494
3DBJ	GH	PHOTOSYNTHESIS	G	1.1	1.1	1	12	VVTKSIVNADAE	20495
3DCT	AB	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	A	1.1	1.1	1	7	PLLCEIW	20496
3DF0	BC	HYDROLASE	B	1.1	1.1	1	15	ATELMNILNKVVTRH	20497
3DHH	AB	OXIDOREDUCTASE	A	1.1	1.1	1	5	EEQLF	20498
3DHH	AB	OXIDOREDUCTASE	A	1.1	1.1	1	7	IVDRFLA	20499
3DIN	CE	MEMBRANE PROTEIN, PROTEIN TRANSPORT	C	1.1	1.1	1	16	IIFTFLALIVFRMGIY	20500
3DL8	BF	PROTEIN TRANSPORT	B	1.1	1.1	1	12	KTEEEEFRNIYN	20501
3DL8	GE	PROTEIN TRANSPORT	G	1.1	1.1	1	33	DYGRYKINEYTKYLTLFVATVQSLGIAFWIRGQ	20502
3DMT	BC	OXIDOREDUCTASE	B	1.1	1.1	1	13	RIGRMVFQALCED	20503
3DOM	AB	TRANSCRIPTION	B	1.1	1.1	1	15	PSIKALILQIDAKMS	20504
3DW8	AB	HYDROLASE	A	1.1	1.1	1	13	DEVLLALAEQLGT	20505
3DW8	AC	HYDROLASE	A	1.1	1.1	1	13	YAIREAATSNLKK	20506
3DW8	DF	HYDROLASE	D	1.1	1.1	1	12	YLHRMTTLFCIN	20507
3DWL	BC	STRUCTURAL PROTEIN	B	1.1	1.1	1	6	NDALKK	20508
3DXA	IJ	IMMUNE SYSTEM	J	1.1	1.1	1	7	EAEISHT	20509
3DZU	AD	TRANSCRIPTION/DNA	A	1.1	1.1	1	7	LVSKMRD	20510
3E0J	EF	TRANSFERASE	F	1.1	1.1	1	8	YKWLSYTL	20511
3E0J	EF	TRANSFERASE	F	1.1	1.1	1	20	VNQAKQMLYDYVERKRKENS	20512
3E1K	GH	TRANSCRIPTION	G	1.1	1.1	1	18	SVVGNILRIYESIADYHF	20513
3E1K	MN	TRANSCRIPTION	N	1.1	1.1	1	8	MDDVYNYI	20514
3E1Y	BE	TRANSLATION	B	1.1	1.1	1	16	NVKFIQEKKLIGRYFD	20515
3E2Z	AB	TRANSFERASE, LYASE	B	1.1	1.1	1	12	SYVKEELSKAAF	20516
3E3Q	LN	IMMUNE SYSTEM	L	1.1	1.1	1	29	PEYWERITQVAKGQEQWFRVNLRTLLGYY	20517
3E9J	BC	OXIDOREDUCTASE	B	1.1	1.1	1	17	MDVFVQQYADTVKYLSE	20518

3EA5	AB	TRANSPORT PROTEIN	B	1.1	1.1	1	14	TAEFAQLLENSILS	20519
3EA5	CD	TRANSPORT PROTEIN	D	1.1	1.1	1	16	ENVKRASLLALGYMCE	20520
3ECH	AC	TRANSCRIPTION, TRANSCRIPTION REGULATION	C	1.1	1.1	1	12	YTEQLRRAARRN	20521
3EDL	DF	STRUCTURAL PROTEIN	F	1.1	1.1	1	22	EGEFSEAREDMAALEKDYEEVG	20522
3EG5	AB	SIGNALING PROTEIN	B	1.1	1.1	1	10	EEKQQPLREK	20523
3EG5	CD	SIGNALING PROTEIN	D	1.1	1.1	1	15	SRNQHEIIRCLKAFM	20524
3EG5	CD	SIGNALING PROTEIN	D	1.1	1.1	1	10	EEKQQPLREK	20525
3EJB	EF	OXIDOREDUCTASE/LIPID TRANSPORT	E	1.1	1.1	1	7	DEEAEKI	20526
3ERC	BC	TRANSCRIPTION, TRANSFERASE/DNA, RNA	B	1.1	1.1	1	17	LKLLLGELFFLSKLQRH	20527
3ETR	AC	OXIDOREDUCTASE	A	1.1	1.1	1	11	RPILQGFRTFA	20528
3ETR	BC	OXIDOREDUCTASE	C	1.1	1.1	1	8	PEKIRNAC	20529
3ETR	LM	OXIDOREDUCTASE	L	1.1	1.1	1	8	VEEIEDAF	20530
3EUB	23	OXIDOREDUCTASE	3	1.1	1.1	1	7	KQVKSVA	20531
3EUH	AC	CELL CYCLE	C	1.1	1.1	1	5	RLANE	20532
3EUH	BE	CELL CYCLE	E	1.1	1.1	1	6	ESVFRF	20533
3EUK	HL	CELL CYCLE	H	1.1	1.1	1	10	DTHSILLNAL	20534
3EXG	CB	OXIDOREDUCTASE	B	1.1	1.1	1	7	FNFSMQA	20535
3EXG	Y2	OXIDOREDUCTASE	2	1.1	1.1	1	12	VKDIIFAIKKTL	20536
3EXH	AB	OXIDOREDUCTASE	A	1.1	1.1	1	13	GQIFEAYNMAALW	20537
3EXH	FC	OXIDOREDUCTASE	C	1.1	1.1	1	11	REEIQEVRSKS	20538
3EYJ	AB	VIRAL PROTEIN	B	1.1	1.1	1	9	NNCIESIRN	20539
3EYJ	AB	VIRAL PROTEIN	B	1.1	1.1	1	28	RIQDLEKYVEDTKIDLWSYNAELLVALE	20540
3EYM	AB	VIRAL PROTEIN	B	1.1	1.1	1	19	LKSTQAAIDQINGKLNRVI	20541
3EYM	CB	VIRAL PROTEIN	B	1.1	1.1	1	52	RIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLR	20542
3F1S	AB	HYDROLASE INHIBITOR/HYDROLASE	B	1.1	1.1	1	7	HLLIPRT	20543
3F3P	BD	STRUCTURAL PROTEIN	D	1.1	1.1	1	9	NSFAFELCS	20544
3F3P	EG	STRUCTURAL PROTEIN	G	1.1	1.1	1	7	IAELLPH	20545
3F3P	IK	STRUCTURAL PROTEIN	K	1.1	1.1	1	9	NSFAFELCS	20546
3F3P	JL	STRUCTURAL PROTEIN	L	1.1	1.1	1	7	IAELLPH	20547
3F6Z	CD	HYDROLASE	C	1.1	1.1	1	8	VAWRNRCK	20548
3F9K	FK	VIRAL PROTEIN, RECOMBINATION	K	1.1	1.1	1	21	QVIMEKSTMLYNKFKNMFLVG	20549
3F9K	JK	VIRAL PROTEIN, RECOMBINATION	J	1.1	1.1	1	13	GRQTALFLLKLAS	20550
3F9K	Vi	VIRAL PROTEIN, RECOMBINATION	i	1.1	1.1	1	6	VLEVLF	20551
3F9K	Za	VIRAL PROTEIN, RECOMBINATION	Z	1.1	1.1	1	13	GRQTALFLLKLAS	20552
3FAL	AD	SIGNALING PROTEIN	D	1.1	1.1	1	23	REDQIALLKTSAIEVMLLETSRR	20553
3FAL	CB	SIGNALING PROTEIN	B	1.1	1.1	1	23	REDQIALLKTSAIEVMLLETSRR	20554
3FAL	CB	SIGNALING PROTEIN	C	1.1	1.1	1	11	LFTLVEWAKRI	20555

3FCU	CD	CELL ADHESION/BLOOD CLOTTING	D	1.1	1.1	1	10	VNLYQNYSEL	20556
3FGC	AD	OXIDOREDUCTASE	A	1.1	1.1	1	24	SNRAKDICRNFLGHWYDSYVNATK	20557
3FH6	HD	TRANSPORT PROTEIN	D	1.1	1.1	1	10	KSTLLRMIAG	20558
3FIC	CN	RIBOSOME	N	1.1	1.1	1	11	RICLRELAHKG	20559
3FKS	KN	HYDROLASE	K	1.1	1.1	1	15	LSKQAVAYRQLSLLL	20560
3FKS	KO	HYDROLASE	O	1.1	1.1	1	7	RGISELG	20561
3FKS	TW	HYDROLASE	W	1.1	1.1	1	10	PAPATTFAHL	20562
3FKS	TX	HYDROLASE	T	1.1	1.1	1	10	YIPTNVISIT	20563
3FKS	Y1	HYDROLASE	Y	1.1	1.1	1	11	FQESALIADKL	20564
3FKU	CB	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.1	1.1	1	22	KESTQKAIDGVTNKVNSIIDKM	20565
3FKU	EF	VIRAL PROTEIN/IMMUNE SYSTEM	E	1.1	1.1	1	10	YEELKHLLSR	20566
3FLO	GH	TRANSFERASE	H	1.1	1.1	1	18	RELMETGRSVVQKYLNDC	20567
3FS4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	D	1.1	1.1	1	19	PECQAAWQKLVRVVAHALA	20568
3FWC	AB	CELL CYCLE, TRANSCRIPTION	A	1.1	1.1	1	11	IKNLRRVAKEL	20569
3G43	CE	METAL BINDING PROTEIN	C	1.1	1.1	1	11	AAELRHVMTNL	20570
3G4S	FM	RIBOSOME	M	1.1	1.1	1	5	IRDAW	20571
3G6A	LH	IMMUNE SYSTEM	L	1.1	1.1	1	6	SEELQA	20572
3G6D	LA	IMMUNE SYSTEM	A	1.1	1.1	1	16	VAQFVKDLLLHLKKLF	20573
3G6J	AB	IMMUNE SYSTEM	A	1.1	1.1	1	11	QSKIWDVVEKA	20574
3GBM	AB	VIRAL PROTEIN / IMMUNE SYSTEM	A	1.1	1.1	1	10	YEELKHLLSR	20575
3GE8	AE	OXIDOREDUCTASE	A	1.1	1.1	1	22	WDLFLKDIDELHHSYHMGVWYW	20576
3GE8	DF	OXIDOREDUCTASE	D	1.1	1.1	1	5	EEQLF	20577
3GE8	DH	OXIDOREDUCTASE	D	1.1	1.1	1	19	YTFANLISSIQTDESRHAQ	20578
3GHG	AB	BLOOD CLOTTING	B	1.1	1.1	1	6	NVEAVS	20579
3GHG	AC	BLOOD CLOTTING	C	1.1	1.1	1	23	LHQVENKTSEVKQLIKAIQLTYN	20580
3GHG	DE	BLOOD CLOTTING	D	1.1	1.1	1	14	LKDYEDQQKQLEQV	20581
3GHG	EF	BLOOD CLOTTING	E	1.1	1.1	1	24	RVLRSILENLRSKIQKLESDVSAQ	20582
3GHG	GH	BLOOD CLOTTING	G	1.1	1.1	1	29	GCRMKGLIDEVNQDFTNRINKLKNSLFEY	20583
3GHG	GI	BLOOD CLOTTING	I	1.1	1.1	1	14	TCGIADFLSTYQTK	20584
3GHG	JL	BLOOD CLOTTING	L	1.1	1.1	1	23	LHQVENKTSEVKQLIKAIQLTYN	20585
3GJX	CA	PROTEIN TRANSPORT	A	1.1	1.1	1	17	PEHRTNFFLLLQAVNSH	20586
3GJX	FD	PROTEIN TRANSPORT	F	1.1	1.1	1	5	DGYYI	20587
3GLH	FJ	TRANSFERASE	F	1.1	1.1	1	19	QTQLRQAVQLLTRTELTLK	20588
3GLH	KL	TRANSFERASE	K	1.1	1.1	1	12	VWAELEGLSLLL	20589
3GLI	AB	TRANSFERASE/DNA	A	1.1	1.1	1	15	LLALAQALERLSLLW	20590
3GLI	CO	TRANSFERASE/DNA	O	1.1	1.1	1	9	RRDWQLQQL	20591
3GLI	FG	TRANSFERASE/DNA	F	1.1	1.1	1	14	SKRALHILQQLRLE	20592
3GLI	FG	TRANSFERASE/DNA	F	1.1	1.1	1	11	WAELEGLSLLL	20593
3GLI	FG	TRANSFERASE/DNA	G	1.1	1.1	1	13	EHVLTALANGLSL	20594

3GM1	AE	TRANSFERASE	A	1.1	1.1	1	18	LVYLNVMELVRAVLELKN	20595
3GM1	BC	TRANSFERASE	B	1.1	1.1	1	17	LVYLNVMELVRAVLELK	20596
3GMW	AB	PROTEIN BINDING	A	1.1	1.1	1	5	PVTEK	20597
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	7	KSIAKTL	20598
3GTM	AF	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	6	EETRAE	20599
3GTM	AS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	8	DEEIIQLH	20600
3GTM	CJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.1	1.1	1	8	KWESYLNL	20601
3GZ1	BP	CHAPERONE	B	1.1	1.1	1	14	VDYIMGLAAIYQIK	20602
3GZD	BC	LYASE	B	1.1	1.1	1	6	FDVARN	20603
3H0L	AB	LIGASE	A	1.1	1.1	1	19	YLKAQKVRRLITNDFLKAF	20604
3H0L	PU	LIGASE	P	1.1	1.1	1	17	PQVKEAFENFIKELEKE	20605
3H0L	VT	LIGASE	T	1.1	1.1	1	15	TKIGKEVIKEMVETG	20606
3H2V	CG	CELL ADHESION	C	1.1	1.1	1	20	DIIAAAKRMALLMAEMSRLV	20607
3H4S	AE	MOTOR PROTEIN/CALCIUM BINDING PROTEIN	E	1.1	1.1	1	7	AESLRRN	20608
3H6P	AC	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	C	1.1	1.1	1	24	YQGWQTQWNQALEDLVRAYQSMSG	20609
3H87	BC	TOXIN/ANTITOXIN	B	1.1	1.1	1	13	IPDLLIAATAELS	20610
3HE7	AC	IMMUNE SYSTEM	A	1.1	1.1	1	28	NQQWEKLQHMFQVYRVSFTRDIQELVKM	20611
3HG1	AD	IMMUNE SYSTEM	A	1.1	1.1	1	24	VAEQLRAYLEGTCVEWLRRYLENG	20612
3HGK	AH	TRANSFERASE	A	1.1	1.1	1	7	PEYFIKG	20613
3HHZ	EO	VIRAL PROTEIN/RNA	O	1.1	1.1	1	11	VVEWLGWFEDQ	20614
3HKZ	AC	TRANSFERASE	A	1.1	1.1	1	10	VKHIYEFLKA	20615
3HKZ	AC	TRANSFERASE	C	1.1	1.1	1	6	QSVGEP	20616
3HKZ	BD	TRANSFERASE	D	1.1	1.1	1	10	DEILAHRLAL	20617
3HKZ	IJ	TRANSFERASE	I	1.1	1.1	1	11	PTELFFHAAGG	20618
3HKZ	IJ	TRANSFERASE	I	1.1	1.1	1	8	YMQRRLIN	20619
3HKZ	IM	TRANSFERASE	M	1.1	1.1	1	8	VVENIIIG	20620
3HKZ	JO	TRANSFERASE	J	1.1	1.1	1	12	IEQLQNEILRYG	20621
3HKZ	TZ	TRANSFERASE	T	1.1	1.1	1	5	IDEAY	20622
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	5	KSIAK	20623
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	11	EETRAELSQLC	20624
3HOU	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	B	1.1	1.1	1	10	VEGISKLLRE	20625

3HOU	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	25	LKLQVLLDEEYKQLVKDRKFLREVF	20626
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.1	1.1	1	5	KSIAK	20627
3HOY	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	11	EIIQNAQRDAV	20628
3HOY	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.1	1.1	1	15	YRHMALLVDVMTTQG	20629
3HOY	BJ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	J	1.1	1.1	1	7	LIEKFLR	20630
3HOY	FG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	F	1.1	1.1	1	17	KYERARILGTRALQISM	20631
3HRD	EF	OXIDOREDUCTASE	E	1.1	1.1	1	8	PIDIRILN	20632
3HRD	EH	OXIDOREDUCTASE	H	1.1	1.1	1	10	LLQQCFLEAG	20633
3HS0	FG	IMMUNE SYSTEM	F	1.1	1.1	1	11	QAKIWDTIEKS	20634
3HUJ	CE	IMMUNE SYSTEM	C	1.1	1.1	1	29	DQQWETLQHIFRVYRSSFTRDVKEFAKML	20635
3I1H	AB	APOPTOSIS	A	1.1	1.1	1	16	VDTARTLFNQVMEKEF	20636
3YGS	CP	APOPTOSIS	P	1.1	1.1	1	8	RLRLVEEL	20637
3YGS	CP	APOPTOSIS	P	1.1	1.1	1	14	RRDQARQLIIDLET	20638
4RUB	AS	LYASE(CARBON-CARBON)	A	1.1	1.1	1	8	IQVERDKL	20639
7INS	AB	HORMONE	A	1.1	1.1	1	7	LYQLENY	20640
7INS	AD	HORMONE	D	1.1	1.1	1	19	VNQHLCGSHLVEALYLVCG	20641
1NOV	CF	VIRUS	C	1.0	1.0	1	12	APGLDFLKCAFA	20642
1A0O	EF	CHEMOTAXIS	F	1.0	1.0	1	13	EVDLLEEELGHLT	20643
1A0O	GH	CHEMOTAXIS	G	1.0	1.0	1	15	AATLEEKLNKIFEKL	20644
1A0O	GH	CHEMOTAXIS	H	1.0	1.0	1	13	EVDLLEEELGHLT	20645
1A2X	AB	COMPLEX (SKELETAL MUSCLE/MUSCLE PROTEIN)	A	1.0	1.0	1	8	AEELAEIF	20646
1A7F	AB	HORMONE	A	1.0	1.0	1	6	LYQLEN	20647
1A9W	CE	OXYGEN TRANSPORT	E	1.0	1.0	1	20	PENFKLLGNVMVIILATHFG	20648
1AFV	BK	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.0	1.0	1	21	QAAMQMLKETINEEAAEWDRL	20649
1AHJ	AB	LYASE	A	1.0	1.0	1	9	PRKVLSEMG	20650
1AIP	AC	COMPLEX OF TWO ELONGATION FACTORS	A	1.0	1.0	1	14	PQTREHILLARQVG	20651
1AM4	AD	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)	A	1.0	1.0	1	7	VFGPNLL	20652
1AM4	BE	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)	B	1.0	1.0	1	6	NTNLAV	20653
1AM4	BE	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)	B	1.0	1.0	1	7	VFGPNLL	20654

1AM4	CF	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)	F	1.0	1.0	1	6	DRLRPL	20655
1AON	GU	COMPLEX (GROEL/GROES)	G	1.0	1.0	1	11	LPVLEAVAKAG	20656
1AQD	DE	COMPLEX (MHC PROTEIN/ANTIGEN)	E	1.0	1.0	1	10	RPDAEYWNSQ	20657
1AWC	AB	TRANSCRIPTION/DNA	A	1.0	1.0	1	7	KDARDCI	20658
1B0N	AB	TRANSCRIPTION REGULATOR	A	1.0	1.0	1	5	VHTLL	20659
1B33	HI	PHOTOSYNTHESIS	I	1.0	1.0	1	14	GELRVRAATTIAAN	20660
1B33	LM	PHOTOSYNTHESIS	M	1.0	1.0	1	14	GELRVRAATTIAAN	20661
1B4U	CB	DIOXYGENASE	C	1.0	1.0	1	7	AQRARKG	20662
1B5F	CD	HYDROLASE	C	1.0	1.0	1	8	VWYNMLNQ	20663
1B6C	GH	COMPLEX (ISOMERASE/PROTEIN KINASE)	H	1.0	1.0	1	14	ERSWFREAEIYQTV	20664
1BCC	EG	OXIDOREDUCTASE	E	1.0	1.0	1	35	SRESDPSRKGFSYLVTAVTTLGVAYAAKNVVTQFV	20665
1BCP	HJ	TOXIN	H	1.0	1.0	1	13	YSRLRKMLYLIYV	20666
1BCP	IJ	TOXIN	I	1.0	1.0	1	14	YDALRRLLYMIYMS	20667
1BGY	AI	ELECTRON TRANSPORT	A	1.0	1.0	1	20	DSQIEKERDVILQELQENDT	20668
1BOM	AB	INSULIN-LIKE BRAIN-SECRETORY PEPTIDE	B	1.0	1.0	1	8	ADLCWEAG	20669
1BR1	CD	MUSCLE PROTEIN	D	1.0	1.0	1	9	FEDYVEGLR	20670
1BR1	GH	MUSCLE PROTEIN	G	1.0	1.0	1	5	FQEFR	20671
1BSX	AX	HORMONE/GROWTH FACTOR	A	1.0	1.0	1	8	PLFLEVFE	20672
1BSX	BY	HORMONE/GROWTH FACTOR	B	1.0	1.0	1	8	PLFLEVFE	20673
1BVY	AF	OXIDOREDUCTASE	A	1.0	1.0	1	6	YKQVKQ	20674
1BXN	CJ	LYASE	C	1.0	1.0	1	20	WRDRFLFVMDAVNKASAATG	20675
1C8O	AB	VIRAL PROTEIN	A	1.0	1.0	1	15	PPSISSVLTILYYGA	20676
1CAX	AD	SEED STORAGE PROTEIN	A	1.0	1.0	1	8	KNFLEASY	20677
1CAX	EB	SEED STORAGE PROTEIN	B	1.0	1.0	1	8	EEVEELLE	20678
1CDL	AE	CALCIUM-BINDING PROTEIN	A	1.0	1.0	1	11	EAELQDMINEV	20679
1CDL	CG	CALCIUM-BINDING PROTEIN	C	1.0	1.0	1	15	EEQIAEFKEAFSLFD	20680
1CDL	CG	CALCIUM-BINDING PROTEIN	C	1.0	1.0	1	16	DTDSEEEIREAFRVFD	20681
1CJF	BC	STRUCTURAL REGULATION PROTEIN	B	1.0	1.0	1	18	GGLINKKCYEMASHLRRS	20682
1CKK	AB	CALMODULIN-PEPTIDE COMPLEX	A	1.0	1.0	1	12	EAELQDMINEVD	20683
1CLY	LH	IMMUNOGLOBULIN	L	1.0	1.0	1	7	DEQLKSG	20684
1CM1	AB	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	A	1.0	1.0	1	12	DEEVDEMIREAD	20685
1CM1	AB	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	A	1.0	1.0	1	10	FPEFLTMMAR	20686
1CQT	BJ	GENE REGULATION/DNA	J	1.0	1.0	1	5	VKELL	20687
1CXZ	AB	SIGNALING PROTEIN	B	1.0	1.0	1	39	PGVQQQLELERERLRREIRKELKLKEGAENLRRATTDLG	20688
1D3U	AB	GENE REGULATION/DNA	B	1.0	1.0	1	15	KKEIGRSYRFIARNL	20689

1D8D	AB	TRANSFERASE	B	1.0	1.0	1	15	QIVATDVCQFLELCQ	20690
1DCE	AB	TRANSFERASE	A	1.0	1.0	1	20	EQKLKLYQSATQAVFQKRQA	20691
1DGH	AD	OXIDOREDUCTASE	A	1.0	1.0	1	9	FPSFIHSQK	20692
1DGH	AD	OXIDOREDUCTASE	D	1.0	1.0	1	9	FPSFIHSQK	20693
1DGR	AX	PLANT PROTEIN	X	1.0	1.0	1	6	SQLRDL	20694
1DIO	AB	LYASE	B	1.0	1.0	1	11	VAFVAVEGNRL	20695
1DIO	AG	LYASE	A	1.0	1.0	1	10	EATELKLGML	20696
1DML	AB	DNA BINDING PROTEIN/TRANSFERASE	B	1.0	1.0	1	9	DVAARLRAA	20697
1DOW	AB	CELL ADHESION	A	1.0	1.0	1	9	SAAGEFADD	20698
1DX5	AO	SERINE PROTEINASE	O	1.0	1.0	1	8	RETAASLL	20699
1DZB	BY	IMMUNE SYSTEM	Y	1.0	1.0	1	6	VAWRNR	20700
1E 50	AB	TRANSCRIPTION	B	1.0	1.0	1	5	EFFRK	20701
1E3A	AB	ANTIBIOTIC RESISTANCE	B	1.0	1.0	1	12	VGAKILYEAVQG	20702
1E3D	AB	HYDROGENASE	B	1.0	1.0	1	18	TEEFAAVQAKLKTFVASG	20703
1E3D	CD	HYDROGENASE	D	1.0	1.0	1	18	TEEFAAVQAKLKTFVASG	20704
1E6V	AE	OXIDOREDUCTASE	E	1.0	1.0	1	18	PYSGTLQAGMAVVHAIID	20705
1E6V	BC	OXIDOREDUCTASE	B	1.0	1.0	1	14	FERLHLLGYAYQGL	20706
1E6V	DB	OXIDOREDUCTASE	D	1.0	1.0	1	17	HLGEYAGIVQAAHAARG	20707
1E6V	EF	OXIDOREDUCTASE	E	1.0	1.0	1	14	FERLHLLGYAYQGL	20708
1E6Y	EF	OXIDOREDUCTASE	E	1.0	1.0	1	15	MFERHQLLGLAYQGL	20709
1E7P	AB	OXIDOREDUCTASE	B	1.0	1.0	1	6	GMSQRV	20710
1E7P	AB	OXIDOREDUCTASE	B	1.0	1.0	1	13	IFIVLNMIRETYD	20711
1E7P	DE	OXIDOREDUCTASE	E	1.0	1.0	1	6	GMSQRV	20712
1E7P	GH	OXIDOREDUCTASE	H	1.0	1.0	1	6	GMSQRV	20713
1E7P	JK	OXIDOREDUCTASE	K	1.0	1.0	1	6	GMSQRV	20714
1EAH	13	VIRUS	3	1.0	1.0	1	5	PRLAH	20715
1EAY	BD	SIGNAL TRANSDUCTION COMPLEX	B	1.0	1.0	1	11	KENIIAAAQAG	20716
1EAY	BD	SIGNAL TRANSDUCTION COMPLEX	D	1.0	1.0	1	9	EDDITAVLC	20717
1EF1	AC	MEMBRANE PROTEIN	C	1.0	1.0	1	9	KYKTLRQIR	20718
1EFP	AB	ELECTRON TRANSPORT	A	1.0	1.0	1	6	IQHLAG	20719
1EGP	AB	PROTEINASE INHIBITOR	A	1.0	1.0	1	12	VDQAREYFTLHY	20720
1EIY	AB	LIGASE/RNA	A	1.0	1.0	1	16	PITLMERELVEIFRAL	20721
1EIY	AB	LIGASE/RNA	B	1.0	1.0	1	6	EEDLVE	20722
1EJH	CG	TRANSLATION	C	1.0	1.0	1	18	RRSDLDRFWLETLLCLIG	20723
1EMU	AB	SIGNALING PROTEIN	A	1.0	1.0	1	15	ADLLDFWFACTGFRK	20724
1EP3	AB	OXIDOREDUCTASE	A	1.0	1.0	1	7	EEYAKYY	20725
1EQZ	AG	STRUCTURAL PROTEIN/DNA	G	1.0	1.0	1	11	TVALREIRRYQ	20726
1ETZ	LB	IMMUNE SYSTEM	L	1.0	1.0	1	5	ARAWE	20727
1ETZ	LH	IMMUNE SYSTEM	L	1.0	1.0	1	6	SEELET	20728
1EYS	LM	ELECTRON TRANSPORT	L	1.0	1.0	1	13	ILSHLDWVSNVGY	20729

1EYS	LM	ELECTRON TRANSPORT	M	1.0	1.0	1	7	EIDQITH	20730
1EYS	MH	ELECTRON TRANSPORT	M	1.0	1.0	1	26	PFHMLSIAFLYGSALLFAMHGATILS	20731
1EYX	KL	PHOTOSYNTHESIS	L	1.0	1.0	1	12	GNKRLDAVNYIV	20732
1EYX	KL	PHOTOSYNTHESIS	L	1.0	1.0	1	12	AFSRVISNADAK	20733
1F51	BE	TRANSFERASE	B	1.0	1.0	1	22	DRVFEMIEEMVIDAKHESKLSN	20734
1F58	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.0	1.0	1	6	SEQLTS	20735
1F66	CD	STRUCTURAL PROTEIN/DNA	C	1.0	1.0	1	5	RSQRA	20736
1F80	BD	TRANSFERASE	B	1.0	1.0	1	23	EARKNEFLAGRFAAKEAFSKAFG	20737
1F80	BD	TRANSFERASE	D	1.0	1.0	1	7	DEDAEKI	20738
1F8V	BD	VIRUS/RNA	B	1.0	1.0	1	12	PLALECYHNLKM	20739
1F90	LH	IMMUNE SYSTEM	L	1.0	1.0	1	6	SEQLTS	20740
1F93	AE	TRANSCRIPTION	E	1.0	1.0	1	13	QLQTELLAALLES	20741
1F93	AF	TRANSCRIPTION	A	1.0	1.0	1	10	RVALQAEKLD	20742
1F93	CG	TRANSCRIPTION	G	1.0	1.0	1	13	QLQTELLAALLES	20743
1F93	DG	TRANSCRIPTION	D	1.0	1.0	1	10	RVALQAEKLD	20744
1F99	KL	PHOTOSYNTHESIS	L	1.0	1.0	1	13	NTQIDALLAIVSE	20745
1FCD	AC	ELECTRON TRANSPORT (FLAVOCYTOCHROME)	C	1.0	1.0	1	9	TIMGRIAKG	20746
1FE8	BI	IMMUNE SYSTEM	B	1.0	1.0	1	10	KAHLLSLVDV	20747
1FFT	AC	OXIDOREDUCTASE	A	1.0	1.0	1	13	TWASLCANVLIIA	20748
1FFT	FG	OXIDOREDUCTASE	F	1.0	1.0	1	14	ANVNAFFGITTMII	20749
1FFU	DF	HYDROLASE	F	1.0	1.0	1	6	ENDLIS	20750
1FHJ	CD	OXYGEN STORAGE/TRANSPORT	D	1.0	1.0	1	20	PENFKLLGNVLVCVLAHHFG	20751
1FIQ	BC	OXIDOREDUCTASE	C	1.0	1.0	1	10	PEHAERAAHV	20752
1FLC	CB	HYDROLASE	B	1.0	1.0	1	24	KGFEKIGNDIQILKSSINIAIEKL	20753
1FLC	ED	HYDROLASE	D	1.0	1.0	1	24	KGFEKIGNDIQILKSSINIAIEKL	20754
1FM6	AD	TRANSCRIPTION	D	1.0	1.0	1	23	VKPIEDIQDNLLQALELQLKLNH	20755
1FM6	UV	TRANSCRIPTION	U	1.0	1.0	1	21	TNICQAADKQLFTLVEWAKRI	20756
1FNT	CJ	HYDROLASE/HYDROLASE ACTIVATOR	C	1.0	1.0	1	22	TADAEILINTARIHAQNYLKTY	20757
1FNT	Hb	HYDROLASE/HYDROLASE ACTIVATOR	b	1.0	1.0	1	11	FGAHMANPLLR	20758
1FNT	HI	HYDROLASE/HYDROLASE ACTIVATOR	H	1.0	1.0	1	20	AADTQAIADIVQYHLELYTS	20759
1FNT	Ib	HYDROLASE/HYDROLASE ACTIVATOR	b	1.0	1.0	1	11	FGAHMANPLLR	20760
1FNT	IJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.0	1.0	1	15	PETFTQLVSSSLYER	20761
1FNT	KL	HYDROLASE/HYDROLASE ACTIVATOR	K	1.0	1.0	1	23	AGDTVQFAEYIQANIQLYSIRED	20762
1FNT	LM	HYDROLASE/HYDROLASE ACTIVATOR	L	1.0	1.0	1	13	VGELFWKVKEEEG	20763
1FNT	QY	HYDROLASE/HYDROLASE ACTIVATOR	Y	1.0	1.0	1	17	PQAVSSFVRQELAKSIR	20764
1FNT	SZ	HYDROLASE/HYDROLASE ACTIVATOR	S	1.0	1.0	1	22	TADARSMIEHARTAAVTHNLYY	20765
1FNT	VN	HYDROLASE/HYDROLASE ACTIVATOR	V	1.0	1.0	1	7	PDEYEQL	20766
1FNT	VW	HYDROLASE/HYDROLASE ACTIVATOR	W	1.0	1.0	1	9	SLAAMAVLE	20767
1FNT	WM	HYDROLASE/HYDROLASE ACTIVATOR	M	1.0	1.0	1	11	LIMPFLDNQVN	20768

1FNT	WN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.0	1.0	1	18	VQVAEEAIVNAMRVLYYR	20769
1FNT	WX	HYDROLASE/HYDROLASE ACTIVATOR	X	1.0	1.0	1	12	SDQLFGMCESLY	20770
1FOE	GH	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	G	1.0	1.0	1	5	LESYL	20771
1FOE	GH	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	G	1.0	1.0	1	12	KYPLLLRELFAL	20772
1FQV	AF	LIGASE	F	1.0	1.0	1	7	VWDQEFL	20773
1FQV	EF	LIGASE	F	1.0	1.0	1	16	KGLLDVTCKTVANMIK	20774
1FQV	GH	LIGASE	G	1.0	1.0	1	8	KRWYRLAS	20775
1FQV	IJ	LIGASE	I	1.0	1.0	1	11	PDVTGRLLSQV	20776
1FQV	KL	LIGASE	K	1.0	1.0	1	10	DELLLGIFSC	20777
1FQV	OL	LIGASE	L	1.0	1.0	1	14	AAILKKVIQWCTHH	20778
1FQV	OP	LIGASE	P	1.0	1.0	1	16	KGLLDVTCKTVANMIK	20779
1FS1	AB	LIGASE	B	1.0	1.0	1	8	PEEIRKTF	20780
1FXW	AF	HYDROLASE	F	1.0	1.0	1	15	RWMSQHNRFVLDCKD	20781
1FYH	AB	IMMUNE SYSTEM	A	1.0	1.0	1	5	SDVAD	20782
1G0U	1N	HYDROLASE	1	1.0	1.0	1	6	WDFAKD	20783
1G0U	FG	HYDROLASE	F	1.0	1.0	1	15	IPAFADRLGQYVQAH	20784
1G0U	M2	HYDROLASE	2	1.0	1.0	1	6	PDEYEQ	20785
1G0U	QR	HYDROLASE	R	1.0	1.0	1	22	TADARSMIEHARTAAVTHNLYY	20786
1G0U	QX	HYDROLASE	Q	1.0	1.0	1	22	NADSRILIEKARVEAQSHRLTL	20787
1G0U	S1	HYDROLASE	S	1.0	1.0	1	15	VERAGHLLCDKAQKN	20788
1G0U	TU	HYDROLASE	T	1.0	1.0	1	15	RQSAKAELEKLVDHH	20789
1G1X	FH	RIBOSOME	H	1.0	1.0	1	12	ILAKTIKRARIL	20790
1G20	AB	OXIDOREDUCTASE	A	1.0	1.0	1	12	GYEFEEFVKRIK	20791
1G20	CB	OXIDOREDUCTASE	B	1.0	1.0	1	17	ASLTKERGRLVDMMTDS	20792
1G20	CD	OXIDOREDUCTASE	D	1.0	1.0	1	11	KFIQRDTLHKG	20793
1G3I	BH	CHAPERONE/HYDROLASE	H	1.0	1.0	1	13	LLKSAVELAKDWR	20794
1G3I	SM	CHAPERONE/HYDROLASE	M	1.0	1.0	1	13	LLKSAVELAKDWR	20795
1G3I	TN	CHAPERONE/HYDROLASE	N	1.0	1.0	1	13	LLKSAVELAKDWR	20796
1G3I	UO	CHAPERONE/HYDROLASE	O	1.0	1.0	1	13	LLKSAVELAKDWR	20797
1G3I	VP	CHAPERONE/HYDROLASE	P	1.0	1.0	1	13	LLKSAVELAKDWR	20798
1G3N	EG	CELL CYCLE, SIGNALING PROTEIN	G	1.0	1.0	1	7	TSSLCYA	20799
1G4Y	BR	SIGNALING PROTEIN	R	1.0	1.0	1	11	TKELGTVMRSL	20800
1G8K	AB	OXIDOREDUCTASE	A	1.0	1.0	1	14	TNYFLNHWLPNLQG	20801
1GCV	AD	OXYGEN STORAGE/TRANSPORT	A	1.0	1.0	1	7	PGSKSYF	20802
1GCV	AD	OXYGEN STORAGE/TRANSPORT	D	1.0	1.0	1	17	SFHLLTDCIIVELAYLR	20803
1GH0	CD	PHOTOSYNTHESIS	C	1.0	1.0	1	10	TGPMDEYLIA	20804
1GH0	MP	PHOTOSYNTHESIS	P	1.0	1.0	1	25	SRRMAACLRDMEIILRYVTYAVFAG	20805
1GH0	QR	PHOTOSYNTHESIS	R	1.0	1.0	1	14	SNKRLDVVNRITSN	20806

1GH0	UX	PHOTOSYNTHESIS	X	1.0	1.0	1	25	SRRMAACLRDMEIILRYVTYAVFAG	20807
1GK0	CD	HYDROLASE	D	1.0	1.0	1	5	EQYFD	20808
1GPQ	AC	HYDROLASE/INHIBITOR	A	1.0	1.0	1	14	SIDGKTVLFAALTG	20809
1GPW	EF	LYASE/TRANSFERASE	F	1.0	1.0	1	11	MNLYRGVKRAS	20810
1GX7	AE	OXIDOREDUCTASE	E	1.0	1.0	1	7	YYHVMHD	20811
1GZL	AC	GLYCOPROTEIN	C	1.0	1.0	1	10	EEWDREIENY	20812
1H1L	CD	OXIDOREDUCTASE	D	1.0	1.0	1	14	SYGKFIQRDTLAKG	20813
1H1V	GA	ACTIN-BINDING	A	1.0	1.0	1	9	QAVLSLYAS	20814
1H2R	SL	OXIDOREDUCTASE	S	1.0	1.0	1	9	IDTLILDTL	20815
1H3O	AD	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	D	1.0	1.0	1	5	EDVEE	20816
1H4J	AB	OXIDOREDUCTASE	A	1.0	1.0	1	5	LGTGT	20817
1H4J	CD	OXIDOREDUCTASE	C	1.0	1.0	1	5	LGTGT	20818
1H4J	EF	OXIDOREDUCTASE	E	1.0	1.0	1	5	LGTGT	20819
1H4J	GH	OXIDOREDUCTASE	G	1.0	1.0	1	5	LGTGT	20820
1HBM	EC	METHANOGENESIS	E	1.0	1.0	1	12	MYDANMVKAAVL	20821
1HBR	AD	OXYGEN STORAGE/TRANSPORT	A	1.0	1.0	1	20	PVNFKLLSQCIQVVLAVHMG	20822
1HQM	AC	TRANSCRIPTION	C	1.0	1.0	1	6	EELLKR	20823
1HR0	EH	RIBOSOME	E	1.0	1.0	1	8	KADVERLR	20824
1HR8	AB	HYDROLASE	A	1.0	1.0	1	19	EDEVSRAKNQLKSSLLMNL	20825
1HR8	AB	HYDROLASE	B	1.0	1.0	1	11	QQGIELEIENI	20826
1HR8	CD	HYDROLASE	C	1.0	1.0	1	19	EDEVSRAKNQLKSSLLMNL	20827
1HR8	CD	HYDROLASE	D	1.0	1.0	1	11	PEEVFEQVDKI	20828
1HRT	LH	HYDROLASE (SERINE PROTEINASE)	L	1.0	1.0	1	7	QTEKELF	20829
1HVU	AB	TRANSFERASE/RNA	A	1.0	1.0	1	9	QYALGIIQA	20830
1HVU	DE	TRANSFERASE/RNA	E	1.0	1.0	1	8	RQLCKLLR	20831
1HVU	GH	TRANSFERASE/RNA	H	1.0	1.0	1	8	RQLCKLLR	20832
1I3O	AE	APOPTOSIS	E	1.0	1.0	1	8	HADYLLRT	20833
1I3O	BE	APOPTOSIS	B	1.0	1.0	1	13	WFIQSLCAMLKQY	20834
1I3O	DF	APOPTOSIS	D	1.0	1.0	1	13	WFIQSLCAMLKQY	20835
1I3Q	AB	TRANSCRIPTION	A	1.0	1.0	1	8	PEEVRAIS	20836
1I3Q	AB	TRANSCRIPTION	A	1.0	1.0	1	11	EETRAELSQLC	20837
1I3Q	AE	TRANSCRIPTION	E	1.0	1.0	1	6	PVALYL	20838
1I3Q	AF	TRANSCRIPTION	F	1.0	1.0	1	17	KYERARILGTRALQISM	20839
1I3Q	BL	TRANSCRIPTION	B	1.0	1.0	1	7	PQEARLR	20840
1I3Q	CK	TRANSCRIPTION	K	1.0	1.0	1	12	HTLGNLIRAELL	20841
1I3R	ED	IMMUNE SYSTEM	D	1.0	1.0	1	23	PEFLEQKRAEVDTVCRHNYEIFD	20842
1I7Q	CD	LYASE	C	1.0	1.0	1	7	EDARLRS	20843
1I7W	CD	CELL ADHESION	C	1.0	1.0	1	14	EGVATYAAAVLFRM	20844
1I84	VW	CONTRACTILE PROTEIN	W	1.0	1.0	1	9	EEEVEQLVA	20845

1IB1	AE	SIGNALING PROTEIN/TRANSFERASE	A	1.0	1.0	1	21	AESKVFYLKMKGDYYRYLAEV	20846
1ID3	AB	STRUCTURAL PROTEIN/DNA	B	1.0	1.0	1	9	DVVYALKRQ	20847
1ID3	CD	STRUCTURAL PROTEIN/DNA	C	1.0	1.0	1	10	PRHLQLAIRN	20848
1ID3	GH	STRUCTURAL PROTEIN/DNA	G	1.0	1.0	1	7	DELNKLL	20849
1IGC	HA	COMPLEX (ANTIBODY/BINDING PROTEIN)	A	1.0	1.0	1	15	AETAEKAFKQYANDN	20850
1IO4	CD	TRANSCRIPTION/DNA	D	1.0	1.0	1	8	EFFRKLSR	20851
1IR2	V4	LYASE	V	1.0	1.0	1	21	NAPGAAANRVALEACTQARNE	20852
1IR2	Y7	LYASE	Y	1.0	1.0	1	9	IQVERDKLN	20853
1IRE	AB	LYASE	B	1.0	1.0	1	10	LDEFRFGIEQ	20854
1IRU	BJ	HYDROLASE	B	1.0	1.0	1	23	GPDYRVLVHRARKLAQQYYLVYQ	20855
1IRU	EM	HYDROLASE	M	1.0	1.0	1	15	TGAIAAMLSTILYSR	20856
1IRU	HN	HYDROLASE	H	1.0	1.0	1	8	YGYVDATY	20857
1IRU	KL	HYDROLASE	K	1.0	1.0	1	22	AGDTVQFAEYIQKNVQLYKMRN	20858
1IRU	PQ	HYDROLASE	P	1.0	1.0	1	15	TAQLVQRVASVMQEY	20859
1IRU	PX	HYDROLASE	X	1.0	1.0	1	22	ATDVQTVAQRLKFRLNLYELKE	20860
1IRU	S1	HYDROLASE	1	1.0	1.0	1	15	TGAIAAMLSTILYSR	20861
1IRU	T2	HYDROLASE	T	1.0	1.0	1	12	VSRLVSLIGSKT	20862
1IRU	TU	HYDROLASE	T	1.0	1.0	1	6	MSEFME	20863
1IRU	V2	HYDROLASE	V	1.0	1.0	1	8	YGYVDATY	20864
1IRU	WN	HYDROLASE	N	1.0	1.0	1	19	QTEARDLVERCMRVLYYRD	20865
1IRU	WN	HYDROLASE	W	1.0	1.0	1	11	SLAAMAVFEDK	20866
1IRU	YZ	HYDROLASE	Y	1.0	1.0	1	22	AGDTVQFAEYIQKNVQLYKMRN	20867
1IW7	DF	TRANSFERASE	D	1.0	1.0	1	6	DEEYRE	20868
1IW7	DF	TRANSFERASE	F	1.0	1.0	1	19	FLDLIQEGNQGLIRAVEKF	20869
1IW7	DF	TRANSFERASE	F	1.0	1.0	1	12	AKRVEETLKIAQ	20870
1IW7	KM	TRANSFERASE	M	1.0	1.0	1	14	KREVEVLRRAEKLG	20871
1IW7	MN	TRANSFERASE	M	1.0	1.0	1	17	LGQILETHLGLAGYFLG	20872
1IW7	NO	TRANSFERASE	N	1.0	1.0	1	15	QKTLKAIEEARKEAV	20873
1IW7	NP	TRANSFERASE	N	1.0	1.0	1	8	VKAARRML	20874
1IW7	NP	TRANSFERASE	P	1.0	1.0	1	19	VDAATQSLLSEELEKALSK	20875
1IWA	CH	LYASE	C	1.0	1.0	1	18	WRERYLFTMEAVNKASAA	20876
1IWA	GB	LYASE	G	1.0	1.0	1	18	WRERYLFTMEAVNKASAA	20877
1IWA	GP	LYASE	P	1.0	1.0	1	15	PAAVLFEINACRKAR	20878
1IWA	IN	LYASE	N	1.0	1.0	1	15	PAAVLFEINACRKAR	20879
1IWA	MJ	LYASE	M	1.0	1.0	1	21	IQAGATANRVALEAMILARNE	20880
1IWA	ON	LYASE	O	1.0	1.0	1	18	WRERYLFTMEAVNKASAA	20881
1IWP	AB	LYASE	B	1.0	1.0	1	12	VSFMAWDAANLS	20882
1IWP	AG	LYASE	G	1.0	1.0	1	13	RQTLEYQAQIAEQ	20883
1IWP	LM	LYASE	L	1.0	1.0	1	10	EATELELGMR	20884

1IXX	EF	COAGULATION FACTOR BINDING	F	1.0	1.0	1	12	WADAENFCTQQH	20885
1IYJ	CD	GENE REGULATION/ANTITUMOR PROTEIN	D	1.0	1.0	1	8	SLYLTKSS	20886
1IZL	JN	PHOTOSYNTHESIS	J	1.0	1.0	1	9	LHFFLAAWR	20887
1J1D	AC	CONTRACTILE PROTEIN	A	1.0	1.0	1	8	YDEFLEFM	20888
1J1E	AB	CONTRACTILE PROTEIN	B	1.0	1.0	1	46	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN	20889
1J1E	AC	CONTRACTILE PROTEIN	A	1.0	1.0	1	11	TKELGKVMRML	20890
1J1E	DF	CONTRACTILE PROTEIN	D	1.0	1.0	1	12	TKELGKVMRMLN	20891
1J34	AB	PROTEIN BINDING/BLOOD CLOTTING	B	1.0	1.0	1	10	WADAENFCTQ	20892
1J8H	AE	IMMUNE SYSTEM	A	1.0	1.0	1	22	AQGALANIAVDKANLEIMTKRS	20893
1JB0	AB	PHOTOSYNTHESIS	A	1.0	1.0	1	5	QGILN	20894
1JB0	AB	PHOTOSYNTHESIS	A	1.0	1.0	1	5	SQVIG	20895
1JB0	AB	PHOTOSYNTHESIS	A	1.0	1.0	1	31	IIQGRAVGVAHYLLGGIATTWAFFLARIISV	20896
1JB0	AB	PHOTOSYNTHESIS	B	1.0	1.0	1	31	IVQARLVGLAHFSVGYILTYAAFLIASTAAK	20897
1JB0	AK	PHOTOSYNTHESIS	K	1.0	1.0	1	14	TTSFGHLLAAGVVS	20898
1JB0	BD	PHOTOSYNTHESIS	B	1.0	1.0	1	17	RGYWQELIETLVWAHER	20899
1JB0	BL	PHOTOSYNTHESIS	L	1.0	1.0	1	28	SEGWSQFTAGFFVGAMGSAFVAFFLLEN	20900
1JBU	HX	HYDROLASE	H	1.0	1.0	1	10	IEWLQKLMRS	20901
1JD2	12	HYDROLASE	1	1.0	1.0	1	15	RQSAKAELEKLVDHH	20902
1JD2	AB	HYDROLASE	B	1.0	1.0	1	22	TADAEILINTARIHAQNYLKTY	20903
1JD2	AG	HYDROLASE	A	1.0	1.0	1	18	GPDYRVLVDKSRKVAHTS	20904
1JD2	BJ	HYDROLASE	J	1.0	1.0	1	17	PQAVSSFVRQELAKSIR	20905
1JD2	DL	HYDROLASE	D	1.0	1.0	1	22	TADARSMIEHARTAAVTHNLYY	20906
1JD2	HI	HYDROLASE	I	1.0	1.0	1	18	PEDLFETISQALLNAADR	20907
1JD2	HN	HYDROLASE	N	1.0	1.0	1	22	AADTQAIADIVQYHLELYTSQY	20908
1JD2	IS	HYDROLASE	S	1.0	1.0	1	19	VEEVIKLVRDSFTSATERH	20909
1JD2	LM	HYDROLASE	M	1.0	1.0	1	14	FGAHMANPLLRKVV	20910
1JD2	OP	HYDROLASE	P	1.0	1.0	1	12	SDQLFGMCESLY	20911
1JD2	TN	HYDROLASE	N	1.0	1.0	1	6	PDEYEQ	20912
1JD2	TN	HYDROLASE	T	1.0	1.0	1	19	VQVAEEAIVNAMRVLYYRD	20913
1JD2	Z1	HYDROLASE	1	1.0	1.0	1	21	IPDGRHLVNRGREEAASFKKL	20914
1JDP	BH	SIGNALING PROTEIN	B	1.0	1.0	1	17	NCYFTLEGVHEVFQEEG	20915
1JEY	AB	DNA BINDING PROTEIN/DNA	A	1.0	1.0	1	7	KEETEEL	20916
1JFI	AB	TRANSCRIPTION/DNA	A	1.0	1.0	1	6	TSHLKQ	20917
1JGN	AB	RNA BINDING PROTEIN	A	1.0	1.0	1	21	PESLRSKVDEAVAVLQAHQAK	20918
1JJO	BC	SIGNALING PROTEIN	B	1.0	1.0	1	12	PLSIALAMGMME	20919
1JL4	AC	IMMUNE SYSTEM	A	1.0	1.0	1	22	PQGGLQNIATGKHNLEILTKRS	20920
1JMU	AB	VIRAL PROTEIN	B	1.0	1.0	1	17	EHAIANFTKAEMALEFN	20921
1JMU	FG	VIRAL PROTEIN	G	1.0	1.0	1	19	LDTKLDQYWTALNLMIDSS	20922

1JMU	FI	VIRAL PROTEIN	F	1.0	1.0	1	5	PAELI	20923
1JMU	FI	VIRAL PROTEIN	I	1.0	1.0	1	5	APIVL	20924
1JMX	AB	OXIDOREDUCTASE	A	1.0	1.0	1	15	AKEWEHLVNFHLGQW	20925
1JNR	CB	OXIDOREDUCTASE	C	1.0	1.0	1	16	PWQGLVRLQKIMDEYA	20926
1JNR	CD	OXIDOREDUCTASE	D	1.0	1.0	1	5	SCVKM	20927
1JOU	AB	BLOOD CLOTTING	B	1.0	1.0	1	8	RETAASLL	20928
1JPW	BE	CELL ADHESION	B	1.0	1.0	1	17	QRLVQNCLWTLRNLSDA	20929
1JQJ	AC	TRANSFERASE	C	1.0	1.0	1	9	WNAIFSLCQ	20930
1JR3	CD	TRANSFERASE	C	1.0	1.0	1	13	EHVLTALANGLSL	20931
1JR3	DE	TRANSFERASE	D	1.0	1.0	1	15	TLQRELLLLVNLKRQ	20932
1JRO	EF	OXIDOREDUCTASE	F	1.0	1.0	1	19	PALDIGQIEGAYVQGAGWL	20933
1JTO	AL	ANTIBODY, HYDROLASE	L	1.0	1.0	1	6	VAWRNR	20934
1JY7	AB	OXYGEN STORAGE/TRANSPORT	B	1.0	1.0	1	14	EVGGEALGRLLVVY	20935
1JY7	RQ	OXYGEN STORAGE/TRANSPORT	Q	1.0	1.0	1	19	PENFRLLGNVLVCVLAHHF	20936
1JY7	RS	OXYGEN STORAGE/TRANSPORT	R	1.0	1.0	1	18	AHAGEYGAEALERMFLSF	20937
1JYO	AF	CHAPERONE	F	1.0	1.0	1	9	TECVKAADE	20938
1JYO	DE	CHAPERONE	D	1.0	1.0	1	15	QAHQDIIANIGEKLG	20939
1K3Z	AD	TRANSCRIPTION	D	1.0	1.0	1	9	ALHLAAILG	20940
1K7L	GH	TRANSCRIPTION	G	1.0	1.0	1	26	AEVRIFHCCQCTSVETVTELTEFAKA	20941
1K8I	AB	IMMUNE SYSTEM	B	1.0	1.0	1	11	LQDCATHTQPF	20942
1KF6	AB	OXIDOREDUCTASE	B	1.0	1.0	1	10	PAQMAKYHQF	20943
1KF6	BD	OXIDOREDUCTASE	B	1.0	1.0	1	6	PQFGLN	20944
1KF9	DC	HORMONE/GROWTH FACTOR	D	1.0	1.0	1	7	LEPVQFL	20945
1KF9	DF	HORMONE/GROWTH FACTOR	D	1.0	1.0	1	47	NVYDLLKDLEEGIQTLMGRLLLKNYGLLYCFNKDMSKVSTYLRTVQC	20946
1KFY	BP	OXIDOREDUCTASE	P	1.0	1.0	1	23	GKWVFYGLAAILTVVTLIGVVTI	20947
1KFY	MN	OXIDOREDUCTASE	M	1.0	1.0	1	13	TGFHMLHTLFQTS	20948
1KFY	MN	OXIDOREDUCTASE	N	1.0	1.0	1	13	LLDALGYIKDNLA	20949
1KFY	ND	OXIDOREDUCTASE	N	1.0	1.0	1	21	PAAAIQQGKVESSKDFLIATL	20950
1KI1	CB	SIGNALING PROTEIN	B	1.0	1.0	1	37	PTERKRQGYIHELIVTEENYVNDLQLVTEIFQKPLME	20951
1KI1	CD	SIGNALING PROTEIN	D	1.0	1.0	1	36	HSHLKHALEKAEELCSQVNEGVREKENSDRLEWIQA	20952
1KIL	BE	MEMBRANE PROTEIN	B	1.0	1.0	1	39	SEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID	20953
1KQS	AY	RIBOSOME	Y	1.0	1.0	1	15	LKIRVRVADVEIKHK	20954
1KQS	FL	RIBOSOME	L	1.0	1.0	1	15	QIAELMWHRMQEWRN	20955
1KV6	AC	GENE REGULATION	A	1.0	1.0	1	8	KLFLEMLE	20956
1KV6	AC	GENE REGULATION	C	1.0	1.0	1	9	KILHRLLQE	20957
1KX4	GH	STRUCTURAL PROTEIN/DNA	H	1.0	1.0	1	12	AIYVYKVLKQVH	20958
1KYO	AB	OXIDOREDUCTASE/ELECTRON TRANSPORT	B	1.0	1.0	1	12	ALKLVRESELLG	20959

1KYO	CP	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.0	1.0	1	14	KLLGVITMFAAILV	20960
1KYO	LM	OXIDOREDUCTASE/ELECTRON TRANSPORT	L	1.0	1.0	1	11	LGEAFKKIDAI	20961
1KYO	LP	OXIDOREDUCTASE/ELECTRON TRANSPORT	L	1.0	1.0	1	20	NFEATKKSVLKQVQDFEDND	20962
1KYO	LP	OXIDOREDUCTASE/ELECTRON TRANSPORT	L	1.0	1.0	1	5	LESLE	20963
1KZ7	CD	SIGNALING PROTEIN	D	1.0	1.0	1	19	PSSFENVKEKWVPEITHHC	20964
1L0O	AC	PROTEIN BINDING	A	1.0	1.0	1	23	MDELTEIKTVVSEAVTNAIIHGY	20965
1L0O	BC	PROTEIN BINDING	B	1.0	1.0	1	15	ESFARVTVAAFVAQL	20966
1L3E	AB	TRANSCRIPTION	B	1.0	1.0	1	22	PEKRKLIQQQLVLLLHAHKCQR	20967
1L9B	MH	PHOTOSYNTHESIS	H	1.0	1.0	1	18	LLEEDKICGYVAGGLMYA	20968
1L9J	MH	PHOTOSYNTHESIS	M	1.0	1.0	1	12	VTLTGGIGILLS	20969
1LB1	AB	SIGNALING PROTEIN	A	1.0	1.0	1	24	MEEFQIYEKYCQNKPRSESLWRQC	20970
1LB1	AB	SIGNALING PROTEIN	A	1.0	1.0	1	12	KYQLLLKEMLKY	20971
1LDK	DE	LIGASE	D	1.0	1.0	1	14	KGLLDVTCKTVANM	20972
1LIA	AB	LIGHT HARVESTING PROTEIN	A	1.0	1.0	1	16	HEAVVKEAGDACFSKY	20973
1LJ2	BC	VIRAL PROTEIN/ TRANSLATION	B	1.0	1.0	1	33	PLHAFDDLESVIRNLISDYDKLFLMFKGLIQRS	20974
1LJ2	BC	VIRAL PROTEIN/ TRANSLATION	C	1.0	1.0	1	5	TEEIM	20975
1LJ2	BD	VIRAL PROTEIN/ TRANSLATION	B	1.0	1.0	1	33	PLHAFDDLESVIRNLISDYDKLFLMFKGLIQRS	20976
1LKY	AB	TRANSCRIPTION	B	1.0	1.0	1	17	PHSGDVLYELLQHILKQ	20977
1LO5	AB	IMMUNE SYSTEM/TOXIN	B	1.0	1.0	1	9	ELGRPDAEY	20978
1LO5	BC	IMMUNE SYSTEM/TOXIN	B	1.0	1.0	1	10	VDTYCRHNYG	20979
1LP1	AB	IMMUNE SYSTEM	A	1.0	1.0	1	13	NKELSVAGREIVT	20980
1LVC	CF	LYASE	C	1.0	1.0	1	8	LTEIKKQI	20981
1LVC	CF	LYASE	C	1.0	1.0	1	18	QEKKRKISIFRGIQAYNE	20982
1LWU	AB	BLOOD CLOTTING	B	1.0	1.0	1	15	VKIRIESTVAGSLRS	20983
1LWU	AC	BLOOD CLOTTING	A	1.0	1.0	1	21	QVSQILRVEVDIDVALRACKG	20984
1LWU	GH	BLOOD CLOTTING	H	1.0	1.0	1	16	RSMKSVLEHLRAKMQR	20985
1LWU	GI	BLOOD CLOTTING	I	1.0	1.0	1	8	LEEVRILE	20986
1LWU	JK	BLOOD CLOTTING	K	1.0	1.0	1	7	IRIESTV	20987
1LWU	JL	BLOOD CLOTTING	J	1.0	1.0	1	37	NMQLQQLTLLQHNIKTQVSQILRVEVDIDVALRACKG	20988
1LWU	JL	BLOOD CLOTTING	L	1.0	1.0	1	8	LEEVRILE	20989
1M1J	BC	BLOOD CLOTTING	C	1.0	1.0	1	7	WVQYKEG	20990
1M1J	EF	BLOOD CLOTTING	F	1.0	1.0	1	5	YRLTT	20991
1M1Y	IJ	OXIDOREDUCTASE	J	1.0	1.0	1	14	SYGKFIQRDTLHKG	20992
1M1Y	KL	OXIDOREDUCTASE	K	1.0	1.0	1	16	FDGFAIFARDMDMTLN	20993
1M2O	AB	PROTEIN TRANSPORT/SIGNALING PROTEIN	B	1.0	1.0	1	8	KTTLLHML	20994

1M46	AB	CELL CYCLE PROTEIN	A	1.0	1.0	1	11	VGDLRYMLTGL	20995
1M46	AB	CELL CYCLE PROTEIN	A	1.0	1.0	1	10	DAEVDELLKG	20996
1M46	AB	CELL CYCLE PROTEIN	A	1.0	1.0	1	10	YKKFIEDVLR	20997
1M56	GI	OXIDOREDUCTASE	G	1.0	1.0	1	7	STDLAIF	20998
1M63	EF	HYDROLASE/ISOMERASE	F	1.0	1.0	1	13	EIKRLGKRFKKLD	20999
1M8Q	PR	CONTRACTILE PROTEIN	R	1.0	1.0	1	9	EDFVEGLRV	21000
1MF8	AC	HYDROLASE, LIGASE	A	1.0	1.0	1	7	RHLTEYF	21001
1MHP	HL	IMMUNE SYSTEM	L	1.0	1.0	1	5	DEQLK	21002
1MIM	LH	IMMUNOGLOBULIN	L	1.0	1.0	1	6	DEQLKS	21003
1MJG	AN	OXIDOREDUCTASE	N	1.0	1.0	1	14	LGDLPPILNRKRAQ	21004
1MMO	DG	OXIDOREDUCTASE (MONOOXYGENASE)	D	1.0	1.0	1	5	IFEQY	21005
1MTY	EB	MONOOXYGENASE	B	1.0	1.0	1	30	LTPFFINQAQTYFQIAKQGVQDLYYNCLGD	21006
1MUJ	AB	IMMUNE SYSTEM	B	1.0	1.0	1	7	PETHTSL	21007
1MVF	BD	IMMUNE SYSTEM	D	1.0	1.0	1	7	ATLMQAL	21008
1MVW	GI	CONTRACTILE PROTEIN	G	1.0	1.0	1	10	SAIPEGQFMD	21009
1MVW	PQ	CONTRACTILE PROTEIN	Q	1.0	1.0	1	12	FTVFLTMFGEKL	21010
1MWA	DI	IMMUNE SYSTEM	I	1.0	1.0	1	28	EYWERETQKAKGNEQSFRVSLRTLLGYY	21011
1MXE	BF	METAL BINDING PROTEIN	B	1.0	1.0	1	14	FPEFLTMMARKMKD	21012
1MXE	BF	METAL BINDING PROTEIN	B	1.0	1.0	1	13	SEEEIREAFRVFD	21013
1N2D	AC	CELL CYCLE	A	1.0	1.0	1	12	TRANKDIFTLFD	21014
1N4M	BE	CELL CYCLE	B	1.0	1.0	1	8	KTNILQYA	21015
1N86	DF	BLOOD CLOTTING	D	1.0	1.0	1	18	LVDMKRLEVDIDIKIRSC	21016
1NBW	AB	HYDROLASE	A	1.0	1.0	1	7	GVLVNNR	21017
1NDO	AB	NON-HEME IRON DIOXYGENASE	A	1.0	1.0	1	15	EDLKRRLADSVQRTF	21018
1NDO	EF	NON-HEME IRON DIOXYGENASE	E	1.0	1.0	1	15	EDLKRRLADSVQRTF	21019
1NEK	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	C	1.0	1.0	1	30	FFVKFIMWGILTALAYHVVVGIRHMMMDFG	21020
1NEX	CD	LIGASE, CELL CYCLE	D	1.0	1.0	1	9	FEDIINSLG	21021
1NF5	AB	TRANSFERASE/TRANSFERASE	A	1.0	1.0	1	7	KAYKPMC	21022
1NGW	AB	IMMUNE SYSTEM	A	1.0	1.0	1	6	DEQLKS	21023
1NGW	LH	IMMUNE SYSTEM	L	1.0	1.0	1	6	DEQLKS	21024
1NIK	AB	TRANSCRIPTION	A	1.0	1.0	1	11	KKIENTMLENI	21025
1NIK	AI	TRANSCRIPTION	A	1.0	1.0	1	28	LRESFEDNVVRFLNEARDKAGRLAEVNL	21026
1NIW	AB	SIGNALING PROTEIN/OXIDOREDUCTASE	A	1.0	1.0	1	6	YEEFVQ	21027
1NIW	EF	SIGNALING PROTEIN/OXIDOREDUCTASE	E	1.0	1.0	1	6	YEEFVQ	21028
1NIW	GH	SIGNALING PROTEIN/OXIDOREDUCTASE	G	1.0	1.0	1	7	AAELRHV	21029

1NIW	GH	SIGNALING PROTEIN/OXIDOREDUCTASE	G	1.0	1.0	1	6	YEEFVQ	21030
1NLD	LH	IMMUNOGLOBULIN	L	1.0	1.0	1	6	SEQLTS	21031
1NTK	BI	OXIDOREDUCTASE	B	1.0	1.0	1	19	RWEVAALQPQLRIDKAVAL	21032
1NTK	CF	OXIDOREDUCTASE	F	1.0	1.0	1	20	ENLYDDRVFRIKRALDLSMR	21033
1NTK	DE	OXIDOREDUCTASE	E	1.0	1.0	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	21034
1NTK	DH	OXIDOREDUCTASE	H	1.0	1.0	1	23	TEELLDFLHARDHCVAHKLFNSL	21035
1NU7	BD	HYDROLASE/PROTEIN BINDING	D	1.0	1.0	1	23	ERIEKEMIKDLESIIEDFFIETG	21036
1NU7	FH	HYDROLASE/PROTEIN BINDING	H	1.0	1.0	1	23	DWYLKGRLTSLESQFINALGILE	21037
1NWD	AB	BINDING PROTEIN/HYDROLASE	A	1.0	1.0	1	12	EEEIREAFRVFD	21038
1NZY	AB	LYASE	B	1.0	1.0	1	7	YSLARIV	21039
1NZY	CB	LYASE	C	1.0	1.0	1	7	YSLARIV	21040
1O18	A8	CONTRACTILE PROTEIN	8	1.0	1.0	1	9	QAVLSLYAS	21041
1O18	P3	CONTRACTILE PROTEIN	P	1.0	1.0	1	5	YDEHL	21042
1O18	PR	CONTRACTILE PROTEIN	R	1.0	1.0	1	10	DFKEAFLLFD	21043
1O2F	AB	TRANSFERASE	B	1.0	1.0	1	13	SDNLKTEMDEYIR	21044
1O4X	AB	TRANSCRIPTION/DNA	B	1.0	1.0	1	22	ETEKRPFIDEAKRLRALHMKEH	21045
1O96	AB	ELECTRON TRANSFER	B	1.0	1.0	1	9	YASSLASKT	21046
1O96	CD	ELECTRON TRANSFER	C	1.0	1.0	1	17	EWDDFSLEEAMKIKESS	21047
1OCC	AM	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	A	1.0	1.0	1	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	21048
1OCC	DK	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	1.0	1.0	1	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	21049
1OCC	DM	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	D	1.0	1.0	1	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	21050
1OCC	GH	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	H	1.0	1.0	1	13	ISWVSTWDDRRAE	21051
1OCC	JL	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	L	1.0	1.0	1	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	21052
1OCC	NZ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	N	1.0	1.0	1	28	DTWAKIHFAIMFVGVNMTFFPQHFLGLS	21053
1OCC	QZ	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Q	1.0	1.0	1	28	EWKTVVGAAMFFIGFTALLLIWEKHYVY	21054
1OCC	WY	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)	Y	1.0	1.0	1	28	KWRLLAMMTLFFGSGFAAPFFIVRHQLL	21055
1OIJ	AB	OXIDOREDUCTASE	B	1.0	1.0	1	12	DQSQEGFAKLLG	21056
1ONK	AB	HYDROLASE/SUGER BINDING PROTEIN	A	1.0	1.0	1	8	VYMLELET	21057
1OOP	BC	VIRUS	C	1.0	1.0	1	7	LLGEILN	21058
1OQO	BD	IMMUNE SYSTEM	D	1.0	1.0	1	14	EEQRNAKIKSIRDD	21059
1OQS	AF	HYDROLASE	F	1.0	1.0	1	19	CLRTICECDRVAANCFHQN	21060

1OQS	CD	HYDROLASE	D	1.0	1.0	1	13	LFQFARMINGKLG	21061
1OQS	GD	HYDROLASE	D	1.0	1.0	1	16	ATDRCCFVHDCCYGGV	21062
1OQS	GH	HYDROLASE	H	1.0	1.0	1	13	LFQFARMINGKLG	21063
1OR7	BF	TRANSCRIPTION	B	1.0	1.0	1	13	EDLRMAITLRELD	21064
1OR7	BF	TRANSCRIPTION	F	1.0	1.0	1	9	SELLNELAH	21065
1OSV	BE	DNA BINDING PROTEIN	B	1.0	1.0	1	8	PLLCEIWD	21066
1OVL	AB	TRANSCRIPTION	B	1.0	1.0	1	11	ISAFSCIAALA	21067
1OVL	DE	TRANSCRIPTION	D	1.0	1.0	1	12	LISALVRAHVDS	21068
1OVL	DE	TRANSCRIPTION	E	1.0	1.0	1	12	LISALVRAHVDS	21069
1OW3	AB	GENE REGULATION/SIGNALING PROTEIN	B	1.0	1.0	1	6	PDSLEN	21070
1OW7	CF	TRANSFERASE	C	1.0	1.0	1	27	EYVPMVKEVGLALRTLLATVDETIPLL	21071
1OXK	CF	SIGNALING PROTEIN	C	1.0	1.0	1	5	KSIIN	21072
1OXK	IJ	SIGNALING PROTEIN	I	1.0	1.0	1	10	WTILNEIISM	21073
1OXK	IJ	SIGNALING PROTEIN	I	1.0	1.0	1	26	FSKGLIIQFIDQAQTTFAQMQRQLDG	21074
1OYV	AI	HYDROLASE	A	1.0	1.0	1	13	TAMKQAVDNAYAR	21075
1P27	CD	RNA BINDING PROTEIN	C	1.0	1.0	1	15	KSVMEELKRIIDDSE	21076
1P4B	LP	IMMUNE SYSTEM	P	1.0	1.0	1	10	HLENEVARLK	21077
1P8D	BD	MEMBRANE PROTEIN/PROTEIN BINDING	B	1.0	1.0	1	28	RDARQQRFAHFTELAIISVQEIVDFAKQ	21078
1P9M	BC	SIGNALING PROTEIN/CYTOKINE	B	1.0	1.0	1	28	QWLQDMTTHLILRSFKEFLQSSLRALRQ	21079
1PCQ	DR	CHAPERONE	D	1.0	1.0	1	13	EALATLVVNTMRG	21080
1PCQ	ES	CHAPERONE	E	1.0	1.0	1	13	IREMLPVLEAVAK	21081
1PGR	CD	CYTOKINE	C	1.0	1.0	1	28	PELGPTLDTLQLDVADFATTIWQQMEEL	21082
1PIV	14	VIRUS	1	1.0	1.0	1	5	IESFF	21083
1PIV	23	VIRUS	3	1.0	1.0	1	5	MDMYR	21084
1PMA	ER	PROTEASE	E	1.0	1.0	1	23	VADARVLVDFARISAQQEKVTYG	21085
1PMA	GU	PROTEASE	G	1.0	1.0	1	23	VADARVLVDFARISAQQEKVTYG	21086
1PMA	O2	PROTEASE	O	1.0	1.0	1	23	VADARVLVDFARISAQQEKVTYG	21087
1PNS	GK	RIBOSOME	K	1.0	1.0	1	18	PYAAQLAALDAAKKAMAY	21088
1POI	AD	TRANSFERASE	A	1.0	1.0	1	8	DVDIAEAA	21089
1POI	AD	TRANSFERASE	A	1.0	1.0	1	7	DEEIRRD	21090
1PSK	LH	IMMUNOGLOBULIN	L	1.0	1.0	1	7	SEQLTSG	21091
1PSS	LM	PHOTOSYNTHETIC REACTION CENTER	L	1.0	1.0	1	7	WWQWWVK	21092
1PSS	MH	PHOTOSYNTHETIC REACTION CENTER	M	1.0	1.0	1	7	WYVWGQN	21093
1PTO	AE	TOXIN	A	1.0	1.0	1	22	RRYTEVYLEHRMQEAVEAERAG	21094
1PTO	IJ	TOXIN	I	1.0	1.0	1	14	YDALRRLLYMIYMS	21095
1PUM	AB	SUGAR BINDING PROTEIN	A	1.0	1.0	1	8	VYMLELET	21096
1Q16	AB	OXIDOREDUCTASE	B	1.0	1.0	1	5	VCSET	21097
1Q5Q	FN	HYDROLASE	F	1.0	1.0	1	22	YNEFENLRRAGIVHADMRGYSY	21098

1Q86	C1	RIBOSOME	1	1.0	1.0	1	15	LKIRVRVADVEIKHK	21099
1Q90	BD	PHOTOSYNTHESIS	B	1.0	1.0	1	22	CIGGITFTCFLVQVATGFAMTF	21100
1Q90	BD	PHOTOSYNTHESIS	D	1.0	1.0	1	25	NDLLYMFPVVILGTFACVIGLSVLD	21101
1QGW	AC	PHOTOSYNTHESIS	C	1.0	1.0	1	9	SVLEDRCLN	21102
1QO0	AD	BINDING PROTEIN	D	1.0	1.0	1	11	PAVLSQIIELE	21103
1QO0	BD	BINDING PROTEIN	D	1.0	1.0	1	49	AHRVLPVLVSARRISEEMAKLKQKTEQLQDRIAGQARINQAKVLLMQRH	21104
1QPW	CB	OXYGEN TRANSPORT	B	1.0	1.0	1	20	PENFRLLGNVIVVVLARRLG	21105
1QS7	AB	METAL BINDING PROTEIN/PEPTIDE	A	1.0	1.0	1	12	DEEVDEMIREAD	21106
1QUQ	AB	DNA-BINDING PROTEIN	A	1.0	1.0	1	5	ISQLL	21107
1R1A	13	VIRUS	3	1.0	1.0	1	6	LIEMCQ	21108
1R24	CD	IMMUNE SYSTEM	C	1.0	1.0	1	7	SEQLTSG	21109
1R2B	AC	TRANSCRIPTION	A	1.0	1.0	1	7	GLFYSIF	21110
1R4A	AE	PROTEIN TRANSPORT	A	1.0	1.0	1	6	TSIRPY	21111
1R4A	DH	PROTEIN TRANSPORT	H	1.0	1.0	1	12	TKTMAKVITTVL	21112
1R4M	CH	CELL CYCLE	C	1.0	1.0	1	22	NYQVEEDIGKLKSCLTGFLQEY	21113
1R4M	EF	CELL CYCLE	E	1.0	1.0	1	32	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS	21114
1R4M	EK	CELL CYCLE	K	1.0	1.0	1	13	VERIKERVEEKEG	21115
1R4M	GH	CELL CYCLE	G	1.0	1.0	1	32	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS	21116
1R4P	AF	TOXIN	F	1.0	1.0	1	13	WNLQPLLQSAQLT	21117
1R4Q	AB	TOXIN	B	1.0	1.0	1	13	WNLQSLLLSAQIT	21118
1R4Q	LI	TOXIN	I	1.0	1.0	1	11	QSLLLSAQITG	21119
1R5W	AE	SIGNALING PROTEIN	A	1.0	1.0	1	23	AQGALANIAVDKANLDVMKERSN	21120
1R5W	BE	SIGNALING PROTEIN	B	1.0	1.0	1	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	21121
1R5W	DF	SIGNALING PROTEIN	D	1.0	1.0	1	28	PEFLEQKRAEVDTVCRHNYEIFDNFLVP	21122
1RCO	VP	LYASE	V	1.0	1.0	1	15	CEDMMKRAVFARELG	21123
1RD8	EB	VIRAL PROTEIN	B	1.0	1.0	1	29	RRIENLNKKVDDGFLDIWTYNAELLVLLE	21124
1RDT	AD	HORMONE/GROWTH FACTOR	A	1.0	1.0	1	7	RFAKLLL	21125
1RH5	AC	PROTEIN TRANSPORT	A	1.0	1.0	1	28	PLLAFLVIIQIAFGSIILIYLDEIVSKY	21126
1RHH	CD	IMMUNE SYSTEM	C	1.0	1.0	1	6	DEQLKS	21127
1RIO	HB	TRANSCRIPTION/DNA	B	1.0	1.0	1	9	QSGVGALFN	21128
1RLD	BT	LYASE(CARBON-CARBON)	B	1.0	1.0	1	14	AKNYGRAVYECLRG	21129
1RM1	AC	TRANSCRIPTION/DNA	A	1.0	1.0	1	19	EDDSKLASRKYARIIQKIG	21130
1RM6	AC	OXIDOREDUCTASE	C	1.0	1.0	1	8	RDEIKAAL	21131
1RP3	EF	TRANSCRIPTION	E	1.0	1.0	1	21	PKRAEAYIKLRIKGAIYDYLR	21132
1RP3	GD	TRANSCRIPTION	G	1.0	1.0	1	14	EREKLVIQLIFYEE	21133
1RSO	AB	NEUROPEPTIDE/MEMBRANE PROTEIN	A	1.0	1.0	1	15	RQLRSSIERVISIFQ	21134
1RTD	AB	TRANSFERASE/DNA	B	1.0	1.0	1	18	VNDIQKLVGKLNWASQIY	21135
1RU7	CD	VIRAL PROTEIN	D	1.0	1.0	1	9	NECMESVRN	21136

1RU7	CF	VIRAL PROTEIN	F	1.0	1.0	1	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	21137
1RU7	EB	VIRAL PROTEIN	B	1.0	1.0	1	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	21138
1RU7	GH	VIRAL PROTEIN	H	1.0	1.0	1	22	QKSTQNAINGITNKVNSVIEKM	21139
1RU7	GJ	VIRAL PROTEIN	J	1.0	1.0	1	22	QKSTQNAINGITNKVNSVIEKM	21140
1RU7	GJ	VIRAL PROTEIN	J	1.0	1.0	1	52	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQL	21141
1RU7	IL	VIRAL PROTEIN	L	1.0	1.0	1	53	KRMENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLK	21142
1RU7	KH	VIRAL PROTEIN	H	1.0	1.0	1	22	QKSTQNAINGITNKVNSVIEKM	21143
1RUY	JK	VIRAL PROTEIN	K	1.0	1.0	1	9	NECMESVRN	21144
1RUY	JM	VIRAL PROTEIN	M	1.0	1.0	1	50	KRIENLNNKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRS	21145
1RUY	LM	VIRAL PROTEIN	M	1.0	1.0	1	22	QKSTQNAIDGITNKVNSVIEKM	21146
1RUZ	HI	VIRAL PROTEIN	I	1.0	1.0	1	22	QKSTQNAIDGITNKVNSVIEKM	21147
1RUZ	JI	VIRAL PROTEIN	I	1.0	1.0	1	46	RRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYE	21148
1RUZ	JK	VIRAL PROTEIN	K	1.0	1.0	1	22	QKSTQNAIDGITNKVNSVIEKM	21149
1RUZ	LM	VIRAL PROTEIN	L	1.0	1.0	1	10	YEELREQLSS	21150
1RUZ	LM	VIRAL PROTEIN	M	1.0	1.0	1	22	QKSTQNAIDGITNKVNSVIEKM	21151
1RY1	WS	TRANSLATION	S	1.0	1.0	1	15	GFPINFLTLYVTVQH	21152
1RYP	12	MULTICATALYTIC PROTEINASE	1	1.0	1.0	1	22	AADGDALVKRFKNSVKWYHFDH	21153
1RYP	AH	MULTICATALYTIC PROTEINASE	A	1.0	1.0	1	22	IPDARNAALRAKAEAAEFRYKY	21154
1RYP	EM	MULTICATALYTIC PROTEINASE	E	1.0	1.0	1	13	VESLTQSVCDLAL	21155
1RYP	FN	MULTICATALYTIC PROTEINASE	F	1.0	1.0	1	15	VERAGHLLCDKAQKN	21156
1RYP	SZ	MULTICATALYTIC PROTEINASE	Z	1.0	1.0	1	22	AADCQFWETWLGSQCRLHELRE	21157
1RYP	T2	MULTICATALYTIC PROTEINASE	T	1.0	1.0	1	15	VERAGHLLCDKAQKN	21158
1RYP	VN	MULTICATALYTIC PROTEINASE	V	1.0	1.0	1	19	KEETVDFIKHSLSQAIKWD	21159
1RZI	CD	IMMUNE SYSTEM	C	1.0	1.0	1	7	DEQLKSG	21160
1RZI	IJ	IMMUNE SYSTEM	I	1.0	1.0	1	7	DEQLKSG	21161
1RZR	AS	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	A	1.0	1.0	1	15	IFYAELARGIEDIAT	21162
1RZR	CT	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	C	1.0	1.0	1	15	IFYAELARGIEDIAT	21163
1S0Y	IL	LYASE	L	1.0	1.0	1	20	VARKQQLIRDVIDVTNKSIG	21164
1S5E	AE	TRANSERASE,TOXIN	A	1.0	1.0	1	30	TCDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	21165
1S5E	AE	TRANSERASE,TOXIN	E	1.0	1.0	1	20	DSQKKAIERMKDTLRIAYLT	21166
1S5E	BK	TRANSERASE,TOXIN	B	1.0	1.0	1	29	CDEKTQSLGVKFLDEYQSKVKRQIFSGYQ	21167
1S5E	BN	TRANSERASE,TOXIN	B	1.0	1.0	1	7	PDEIKQS	21168

1S5L	ac	PHOTOSYNTHESIS	c	1.0	1.0	1	26	PRSWLATSHFVLAFFFLVGHLWHAGR	21169
1S5L	AD	PHOTOSYNTHESIS	A	1.0	1.0	1	25	WICVAYSAPLASAFAVFLIYPIGQG	21170
1S5L	AD	PHOTOSYNTHESIS	D	1.0	1.0	1	25	LWTFIALHGAFGLIGFMLRQFEIAR	21171
1S5L	ad	PHOTOSYNTHESIS	d	1.0	1.0	1	17	YNAIAFSAPIAVFVSVF	21172
1S5L	AD	PHOTOSYNTHESIS	D	1.0	1.0	1	7	RWLHFFM	21173
1S5L	ai	PHOTOSYNTHESIS	a	1.0	1.0	1	21	VIMIPTLLAATICFVIAFIAA	21174
1S5L	AI	PHOTOSYNTHESIS	A	1.0	1.0	1	21	VIMIPTLLAATICFVIAFIAA	21175
1S5L	bo	PHOTOSYNTHESIS	b	1.0	1.0	1	13	PPTVKSYARKAIF	21176
1S5L	BU	PHOTOSYNTHESIS	U	1.0	1.0	1	6	VDEKLG	21177
1S5L	DE	PHOTOSYNTHESIS	E	1.0	1.0	1	13	AKQQVETFLEQLK	21178
1S5L	df	PHOTOSYNTHESIS	f	1.0	1.0	1	27	TVRWVAVHTLAVPTIFFLGAIAAMQFI	21179
1S5L	DL	PHOTOSYNTHESIS	D	1.0	1.0	1	27	PFHMMGVAGVLGGALLCAIHGATVENT	21180
1S5L	dl	PHOTOSYNTHESIS	d	1.0	1.0	1	27	PFHMMGVAGVLGGALLCAIHGATVENT	21181
1S5L	DO	PHOTOSYNTHESIS	O	1.0	1.0	1	8	EEELARAN	21182
1S5L	do	PHOTOSYNTHESIS	o	1.0	1.0	1	8	EEELARAN	21183
1S5L	dv	PHOTOSYNTHESIS	d	1.0	1.0	1	21	FYTKNLLLNEGIRAWMAPQDQ	21184
1S5L	lm	PHOTOSYNTHESIS	m	1.0	1.0	1	26	QLGLIATALFVLVPSVFLIILYVQTE	21185
1S5R	AB	TRANSCRIPTION	B	1.0	1.0	1	25	PDIYKAFLEILHTYQKEQRNAKEAG	21186
1S5R	AB	TRANSCRIPTION	B	1.0	1.0	1	11	EDLLSEFGQFL	21187
1SB2	AB	TOXIN	A	1.0	1.0	1	10	WEEAERFCTE	21188
1SB3	AB	OXIDOREDUCTASE	A	1.0	1.0	1	14	PDRITELLDAKEAA	21189
1SB3	BC	OXIDOREDUCTASE	C	1.0	1.0	1	10	LLDYLRETVG	21190
1SB3	EF	OXIDOREDUCTASE	E	1.0	1.0	1	7	PTHRAAA	21191
1SCT	CD	OXYGEN TRANSPORT	C	1.0	1.0	1	16	IEATGLMLMSNLFTLR	21192
1SCT	CD	OXYGEN TRANSPORT	D	1.0	1.0	1	18	VERLKCVVEKFAVNHINR	21193
1SHZ	AC	SIGNALING PROTEIN	A	1.0	1.0	1	6	RSERKK	21194
1SHZ	AC	SIGNALING PROTEIN	A	1.0	1.0	1	22	RPTIYSNVIKGMRVLVDAREKL	21195
1SKY	BE	ATP SYNTHASE	B	1.0	1.0	1	14	ESTVATVVETLAKH	21196
1SQB	AE	OXIDOREDUCTASE	A	1.0	1.0	1	14	MRDVVFNYLHATAF	21197
1SQB	AK	OXIDOREDUCTASE	K	1.0	1.0	1	10	PRYRQLARNW	21198
1SQB	DE	OXIDOREDUCTASE	E	1.0	1.0	1	33	SEARKGFSYLVTATTTVGVAYAAKNVVSQFVSS	21199
1SQB	FG	OXIDOREDUCTASE	F	1.0	1.0	1	20	ENLYDDRVFRIKRALDLSMR	21200
1SQX	AE	OXIDOREDUCTASE	A	1.0	1.0	1	14	MRDVVFNYLHATAF	21201
1SQX	AG	OXIDOREDUCTASE	A	1.0	1.0	1	7	YNRIRSG	21202
1SQX	DH	OXIDOREDUCTASE	D	1.0	1.0	1	10	EDYVFSLLTG	21203
1SSE	AB	TRANSCRIPTION ACTIVATOR	A	1.0	1.0	1	10	EFCSKMNQVC	21204
1SV0	BD	TRANSCRIPTION	D	1.0	1.0	1	7	GKALCLM	21205
1SXJ	BC	REPLICATION	B	1.0	1.0	1	15	MRQAINNLQSTVAGH	21206
1T0J	BC	SIGNALING PROTEIN	B	1.0	1.0	1	20	LEDACEHLADYLEAYWKATH	21207
1T0K	AB	RIBOSOME	B	1.0	1.0	1	15	VLRKSELEYYAMLSK	21208

1T0Q	AB	OXIDOREDUCTASE	A	1.0	1.0	1	5	ENELF	21209
1T2V	AF	ANTITUMOR PROTEIN	A	1.0	1.0	1	10	LKYFLGIAGG	21210
1T2V	CH	ANTITUMOR PROTEIN	C	1.0	1.0	1	14	PEEFMLVYKFARKH	21211
1T34	AH	SIGNALING PROTEIN,MEMBRANE PROTEIN	A	1.0	1.0	1	17	PCFFIVEGLYMRVRERL	21212
1T3Q	AC	OXIDOREDUCTASE	C	1.0	1.0	1	7	QAVRNRG	21213
1T60	HI	STRUCTURAL PROTEIN	H	1.0	1.0	1	7	ENIRPFI	21214
1T6V	MO	HYDROLASE/IMMUNE SYSTEM	M	1.0	1.0	1	8	VAWRNRCK	21215
1TBA	AB	COMPLEX (TRANSCRIPTION FACTORS)	A	1.0	1.0	1	6	LGLDSM	21216
1TBQ	KS	COMPLEX (SERINE PROTEASE/INHIBITOR)	S	1.0	1.0	1	10	PCTLNCAKFN	21217
1TH1	AC	CELL ADHESION/ANTITUMOR PROTEIN	A	1.0	1.0	1	17	EKLLWTTSRVLKVLSVC	21218
1TH1	BD	CELL ADHESION/ANTITUMOR PROTEIN	D	1.0	1.0	1	10	AVNAAVQRVQ	21219
1TI2	CD	OXIDOREDUCTASE	C	1.0	1.0	1	5	PETNS	21220
1TI2	GH	OXIDOREDUCTASE	G	1.0	1.0	1	14	ACEIRALARQWAKK	21221
1TME	13	VIRUS	3	1.0	1.0	1	5	SCMCN	21222
1TN6	AB	TRANSFERASE	B	1.0	1.0	1	11	LKSLLQWVTSR	21223
1TOC	BR	COMPLEX (HYDROLASE/INHIBITOR)	R	1.0	1.0	1	8	EVECQVAC	21224
1TQE	PX	TRANSCRIPTION/PROTEIN BINDING/DNA	P	1.0	1.0	1	8	MDRVLLKY	21225
1TU3	BG	PROTEIN TRANSPORT	B	1.0	1.0	1	6	HSLAPM	21226
1TX4	AB	COMPLEX (GTPASE ACTIVATN/PROTO-ONCOGENE)	B	1.0	1.0	1	6	PDSLEN	21227
1TZH	LH	IMMUNE SYSTEM	L	1.0	1.0	1	7	DEQLKSG	21228
1TZN	Aa	TOXIN RECEPTOR/TOXIN	a	1.0	1.0	1	16	IHEGLKLANEQIQKAG	21229
1U0N	CD	BLOOD CLOTTING	D	1.0	1.0	1	10	LYFRRWLQDN	21230
1U35	CD	STRUCTURAL PROTEIN/DNA	C	1.0	1.0	1	5	RSAKA	21231
1U3H	BD	IMMUNE SYSTEM	D	1.0	1.0	1	34	DAEYYNKQYLERTRAELDTVCRYNYEETEVPTSL	21232
1U6G	BC	LIGASE	C	1.0	1.0	1	15	KDFRFMATNDLMTEL	21233
1UCY	LH	COMPLEX (SERINE PROTEASE/COAGULATION)	L	1.0	1.0	1	7	EKELFES	21234
1UF2	BE	VIRUS	E	1.0	1.0	1	14	GDFNALSNMFTQLS	21235
1UHE	BA	LYASE	A	1.0	1.0	1	7	EDLAKLA	21236
1UHL	AB	DNA BINDING PROTEIN	A	1.0	1.0	1	7	RFAKLLL	21237
1UPT	BA	HYDROLASE/PROTEIN-BINDING	B	1.0	1.0	1	7	KVITTVL	21238
1UPT	DE	HYDROLASE/PROTEIN-BINDING	E	1.0	1.0	1	10	IGISKSELVA	21239
1UPT	FE	HYDROLASE/PROTEIN-BINDING	F	1.0	1.0	1	7	KVITTVL	21240
1UR6	AB	LIGASE	B	1.0	1.0	1	6	CWHRIR	21241

1URQ	AC	TRANSPORT PROTEIN	A	1.0	1.0	1	56	EGVKGAASGVVGELARARLALDERGQKLSDLEERTAAMMSSADSFSK HAHEMMLKY	21242
1UZH	HW	LYASE	H	1.0	1.0	1	20	WRDRFLFVAEAIYKAQAETG	21243
1UZH	KP	LYASE	K	1.0	1.0	1	10	PELAAACEVW	21244
1UZH	VC	LYASE	V	1.0	1.0	1	20	WRDRFLFVAEAIYKAQAETG	21245
1UZH	VW	LYASE	V	1.0	1.0	1	14	AKNYGRAVYECLRG	21246
1V54	DE	OXIDOREDUCTASE	E	1.0	1.0	1	14	PKIIDAALRACRRL	21247
1V7N	MZ	IMMUNE SYSTEM/CYTOKINE	M	1.0	1.0	1	6	KDEYER	21248
1VF5	AB	PHOTOSYNTHESIS	A	1.0	1.0	1	21	CLGGITLTCFLIQFATGFAMT	21249
1VF5	AD	PHOTOSYNTHESIS	A	1.0	1.0	1	29	GWLIRSIHRWSASMMVLMMILHVFRVYLT	21250
1VF5	AQ	PHOTOSYNTHESIS	A	1.0	1.0	1	10	GVLISDLLRG	21251
1VF5	CG	PHOTOSYNTHESIS	C	1.0	1.0	1	25	PNRVKWMIAFICLVMLAQLMLILKK	21252
1VF5	ND	PHOTOSYNTHESIS	N	1.0	1.0	1	10	QVGYWAVKIV	21253
1VF5	OR	PHOTOSYNTHESIS	R	1.0	1.0	1	25	ILGAVFYIVFIALFFGIAVGIIFAI	21254
1VF5	OT	PHOTOSYNTHESIS	T	1.0	1.0	1	6	TLGGLF	21255
1VF5	PT	PHOTOSYNTHESIS	T	1.0	1.0	1	10	YAAYQQYKRP	21256
1VG0	AB	PROTEIN BINDING/PROTEIN TRANSPORT	A	1.0	1.0	1	10	LLIDLLIKSN	21257
1VOQ	BH	RIBOSOME	B	1.0	1.0	1	6	TMEELE	21258
1VQP	NQ	RIBOSOME	N	1.0	1.0	1	11	YHQRLRLLKSG	21259
1VQP	SV	RIBOSOME	V	1.0	1.0	1	24	PAEREAELDDLKTELLNARAVQAA	21260
1VRA	AB	TRANSFERASE	A	1.0	1.0	1	13	APLKVTQESIAVE	21261
1VSA	RW	RIBOSOME	W	1.0	1.0	1	14	SPVELEKLVREKKR	21262
1VYW	AD	TRANSFERASE	A	1.0	1.0	1	5	VDMEN	21263
1W2B	R5	RIBOSOME	R	1.0	1.0	1	10	EKAMNDMDFQ	21264
1W2W	MN	ISOMERASE	N	1.0	1.0	1	11	TLQLAVICKQF	21265
1W5C	AD	PHOTOSYNTHESIS	D	1.0	1.0	1	9	QFEIARLVG	21266
1W5C	BD	PHOTOSYNTHESIS	B	1.0	1.0	1	6	PRGWFT	21267
1W5C	BD	PHOTOSYNTHESIS	B	1.0	1.0	1	6	RDVFSG	21268
1W5C	CV	PHOTOSYNTHESIS	V	1.0	1.0	1	5	PKMRN	21269
1W5C	DE	PHOTOSYNTHESIS	E	1.0	1.0	1	12	KQQVETFLEQLK	21270
1W5C	GJ	PHOTOSYNTHESIS	J	1.0	1.0	1	9	QFEIARLVG	21271
1W5C	HJ	PHOTOSYNTHESIS	H	1.0	1.0	1	7	QRLYKAL	21272
1W5C	HJ	PHOTOSYNTHESIS	H	1.0	1.0	1	6	PRGWFT	21273
1W5C	HJ	PHOTOSYNTHESIS	H	1.0	1.0	1	6	RDVFSG	21274
1W5C	JK	PHOTOSYNTHESIS	K	1.0	1.0	1	12	KQQVETFLEQLK	21275
1W63	BM	ENDOCYTOSIS	M	1.0	1.0	1	12	FVIIYELLDELM	21276
1W63	DN	ENDOCYTOSIS	D	1.0	1.0	1	15	MVVANRVAALSEIAE	21277
1W63	DN	ENDOCYTOSIS	D	1.0	1.0	1	10	WAQIFILDCL	21278
1W63	DN	ENDOCYTOSIS	N	1.0	1.0	1	12	FVIIYELLDELM	21279

1W63	DN	ENDOCYTOSIS	N	1.0	1.0	1	18	SLVFSFLYKVVQVFSEYF	21280
1W63	EM	ENDOCYTOSIS	E	1.0	1.0	1	11	LRELIRTIRTA	21281
1W63	FO	ENDOCYTOSIS	F	1.0	1.0	1	15	MVVANRVAALSEIAE	21282
1W63	FO	ENDOCYTOSIS	O	1.0	1.0	1	12	FVIIYELLDELM	21283
1W63	GP	ENDOCYTOSIS	G	1.0	1.0	1	17	PEFKADCASGIFLAAEK	21284
1W63	HP	ENDOCYTOSIS	H	1.0	1.0	1	15	MVVANRVAALSEIAE	21285
1W63	HP	ENDOCYTOSIS	P	1.0	1.0	1	12	FVIIYELLDELM	21286
1W63	JR	ENDOCYTOSIS	J	1.0	1.0	1	15	MVVANRVAALSEIAE	21287
1W63	JR	ENDOCYTOSIS	J	1.0	1.0	1	18	VDFVRKAVRAIGRCAIKV	21288
1W63	JR	ENDOCYTOSIS	R	1.0	1.0	1	18	SLVFSFLYKVVQVFSEYF	21289
1W63	KV	ENDOCYTOSIS	V	1.0	1.0	1	7	EESIRDN	21290
1W63	LV	ENDOCYTOSIS	L	1.0	1.0	1	15	MVVANRVAALSEIAE	21291
1W63	LV	ENDOCYTOSIS	L	1.0	1.0	1	18	KEKKKEAVKKVIASMTVG	21292
1W63	LV	ENDOCYTOSIS	V	1.0	1.0	1	12	FVIIYELLDELM	21293
1W72	AL	IMMUNE SYSTEM	A	1.0	1.0	1	29	PEYWDQETRNMKAHSQTDRANLGTLRGYY	21294
1W7P	AD	PROTEIN TRANSPORT	D	1.0	1.0	1	14	LGILMEVLQNCVDE	21295
1WCM	AE	TRANSCRIPTION	A	1.0	1.0	1	10	QLVKDRKFLR	21296
1WDC	AB	MUSCLE PROTEIN	B	1.0	1.0	1	9	YVKFTAMIK	21297
1WDW	ED	LYASE	E	1.0	1.0	1	15	KQSTLNFLLALDEYA	21298
1WE3	BP	CHAPERONE	B	1.0	1.0	1	15	VRELLPILEQVAQTG	21299
1WMI	AB	HYDROLASE/HYDROLASE INHIBITOR	A	1.0	1.0	1	17	KAHYRRFLEFRDILEYE	21300
1WX5	CD	OXIDOREDUCTASE/METAL TRANSPORT	C	1.0	1.0	1	16	RYDEFVRTHNEFIMSD	21301
1WYU	AB	OXIDOREDUCTASE	B	1.0	1.0	1	10	KLHEEAARLF	21302
1WYU	CB	OXIDOREDUCTASE	C	1.0	1.0	1	11	EEEIREMLRRV	21303
1WYU	EF	OXIDOREDUCTASE	F	1.0	1.0	1	11	ALDLAKGLLEL	21304
1X2T	AB	PROTEIN BINDING	B	1.0	1.0	1	10	WADAENFCTQ	21305
1X2T	CD	PROTEIN BINDING	C	1.0	1.0	1	10	WDDAERFCTE	21306
1XCG	EF	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	E	1.0	1.0	1	38	QREIDRQEVINELFVTEASHLRTLRVLDLIFYQRMKKE	21307
1XCT	AL	IMMUNE SYSTEM	L	1.0	1.0	1	18	FEEATAEAYRYAALHAKV	21308
1XDK	EF	HORMONE/GROWTH FACTOR RECEPTOR	E	1.0	1.0	1	17	GAIFDRVLTELVSKMRD	21309
1XDK	EF	HORMONE/GROWTH FACTOR RECEPTOR	F	1.0	1.0	1	8	PTKVDKLQ	21310
1XFU	AO	LYASE/METAL BINDING PROTEIN	A	1.0	1.0	1	23	PEYKNYFQYLKERITNQVQLLLT	21311
1XFU	BP	LYASE/METAL BINDING PROTEIN	B	1.0	1.0	1	23	PEYKNYFQYLKERITNQVQLLLT	21312
1XFU	CQ	LYASE/METAL BINDING PROTEIN	C	1.0	1.0	1	23	PEYKNYFQYLKERITNQVQLLLT	21313
1XFU	DR	LYASE/METAL BINDING PROTEIN	D	1.0	1.0	1	23	PEYKNYFQYLKERITNQVQLLLT	21314
1XFU	ES	LYASE/METAL BINDING PROTEIN	E	1.0	1.0	1	23	PEYKNYFQYLKERITNQVQLLLT	21315

1XFV	ES	LYASE/METAL BINDING PROTEIN	E	1.0	1.0	1	7	GYLSDYY	21316
1XG2	AB	HYDROLASE/HYDROLASE INHIBITOR	B	1.0	1.0	1	24	TQLHQADLKLEDLCDIVLVISNLL	21317
1XK4	FL	METAL BINDING PROTEIN	L	1.0	1.0	1	12	QGEFKELVRKDL	21318
1XK4	IK	METAL BINDING PROTEIN	I	1.0	1.0	1	12	RDDLKKLLETES	21319
1XK4	JK	METAL BINDING PROTEIN	K	1.0	1.0	1	12	EKVIEHIMEDLD	21320
1XL3	BD	CELL INVASION	D	1.0	1.0	1	5	MFRLF	21321
1XLS	BF	TRANSCRIPTION	B	1.0	1.0	1	23	PAEVEALREKVYASLEAYCKHKY	21322
1XLS	CG	TRANSCRIPTION	C	1.0	1.0	1	16	IFDRVLTELVSKMRDM	21323
1XLS	CG	TRANSCRIPTION	G	1.0	1.0	1	21	REEIDQLQEEMALILNNHIME	21324
1XLT	DF	OXIDOREDUCTASE	F	1.0	1.0	1	9	HMNVLLAEA	21325
1XME	AC	OXIDOREDUCTASE	A	1.0	1.0	1	22	AWVPGHFHLQVASLVTLTAMGS	21326
1XOU	AB	STRUCTURAL PROTEIN/CHAPERONE	A	1.0	1.0	1	15	NLTTTVNNSQLEIQQ	21327
1XPK	DC	TRANSFERASE	D	1.0	1.0	1	24	GALSKDAYIRSFQQSWNEYAKRQG	21328
1XQ5	AD	OXYGEN STORAGE/TRANSPORT	A	1.0	1.0	1	19	PANFKILSHCILVLLAVKF	21329
1XRS	AB	ISOMERASE	A	1.0	1.0	1	18	IFKGHIQDALFNMVTIMT	21330
1XTC	AH	TOXIN	A	1.0	1.0	1	8	PDEIKQSG	21331
1XTC	CH	TOXIN	H	1.0	1.0	1	17	KKAIERMKDTLRIAYLT	21332
1XTG	AB	TOXIN	A	1.0	1.0	1	12	LQYMKNVFKEKY	21333
1XV9	CG	DNA BINDING PROTEIN	C	1.0	1.0	1	10	LFTLVEWAKR	21334
1XV9	DH	DNA BINDING PROTEIN	D	1.0	1.0	1	25	VLPLVTHFADINTFMVLQVIKFTKD	21335
1XXH	AB	TRANSFERASE	A	1.0	1.0	1	15	LLALAQALERLSLLW	21336
1XXH	DE	TRANSFERASE	E	1.0	1.0	1	5	PSRLQ	21337
1XXI	AB	TRANSFERASE	B	1.0	1.0	1	21	WEALLVEMLGLLHRIAMVQLS	21338
1XXI	AB	TRANSFERASE	B	1.0	1.0	1	21	PTDIQLYYQTLLIGRKELPYA	21339
1XXI	AE	TRANSFERASE	A	1.0	1.0	1	15	TLQRELLLLVNLKRQ	21340
1Y74	AD	TRANSPORT PROTEIN	D	1.0	1.0	1	18	PHFMALLQTHDVVAHEVY	21341
1Y74	CB	TRANSPORT PROTEIN	B	1.0	1.0	1	10	NDAKELKRIL	21342
1Y76	AD	TRANSPORT PROTEIN	D	1.0	1.0	1	20	KDFQNAFKIHNAITVHMNKA	21343
1Y8H	CD	OXYGEN STORAGE/TRANSPORT	C	1.0	1.0	1	19	PVNFKLLSHCLLSTLAVHL	21344
1Y8R	AB	LIGASE	A	1.0	1.0	1	5	DRQIR	21345
1YA7	AN	HYDROLASE/HYDROLASE ACTIVATOR	A	1.0	1.0	1	22	VADARVLVDFARISAQQEKVTY	21346
1YA7	CI	HYDROLASE/HYDROLASE ACTIVATOR	C	1.0	1.0	1	23	VADARVLVDFARISAQQEKVTYG	21347
1YA7	DU	HYDROLASE/HYDROLASE ACTIVATOR	D	1.0	1.0	1	13	FQVEYAREAVKKG	21348
1YBQ	AB	HYDROLASE	A	1.0	1.0	1	8	VEKDVAII	21349
1YBQ	AB	HYDROLASE	B	1.0	1.0	1	15	PESLLAKTRALNEEG	21350
1YCS	AB	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)	A	1.0	1.0	1	10	PGRDRRTEEE	21351
1YE9	BE	OXIDOREDUCTASE	B	1.0	1.0	1	9	FPDFVHAVK	21352
1YE9	CF	OXIDOREDUCTASE	C	1.0	1.0	1	12	FILREKITHFDH	21353
1YE9	JN	OXIDOREDUCTASE	N	1.0	1.0	1	7	FFAENEQ	21354

1YED	LH	CATALYTIC ANTIBODY	L	1.0	1.0	1	6	SEQLTS	21355
1YEW	BC	OXIDOREDUCTASE, MEMBRANE PROTEIN	C	1.0	1.0	1	19	LSYPIYIITGFAAFIYAKT	21356
1YEW	FG	OXIDOREDUCTASE, MEMBRANE PROTEIN	G	1.0	1.0	1	19	LSYPIYIITGFAAFIYAKT	21357
1YHU	AC	OXYGEN STORAGE/TRANSPORT	A	1.0	1.0	1	20	IGAARSKFGDALWRNVFNYA	21358
1YHU	BD	OXYGEN STORAGE/TRANSPORT	B	1.0	1.0	1	16	EPVLNTQLAHLAKQHE	21359
1YHU	BD	OXYGEN STORAGE/TRANSPORT	D	1.0	1.0	1	18	GRRIAIAQAVFKDLFANV	21360
1YHU	EG	OXYGEN STORAGE/TRANSPORT	E	1.0	1.0	1	20	IGAARSKFGDALWRNVFNYA	21361
1YHU	FH	OXYGEN STORAGE/TRANSPORT	F	1.0	1.0	1	16	EPVLNTQLAHLAKQHE	21362
1YHU	IK	OXYGEN STORAGE/TRANSPORT	I	1.0	1.0	1	20	IGAARSKFGDALWRNVFNYA	21363
1YHU	JL	OXYGEN STORAGE/TRANSPORT	J	1.0	1.0	1	16	EPVLNTQLAHLAKQHE	21364
1YHU	JL	OXYGEN STORAGE/TRANSPORT	L	1.0	1.0	1	17	PATLNEQLSHLATQHKA	21365
1YHU	NP	OXYGEN STORAGE/TRANSPORT	P	1.0	1.0	1	17	PATLNEQLSHLATQHKA	21366
1YHU	QS	OXYGEN STORAGE/TRANSPORT	Q	1.0	1.0	1	20	IGAARSKFGDALWRNVFNYA	21367
1YHU	QS	OXYGEN STORAGE/TRANSPORT	S	1.0	1.0	1	19	AASRVSAGEEVFAALFKMV	21368
1YHU	RT	OXYGEN STORAGE/TRANSPORT	R	1.0	1.0	1	16	EPVLNTQLAHLAKQHE	21369
1YHU	UW	OXYGEN STORAGE/TRANSPORT	U	1.0	1.0	1	20	IGAARSKFGDALWRNVFNYA	21370
1YHU	VW	OXYGEN STORAGE/TRANSPORT	V	1.0	1.0	1	15	PLQRLKVKRQWAEAY	21371
1YHU	VW	OXYGEN STORAGE/TRANSPORT	W	1.0	1.0	1	15	DAAAAIVQAQWEDVW	21372
1YKK	AB	OXIDOREDUCTASE	A	1.0	1.0	1	5	VHIGL	21373
1YKK	CD	OXIDOREDUCTASE	C	1.0	1.0	1	5	VHIGL	21374
1YM0	AB	HYDROLASE	A	1.0	1.0	1	10	AGWITDTITN	21375
1YMM	AC	IMMUNE SYSTEM	A	1.0	1.0	1	22	AQGALANIAVDKANLEIMTKRS	21376
1YNJ	CD	TRANSFERASE	C	1.0	1.0	1	7	PLGVPSR	21377
1YR5	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.0	1.0	1	11	FPEFLTMMARK	21378
1YU6	BD	HYDROLASE	B	1.0	1.0	1	10	HGTHVAGTVA	21379
1YV0	TI	CONTRACTILE PROTEIN	T	1.0	1.0	1	8	QTEKYDFA	21380
1YYL	LH	VIRAL PROTEIN/IMMUNE SYSTEM	L	1.0	1.0	1	5	DEQLK	21381
1Z00	AB	HYDROLASE	B	1.0	1.0	1	11	AKNCRSLMHHV	21382
1Z0K	AB	PROTEIN TRANSPORT	A	1.0	1.0	1	9	RSVTRSYYR	21383
1Z0K	CB	PROTEIN TRANSPORT	B	1.0	1.0	1	22	MDEVRTLQENLRQLQDEYDQQQ	21384
1Z56	AC	LIGASE	C	1.0	1.0	1	10	IEMKIKLFGG	21385
1Z6O	DR	METAL BINDING PROTEIN	R	1.0	1.0	1	13	EALGEFIFDKKLL	21386
1Z6O	LV	METAL BINDING PROTEIN	V	1.0	1.0	1	13	EALGEFIFDKKLL	21387
1Z7Q	BJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.0	1.0	1	22	ATDVTTLNEMFRYKTNLYKLKE	21388
1Z7Q	DK	HYDROLASE/HYDROLASE ACTIVATOR	D	1.0	1.0	1	21	NADSRILIEKARVEAQSHRLT	21389
1Z7Q	FN	HYDROLASE/HYDROLASE ACTIVATOR	N	1.0	1.0	1	20	ISDMQHIERLLKDLVTENAY	21390
1Z7Q	Gg	HYDROLASE/HYDROLASE ACTIVATOR	G	1.0	1.0	1	22	IPDGRHLVNRGREEAASFKKLY	21391

1Z7Q	Hb	HYDROLASE/HYDROLASE ACTIVATOR	b	1.0	1.0	1	18	VQVAEEAIVNAMRVLYYR	21392
1Z7Q	IJ	HYDROLASE/HYDROLASE ACTIVATOR	J	1.0	1.0	1	15	PETFTQLVSSSLYER	21393
1Z7Q	PW	HYDROLASE/HYDROLASE ACTIVATOR	P	1.0	1.0	1	14	GPDYRVLVDKSRKV	21394
1Z7Q	QX	HYDROLASE/HYDROLASE ACTIVATOR	Q	1.0	1.0	1	22	TADAEILINTARIHAQNYLKTY	21395
1Z7Q	RS	HYDROLASE/HYDROLASE ACTIVATOR	S	1.0	1.0	1	23	TADARSMIEHARTAAVTHNLYYD	21396
1Z7Q	Tb	HYDROLASE/HYDROLASE ACTIVATOR	b	1.0	1.0	1	17	PSYIFEYLATVMYQRRS	21397
1Z7Q	Tb	HYDROLASE/HYDROLASE ACTIVATOR	T	1.0	1.0	1	5	SLVFN	21398
1Z7Q	XM	HYDROLASE/HYDROLASE ACTIVATOR	X	1.0	1.0	1	9	SDQLFGMCE	21399
1Z7Q	XM	HYDROLASE/HYDROLASE ACTIVATOR	X	1.0	1.0	1	18	PEDLFETISQALLNAADR	21400
1Z7S	13	VIRUS	1	1.0	1.0	1	5	PSDVV	21401
1Z7S	14	VIRUS	1	1.0	1.0	1	5	LESFF	21402
1Z8Y	IJ	VIRUS	I	1.0	1.0	1	5	GLMIF	21403
1Z8Y	KL	VIRUS	K	1.0	1.0	1	5	GLMIF	21404
1Z8Y	MN	VIRUS	M	1.0	1.0	1	5	GLMIF	21405
1Z8Y	OP	VIRUS	O	1.0	1.0	1	5	GLMIF	21406
1ZA6	CD	IMMUNE SYSTEM	C	1.0	1.0	1	7	DEQLKSG	21407
1ZBB	AG	STRUCTURAL PROTEIN/DNA	G	1.0	1.0	1	10	PRHLQLAVRN	21408
1ZBB	CD	STRUCTURAL PROTEIN/DNA	C	1.0	1.0	1	5	RSSRA	21409
1ZGL	ES	IMMUNE SYSTEM	E	1.0	1.0	1	8	DFLEDRRA	21410
1ZGL	ET	IMMUNE SYSTEM	E	1.0	1.0	1	8	RPDAEYWN	21411
1ZGL	GI	IMMUNE SYSTEM	G	1.0	1.0	1	20	GALANIAVDKANLEIMTKRS	21412
1ZOY	AB	OXIDOREDUCTASE	A	1.0	1.0	1	26	TDLVETLELQNLMLCALQTIYGAEAR	21413
1ZRT	QR	OXIDOREDUCTASE/METAL TRANSPORT	R	1.0	1.0	1	27	RDFLYHATAATGVVVTGAAVWPLINQM	21414
1ZT2	AB	REPLICATION, TRANSFERASE	A	1.0	1.0	1	12	SDERKEIAEYVM	21415
1ZUD	12	TRANSFERASE/BIOSYNTHETIC PROTEIN	1	1.0	1.0	1	5	YRCLW	21416
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.0	1.0	1	15	EEQIAEFKEAFSLFD	21417
1ZUZ	AB	METAL BINDING PROTEIN/TRANSFERASE	A	1.0	1.0	1	11	FPEFLTMMARK	21418
1ZV8	IF	VIRAL PROTEIN	F	1.0	1.0	1	17	QKEIDRLNEVAKNLNES	21419
1ZVV	GJ	TRANSCRIPTION/DNA	G	1.0	1.0	1	14	AELARGIEDIASMY	21420
1ZY3	AB	APOPTOSIS	A	1.0	1.0	1	9	TFSDLAAQL	21421
2A1T	RS	OXIDOREDUCTASE/ELECTRON TRANSPORT	S	1.0	1.0	1	15	PLQVARVLAKLAEKE	21422
2A40	AC	STRUCTURAL PROTEIN	A	1.0	1.0	1	12	SVWIGGSILASL	21423
2A40	DE	STRUCTURAL PROTEIN	E	1.0	1.0	1	11	VAVGKLLDYLN	21424
2A45	JK	BLOOD CLOTTING	K	1.0	1.0	1	6	LNNNVE	21425

2A5T	AB	METAL TRANSPORT,MEMBRANE PROTEIN	A	1.0	1.0	1	9	SVDIYFRRQ	21426
2A79	AB	MEMBRANE PROTEIN	B	1.0	1.0	1	7	PKKRMRY	21427
2ACL	AB	TRANSCRIPTION	A	1.0	1.0	1	18	GAIFDRVLTELVSKMRDM	21428
2ACL	AF	TRANSCRIPTION	A	1.0	1.0	1	23	PVTNICQAADKQLFTLVEWAKRI	21429
2ACL	AF	TRANSCRIPTION	A	1.0	1.0	1	11	LDDQVILLRAG	21430
2ACL	CD	TRANSCRIPTION	C	1.0	1.0	1	18	GAIFDRVLTELVSKMRDM	21431
2ACL	CD	TRANSCRIPTION	C	1.0	1.0	1	7	RFAKLLL	21432
2ACL	EF	TRANSCRIPTION	E	1.0	1.0	1	7	RFAKLLL	21433
2ACL	EF	TRANSCRIPTION	F	1.0	1.0	1	7	PLLSEIW	21434
2ACL	GD	TRANSCRIPTION	G	1.0	1.0	1	11	LDDQVILLRAG	21435
2ACL	GH	TRANSCRIPTION	G	1.0	1.0	1	6	FLMEML	21436
2ACZ	CD	OXIDOREDUCTASE/ELECTRON TRANSPORT	D	1.0	1.0	1	27	GVHDFILVRATAIVLTLYIIYMVGFFA	21437
2AFH	AB	OXIDOREDUCTASE	A	1.0	1.0	1	8	ISEIELTP	21438
2AFH	AB	OXIDOREDUCTASE	A	1.0	1.0	1	16	FDGFAIFARDMDMTLN	21439
2AFH	AD	OXIDOREDUCTASE	D	1.0	1.0	1	16	LDWTDEFLMKVSEISG	21440
2AFH	BF	OXIDOREDUCTASE	B	1.0	1.0	1	13	KRWKKAVDAILAA	21441
2AFH	CD	OXIDOREDUCTASE	C	1.0	1.0	1	8	ISEIELTP	21442
2AK4	FJ	IMMUNE SYSTEM	F	1.0	1.0	1	29	PEYWDRNTQIFKTNTQTYRESLRNLRGYY	21443
2AKA	AB	CONTRACTILE PROTEIN	A	1.0	1.0	1	16	QLARIEEAREQRISEI	21444
2AP2	CQ	IMMUNE SYSTEM	Q	1.0	1.0	1	12	VQEALDKAREGR	21445
2ARJ	LH	IMMUNE SYSTEM	L	1.0	1.0	1	6	MEQLTS	21446
2AST	AB	CELL CYCLE/LIGASE/PROTEIN TURNOVER	A	1.0	1.0	1	10	EEEAQVRKEN	21447
2AUH	AB	TRANSFERASE/SIGNALING PROTEIN	A	1.0	1.0	1	11	NEQVLKFVMDG	21448
2AXT	BD	ELECTRON TRANSPORT	D	1.0	1.0	1	21	FYTKNLLLNEGIRAWMAPQDQ	21449
2AXT	bT	ELECTRON TRANSPORT	b	1.0	1.0	1	25	FEGVALAHIVLSGLLFLAACWHWVY	21450
2AXT	CV	ELECTRON TRANSPORT	V	1.0	1.0	1	6	PKMRNL	21451
2AXT	de	ELECTRON TRANSPORT	e	1.0	1.0	1	12	AKQQVETFLEQL	21452
2AXT	DF	ELECTRON TRANSPORT	D	1.0	1.0	1	20	LLFPCAYLALGGWLTGTTFV	21453
2AXT	df	ELECTRON TRANSPORT	d	1.0	1.0	1	14	YLALGGWLTGTTFV	21454
2AXT	DH	ELECTRON TRANSPORT	D	1.0	1.0	1	10	WFDILDDWLK	21455
2AXT	dh	ELECTRON TRANSPORT	d	1.0	1.0	1	10	WFDILDDWLK	21456
2AXT	DL	ELECTRON TRANSPORT	D	1.0	1.0	1	17	PFHMMGVAGVLGGALLC	21457
2AXT	dl	ELECTRON TRANSPORT	d	1.0	1.0	1	17	PFHMMGVAGVLGGALLC	21458
2AXT	DV	ELECTRON TRANSPORT	D	1.0	1.0	1	21	FYTKNLLLNEGIRAWMAPQDQ	21459
2AXT	dv	ELECTRON TRANSPORT	d	1.0	1.0	1	21	FYTKNLLLNEGIRAWMAPQDQ	21460
2AZE	AB	CELL CYCLE, TRANSCRIPTION	A	1.0	1.0	1	9	EPYVTEMAQ	21461

2AZE	AC	CELL CYCLE, TRANSCRIPTION	A	1.0	1.0	1	48	AQECQNLEVERQRRLERIKQKQSQLQELILQQIAFKNLVQRNRHAEQQ	21462
2BE7	BE	TRANSFERASE	B	1.0	1.0	1	7	AARLASE	21463
2BEX	AC	HYDROLASE/INHIBITOR	C	1.0	1.0	1	12	CTNAMQVINNYQ	21464
2BG9	AB	ION CHANNEL/RECEPTOR	B	1.0	1.0	1	27	SLSISALLALTVFLLLLADKVPETSLS	21465
2BL0	AB	MUSCLE PROTEIN	B	1.0	1.0	1	11	SKEMLDAFRAL	21466
2BOV	AB	TRANSFERASE	B	1.0	1.0	1	16	IDQAKAWGNAQYKKYG	21467
2BR2	ST	HYDROLASE	T	1.0	1.0	1	18	RREIELSKVIREALESAV	21468
2BRU	BC	OXIDOREDUCTASE	B	1.0	1.0	1	7	SRAQSLD	21469
2BSK	CD	PROTEIN TRANSPORT	C	1.0	1.0	1	19	KEFLGTYNKLTETCFLDCV	21470
2BSK	CF	PROTEIN TRANSPORT	F	1.0	1.0	1	6	AELEVE	21471
2BV8	AB	PHOTOSYNTHESIS	A	1.0	1.0	1	10	TGPMDEYLIA	21472
2BV8	AF	PHOTOSYNTHESIS	A	1.0	1.0	1	8	LSEINRSF	21473
2BV8	AF	PHOTOSYNTHESIS	A	1.0	1.0	1	24	ATGKAKCARDIGYYLRMVTYCLVV	21474
2BV8	ML	PHOTOSYNTHESIS	M	1.0	1.0	1	24	ATGKAKCARDIGYYLRMVTYCLVV	21475
2BWE	KT	SIGNALING PROTEIN	K	1.0	1.0	1	11	FDRNVAALRRS	21476
2CCI	CD	CELL CYCLE	C	1.0	1.0	1	12	STAIREISLLKE	21477
2CLY	AB	HYDROLASE	A	1.0	1.0	1	39	EFADKLNEQKIAQLEEVKQASIKQIQDAIDMEKSQQALV	21478
2CLY	AC	HYDROLASE	C	1.0	1.0	1	14	LFVDKIREYRTKRQ	21479
2CLY	DE	HYDROLASE	E	1.0	1.0	1	14	AQVDAEEKEDVKSC	21480
2CMR	HA	IMMUNE SYSTEM	A	1.0	1.0	1	40	QLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILA	21481
2CZV	AC	HYDROLASE	A	1.0	1.0	1	6	LRPLLY	21482
2CZV	AD	HYDROLASE	D	1.0	1.0	1	8	ETGTAIVK	21483
2D1P	EF	TRANSLATION	E	1.0	1.0	1	7	AASLRER	21484
2D1P	HF	TRANSLATION	F	1.0	1.0	1	8	RYLESLRN	21485
2D7D	AB	HYDROLASE/DNA	A	1.0	1.0	1	21	KKERQKVVEQMEHEMKEAAKA	21486
2DBU	CD	TRANSFERASE	C	1.0	1.0	1	12	TVAGFSLALDKY	21487
2DD4	DF	HYDROLASE	D	1.0	1.0	1	6	AEDEAF	21488
2DD4	GI	HYDROLASE	I	1.0	1.0	1	5	WVTSP	21489
2DD4	HI	HYDROLASE	I	1.0	1.0	1	8	PRQVLAEF	21490
2DD4	JL	HYDROLASE	L	1.0	1.0	1	5	WVTSP	21491
2DFK	CB	CELL CYCLE	C	1.0	1.0	1	7	GPCFLEH	21492
2DFS	AF	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	F	1.0	1.0	1	9	AAELRHVMT	21493
2DFS	MR	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	M	1.0	1.0	1	29	LARVHYHRTLKAIVYLQCCYRRMMAKREL	21494
2DFS	MS	CONTRACTILE PROTEIN/TRANSPORT PROTEIN	S	1.0	1.0	1	7	EAELQDM	21495
2DOQ	AD	CELL CYCLE	A	1.0	1.0	1	11	IKNLRRVAKEL	21496
2DPP	AB	LYASE	B	1.0	1.0	1	16	YYGHWIATVAYNLVDT	21497

2DSR	GI	PROTEIN BINDING/HORMONE/GROWTH FACTOR	G	1.0	1.0	1	7	HEDLYII	21498
2DWZ	CD	ONCOPROTEIN	C	1.0	1.0	1	8	AMHRAAAK	21499
2DXB	AC	HYDROLASE	A	1.0	1.0	1	5	AEDEA	21500
2DXB	AC	HYDROLASE	C	1.0	1.0	1	5	WVTSP	21501
2DXB	DF	HYDROLASE	F	1.0	1.0	1	5	WVTSP	21502
2DXB	GI	HYDROLASE	G	1.0	1.0	1	6	AEDEAF	21503
2DXB	GI	HYDROLASE	I	1.0	1.0	1	5	WVTSP	21504
2DXB	JL	HYDROLASE	J	1.0	1.0	1	5	AEDEA	21505
2DXB	JL	HYDROLASE	L	1.0	1.0	1	5	WVTSP	21506
2DXB	PR	HYDROLASE	R	1.0	1.0	1	5	WVTSP	21507
2DXB	VX	HYDROLASE	X	1.0	1.0	1	5	WVTSP	21508
2DZN	AB	PROTEIN BINDING	A	1.0	1.0	1	9	PFHIACSVG	21509
2DZN	EF	PROTEIN BINDING	E	1.0	1.0	1	9	PFHIACSVG	21510
2E 30	AB	METAL BINDING PROTEIN/TRANSPORT PROTEIN	A	1.0	1.0	1	12	SFTEFVKVLEKV	21511
2E 74	BG	PHOTOSYNTHESIS	B	1.0	1.0	1	22	PVATTIFLFGTLVTIWLGIGAT	21512
2E3X	BC	HYDROLASE, BLOOD CLOTTING, TOXIN	B	1.0	1.0	1	9	WEAAERFCM	21513
2E9X	EF	REPLICATION	F	1.0	1.0	1	9	AAEVEFLAE	21514
2E9X	EH	REPLICATION	H	1.0	1.0	1	17	PEIVECVMEQLEHMEEN	21515
2EC6	AB	CONTRACTILE PROTEIN	B	1.0	1.0	1	6	RFVAMI	21516
2EC6	AC	CONTRACTILE PROTEIN	A	1.0	1.0	1	5	GYLIR	21517
2EFC	AB	TRANSPORT PROTEIN	A	1.0	1.0	1	26	PRDKLVCILNCCKVINNLLLNASIAS	21518
2EHO	BD	REPLICATION	D	1.0	1.0	1	8	LWLAKGLF	21519
2EHO	IJ	REPLICATION	J	1.0	1.0	1	10	EDGLRQVLEE	21520
2EKV	AB	CONTRACTILE PROTEIN	B	1.0	1.0	1	10	DALRNAFSMF	21521
2EKV	AC	CONTRACTILE PROTEIN	C	1.0	1.0	1	11	SAEIRNVLKML	21522
2EQ7	BC	OXIDOREDUCTASE	C	1.0	1.0	1	7	KEDVMRH	21523
2ES4	AD	HYDROLASE	D	1.0	1.0	1	20	PAAMQLALDQRAALADRTLG	21524
2ES4	BE	HYDROLASE	B	1.0	1.0	1	16	PSTLALLATGAVMINR	21525
2ESV	AE	IMMUNE SYSTEM	A	1.0	1.0	1	30	SEYWDRETRSARDTAQIFRVNLRTLRGYYN	21526
2F43	AB	HYDROLASE	B	1.0	1.0	1	23	SEHYDVARGVQKILQDYKSLQDI	21527
2F54	AE	IMMUNE SYSTEM	A	1.0	1.0	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	21528
2F66	AC	TRANSPORT PROTEIN	C	1.0	1.0	1	29	KYGDIALKKKLEQNTKKLDEESSQLETTT	21529
2F8N	BD	STRUCTURAL PROTEIN/DNA	B	1.0	1.0	1	10	AMDVVYALKR	21530
2F8N	FD	STRUCTURAL PROTEIN/DNA	D	1.0	1.0	1	29	SKAMGIMNSFVNDIFERIASEASRLAHYN	21531
2F9D	AP	RNA BINDING PROTEIN	A	1.0	1.0	1	12	IFDAKNACDHLS	21532
2F9I	AD	TRANSFERASE	D	1.0	1.0	1	7	AEFLLEH	21533

2F9I	CB	TRANSFERASE	C	1.0	1.0	1	17	PEGYRKALRLMKQAEKF	21534
2FBW	OP	OXIDOREDUCTASE	P	1.0	1.0	1	30	PALIYSAKFALVFPLSYHTWNGIRHLVWDM	21535
2FEW	AB	TRANSFERASE	A	1.0	1.0	1	14	PEYVQAMLDREKLT	21536
2FEW	AB	TRANSFERASE	B	1.0	1.0	1	16	SSAMGAGVLRKKIQDA	21537
2FHH	DR	HYDROLASE	D	1.0	1.0	1	22	FNEFDNLRRGGIQFADTRGYAY	21538
2FHH	KE	HYDROLASE	E	1.0	1.0	1	23	AAVAVEFARLYAVELEHYEKLEG	21539
2FHH	QZ	HYDROLASE	Z	1.0	1.0	1	14	FAGKINRLAIMVRG	21540
2FJ7	AG	STRUCTURAL PROTEIN/DNA	A	1.0	1.0	1	29	SSAVMALQEASEAYLVALFEDTNLCAIHA	21541
2FJ7	GH	STRUCTURAL PROTEIN/DNA	G	1.0	1.0	1	10	PRHLQLAVRN	21542
2FJF	GI	IMMUNE SYSTEM	G	1.0	1.0	1	6	DEQLKS	21543
2FJF	ST	IMMUNE SYSTEM	S	1.0	1.0	1	5	DEQLK	21544
2FKW	AD	MEMBRANE PROTEIN, PHOTOSYNTHESIS	D	1.0	1.0	1	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	21545
2FKW	CF	MEMBRANE PROTEIN, PHOTOSYNTHESIS	F	1.0	1.0	1	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	21546
2FKW	OS	MEMBRANE PROTEIN, PHOTOSYNTHESIS	S	1.0	1.0	1	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	21547
2FKW	RB	MEMBRANE PROTEIN, PHOTOSYNTHESIS	B	1.0	1.0	1	32	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA	21548
2FL5	AB	IMMUNE SYSTEM	A	1.0	1.0	1	6	SEELQA	21549
2FL5	EF	IMMUNE SYSTEM	E	1.0	1.0	1	6	SEELQA	21550
2FM8	AC	CHAPERONE/CELL INVASION	A	1.0	1.0	1	13	IAELVRSALEVSG	21551
2FMM	EC	TRANSCRIPTION	E	1.0	1.0	1	14	TERHRAEVRRAVND	21552
2FO1	DE	GENE REGULATION/SIGNALLING PROTEIN/DNA	D	1.0	1.0	1	6	AFHSGE	21553
2FO1	DE	GENE REGULATION/SIGNALLING PROTEIN/DNA	E	1.0	1.0	1	7	RRLVAYL	21554
2FSE	CF	IMMUNE SYSTEM, STRUCTURAL PROTEIN	C	1.0	1.0	1	19	AQGALANIAVDKANLEIMT	21555
2FSE	DF	IMMUNE SYSTEM, STRUCTURAL PROTEIN	D	1.0	1.0	1	12	YCRHNYGVGESF	21556
2FTK	AE	TRANSFERASE	E	1.0	1.0	1	12	GLQALDIVTKER	21557
2FUG	12	OXIDOREDUCTASE	2	1.0	1.0	1	12	IMPLLRRVQQEE	21558
2FUG	12	OXIDOREDUCTASE	2	1.0	1.0	1	13	AEELWDYLTETLG	21559
2FUG	49	OXIDOREDUCTASE	9	1.0	1.0	1	6	LCAAAC	21560
2FUG	AB	OXIDOREDUCTASE	B	1.0	1.0	1	11	QDFLEETFAKY	21561
2FUG	AC	OXIDOREDUCTASE	A	1.0	1.0	1	19	TPCREGVAGFMVNLFAKIG	21562
2FUG	MP	OXIDOREDUCTASE	P	1.0	1.0	1	6	LCAAAC	21563
2FUG	ST	OXIDOREDUCTASE	T	1.0	1.0	1	11	QDFLEETFAKY	21564

2FV4	AB	STRUCTURAL PROTEIN, PROTEIN BINDING	A	1.0	1.0	1	13	DAAEVALYERLLQ	21565
2FYN	AB	OXIDOREDUCTASE	A	1.0	1.0	1	22	PMFKIYFWLLAADFVILTWVGA	21566
2FYN	GH	OXIDOREDUCTASE	H	1.0	1.0	1	5	ISQLF	21567
2FYN	GI	OXIDOREDUCTASE	I	1.0	1.0	1	22	YATAGAGAVATGAAVWPLINQM	21568
2FYN	PR	OXIDOREDUCTASE	R	1.0	1.0	1	23	YATAGAGAVATGAAVWPLINQMN	21569
2G2R	LH	IMMUNE SYSTEM	L	1.0	1.0	1	7	SEQLTSG	21570
2G3Q	AB	ENDOCYTOSIS/SIGNALING PROTEIN	A	1.0	1.0	1	11	LEAATNFLLDS	21571
2G5B	AB	APOPTOSIS	A	1.0	1.0	1	6	SEQLTS	21572
2G5B	CD	APOPTOSIS	C	1.0	1.0	1	6	SEQLTS	21573
2G60	LH	IMMUNE SYSTEM	L	1.0	1.0	1	7	SEQLTSG	21574
2G75	CD	IMMUNE SYSTEM	D	1.0	1.0	1	5	SEEFQ	21575
2G9H	AB	IMMUNE SYSTEM	B	1.0	1.0	1	22	KDLLEQRRAAVDTYCRHNYGVG	21576
2GAG	BD	OXIDOREDUCTASE	D	1.0	1.0	1	9	DKQWSRYLF	21577
2GBW	CD	OXIDOREDUCTASE	C	1.0	1.0	1	8	GYHVGWTH	21578
2GCO	AB	SIGNALING PROTEIN	B	1.0	1.0	1	14	VREVFEMATRAGLQ	21579
2GEZ	GF	HYDROLASE	F	1.0	1.0	1	7	GEEIIRA	21580
2GFB	EB	IMMUNOGLOBULIN	E	1.0	1.0	1	5	KDEYE	21581
2GGM	BC	CELL CYCLE	C	1.0	1.0	1	16	WKLLAKGLLIRERLKR	21582
2GGP	AB	CHAPERONE, METAL TRANSPORT	B	1.0	1.0	1	12	SACTNTINTQLR	21583
2GHO	AC	TRANSFERASE	A	1.0	1.0	1	10	VEIILNLKEL	21584
2GHO	BD	TRANSFERASE	D	1.0	1.0	1	13	PGRILFARIVGEA	21585
2GID	PK	TRANSLATION	P	1.0	1.0	1	5	VAESL	21586
2GKV	EA	HYDROLASE/HYDROLASE INHIBITOR	E	1.0	1.0	1	5	GHCTD	21587
2GL7	AC	TRANSCRIPTION	A	1.0	1.0	1	19	QDDAELATRAIPELTKLLN	21588
2GOO	AB	TRANSFERASE	B	1.0	1.0	1	7	SDFQCKD	21589
2GOX	AB	CELL ADHESION/TOXIN	B	1.0	1.0	1	18	KVKKMVLQERIDNVLKQG	21590
2GOX	CD	CELL ADHESION/TOXIN	C	1.0	1.0	1	21	LEKRQGALELIKKGYTQQLAF	21591
2GPV	BH	TRANSCRIPTION	B	1.0	1.0	1	13	WMEILILGVVYRS	21592
2GPV	CI	TRANSCRIPTION	C	1.0	1.0	1	11	LADQMSLLQSA	21593
2GTL	AD	OXYGEN STORAGE/TRANSPORT	A	1.0	1.0	1	16	LVLQSHLGHLADQHIQ	21594
2GTL	BC	OXYGEN STORAGE/TRANSPORT	B	1.0	1.0	1	16	PATLKEELDHLQVQHE	21595
2GTL	EN	OXYGEN STORAGE/TRANSPORT	E	1.0	1.0	1	12	YEDRREIRHIWD	21596
2GTL	FG	OXYGEN STORAGE/TRANSPORT	F	1.0	1.0	1	16	VLEGLKVKSEWGRAYG	21597
2GTL	MO	OXYGEN STORAGE/TRANSPORT	M	1.0	1.0	1	15	KKTIRQLKARISNLE	21598
2GUZ	AB	CHAPERONE, PROTEIN TRANSPORT	B	1.0	1.0	1	8	LDESCKIL	21599
2GUZ	AF	CHAPERONE, PROTEIN TRANSPORT	F	1.0	1.0	1	15	MDKINNRFNYLFEVN	21600
2GUZ	CD	CHAPERONE, PROTEIN TRANSPORT	C	1.0	1.0	1	8	SKEALQIL	21601
2GUZ	IJ	CHAPERONE, PROTEIN TRANSPORT	I	1.0	1.0	1	8	SKEALQIL	21602
2GUZ	KL	CHAPERONE, PROTEIN TRANSPORT	K	1.0	1.0	1	15	KKKLKEVHRKIMLAN	21603

2GV5	BC	CELL CYCLE	B	1.0	1.0	1	9	ENEFIAICT	21604
2GV5	BC	CELL CYCLE	B	1.0	1.0	1	7	YHELKVA	21605
2GV5	EF	CELL CYCLE	E	1.0	1.0	1	7	YHELKVA	21606
2GWF	EF	HYDROLASE/LIGASE	F	1.0	1.0	1	7	RRYYENY	21607
2H1L	HT	VIRAL PROTEIN	T	1.0	1.0	1	11	PGRDRRTEEEN	21608
2H1O	DH	GENE REGULATION/DNA COMPLEX	D	1.0	1.0	1	13	AITVAEMRLGVAL	21609
2H4C	CD	HYDROLASE	D	1.0	1.0	1	10	FQFARLIDAK	21610
2H4C	CD	HYDROLASE	D	1.0	1.0	1	15	ATDRCCFVHDCCYAR	21611
2H4M	AC	PROTEIN TRANSPORT	A	1.0	1.0	1	18	PEVRQSSFALLGDLTKAC	21612
2H4M	BD	PROTEIN TRANSPORT	B	1.0	1.0	1	15	LFPLLECLSSVATAL	21613
2H4M	BD	PROTEIN TRANSPORT	B	1.0	1.0	1	18	KTLLENTAITIGRLGYVC	21614
2H4Q	AB	HYDROLASE INHIBITOR	A	1.0	1.0	1	9	YERLSEWAD	21615
2H61	AD	METAL BINDING PROTEIN, SIGNALING PROTEIN	D	1.0	1.0	1	19	FQEFMAFVAMVTTACHEFF	21616
2H61	BD	METAL BINDING PROTEIN, SIGNALING PROTEIN	B	1.0	1.0	1	18	ELEKAMVALIDVFHQYSG	21617
2H61	FG	METAL BINDING PROTEIN, SIGNALING PROTEIN	F	1.0	1.0	1	20	FQEFMAFVAMVTTACHEFFE	21618
2HGR	FQ	RIBOSOME	Q	1.0	1.0	1	11	RICLRELAHKG	21619
2HH0	LH	IMMUNE SYSTEM	L	1.0	1.0	1	7	DEQLKSG	21620
2HIO	BD	STRUCTURAL PROTEIN,DNA BINDING PROTEIN	D	1.0	1.0	1	11	AMDVVYALKRQ	21621
2HJ9	AC	SIGNALING PROTEIN	C	1.0	1.0	1	15	TDVLNFFFLSIDQSD	21622
2HLD	AG	HYDROLASE	G	1.0	1.0	1	65	FEYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITGA	21623
2HLD	BF	HYDROLASE	F	1.0	1.0	1	14	TREGNDLYREMKET	21624
2HLD	CF	HYDROLASE	F	1.0	1.0	1	9	PAPATTFAH	21625
2HLD	CF	HYDROLASE	F	1.0	1.0	1	20	QEHYDVASKVQETLQTYKSL	21626
2HLD	HI	HYDROLASE	I	1.0	1.0	1	12	YAAYLNVAAQAI	21627
2HLD	JM	HYDROLASE	M	1.0	1.0	1	20	QEHYDVASKVQETLQTYKSL	21628
2HLD	SV	HYDROLASE	S	1.0	1.0	1	7	AELFYKG	21629
2HLD	SV	HYDROLASE	V	1.0	1.0	1	8	QDIIAILG	21630
2HLD	TX	HYDROLASE	X	1.0	1.0	1	22	PGARARVALTGLTIAEYFRDEE	21631
2HLD	UV	HYDROLASE	V	1.0	1.0	1	6	RGISEL	21632
2HLD	UX	HYDROLASE	X	1.0	1.0	1	8	PAPATTFA	21633
2HLD	WY	HYDROLASE	Y	1.0	1.0	1	63	EYTLANQMLTAMAQGYAAEISARRNAMDNASKNAGDMINRYSILYNRTRQAVITNELVDIITG	21634
2HOD	AC	BLOOD CLOTTING	A	1.0	1.0	1	8	DIDIKIRS	21635
2HOD	DE	BLOOD CLOTTING	D	1.0	1.0	1	13	YEDQQKQLEQVIA	21636
2HYB	GH	TRANSFERASE	H	1.0	1.0	1	15	YAWEALEVVLIGAAF	21637

2HZE	AB	ELECTRON TRANSPORT, OXIDOREDUCTASE	B	1.0	1.0	1	10	YSDLLEIDNM	21638
2HZM	EF	TRANSCRIPTION	F	1.0	1.0	1	8	VSSLMNGL	21639
2I2R	AE	TRANSPORT PROTEIN	E	1.0	1.0	1	8	HVDVFFQK	21640
2I2R	BO	TRANSPORT PROTEIN	O	1.0	1.0	1	7	LEQLEAQ	21641
2I2R	CN	TRANSPORT PROTEIN	N	1.0	1.0	1	7	LEQLEAQ	21642
2I2R	IM	TRANSPORT PROTEIN	M	1.0	1.0	1	16	KEEMMDIVKAIYDMED	21643
2I2R	IP	TRANSPORT PROTEIN	P	1.0	1.0	1	7	LEQLEAQ	21644
2I2R	JN	TRANSPORT PROTEIN	N	1.0	1.0	1	15	KEEMMDIVKAIYDMD	21645
2I2R	KN	TRANSPORT PROTEIN	K	1.0	1.0	1	11	ISAYDDELAFY	21646
2I2R	LP	TRANSPORT PROTEIN	P	1.0	1.0	1	13	VHEKLRWTFNLYD	21647
2I2R	LP	TRANSPORT PROTEIN	P	1.0	1.0	1	16	KEEMMDIVKAIYDMMG	21648
2I2T	TY	RIBOSOME	Y	1.0	1.0	1	9	QFNLRMQAA	21649
2I2X	AD	TRANSFERASE	A	1.0	1.0	1	23	PSWGAEVAHAQKTIMEKYHDEYG	21650
2I2X	CD	TRANSFERASE	D	1.0	1.0	1	8	EASLKKVL	21651
2I2X	EH	TRANSFERASE	H	1.0	1.0	1	8	EASLKKVL	21652
2I2X	GH	TRANSFERASE	H	1.0	1.0	1	16	LPNVMMSADAMLEGIE	21653
2I2X	IJ	TRANSFERASE	J	1.0	1.0	1	14	DIGKNIVTALLRAN	21654
2I2X	IJ	TRANSFERASE	J	1.0	1.0	1	6	YNVALE	21655
2I2X	IJ	TRANSFERASE	J	1.0	1.0	1	16	LPNVMMSADAMLEGIE	21656
2I2X	IL	TRANSFERASE	L	1.0	1.0	1	8	EASLKKVL	21657
2I2X	KJ	TRANSFERASE	K	1.0	1.0	1	23	PSWGAEVAHAQKTIMEKYHDEYG	21658
2I2X	KL	TRANSFERASE	L	1.0	1.0	1	17	DALMVGMGVVIRLYDEG	21659
2I2X	KL	TRANSFERASE	L	1.0	1.0	1	19	LPNVMMSADAMLEGIEYCK	21660
2I2X	MN	TRANSFERASE	N	1.0	1.0	1	21	LPNVMMSADAMLEGIEYCKEN	21661
2I9L	BI	IMMUNE SYSTEM/VIRAL PROTEIN	I	1.0	1.0	1	19	ADAQLDAVLSAATETYSGL	21662
2IAE	AB	HYDROLASE	B	1.0	1.0	1	9	QKFVLQLLE	21663
2IAE	EF	HYDROLASE	E	1.0	1.0	1	7	FQVAERA	21664
2IAN	QE	IMMUNE SYSTEM	Q	1.0	1.0	1	11	ELGRPDAEYWN	21665
2IBF	AB	CELL ADHESION, STRUCTURAL PROTEIN	A	1.0	1.0	1	17	EPVAQQISHLVIMHEEG	21666
2ICW	AG	IMMUNE SYSTEM	A	1.0	1.0	1	17	AQGALANIAVDKANLEI	21667
2ICW	DF	IMMUNE SYSTEM	D	1.0	1.0	1	17	AQGALANIAVDKANLEI	21668
2ICW	EF	IMMUNE SYSTEM	E	1.0	1.0	1	9	KDLLEQRRA	21669
2ICW	FG	IMMUNE SYSTEM	G	1.0	1.0	1	7	DFAKAVF	21670
2ICW	HL	IMMUNE SYSTEM	H	1.0	1.0	1	22	YKEIFNMMFLKLSVVFDTQRKE	21671
2IK8	AB	SIGNALING PROTEIN	A	1.0	1.0	1	10	RSERKKWIHC	21672
2INN	AC	OXIDOREDUCTASE	C	1.0	1.0	1	7	GHIARRF	21673
2INN	AF	OXIDOREDUCTASE	A	1.0	1.0	1	7	PEKYIQA	21674
2INN	BD	OXIDOREDUCTASE	D	1.0	1.0	1	5	RYQEA	21675

2IX7	CA	CONTRACTILE PROTEIN/METAL BINDING	A	1.0	1.0	1	10	EAELQDMINE	21676
2J01	FP	RIBOSOME	F	1.0	1.0	1	7	VYDIVRT	21677
2J03	FP	RIBOSOME	F	1.0	1.0	1	7	VYDIVRT	21678
2J0M	AB	TRANSFERASE	A	1.0	1.0	1	12	KSNYEVLEKDVG	21679
2J0Q	BF	HYDROLASE	B	1.0	1.0	1	12	DIRILRDIEQYY	21680
2J3R	AB	TRANSPORT	A	1.0	1.0	1	17	FRETADVIAKVAFKMYL	21681
2J59	FR	HYDROLASE	F	1.0	1.0	1	7	RPLWRHY	21682
2J5G	ED	HYDROLASE	D	1.0	1.0	1	15	LMERAWEIARTLAKQ	21683
2J5L	BC	IMMUNE SYSTEM	B	1.0	1.0	1	5	SEQLT	21684
2J7A	AF	OXIDOREDUCTASE	F	1.0	1.0	1	5	RPFCT	21685
2J7A	MO	OXIDOREDUCTASE	O	1.0	1.0	1	5	SMEAK	21686
2JBY	AB	APOPTOSIS	A	1.0	1.0	1	12	IVNIKNTLTFAL	21687
2JDQ	AE	PROTEIN TRANSPORT	A	1.0	1.0	1	11	NDKIQAVIDAG	21688
2JDQ	AE	PROTEIN TRANSPORT	A	1.0	1.0	1	15	YKVVSPALRAVGNIV	21689
2JDQ	BD	PROTEIN TRANSPORT	B	1.0	1.0	1	25	SKIVQVALNGLENILRLGEQEAKRN	21690
2JIY	LM	PHOTOSYNTHESIS	M	1.0	1.0	1	26	MEGIHRWAIWMAVLVTLTGGIGILLS	21691
2JIZ	AE	HYDROLASE	E	1.0	1.0	1	15	IFRFTQAGSEVSALL	21692
2JIZ	CF	HYDROLASE	C	1.0	1.0	1	14	RSTVAQLVKRLTDA	21693
2JIZ	HN	HYDROLASE	N	1.0	1.0	1	38	LKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKP	21694
2JIZ	JN	HYDROLASE	N	1.0	1.0	1	69	NYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN RTRQAVITKELIEIISGAAA	21695
2JJ0	MH	PHOTOSYNTHESIS	M	1.0	1.0	1	7	TLLGWFG	21696
2JM6	AB	APOPTOSIS	B	1.0	1.0	1	15	EGDVKSFSRVMVHVF	21697
2JSS	AB	CHAPERONE/NUCLEAR PROTEIN	A	1.0	1.0	1	29	AAIYLTAVLEYLTAEVLELAGNAAKDLKV	21698
2JU0	AB	METAL BINDING PROTEIN/SIGNALING PROTEIN	A	1.0	1.0	1	13	EIQQWHKGFLRDC	21699
2JZB	AB	TRANSFERASE/TRANSCRIPTION	A	1.0	1.0	1	6	EVELLK	21700
2K2F	CA	METAL BINDING PROTEIN	C	1.0	1.0	1	11	KAVWHKLLSKQ	21701
2K42	AB	SIGNALING PROTEIN	A	1.0	1.0	1	14	AETSKLIYDFIEDQ	21702
2K6Q	AB	APOPTOSIS INHIBITOR/APOPTOSIS	A	1.0	1.0	1	13	MSELIKIIRRRLQ	21703
2K7L	BA	TRANSCRIPTION	A	1.0	1.0	1	16	SEQTVNVLAQILKRLN	21704
2KA4	AB	TRANSCRIPTION REGULATOR	A	1.0	1.0	1	14	CRTMKNVLNHMTHC	21705
2KC8	AB	TOXIN/TOXIN REPRESSOR	A	1.0	1.0	1	17	STVREQLKKKLVEVLES	21706
2MEV	14	VIRUS	1	1.0	1.0	1	5	VAFFY	21707
2NGR	AB	HYDROLASE	B	1.0	1.0	1	14	LHLPAVILKTFLRE	21708
2NLA	AB	APOPTOSIS	A	1.0	1.0	1	15	EDDVKSLSRVMIHVF	21709
2NNA	AB	IMMUNE SYSTEM	A	1.0	1.0	1	7	PLFRRFR	21710
2NNW	CD	TRANSFERASE	C	1.0	1.0	1	10	PEKVLDQLLK	21711
2NOJ	GH	IMMUNE SYSTEM	G	1.0	1.0	1	22	GEQNMIGMTPTVIAVHYLDETE	21712

2NPI	AC	TRANSCRIPTION	A	1.0	1.0	1	22	KDLYLECISQLGQVVGQRLHLD	21713
2NQB	EC	STRUCTURAL PROTEIN/DNA	E	1.0	1.0	1	29	SSAVMALQEASEAYLVGLFEDTNLCAIHA	21714
2NTI	AC	DNA BINDING PROTEIN	A	1.0	1.0	1	11	SSVKKILSKAS	21715
2NTY	AD	SIGNALING PROTEIN	D	1.0	1.0	1	8	CMLISYTS	21716
2NU9	AG	LIGASE	A	1.0	1.0	1	14	TLDMLTVKVKLDEA	21717
2NU9	AG	LIGASE	A	1.0	1.0	1	12	CKDSILEAIDAG	21718
2NU9	HI	LIGASE	I	1.0	1.0	1	8	IEKVAEET	21719
2NUU	BH	TRANSPORT PROTEIN/SIGNALING PROTEIN	B	1.0	1.0	1	30	EIAALAFVNTVVATAAAILGWIFGEWALRG	21720
2NV2	CD	LYASE/TRANSFERASE	C	1.0	1.0	1	11	AEQAKIAEEAG	21721
2NV2	KL	LYASE/TRANSFERASE	K	1.0	1.0	1	11	AEQAKIAEEAG	21722
2NV2	OP	LYASE/TRANSFERASE	O	1.0	1.0	1	11	AEQAKIAEEAG	21723
2NVU	BC	PROTEIN TURNOVER, LIGASE	B	1.0	1.0	1	7	LQWPKEQ	21724
2NVU	BC	PROTEIN TURNOVER, LIGASE	C	1.0	1.0	1	10	KEAAEVLQNN	21725
2NVU	BI	PROTEIN TURNOVER, LIGASE	B	1.0	1.0	1	15	IIARRWINGMLISLL	21726
2NXX	AE	HORMONE/GROWTH FACTOR	A	1.0	1.0	1	14	YDRVLSELVNKMKE	21727
2NXX	CG	HORMONE/GROWTH FACTOR	C	1.0	1.0	1	23	VQEVEMLREKIYGVLEEYTRTTH	21728
2NYL	EF	HYDROLASE	F	1.0	1.0	1	7	RQITQVY	21729
2NZ0	AB	MEMBRANE PROTEIN	A	1.0	1.0	1	11	EKLRWTFNLYD	21730
2NZ0	AB	MEMBRANE PROTEIN	A	1.0	1.0	1	15	KEEMMDIVKAIYDMM	21731
2NZ0	AB	MEMBRANE PROTEIN	A	1.0	1.0	1	7	VDVFFQK	21732
2NZ0	CD	MEMBRANE PROTEIN	C	1.0	1.0	1	11	STYAHYLFNAF	21733
2NZU	GL	TRANSCRIPTION	G	1.0	1.0	1	17	IFYAELARGIEDIATMY	21734
2O01	AB	PHOTOSYNTHESIS	B	1.0	1.0	1	5	KKDFG	21735
2O25	BC	LIGASE	C	1.0	1.0	1	16	IALSRLAQERKAWRKD	21736
2O26	AX	CYTOKINE/SIGNALING PROTEIN	A	1.0	1.0	1	19	NYSIIDKLGKIVDDLVLCM	21737
2O8A	AI	HYDROLASE/INHIBITOR	I	1.0	1.0	1	18	PEEREKKRQFEMKRKLHY	21738
2O8A	BJ	HYDROLASE/INHIBITOR	B	1.0	1.0	1	7	ASINRIY	21739
2O8F	AB	DNA BINDING PROTEIN/DNA	A	1.0	1.0	1	10	KHVIECAKQK	21740
2O97	AB	DNA BINDING PROTEIN	B	1.0	1.0	1	7	KALKDAV	21741
2ODE	AD	SIGNALING PROTEIN	D	1.0	1.0	1	13	FQTREATRKNLQE	21742
2ODE	CB	SIGNALING PROTEIN	B	1.0	1.0	1	13	FQTREATRKNLQE	21743
2OF5	BH	APOPTOSIS	B	1.0	1.0	1	16	VQSQVVEAFIRWRQRF	21744
2OF5	EL	APOPTOSIS	L	1.0	1.0	1	12	QDVAEEVRAVLE	21745
2OGX	AB	METAL BINDING PROTEIN	A	1.0	1.0	1	13	ADTGAFLLADAFG	21746
2OM0	12	HORMONE	1	1.0	1.0	1	7	LYQLENY	21747
2OM0	ab	HORMONE	a	1.0	1.0	1	7	LYQLENY	21748
2OM0	EJ	HORMONE	J	1.0	1.0	1	19	VNQHLCGSHLVEALYLVCG	21749
2OM0	GB	HORMONE	G	1.0	1.0	1	7	LYQLENY	21750
2OM0	GD	HORMONE	D	1.0	1.0	1	19	VNQHLCGSHLVEALYLVCG	21751

2OM0	gh	HORMONE	g	1.0	1.0	1	7	LYQLENY	21752
2OM0	ij	HORMONE	i	1.0	1.0	1	7	LYQLENY	21753
2OM0	UR	HORMONE	R	1.0	1.0	1	19	VNQHLCGSHLVEALYLVCG	21754
2OM0	XY	HORMONE	X	1.0	1.0	1	7	LYQLENY	21755
2ONK	GI	MEMBRANE PROTEIN	I	1.0	1.0	1	13	PLRVFFTVSLPLS	21756
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	A	1.0	1.0	1	9	DGQKEELIR	21757
2OPL	AB	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	B	1.0	1.0	1	8	TIEQIKAK	21758
2OQJ	DB	IMMUNE SYSTEM	D	1.0	1.0	1	7	DEQLKSG	21759
2OT8	AC	TRANSPORT PROTEIN	A	1.0	1.0	1	17	HKNLLILYDAIGTLADS	21760
2OTJ	FM	RIBOSOME	F	1.0	1.0	1	11	TNETTKSIERG	21761
2OTJ	SV	RIBOSOME	V	1.0	1.0	1	24	PAEREAELDDLKTELLNARAVQAA	21762
2OV2	HN	PROTEIN BINDING/TRANSFERASE	H	1.0	1.0	1	11	YPQGLAMAREI	21763
2OXQ	BD	LIGASE	B	1.0	1.0	1	16	MALKRIQKELQDLQRD	21764
2OXQ	BD	LIGASE	D	1.0	1.0	1	12	RKDIEEHLQRVG	21765
2OZ4	LH	CELL ADHESION	L	1.0	1.0	1	7	SEQLTSG	21766
2P1N	DE	SIGNALING PROTEIN	D	1.0	1.0	1	5	PEEIR	21767
2P1N	DE	SIGNALING PROTEIN	D	1.0	1.0	1	14	QATLFELILAANYL	21768
2P22	AB	TRANSPORT PROTEIN	A	1.0	1.0	1	30	DGLNQLYNLVAQDYALTDTIECLSRMLHRG	21769
2P2C	EF	HYDROLASE	E	1.0	1.0	1	15	GDVDHSTLVTLFKLL	21770
2P2C	IJ	HYDROLASE	J	1.0	1.0	1	13	WYIEALAQVFSER	21771
2P2C	KL	HYDROLASE	K	1.0	1.0	1	15	GDVDHSTLVTLFKLL	21772
2P6A	BC	SIGNALING PROTEIN	B	1.0	1.0	1	6	IAGTSG	21773
2P6A	BC	SIGNALING PROTEIN	C	1.0	1.0	1	9	TLFKWMIFN	21774
2P7V	AB	TRANSCRIPTION	A	1.0	1.0	1	32	NGQLARAAKIWPQLEANTQQIMDYYDSSLETA	21775
2P9V	AB	HYDROLASE	A	1.0	1.0	1	11	KTLQQGIQLAQ	21776
2PCF	AB	COMPLEX (ELECTRON TRANSPORT PROTEINS)	B	1.0	1.0	1	7	PIFAQQN	21777
2PF4	BH	HYDROLASE REGULATOR/VIRAL PROTEIN	B	1.0	1.0	1	10	WRVRLAIIEY	21778
2PMZ	AC	TRANSLATION, TRANSFERASE	A	1.0	1.0	1	9	VKHIYEFLK	21779
2PMZ	GV	TRANSLATION, TRANSFERASE	G	1.0	1.0	1	11	IEAAREIIIRE	21780
2PMZ	QG	TRANSLATION, TRANSFERASE	Q	1.0	1.0	1	5	RFRGN	21781
2PMZ	QR	TRANSLATION, TRANSFERASE	Q	1.0	1.0	1	7	KEEAQQI	21782
2PMZ	QX	TRANSLATION, TRANSFERASE	Q	1.0	1.0	1	7	KEEAQQI	21783
2PMZ	QX	TRANSLATION, TRANSFERASE	X	1.0	1.0	1	13	TLGNLIAGTLRRI	21784
2PQA	CD	REPLICATION	D	1.0	1.0	1	14	LGLYNEAVKIIHDF	21785
2PQR	AC	APOPTOSIS	A	1.0	1.0	1	14	PQQLEILRQQVVSE	21786
2PQR	BD	APOPTOSIS	B	1.0	1.0	1	14	PQQLEILRQQVVSE	21787

2PT7	BG	HYDROLASE/PROTEIN BINDING	G	1.0	1.0	1	18	YRYKALSYLLFNWIHPTY	21788
2PT7	DH	HYDROLASE/PROTEIN BINDING	H	1.0	1.0	1	12	LHEIKQELKDLF	21789
2PT7	EH	HYDROLASE/PROTEIN BINDING	E	1.0	1.0	1	15	LSRLMHFARCCASFK	21790
2Q97	AT	STRUCTURAL PROTEIN/CELL INVASION	A	1.0	1.0	1	12	SVWIGGSILASL	21791
2Q9Q	AD	REPLICATION	A	1.0	1.0	1	11	YMELTKLLLNH	21792
2Q9Q	FG	REPLICATION	F	1.0	1.0	1	10	FPHVLEKEKT	21793
2QA4	FM	RIBOSOME	F	1.0	1.0	1	11	TNETTKSIERG	21794
2QA4	NQ	RIBOSOME	Q	1.0	1.0	1	5	PQRAV	21795
2QAG	BC	CELL CYCLE, STRUCTURAL PROTEIN	B	1.0	1.0	1	5	DQLVN	21796
2QBY	AB	REPLICATION/DNA	B	1.0	1.0	1	6	PRVLSS	21797
2QCS	AB	TRANSFERASE/TRANSFERASE INHIBITOR	B	1.0	1.0	1	11	KWERLTVADAL	21798
2QEX	NQ	RIBOSOME	Q	1.0	1.0	1	5	PQRAV	21799
2QHO	AB	PROTEIN BINDING/LIGASE	B	1.0	1.0	1	10	VNLAVNNLLS	21800
2QHO	CB	PROTEIN BINDING/LIGASE	B	1.0	1.0	1	11	RSVIIRELQRT	21801
2QJ9	BD	CYTOKINE/RECEPTOR	D	1.0	1.0	1	7	SDFQCRD	21802
2QJK	AC	ELECTRON TRANSPORT	C	1.0	1.0	1	29	RRDFLYYATAGAGAVATGAAVWPLINQMN	21803
2QJK	JK	ELECTRON TRANSPORT	J	1.0	1.0	1	22	PMFKIYFWLLAADFVILTWVGA	21804
2QJK	KL	ELECTRON TRANSPORT	K	1.0	1.0	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	21805
2QJK	QR	ELECTRON TRANSPORT	Q	1.0	1.0	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	21806
2QJP	AC	ELECTRON TRANSPORT	C	1.0	1.0	1	28	RRDFLYYATAGAGAVATGAAVWPLINQM	21807
2QJP	GH	ELECTRON TRANSPORT	G	1.0	1.0	1	22	PMFKIYFWLLAADFVILTWVGA	21808
2QJP	JK	ELECTRON TRANSPORT	J	1.0	1.0	1	22	PMFKIYFWLLAADFVILTWVGA	21809
2QJY	GI	OXIDOREDUCTASE	G	1.0	1.0	1	15	VDLAFASVEHIMRNV	21810
2QJY	HI	OXIDOREDUCTASE	H	1.0	1.0	1	32	LMARKQAGFTAVMFLTVLSVLLYLTNKRLWAG	21811
2QJY	JK	OXIDOREDUCTASE	J	1.0	1.0	1	22	PMFKIYFWLLAADFVILTWVGA	21812
2QJY	MN	OXIDOREDUCTASE	N	1.0	1.0	1	6	ISQLFN	21813
2QJY	MO	OXIDOREDUCTASE	M	1.0	1.0	1	15	VDLAFASVEHIMRNV	21814
2QJY	PR	OXIDOREDUCTASE	P	1.0	1.0	1	15	VDLAFASVEHIMRNV	21815
2QKI	DH	IMMUNE SYSTEM	D	1.0	1.0	1	7	RAHEAKI	21816
2QKM	CB	HYDROLASE	B	1.0	1.0	1	5	AEEQS	21817
2QLV	AC	TRANSFERASE/PROTEIN BINDING	C	1.0	1.0	1	6	VGEALM	21818
2QMB	CD	TRANSPORT PROTEIN	C	1.0	1.0	1	15	EEYGAETLERMFITY	21819
2QOG	DB	HYDROLASE	B	1.0	1.0	1	13	LLQFNKMIKFETR	21820
2QOU	MS	RIBOSOME	M	1.0	1.0	1	18	GDLRREISMSIKRLMDLG	21821
2QP0	NS	RIBOSOME	N	1.0	1.0	1	6	NAVLKL	21822
2QY0	CB	HYDROLASE	B	1.0	1.0	1	8	VEELMKLG	21823
2R6C	AG	REPLICATION	G	1.0	1.0	1	10	FLTAARIAKE	21824
2R6C	DH	REPLICATION	H	1.0	1.0	1	13	EQELEDYIRHVLN	21825

2R9R	GH	MEMBRANE PROTEIN, TRANSPORT PROTEIN	G	1.0	1.0	1	15	REKVEVQLPELFHKI	21826
2RAO	AB	OXYGEN BINDING	A	1.0	1.0	1	19	PVNFKLLSHCLLVTLANHH	21827
2RAO	CB	OXYGEN BINDING	C	1.0	1.0	1	19	PVNFKLLSHCLLVTLANHH	21828
2RET	CD	PROTEIN TRANSPORT	C	1.0	1.0	1	7	VGYLEQK	21829
2REX	AB	SIGNALING PROTEIN/LIPOPROTEIN	B	1.0	1.0	1	9	DNVRPLCYS	21830
2RF9	AC	TRANSFERASE	A	1.0	1.0	1	9	SEISSILEK	21831
2RFT	AB	VIRAL PROTEIN	A	1.0	1.0	1	8	LPNLLRGY	21832
2RGN	BC	SIGNALING PROTEIN COMPLEX	B	1.0	1.0	1	8	IKPVQRIM	21833
2RHS	AD	LIGASE	A	1.0	1.0	1	6	VRFLEQ	21834
2RHS	CB	LIGASE	B	1.0	1.0	1	7	PQVAADN	21835
2RHS	CD	LIGASE	C	1.0	1.0	1	16	MSDLKGTLELVAKKLF	21836
2RI4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.0	1.0	1	15	KLLSHSLLVTLACHL	21837
2RI4	CD	OXYGEN STORAGE, OXYGEN TRANSPORT	C	1.0	1.0	1	16	AGAYGAEALERMFLSF	21838
2RI4	IL	OXYGEN STORAGE, OXYGEN TRANSPORT	L	1.0	1.0	1	5	TQRFF	21839
2RMK	AB	MEMBRANE PROTEIN/TRANSFERASE	B	1.0	1.0	1	31	NLSRVAGLEKQLAIELKVKQGAENMIQTYSN	21840
2ROD	AB	APOPTOSIS	A	1.0	1.0	1	22	GAAGRRALETLRRVGDGVQRNH	21841
2UUN	AD	ELECTRON TRANSPORT	D	1.0	1.0	1	25	SDRMAACLRDMEIILRYVTYAVFAG	21842
2UUN	GH	ELECTRON TRANSPORT	G	1.0	1.0	1	10	TGPMDEYLIA	21843
2UUN	GJ	ELECTRON TRANSPORT	J	1.0	1.0	1	25	SDRMAACLRDMEIILRYVTYAVFAG	21844
2UUN	OR	ELECTRON TRANSPORT	O	1.0	1.0	1	25	QRGKDKCARDIGYYLRMVTYCLIAG	21845
2UUN	UX	ELECTRON TRANSPORT	X	1.0	1.0	1	25	SDRMAACLRDMEIILRYVTYAVFAG	21846
2UY1	AB	RNA BINDING PROTEIN	A	1.0	1.0	1	10	FLSLYYGLVM	21847
2UYL	VW	IMMUNE SYSTEM	V	1.0	1.0	1	6	SEQLTS	21848
2UZ1	AB	LYASE	A	1.0	1.0	1	6	GGFTNA	21849
2UZ1	AB	LYASE	A	1.0	1.0	1	10	VTPIANAWLD	21850
2UZ1	AC	LYASE	C	1.0	1.0	1	14	IPRLVMQAIRAALS	21851
2V1D	AB	OXIDOREDUCTASE/REPRESSOR	B	1.0	1.0	1	7	QEDVEAV	21852
2V1S	AK	OXIDOREDUCTASE	A	1.0	1.0	1	11	QQLLQVLQQTL	21853
2V1S	CL	OXIDOREDUCTASE	C	1.0	1.0	1	11	QQLLQVLQQTL	21854
2V36	AB	TRANSFERASE	A	1.0	1.0	1	7	FSERVTK	21855
2V36	AB	TRANSFERASE	A	1.0	1.0	1	10	SVLAEAISDY	21856
2V4J	BC	OXIDOREDUCTASE	B	1.0	1.0	1	6	IPLAVA	21857
2V4J	DB	OXIDOREDUCTASE	D	1.0	1.0	1	8	LGETMKRL	21858
2V52	BM	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	B	1.0	1.0	1	9	QAVLSLYAS	21859
2V5Q	BC	TRANSFERASE	B	1.0	1.0	1	6	ITCLTI	21860

2V7Q	BF	HYDROLASE	F	1.0	1.0	1	5	RAIAE	21861
2V7Q	CJ	HYDROLASE	C	1.0	1.0	1	14	QQLLSRGVRLTELL	21862
2V7Q	DG	HYDROLASE	G	1.0	1.0	1	75	ADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDK LTLTFNRTRQAVITKELIEIISGAAAL	21863
2V7Q	GJ	HYDROLASE	J	1.0	1.0	1	30	AFGKREQAEEERYFRARAKEQLAALKKHHE	21864
2V8S	EV	PROTEIN TRANSPORT	V	1.0	1.0	1	19	EHFEKLHEIFRGLLEDLQG	21865
2VDB	AB	PROTEIN BINDING	A	1.0	1.0	1	21	FAEVSKLVTDLTKVHTECCHG	21866
2VDB	AB	PROTEIN BINDING	A	1.0	1.0	1	5	QDSIS	21867
2VDW	AB	TRANSFERASE	A	1.0	1.0	1	17	PLGILSNYVKTLLISMY	21868
2VE7	BD	CELL CYCLE	B	1.0	1.0	1	26	QIARLEQERSTANKANAERLKRLQKS	21869
2VGL	AM	PROTEIN TRANSPORT	A	1.0	1.0	1	10	EFSHEAVKTH	21870
2VGL	BM	PROTEIN TRANSPORT	B	1.0	1.0	1	6	LASVYH	21871
2VGO	BC	TRANSFERASE	B	1.0	1.0	1	13	EHQLRREIEIQSH	21872
2VIR	AB	COMPLEX (HEMAGGLUTININ/IMMMUNOGLOBULIN)	A	1.0	1.0	1	6	SEELET	21873
2VML	GJ	PHOTOSYNTHESIS	G	1.0	1.0	1	9	GPLDDYIVA	21874
2VOF	AB	APOPTOSIS	A	1.0	1.0	1	21	QACRVLQRVAFSVQKEVEKNL	21875
2VOL	AB	IMMUNE SYSTEM	A	1.0	1.0	1	6	PKDVLT	21876
2VOY	GH	HYDROLASE	H	1.0	1.0	1	17	AVITTCLALGTRRMAKK	21877
2VOY	KL	HYDROLASE	L	1.0	1.0	1	20	VQLLWVNLVTDGLPATALGF	21878
2VPD	AB	GENE REGULATION	A	1.0	1.0	1	6	DTCMAD	21879
2VPD	CD	GENE REGULATION	C	1.0	1.0	1	10	ETAYGLLTAE	21880
2VR0	AC	OXIDOREDUCTASE	C	1.0	1.0	1	5	SMEAK	21881
2VR0	EF	OXIDOREDUCTASE	E	1.0	1.0	1	5	RNEMR	21882
2VSO	AE	HYDROLASE/TRANSLATION	E	1.0	1.0	1	15	FDAISSEILAIANIS	21883
2VU8	EI	HYDROLASE/INHIBITOR	E	1.0	1.0	1	9	RATCRAQYG	21884
2VUS	CK	TRANSCRIPTION	C	1.0	1.0	1	16	MEEYAREVFPIEEEAN	21885
2VUS	GO	TRANSCRIPTION	G	1.0	1.0	1	16	MEEYAREVFPIEEEAN	21886
2VXS	JN	CYTOKINE	N	1.0	1.0	1	6	SEELQA	21887
2VYN	DA	OXIDOREDUCTASE	A	1.0	1.0	1	16	NETGYSNKVLDLIAHI	21888
2VYN	DA	OXIDOREDUCTASE	D	1.0	1.0	1	13	RIGRLVLRVCMEK	21889
2VYR	BF	IMMUNE SYSTEM	B	1.0	1.0	1	15	VKEVMHYLGQYIMVK	21890
2W0C	IS	VIRUS	S	1.0	1.0	1	21	LDALISGWARVEQIKAAKAST	21891
2W73	BL	METAL BINDING PROTEIN	B	1.0	1.0	1	11	AAELRHVMTNL	21892
2W80	BC	IMMUNE SYSTEM	B	1.0	1.0	1	7	ENMRRPY	21893
2W96	BA	CELL CYCLE	A	1.0	1.0	1	15	PEELLQMELLLVNKL	21894
2WAQ	AB	TRANSCRIPTION	A	1.0	1.0	1	5	LEDVS	21895
2WAQ	AL	TRANSCRIPTION	A	1.0	1.0	1	11	KEEAQQILGVA	21896
2WAQ	BD	TRANSCRIPTION	D	1.0	1.0	1	14	LEFVNAIRRAAMLY	21897

2WAQ	CH	TRANSCRIPTION	C	1.0	1.0	1	18	IEAAREIIIREISKVLAE	21898
2WAQ	HK	TRANSCRIPTION	K	1.0	1.0	1	10	HFNEVFISLW	21899
2WB1	AB	TRANSCRIPTION	B	1.0	1.0	1	5	FEARD	21900
2WB1	AK	TRANSCRIPTION	K	1.0	1.0	1	17	RYEIARVISARALQLAM	21901
2WB1	BD	TRANSCRIPTION	D	1.0	1.0	1	11	DEILAHRLALI	21902
2WB1	RX	TRANSCRIPTION	R	1.0	1.0	1	7	PMEARLR	21903
2WB1	WR	TRANSCRIPTION	R	1.0	1.0	1	6	AMLLKD	21904
2WB1	WR	TRANSCRIPTION	R	1.0	1.0	1	9	QLQNEILKY	21905
2WB1	WY	TRANSCRIPTION	W	1.0	1.0	1	9	VKHVYEFLK	21906
2WB1	WY	TRANSCRIPTION	Y	1.0	1.0	1	13	DLKNLISNKEVLV	21907
2WB1	YR	TRANSCRIPTION	Y	1.0	1.0	1	8	VVENIIIG	21908
2WBE	AB	STRUCTURAL PROTEIN	A	1.0	1.0	1	15	AWARLDHKFDLMYAK	21909
2WDI	FP	RIBOSOME	F	1.0	1.0	1	7	VYDIVRT	21910
2WG8	AB	HYDROLASE	B	1.0	1.0	1	15	ALDACCMVHDHCVDT	21911
2WIN	CD	IMMUNE SYSTEM	C	1.0	1.0	1	11	QSKIWDVVEKA	21912
2WIN	EF	IMMUNE SYSTEM	E	1.0	1.0	1	11	QSKIWDVVEKA	21913
2WME	AE	OXIDOREDUCTASE	E	1.0	1.0	1	17	FPHMESVLGYIESGKAQ	21914
2Z2S	EF	TRANSCRIPTION	E	1.0	1.0	1	13	QENARLGRAIARL	21915
2Z3R	ON	CYTOKINE/CYTOKINE RECEPTOR	O	1.0	1.0	1	20	KVTAMKCFLLELQVISLESG	21916
2Z8V	AD	IMMUNE SYSTEM	A	1.0	1.0	1	8	LDEMRHFY	21917
2ZCY	AH	HYDROLASE	H	1.0	1.0	1	23	AADTEAVTQLIGSNIELHSLYTS	21918
2ZCY	IZ	HYDROLASE	I	1.0	1.0	1	12	SDQLFGMCESLY	21919
2ZCY	IZ	HYDROLASE	I	1.0	1.0	1	18	PEDLFETISQALLNAADR	21920
2ZCY	LM	HYDROLASE	M	1.0	1.0	1	14	FGAHMANPLLRKVV	21921
2ZCY	PW	HYDROLASE	P	1.0	1.0	1	22	TADAEILINTARIHAQNYLKTY	21922
2ZCY	RZ	HYDROLASE	R	1.0	1.0	1	22	TADARSMIEHARTAAVTHNLYY	21923
2ZCY	VM	HYDROLASE	V	1.0	1.0	1	15	VVSALQMLKQHLFKY	21924
2ZCY	WL	HYDROLASE	L	1.0	1.0	1	19	VEEVIKLVRDSFTSATERH	21925
2ZHX	IJ	HYDROLASE/HYDROLASE INHIBITOR	I	1.0	1.0	1	14	RSLANIFDEYTADL	21926
2ZHX	IJ	HYDROLASE/HYDROLASE INHIBITOR	J	1.0	1.0	1	9	PEEVEEVIG	21927
2ZIV	AB	HYDROLASE	A	1.0	1.0	1	10	MDDLCGSIID	21928
2ZJS	YE	PROTEIN TRANSPORT/IMMUNE SYSTEM	Y	1.0	1.0	1	22	PELRQRVLFTLLVLAAYRLGAF	21929
2ZJS	YE	PROTEIN TRANSPORT/IMMUNE SYSTEM	Y	1.0	1.0	1	9	VKAFWSALQ	21930
2ZL1	AB	PROTEIN BINDING	A	1.0	1.0	1	5	EHALR	21931
2ZME	AB	PROTEIN TRANSPORT	B	1.0	1.0	1	13	DETIRFKSYLLSM	21932
2ZNE	AC	APOPTOSIS	A	1.0	1.0	1	22	FDDFIQGCIVLQRLTDIFRRYD	21933
2ZNV	AC	HYDROLASE/SIGNALING PROTEIN	A	1.0	1.0	1	14	SVDLHTHCSYQLML	21934
2ZNW	AZ	IMMUNE SYSTEM/HYDROLASE	Z	1.0	1.0	1	5	VQAWI	21935

2ZT9	BG	PHOTOSYNTHESIS	B	1.0	1.0	1	9	PTLRAKLAK	21936
2ZT9	DE	PHOTOSYNTHESIS	D	1.0	1.0	1	31	MGRRQFMNLLTFGTVTGVALGALYPVVNYFI	21937
2ZT9	FG	PHOTOSYNTHESIS	G	1.0	1.0	1	28	PLLSGIVLGLIVVTLAGLFYAAYKQYKR	21938
2ZU6	AB	HYDROLASE	B	1.0	1.0	1	9	VNHLVKEID	21939
2ZU6	AE	HYDROLASE	E	1.0	1.0	1	20	TDVEKSFDKLLKDLPELALD	21940
2ZU6	CB	HYDROLASE	C	1.0	1.0	1	13	RELAQQIQKVVMA	21941
2ZU6	DE	HYDROLASE	E	1.0	1.0	1	9	VNHLVKEID	21942
2ZVN	AB	SIGNALING PROTEIN/TRANSCRIPTION	B	1.0	1.0	1	35	TVPVLKAQADIYKADFQAERHAREKLVEKKEYLQE	21943
3A0B	AD	ELECTRON TRANSPORT	D	1.0	1.0	1	24	IALHGAFGLIGFMLRQFEIARLVG	21944
3A0B	AD	ELECTRON TRANSPORT	D	1.0	1.0	1	12	FYTKNLLLNEGI	21945
3A0B	AV	ELECTRON TRANSPORT	V	1.0	1.0	1	18	EKDLVAIAGHILVEPKIL	21946
3A0B	BD	ELECTRON TRANSPORT	B	1.0	1.0	1	5	HIWHG	21947
3A0B	bT	ELECTRON TRANSPORT	T	1.0	1.0	1	10	CIIALFFFAI	21948
3A0B	Bt	ELECTRON TRANSPORT	t	1.0	1.0	1	9	CIIALFFFA	21949
3A0B	cz	ELECTRON TRANSPORT	c	1.0	1.0	1	20	FPFFVVGVVHLISSAVLGFG	21950
3A0B	de	ELECTRON TRANSPORT	d	1.0	1.0	1	7	FTRWCQL	21951
3A0B	DM	ELECTRON TRANSPORT	D	1.0	1.0	1	9	ISQEIRAAE	21952
3A0B	DX	ELECTRON TRANSPORT	D	1.0	1.0	1	10	WSGILLFPCA	21953
3A0B	dx	ELECTRON TRANSPORT	d	1.0	1.0	1	10	WSGILLFPCA	21954
3A0B	EF	ELECTRON TRANSPORT	F	1.0	1.0	1	17	TLAVPTIFFLGAIAAMQ	21955
3A0B	HX	ELECTRON TRANSPORT	H	1.0	1.0	1	18	VFMGLFLVFLLIILEIYN	21956
3A0B	YZ	ELECTRON TRANSPORT	Y	1.0	1.0	1	9	IIFLLAVRR	21957
3A0B	yz	ELECTRON TRANSPORT	y	1.0	1.0	1	9	IIFLLAVRR	21958
3A1G	AD	TRANSFERASE	D	1.0	1.0	1	10	SRTREILTKT	21959
3B2U	JI	IMMUNE SYSTEM/TRANSFERASE	I	1.0	1.0	1	6	PVAFRG	21960
3B2U	LH	IMMUNE SYSTEM/TRANSFERASE	L	1.0	1.0	1	7	DEQLKSG	21961
3B2U	NM	IMMUNE SYSTEM/TRANSFERASE	M	1.0	1.0	1	6	PVAFRG	21962
3B2U	WV	IMMUNE SYSTEM/TRANSFERASE	V	1.0	1.0	1	6	PVAFRG	21963
3B5N	AK	MEMBRANE PROTEIN	A	1.0	1.0	1	60	SRTAELQAEIDDTVGIMRDNINKVAERGERLTSIEDKADNLAVSAQGFKRGANRVRKAMW	21964
3B5N	FH	MEMBRANE PROTEIN	H	1.0	1.0	1	61	EMELEIDRNLDQIQQVSNRLKKMALTTGKELDSQQKRLNNIEESTDDLDINLHMNTNRLAG	21965
3B63	DF	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	D	1.0	1.0	1	7	DEAQSKR	21966
3B63	NM	CONTRACTILE PROTEIN/STRUCTURAL PROTEIN	N	1.0	1.0	1	14	GRDLTDYLMKILTE	21967
3B9J	AB	OXIDOREDUCTASE	A	1.0	1.0	1	8	VEEIEDAF	21968
3BBN	BH	RIBOSOME	B	1.0	1.0	1	5	CITLG	21969
3BC1	AB	SIGNALING PROTEIN/TRANSPORT PROTEIN	B	1.0	1.0	1	9	DQQLKNMSG	21970

3BC1	EF	SIGNALING PROTEIN/TRANSPORT PROTEIN	F	1.0	1.0	1	8	DQQLKNMS	21971
3BCQ	AD	TRANSPORT PROTEIN/OXYGEN BINDING	A	1.0	1.0	1	15	PANFKILSHNLLVVL	21972
3BL2	AD	VIRAL PROTEIN/APOPTOSIS	D	1.0	1.0	1	17	MENLSRRLKVTGDLFDI	21973
3BL2	BC	VIRAL PROTEIN/APOPTOSIS	C	1.0	1.0	1	17	MENLSRRLKVTGDLFDI	21974
3BL2	BD	VIRAL PROTEIN/APOPTOSIS	B	1.0	1.0	1	5	YGPAL	21975
3BLW	EF	OXIDOREDUCTASE	E	1.0	1.0	1	11	VDNASMQAVAK	21976
3BLW	EF	OXIDOREDUCTASE	E	1.0	1.0	1	15	SMYGTILGNIGAALI	21977
3BLW	MN	OXIDOREDUCTASE	M	1.0	1.0	1	11	VDNASMQAVAK	21978
3BN9	CD	HYDROLASE	C	1.0	1.0	1	5	DEQLK	21979
3BRT	AB	TRANSFERASE/TRANSCRIPTION	A	1.0	1.0	1	21	ELVAEAHNLCTLLENAIQDTV	21980
3BRT	AD	TRANSFERASE/TRANSCRIPTION	A	1.0	1.0	1	5	REQGN	21981
3BRV	CD	TRANSFERASE/TRANSCRIPTION	D	1.0	1.0	1	60	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	21982
3BSZ	MN	TRANSPORT PROTEIN/IMMUNE SYSTEM	M	1.0	1.0	1	5	SEQLT	21983
3BUA	AE	DNA BINDING PROTEIN	E	1.0	1.0	1	6	GLALKY	21984
3BUA	DH	DNA BINDING PROTEIN	D	1.0	1.0	1	16	PLESAINVLEMIKTEF	21985
3BVH	AB	BLOOD CLOTTING	A	1.0	1.0	1	8	QHIQLLQK	21986
3BX4	AB	TOXIN	A	1.0	1.0	1	10	WDEAEKFCRA	21987
3BZ1	BD	ELECTRON TRANSPORT	D	1.0	1.0	1	7	LIYPLGQ	21988
3BZ1	BL	ELECTRON TRANSPORT	L	1.0	1.0	1	24	RTSLYLGLLLILVLALLFSSYFFN	21989
3BZ1	CZ	ELECTRON TRANSPORT	C	1.0	1.0	1	26	FPFFVVGVVHLISSAVLGFGGVYHAI	21990
3BZ1	DX	ELECTRON TRANSPORT	D	1.0	1.0	1	24	WSGILLFPCAYLALGGWLTGTTFV	21991
3BZ4	GH	IMMUNE SYSTEM	G	1.0	1.0	1	7	SEQLTSG	21992
3C1B	CD	STRUCTURAL PROTEIN/DNA	C	1.0	1.0	1	10	VGRVHRLLRK	21993
3C5W	AC	HYDROLASE	A	1.0	1.0	1	19	YAIREAATSNLKKLVEKFG	21994
3C5Z	AD	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	D	1.0	1.0	1	21	PEILERTRAELDTVCRHNYEG	21995
3C60	EH	SUGAR BINDING PROTEIN/IMMUNE SYSTEM	H	1.0	1.0	1	21	PEILERTRAELDTVCRHNYEG	21996
3C66	AC	TRANSFERASE	C	1.0	1.0	1	6	AKLLDS	21997
3C7K	AB	SIGNALING PROTEIN	A	1.0	1.0	1	23	KPVVYSNTIQSLAAIVRAMDTLG	21998
3C91	DK	HYDROLASE	D	1.0	1.0	1	23	VADARVLVDFARISAQQEKVTYG	21999
3C91	FN	HYDROLASE	N	1.0	1.0	1	22	VGDAQVLVRYMKAELELYRLQR	22000
3C91	RY	HYDROLASE	R	1.0	1.0	1	23	VADARVLVDFARISAQQEKVTYG	22001
3C91	T1	HYDROLASE	1	1.0	1.0	1	22	VGDAQVLVRYMKAELELYRLQR	22002
3C98	AB	ENDOCYTOSIS/EXOCYTOSIS	B	1.0	1.0	1	47	ADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRIQRQLEITG	22003

3CDK	CD	TRANSFERASE	C	1.0	1.0	1	8	NPIAAMAG	22004
3CF6	ER	SIGNALING PROTEIN/GTP-BINDING PROTEIN	E	1.0	1.0	1	23	ANLDLFLRRFNEIQFWVVTEVCL	22005
3CFB	LH	IMMUNE SYSTEM	L	1.0	1.0	1	6	SEQLTS	22006
3CFK	AK	IMMUNE SYSTEM	A	1.0	1.0	1	7	DEQLKSG	22007
3CJH	GH	PROTEIN TRANSPORT	H	1.0	1.0	1	28	SQEEQCLSNCVNRFLDTNIRIVNGLQNT	22008
3CJI	AD	VIRUS	A	1.0	1.0	1	5	VKFLF	22009
3CJT	IJ	TRANSFERASE/RIBOSOMAL PROTEIN	J	1.0	1.0	1	9	ASYLIRKAA	22010
3CMA	NQ	RIBOSOME	N	1.0	1.0	1	11	YHQRLRLLKSG	22011
3CUE	AC	PROTEIN TRANSPORT	C	1.0	1.0	1	23	QNEEDAKLLYGMIFSLRSITQKL	22012
3CUE	WX	PROTEIN TRANSPORT	X	1.0	1.0	1	9	KSCLLLRFS	22013
3CVH	MQ	IMMUNE SYSTEM	M	1.0	1.0	1	14	MAALITKHKWEQAG	22014
3CXH	AC	OXIDOREDUCTASE	C	1.0	1.0	1	5	FRKSN	22015
3CXH	CG	OXIDOREDUCTASE	C	1.0	1.0	1	22	VLSKFFFFIFVFNFVLLGQIGA	22016
3CXH	NP	OXIDOREDUCTASE	N	1.0	1.0	1	12	AFSSVEHIMRDV	22017
3CXH	OT	OXIDOREDUCTASE	O	1.0	1.0	1	9	NEEVRNMAE	22018
3CXH	OT	OXIDOREDUCTASE	O	1.0	1.0	1	19	HASIRRGYQVYREVCAACH	22019
3D31	AC	TRANSPORT PROTEIN	C	1.0	1.0	1	13	LWKAFFFVTLPLS	22020
3D32	BD	TRANSPORT PROTEIN	B	1.0	1.0	1	15	FEKRRSEGEKIRKKY	22021
3D3C	BK	TRANSCRIPTION	B	1.0	1.0	1	17	QVEKAVLRIALYELSKR	22022
3D48	PR	HORMONE/HORMONE RECEPTOR	P	1.0	1.0	1	6	FITKAI	22023
3D5B	FP	RIBOSOME	F	1.0	1.0	1	5	VYDIV	22024
3D5B	I1	RIBOSOME	I	1.0	1.0	1	5	YLLPR	22025
3D5D	P8	RIBOSOME	8	1.0	1.0	1	5	KRHLN	22026
3D7V	AB	APOPTOSIS	A	1.0	1.0	1	8	WDGFVEFF	22027
3DA7	BC	PROTEIN BINDING	C	1.0	1.0	1	12	ISDLHQTLKKEL	22028
3DAB	AB	CELL CYCLE	A	1.0	1.0	1	15	VKEVMHYLGQYIMVK	22029
3DAW	AB	STRUCTURAL PROTEIN/STRUCTURAL PROTEIN RE	A	1.0	1.0	1	10	IDIRKDLYAN	22030
3DBH	AB	CELL CYCLE	A	1.0	1.0	1	6	LKEQKY	22031
3DBH	CD	CELL CYCLE	D	1.0	1.0	1	11	LGCELLKNLAL	22032
3DBH	EF	CELL CYCLE	E	1.0	1.0	1	33	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQSI	22033
3DBH	EF	CELL CYCLE	F	1.0	1.0	1	21	ASTNAVIAAVCATEVFKIATS	22034
3DBH	GH	CELL CYCLE	G	1.0	1.0	1	6	GEDAGN	22035
3DD7	AB	RIBOSOME INHIBITOR	A	1.0	1.0	1	16	NKRTALNSALLFLRRN	22036
3DD7	CB	RIBOSOME INHIBITOR	B	1.0	1.0	1	9	EFASLFDTL	22037
3DGC	MR	CYTOKINE/SIGNALING PROTEIN	M	1.0	1.0	1	5	KSNFQ	22038
3DGE	AD	TRANSFERASE/SIGNALING PROTEIN	D	1.0	1.0	1	9	EDESLALSL	22039
3DHW	AC	MEMBRANE PROTEIN/HYDROLASE	A	1.0	1.0	1	6	ASRAMG	22040

3DIN	FG	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	1.0	1.0	1	11	GISILIFAGIV	22041
3DIN	FH	MEMBRANE PROTEIN, PROTEIN TRANSPORT	F	1.0	1.0	1	16	MLAGTMFLLWLGERIT	22042
3DL8	BH	PROTEIN TRANSPORT	B	1.0	1.0	1	18	STKLYVQANAFVRTLKAE	22043
3DMT	AC	OXIDOREDUCTASE	A	1.0	1.0	1	10	AEYFAYQMRY	22044
3DMT	AC	OXIDOREDUCTASE	C	1.0	1.0	1	10	AEYFAYQMRY	22045
3DNL	EF	VIRAL PROTEIN	F	1.0	1.0	1	9	MRDNWRSEL	22046
3DQV	AD	LIGASE	D	1.0	1.0	1	10	KEQIEWLIEH	22047
3DRA	AB	TRANSFERASE	B	1.0	1.0	1	15	KLAIIYFCLHGLQLI	22048
3DRA	AB	TRANSFERASE	B	1.0	1.0	1	16	NQELIYYRNFIINQFM	22049
3DS3	BD	VIRAL PROTEIN	B	1.0	1.0	1	14	FRDYVDRFAKTLRA	22050
3DTP	AC	CONTRACTILE PROTEIN	C	1.0	1.0	1	10	YEELVRMVLS	22051
3DTP	BD	CONTRACTILE PROTEIN	D	1.0	1.0	1	8	EEVEQLVA	22052
3DTU	AB	OXIDOREDUCTASE	B	1.0	1.0	1	7	SPLEIAW	22053
3DTV	AC	LYASE	C	1.0	1.0	1	12	MSTAVLNGLRAL	22054
3DUF	GF	OXIDOREDUCTASE/TRANSFERASE	G	1.0	1.0	1	7	VTDLISI	22055
3DVU	BD	VIRAL PROTEIN/APOPTOSIS	B	1.0	1.0	1	17	SGRIVGFFDVGRYVCEE	22056
3DW8	AC	HYDROLASE	C	1.0	1.0	1	12	FHDLMELFRIGG	22057
3DW8	AF	HYDROLASE	A	1.0	1.0	1	6	KDNTIE	22058
3DXA	AD	IMMUNE SYSTEM	A	1.0	1.0	1	29	PEYWDRETQISKTNTQTYRENLRTALRYY	22059
3DXA	NO	IMMUNE SYSTEM	O	1.0	1.0	1	7	EAEISHT	22060
3E1K	IJ	TRANSCRIPTION	J	1.0	1.0	1	8	MDDVYNYI	22061
3E1Y	AF	TRANSLATION	A	1.0	1.0	1	16	NVKFIQEKKLIGRYFD	22062
3E2Z	AB	TRANSFERASE, LYASE	A	1.0	1.0	1	16	TPLQAALAEAFWIDIK	22063
3EDQ	BD	HYDROLASE	B	1.0	1.0	1	15	FMHILTRVNRKVATE	22064
3EFD	HK	IMMUNE SYSTEM	K	1.0	1.0	1	25	AAEEAYTRTTRALHERFDRLERMLD	22065
3EIQ	DC	HYDROLASE/ANTITUMOR PROTEIN	C	1.0	1.0	1	12	ISEAEHCLKELE	22066
3ENO	BD	HYDROLASE/UNKNOWN FUNCTION	D	1.0	1.0	1	22	SSALRGTVNSYLRWIKAAIDVI	22067
3EPD	14	VIRAL PROTEIN	1	1.0	1.0	1	5	IESFF	22068
3ESW	AB	HYDROLASE	B	1.0	1.0	1	11	VEDLLSLRQVV	22069
3EUB	34	OXIDOREDUCTASE	4	1.0	1.0	1	10	PEHAERAAHV	22070
3EUB	AB	OXIDOREDUCTASE	A	1.0	1.0	1	7	VEEIEDA	22071
3EUB	BC	OXIDOREDUCTASE	C	1.0	1.0	1	10	PEHAERAAHV	22072
3EUB	SU	OXIDOREDUCTASE	S	1.0	1.0	1	7	RPILQGF	22073
3EUB	TU	OXIDOREDUCTASE	U	1.0	1.0	1	8	PEKIRNAC	22074
3EUH	AC	CELL CYCLE	C	1.0	1.0	1	12	QQELYDELLTLA	22075
3EXH	HG	OXIDOREDUCTASE	G	1.0	1.0	1	13	GQIFEAYNMAALW	22076
3EYJ	AB	VIRAL PROTEIN	B	1.0	1.0	1	20	LKSTQAAIDQINGKLNRLIE	22077
3EZQ	CD	APOPTOSIS	D	1.0	1.0	1	13	EEDLCAAFNVICD	22078

3EZQ	GH	APOPTOSIS	H	1.0	1.0	1	13	EEDLCAAFNVICD	22079
3EZQ	MN	APOPTOSIS	N	1.0	1.0	1	13	EEDLCAAFNVICD	22080
3F1E	FR	RIBOSOME	R	1.0	1.0	1	17	AKEQRILAKTIKRARIL	22081
3F1F	G4	RIBOSOME	G	1.0	1.0	1	5	VALPR	22082
3F1F	W5	RIBOSOME	W	1.0	1.0	1	10	LEEARNILRY	22083
3F3P	IL	STRUCTURAL PROTEIN	L	1.0	1.0	1	20	SSTFREWKNLVLKLSQAFGS	22084
3F3P	JK	STRUCTURAL PROTEIN	K	1.0	1.0	1	6	SAEYLQ	22085
3F3P	JL	STRUCTURAL PROTEIN	L	1.0	1.0	1	9	NSFAFELCS	22086
3F5C	AB	TRANSCRIPTION	A	1.0	1.0	1	11	LLIEMLHAKRA	22087
3F9K	AC	VIRAL PROTEIN, RECOMBINATION	C	1.0	1.0	1	15	MDSRLQRIHAEIKNS	22088
3F9K	BK	VIRAL PROTEIN, RECOMBINATION	K	1.0	1.0	1	21	QVIMEKSTMLYNKFKNMFLVG	22089
3F9K	ce	VIRAL PROTEIN, RECOMBINATION	c	1.0	1.0	1	12	IEPAQEEHEKYH	22090
3F9K	dO	VIRAL PROTEIN, RECOMBINATION	d	1.0	1.0	1	10	NLVARQIVNS	22091
3F9K	Vi	VIRAL PROTEIN, RECOMBINATION	V	1.0	1.0	1	10	NLVARQIVNS	22092
3F9K	VO	VIRAL PROTEIN, RECOMBINATION	O	1.0	1.0	1	21	QVIMEKSTMLYNKFKNMFLVG	22093
3FAL	AB	SIGNALING PROTEIN	A	1.0	1.0	1	7	RFAKLLL	22094
3FAL	AD	SIGNALING PROTEIN	A	1.0	1.0	1	14	PVTNICQAADKQLF	22095
3FCS	CD	CELL ADHESION/BLOOD CLOTTING	D	1.0	1.0	1	11	VNLYQNYSELI	22096
3FGC	AD	OXIDOREDUCTASE	D	1.0	1.0	1	12	FEQKMGELLSEN	22097
3FH6	FG	TRANSPORT PROTEIN	F	1.0	1.0	1	8	FVLIQLLT	22098
3FH6	HI	TRANSPORT PROTEIN	H	1.0	1.0	1	8	FVLIQLLT	22099
3FH6	HI	TRANSPORT PROTEIN	I	1.0	1.0	1	27	LWGDFAAAAVMSALPITIVFLLAQRWL	22100
3FH9	AB	OXYGEN TRANSPORT	A	1.0	1.0	1	19	PVNFKLLSHCLLVTLASHL	22101
3FIH	MS	RIBOSOME	M	1.0	1.0	1	18	GDLRREISMSIKRLMDLG	22102
3FIK	QR	RIBOSOME	Q	1.0	1.0	1	12	YRVAFQAVIKAG	22103
3FIN	FP	RIBOSOME	F	1.0	1.0	1	7	VYDIVRT	22104
3FKS	CF	HYDROLASE	C	1.0	1.0	1	7	AELFYKG	22105
3FKS	EG	HYDROLASE	G	1.0	1.0	1	27	MINRYSILYNRTRQAVITNELVDIITG	22106
3FKS	KO	HYDROLASE	O	1.0	1.0	1	5	EVFTG	22107
3FKS	NP	HYDROLASE	P	1.0	1.0	1	5	KIVAS	22108
3FKS	OP	HYDROLASE	P	1.0	1.0	1	29	MINRYSILYNRTRQAVITNELVDIITGAS	22109
3FKS	TW	HYDROLASE	T	1.0	1.0	1	14	LSKQAVAYRQLSLL	22110
3FKS	TX	HYDROLASE	X	1.0	1.0	1	15	IFRFTQAGSEVSALL	22111
3FKU	BY	VIRAL PROTEIN/IMMUNE SYSTEM	B	1.0	1.0	1	22	KESTQKAIDGVTNKVNSIIDKM	22112
3FKU	ED	VIRAL PROTEIN/IMMUNE SYSTEM	D	1.0	1.0	1	50	IENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL	22113
3FKU	FX	VIRAL PROTEIN/IMMUNE SYSTEM	F	1.0	1.0	1	22	KESTQKAIDGVTNKVNSIIDKM	22114
3FKU	GJ	VIRAL PROTEIN/IMMUNE SYSTEM	J	1.0	1.0	1	12	RRIENLNKKMED	22115
3FKU	IJ	VIRAL PROTEIN/IMMUNE SYSTEM	I	1.0	1.0	1	10	YEELKHLLSR	22116
3FLO	AB	TRANSFERASE	B	1.0	1.0	1	17	RELMETGRSVVQKYLND	22117

3FS4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	A	1.0	1.0	1	19	PVNFKLLGQCFLVVVAIHH	22118
3FS4	AB	OXYGEN STORAGE, OXYGEN TRANSPORT	B	1.0	1.0	1	20	PENFRLLGDILIIVLAAHFT	22119
3FSG	BD	HYDROLASE	B	1.0	1.0	1	10	YQEQLKLINH	22120
3FWC	BC	CELL CYCLE, TRANSCRIPTION	C	1.0	1.0	1	11	LKSQIQQYLVE	22121
3FWC	IJ	CELL CYCLE, TRANSCRIPTION	I	1.0	1.0	1	11	IKNLRRVAKEL	22122
3FWC	JL	CELL CYCLE, TRANSCRIPTION	L	1.0	1.0	1	13	WVDKVKDLTKSEM	22123
3FWC	NO	CELL CYCLE, TRANSCRIPTION	O	1.0	1.0	1	14	WVDKVKDLTKSEMN	22124
3G03	AB	CELL CYCLE	A	1.0	1.0	1	11	HRKIYTMIYRN	22125
3G33	CB	CELL CYCLE	B	1.0	1.0	1	16	LQLLGAVCMLLASKLR	22126
3G3B	EF	HYDROLASE/IMMUNE SYSTEM	F	1.0	1.0	1	8	VAWRNRCK	22127
3G43	BE	METAL BINDING PROTEIN	B	1.0	1.0	1	12	DEEVDEMIREAD	22128
3G43	BE	METAL BINDING PROTEIN	B	1.0	1.0	1	9	YEEFVQMMT	22129
3G4S	AZ	RIBOSOME	Z	1.0	1.0	1	5	TVRRS	22130
3G6J	CD	IMMUNE SYSTEM	C	1.0	1.0	1	7	KGVFVLN	22131
3G6J	CD	IMMUNE SYSTEM	C	1.0	1.0	1	11	QSKIWDVVEKA	22132
3G6J	CD	IMMUNE SYSTEM	D	1.0	1.0	1	21	LEKRQGALELIKKGYTQQLAF	22133
3G9K	DF	HYDROLASE	D	1.0	1.0	1	14	TDLARTLKKIQKEG	22134
3G9K	DF	HYDROLASE	D	1.0	1.0	1	16	AVDAAIVVSYVLGVVE	22135
3G9K	LS	HYDROLASE	L	1.0	1.0	1	5	AKGFY	22136
3G9K	LS	HYDROLASE	L	1.0	1.0	1	16	AVDAAIVVSYVLGVVE	22137
3GCG	AB	SIGNALING PROTEIN/TRANSCRIPTION	B	1.0	1.0	1	16	HGKLTNQLLQAVAKQT	22138
3GE8	AB	OXIDOREDUCTASE	A	1.0	1.0	1	5	EEQLF	22139
3GE8	DF	OXIDOREDUCTASE	D	1.0	1.0	1	7	LFFPHEY	22140
3GE8	DG	OXIDOREDUCTASE	D	1.0	1.0	1	14	WGRCWDVITENVLN	22141
3GGR	BC	CELL CYCLE	C	1.0	1.0	1	8	LTVLLDCL	22142
3GHG	AC	BLOOD CLOTTING	C	1.0	1.0	1	19	IDAATLKSRKMLEEIMKYE	22143
3GHG	DE	BLOOD CLOTTING	E	1.0	1.0	1	16	QQERPIRNSVDELNNN	22144
3GHG	EF	BLOOD CLOTTING	E	1.0	1.0	1	9	GCQLQEALL	22145
3GHG	EF	BLOOD CLOTTING	F	1.0	1.0	1	5	LSTYQ	22146
3GHG	HI	BLOOD CLOTTING	H	1.0	1.0	1	9	EYSSELEKH	22147
3GJF	DK	IMMUNE SYSTEM	D	1.0	1.0	1	29	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	22148
3GLH	AB	TRANSFERASE	B	1.0	1.0	1	6	VTILSR	22149
3GLH	FN	TRANSFERASE	F	1.0	1.0	1	8	LRALFDKH	22150
3GLH	KL	TRANSFERASE	L	1.0	1.0	1	13	EHVLTALANGLSL	22151
3GLH	NO	TRANSFERASE	O	1.0	1.0	1	20	APARLHWLATLLMDALKRHH	22152
3GLI	DE	TRANSFERASE/DNA	E	1.0	1.0	1	13	VDAVREVTEKLNE	22153
3GLI	IJ	TRANSFERASE/DNA	J	1.0	1.0	1	6	LKTLEE	22154
3GM1	BD	TRANSFERASE	B	1.0	1.0	1	31	SSSRTEIEGTQKLLNKDLAELINKMRLAQQN	22155

3GNI	AB	SIGNALING PROTEIN/SIGNALING PROTEIN	B	1.0	1.0	1	17	NEMVTFLQGELHVSKLF	22156
3GRW	LH	TRANSFERASE/IMMUNE SYSTEM	L	1.0	1.0	1	6	DEQLKS	22157
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.0	1.0	1	7	VSENVIL	22158
3GTM	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.0	1.0	1	6	IRARLK	22159
3GTM	AE	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	E	1.0	1.0	1	7	PVALYLG	22160
3GTM	AI	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.0	1.0	1	7	FEDNVVR	22161
3GTM	AS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.0	1.0	1	9	AGRLAEVNL	22162
3GTM	AS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	S	1.0	1.0	1	17	LKQKIEEIAKQNLYNAQ	22163
3GTU	CD	TRANSFERASE	D	1.0	1.0	1	12	SNAILRYIARKH	22164
3GZU	BO	VIRUS	O	1.0	1.0	1	15	SDLIQQFNQMIITMN	22165
3H0L	DF	LIGASE	D	1.0	1.0	1	13	IFEMYARTRDEGF	22166
3H0L	DH	LIGASE	H	1.0	1.0	1	10	KEWIEEIKKN	22167
3H0L	GK	LIGASE	G	1.0	1.0	1	20	PKEVVESFYDRYNQTEEKVK	22168
3H0L	JL	LIGASE	J	1.0	1.0	1	11	IIAPSEASSNL	22169
3H0L	MN	LIGASE	M	1.0	1.0	1	24	YYDAYYLKAQKVRRLITNDFLKAF	22170
3H1C	TU	TRANSFERASE	T	1.0	1.0	1	26	KEIMQVALNQAKGARLHILGVMEQAI	22171
3H2U	CD	CELL ADHESION	C	1.0	1.0	1	29	TKRALIQCAKDIAKASDEVTRLAKEVAKQ	22172
3H4P	Bb	HYDROLASE	b	1.0	1.0	1	6	LIAEAK	22173
3H4P	Ee	HYDROLASE	e	1.0	1.0	1	6	LYKMRT	22174
3H4P	Ii	HYDROLASE	i	1.0	1.0	1	6	LYKMRT	22175
3H4P	Nn	HYDROLASE	n	1.0	1.0	1	6	LIAEAK	22176
3HAE	GI	IMMUNE SYSTEM	G	1.0	1.0	1	6	SEELQA	22177
3HC0	HL	IMMUNE SYSTEM	L	1.0	1.0	1	6	DEQLKS	22178
3HEI	OP	TRANSFERASE/SIGNALING PROTEIN	O	1.0	1.0	1	6	SSDFEA	22179
3HKZ	AK	TRANSFERASE	A	1.0	1.0	1	11	EEAIAEAKEIM	22180
3HKZ	CE	TRANSFERASE	E	1.0	1.0	1	8	LNEIALNE	22181
3HKZ	IM	TRANSFERASE	I	1.0	1.0	1	8	ILHWLIKE	22182
3HKZ	JO	TRANSFERASE	O	1.0	1.0	1	6	ECLRYC	22183
3HKZ	MT	TRANSFERASE	M	1.0	1.0	1	11	IEAAREIIIRE	22184
3HKZ	MU	TRANSFERASE	U	1.0	1.0	1	16	RYEIARVISARALQLA	22185
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.0	1.0	1	15	VGVLAAQSIGEPATQ	22186

3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.0	1.0	1	6	IRARLK	22187
3HOU	MN	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	N	1.0	1.0	1	17	VAHLIECLLSKVAALSG	22188
3HOU	MQ	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	M	1.0	1.0	1	22	LKLQVLLDEEYKQLVKDRKFLR	22189
3HOU	PS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	P	1.0	1.0	1	17	EARLVIKEALVERRRAF	22190
3HOU	RS	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	R	1.0	1.0	1	17	KYERARILGTRALQISM	22191
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.0	1.0	1	12	VGVLAAQSIGEP	22192
3HOY	AB	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	A	1.0	1.0	1	5	KSIAK	22193
3HOY	AG	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	G	1.0	1.0	1	14	MKQYLKTKLLEEVE	22194
3HOY	CK	TRANSCRIPTION, TRANSFERASE/DNA-RNA HYBRID	C	1.0	1.0	1	6	TQMDQD	22195
3HQR	AS	OXIDOREDUCTASE/TRANSCRIPTION	A	1.0	1.0	1	5	SKDIR	22196
3HRD	CD	OXIDOREDUCTASE	C	1.0	1.0	1	9	TDLVIEIND	22197
3HRD	GH	OXIDOREDUCTASE	G	1.0	1.0	1	8	DLVIEIND	22198
3HRW	AB	OXYGEN TRANSPORT	B	1.0	1.0	1	17	PAAQAAFQKVVAGVATA	22199
3KIN	CD	MOTOR PROTEIN	C	1.0	1.0	1	8	KQIVKDVL	22200
3KIN	CD	MOTOR PROTEIN	D	1.0	1.0	1	16	KSLSALGNVISALAEG	22201
3PRO	AC	PRO REGION	C	1.0	1.0	1	17	PTQLPQYLQTEKLARTQ	22202
4RUB	BT	LYASE(CARBON-CARBON)	B	1.0	1.0	1	20	WRDRFLFCAEALYKAQAETG	22203
4RUB	DV	LYASE(CARBON-CARBON)	V	1.0	1.0	1	15	QEQLLSEVEYLLKNG	22204
5CSC	AB	OXO-ACID-LYASE	B	1.0	1.0	1	5	VDMSY	22205

[0054] As described *supra*, the collection of protein secondary structures that are at an interface of a two-chain inter-protein interaction can be classified by the biological function of the interacting proteins. These sub-collections of secondary structures at an interface of a two-chain inter-protein interaction provide targeted collections for identifying interactions that are suitable targets for therapeutic drug design and screening purposes. As shown in Figure 5, the representative collection of secondary structures at an interface of a two-chain inter-protein interaction identified using the methods described herein can be classified into several functional categories.

[0055] In one embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating the cell cycle. Table 3 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating cell cycle. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 3.

Table 3: Representative HIPP Interactions Involved in Cell Cycle

CLASSIFICATION	*PDB CODE*
APOPTOSIS	1D2Z, 1F3V, 1F9E, 1G5J, 1I3O, 1NW9, 1PQ1, 1TY4, 1ZY3, 2A5Y, 2G5B, 2JBY, 2JM6, 2K7W, 2NLA, 2OF5, 2P1L, 2PQK, 2PQN, 2PQR, 2ROC, 2ROD, 2V6Q, 2VOF, 2VOG, 2VOH, 2VOI, 2ZNE, 3D7V, 3EZQ, 3FDL, 3H11, 3I1H, 3YGS, 3EB6
APOPTOSIS INHIBITOR/APOPTOSIS	2K6Q, 1G73, 2PON
APOPTOSIS/HYDROLASE	1I4O, 1KMC, 2FUN, 3F2O
CELL CYCLE	1DOA, 1F47, 1GO4, 1I2M, 1N2D, 1N4M, 1OTR, 1R4M, 1SA0, 1XEW, 2AFF, 2CCI, 2DFK, 2DOQ, 2GGM, 2GV5, 2I3S, 2I3T, 2K2I, 2OBH, 2QYF, 2RAW, 2RAX, 2V4Z, 2VE7, 2W96, 3DAB, 3DAC, 3DBH, 3EAB, 3EUH, 3EUK, 3FDO, 3G03, 3G33, 3G65, 3GGR, 1KAT, 3C0R, 1G3N, 2AZE, 3FWB, 3FWC, 1IBR, 2ZXX, 1JOW, 1N4M
CELL CYCLE PROTEIN	1M45, 1M46
CELL CYCLE, STRUCTURAL PROTEIN	2QAG
CELL CYCLE/CELL CYCLE/CELL CYCLE	2QFA
CELL CYCLE/TRANSPORT PROTEIN	3E1R
COMPLEX (CYTOKINE/RECEPTOR)	1EER
COMPLEX (ONCOGENE PROTEIN/PEPTIDE)	1YCR
KINASE/KINASE ACTIVATOR	1H4L
LIGASE,CELL CYCLE	2AST
TRANSFERASE/CELL CYCLE	1OL5, 1WMH
OTHER	1YCS, 1BXL, 1AON

[0056] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating DNA binding. Table 4 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating DNA binding. These two-chain inter-protein interactions include proteins that target DNA but are not involved in transcription. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 4.

Table 4: Representative HIPP Interactions Involved in DNA Binding

CLASSIFICATION	*PDB CODE*
DNA BINDING PROTEIN	1L1O, 1N1J, 1OSV, 1T0F, 1UB4, 1UHL, 1XV9, 2A1J, 2BKY, 2HUE, 2NTI, 2O97, 3BQO, 3BU8, 3BUA, 3EI4, 3FPN, 1QUQ, 1VYJ, 2BYK
DNA BINDING PROTEIN, CHAPERONE	3BTP
DNA BINDING PROTEIN/ DNA	1AKH, 1AOI, 1JEY, 1PH1, 2O8F, 2QSH, 3EI2
DNA BINDING PROTEIN/ RECOMBINATION/ DNA	1P4E
DNA BINDING PROTEIN/ TRANSFERASE	1DML
HYDROLASE/ DNA	2D7D, 2PJR
ISOMERASE/ DNA	2B9S, 3FOE
LEUCINE ZIPPER	1A93
RECOMBINATION	2V1C
REPLICATION	1F2U, 1II8, 1P9D, 1SXJ, 1TUE, 1U7B, 2E9X, 2EHO, 2HII, 2HIK, 2IX2, 2PQA, 2Q9Q, 2R6C
REPLICATION, TRANSFERASE	1ZT2
REPLICATION,DNA BINDING PROTEIN	2PI2, 1YYP
REPLICATION/ DNA	2QBY
REPLICATION/ TRANSFERASE	1ZT2, 1YYP
STRUCTURAL PROTEIN/ DNA	1EQZ, 1F66, 1ID3, 1KX4, 1U35, 1ZBB, 2F8N, 2FJ7, 2I0Q, 2NQB, 2NZD, 3C1B
TRANSCRIPTION,TRANSFERASE/ DNA-RNA HYBRID	3ERC, 3GTM, 3HOU, 3HOY
TRANSFERASE/ DNA	1RTD, 3GLI
TRANSFERASE/ ELECTRON TRANSPORT/ DNA	1SKR
OTHER	1AXC, 1BI4, 1JB7, 2VTB, 1H6K, 2ZYZ

[0057] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating energy metabolism or enzymatic activity. Table 5 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating energy metabolism or enzymatic activity. These two-chain inter-protein interactions include hydrolases, oxidoreductases, and transferases, among other enzymes. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about

20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 5.

Table 5: Representative HIPP Interactions Involved in Energy Metabolism or Enzymatic Activity

CLASSIFICATION	*PDB CODE*
ASPARTYL PROTEASE	1LYW, 1AVF
ATP SYNTHASE	1SKY
COMPLEX (METALLOPROTEASE/ INHIBITOR)	1SMP, 1UEA
COMPLEX (PROTEASE/INHIBITOR)	1HIA
COMPLEX (PROTEINASE/INHIBITOR)	2SNI, 1SBN
COMPLEX (SERINE PROTEASE/INHIBITOR)	1A0H, 1AZZ, 1BCR, 1BTH, 1CA0, 1CBW, 1TBQ, 1CHO, 1CSE, 1MEE, 1TEC, 4SGB
COMPLEX (TRANSFERASE/ PEPTIDE)	1A81
DEHYDROGENASE	1H0H
DIOXYGENASE	1B4U
ELECTRON TRANSPORT	1O96, 1BGY, 1EFP, 1EYS, 1KN1, 1O94, 1PHN, 1Z8U, 2AXT, 2C7J, 2JBL, 2JXM, 2PUK, 2PVG, 2PVO, 2QJK, 2QJP, 2UUN, 3A0B, 3BZ1, 1JJU, 3A0B, 3BZ1
ELECTRON TRANSPORT(FLAVOCYTOCHROME)	1FCD
GLYCOSIDASE	2AAI
GLYCOSIDASE/CARBOHYDRATE	1ABR
GLYCOSYLASE	1UGH
HYDROGENASE	1E08, 13DE
HYDROLASE	1AOK, 1APY, 1AYY, 1B5F, 1CLV, 1CP9, 1E1H, 1E9Y, 1EJR, 1EUV, 1EZQ, 1FFU, 1FLC, 1FS0, 1FWA, 1FX0, 1FXW, 1G0U, 1GK0, 1HR8, 1HWM, 1ICF, 1ID5, 1IRU, 1IXR, 1IXS, 1JBU, 1JD2, 1JTG, 1K3B, 1KFU, 1KLI, 1N8O, 1N9G, 1NB3, 1NBF, 1NBW, 1NFU, 1NX0, 1OOK, 1OQS, 1OR0, 1OWS, 1OYV, 1P0S, 1PC8, 1Q5Q, 1Q5R, 1Q7L, 1QHH, 1R6O, 1RZO, 1S70, 1SCJ, 1SP4, 1T3M, 1V02, 1VZJ, 1W0Y, 1W1I, 1WPX, 1WYW, 1X3Z, 1XD3, 1XM4, 1XZP, 1Y75, 1YBQ, 1YM0, 1YU6, 1Z00, 2A1D, 2A7U, 2ADV, 2AYO, 2BFZ, 2BGN, 2BO9, 2BR2, 2C4F, 2CLY, 2CMY, 2CZV, 2D07, 2DD4, 2DFX, 2DOI, 2DXB, 2ES4, 2F43, 2F4O, 2FHH, 2GD4, 2GEZ, 2GJX, 2H4C, 2HD5, 2HLD, 2IAE, 2IBI, 2IOF, 2IUC, 2IZO, 2J0Q, 2J0S, 2J0T, 2J0U, 2J59, 2J5G, 2J7Q, 2J88, 2JE6, 2JEA, 2JET, 2JIZ, 2NGR, 2NP0, 2NYL, 2P2C, 2P3F, 2P9V, 2PV9, 2QE7, 2QKL, 2QKM, 2QL5, 2QOG, 2QY0, 2RD4, 2V7Q, 2VBL, 2VBN, 2VBO, 2VOY, 2VSK, 2WAX, 2WG8, 2WHP, 2WJV, 2Z2Y, 2ZAE, 2ZAL, 2ZCY, 2ZIV, 2ZIX, 2ZLE, 2ZU6, 3BGO, 3BN9, 3C5W, 3C91, 3D7W, 3DF0, 3DW8, 3E6P, 3EDQ, 3EDX, 3ESW, 3F6Z, 3F75, 3FKS, 3FSG, 3G9K, 3H4P, 3HKI, 3HKJ, 3I3T, 3UBP, 1AYY, 1IRU, 2HLD, 2VOY, 2ZCY, 2ZLE, 3C91
HYDROLASE (SERINE PROTEASE)	1EPT
HYDROLASE (SERINE PROTEINASE)	1HLE, 1HRT, 1HPP
HYDROLASE ACTIVATOR	1FNT, 1YA7, 1Z7Q, 2IY0
HYDROLASE INHIBITOR/HYDROLASE	1CQ4, 2H4P, 2H4Q, 3F02, 9PAI, 1TA3, 2NQD, 3F1S, 1B27, 1DP5, 1DPJ, 1DTD, 1EZX, 1F34, 1I51, 1IBX, 1LQM, 1SR5, 1WMI, 1XG2, 1Z7X, 1ZLH, 1ZLI, 2ABZ, 2D26, 2E2D, 2G2U, 2GKV, 2O3B, 2OUL, 2ZHX, 3B9F, 3BG4, 3BOW, 3CBJ, 3D4U, 3E2K, 1JIW
HYDROLASE(O-GLYCOSYL)	1NCA
HYDROLASE/HYDROLASE ACTIVATOR	1FNT, 1YA7, 1Z7Q, 2IY0
HYDROLASE/HYDROLASE INHIBITOR	1TA3, 2NQD, 3F1S, 1B27, 1DP5, 1DPJ, 1DTD, 1EZX, 1F34, 1I51, 1IBX, 1LQM, 1SR5, 1WMI, 1XG2, 1Z7X, 1ZLH, 1ZLI, 2ABZ, 2D26, 2E2D, 2G2U, 2GKV, 2O3B, 2OUL, 2ZHX, 3B9F, 3BG4, 3BOW, 3CBJ, 3D4U, 3E2K, 1JIW

HYDROLASE/HYDROLASE INHIBITOR/DNA	
HYDROLASE/INHIBITOR	1EJM, 1GPQ, 1JTD, 1OC0, 1UDI, 1UUZ, 2BEX, 2J8X, 2O8A, 2VU8
HYDROLASE/LIGASE	2GWF
HYDROLASE/PROTEIN BINDING	1NU7, 1NU9, 1V5I, 1ZNV, 2G4D, 2PT7, 1UPT
HYDROLASE/TRANSFERASE	1FQ1, 2NN6, 3D6N
HYDROLASE/UNKNOWN FUNCTION	3ENO
ISOMERASE	1CB7, 1E1C, 1W2W, 1XRS, 2HP0, 2PV2, 2ZBK, 3FDZ
LIGASE	1C4Z, 1EUC, 1FBV, 1FQV, 1FS1, 1FS2, 1FXT, 1JW9, 1LDK, 1U6G, 1UR6, 1Y8R, 1Y8X, 1Z56, 1Z5S, 2AKW, 2C4O, 2DF4, 2E 32, 2EJF, 2F9Y, 2GRN, 2NU9, 2O25, 2OOB, 2OXQ, 2RHS, 2VJE, 3D54, 3DQV, 3E 95, 3EQS, 3FN1, 3FSH, 3H0L
LIGHT HARVESTING COMPLEX	1LGH, 1CPCP, 1LIA, 1ALL
LUMINESCENCE	2G2S, 2GW4
LYASE	1AHJ, 1BXN, 1DIO, 1GXS, 1I1Q, 1I7M, 1I7Q, 1IBT, 1IR2, 1IRE, 1IWA, 1IWP, 1LVC, 1MHM, 1MT1, 1NBU, 1NZY, 1P7T, 1PYU, 1QDL, 1RCO, 1S0Y, 1SVD, 1UHE, 1UZD, 1UZH, 1V29, 1WDD, 1WDW, 1YSL, 1ZQ1, 2AL2, 2DPP, 2FYM, 2QCD, 2QQD, 2UZ1, 2VLH, 3DTV, 3ET6, 3GZD
LYASE (CARBON-CARBON)	1RLD, 4RUB
LYASE,OXIDOREDUCTASE/TRANSFERASE	1WDK
LYASE/OXIDOREDUCTASE	1NVM
LYASE/TRANSFERASE	2ISS
METHANOGENESIS	1HBM
MOLYBDENUM-IRON PROTEIN	1MIO
MONOOXYGENASE	1MTY
OXIDOREDUCTASE	1BCC, 1BIQ, 1BVY, 1CC1, 1DGH, 1DII, 1E6E, 1E6V, 1E6Y, 1E7P, 1EO2, 1EP3, 1F6M, 1FFT, 1FIQ, 1FYZ, 1G20, 1G72, 1G8K, 1GX7, 1H1L, 1H2A, 1H2R, 1H4J, 1JK0, 1JK9, 1JMX, 1JNR, 1JRO, 1JZD, 1KF6, 1KFY, 1KQF, 1LRW, 1M1Y, 1M56, 1MG2, 1MHY, 1MJG, 1N5W, 1NHG, 1NI4, 1NTK, 1OAO, 1OIJ, 1Q16, 1R1R, 1R27, 1RM6, 1SB3, 1SQB, 1SQX, 1T0Q, 1T3Q, 1TI2, 1ULI, 1UM9, 1USP, 1V54, 1VRQ, 1VRS, 1WQL, 1WYU, 1XLT, 1XME, 1Y56, 1YE9, 1YKK, 1YQ3, 1ZOY, 1ZY8, 2AFH, 2BMO, 2BP7, 2BRU, 2BS4, 2CKF, 2D0V, 2DE5, 2E1M, 2EQ7, 2EQ9, 2FBW, 2FOI, 2FRV, 2FUG, 2FYN, 2GAG, 2GBW, 2H9A, 2HT9, 2IBZ, 2IFQ, 2INN, 2INP, 2IVF, 2J55, 2J57, 2J7A, 2JGD, 2K9F, 2O8V, 2PKQ, 2QJY, 2R00, 2UW1, 2V1S, 2V3B, 2V4J, 2VDC, 2VL2, 2VR0, 2VRC, 2VVL, 2VYN, 2WD7, 2WD7, 2WME, 3B9J, 3BLW, 3BMC, 3C75, 3C7B, 3CF4, 3CWB, 3CXH, 3DHH, 3DMT, 3DTU, 3E7S, 3E9J, 3EH3, 3EN1, 3ETR, 3EUB, 3EXG, 3EXH, 3FGC, 3GE8, 3HRD, 1G20, 2P80, 1ZRT
OXIDOREDUCTASE COMPLEX	2RII
OXIDOREDUCTASE, TRANSFERASE	3DUF, 1J31
OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN	1Z5Y, 2FHS
OXIDOREDUCTASE/ELECTRON TRANSPORT	1KYO, 1NEK, 2A1T, 2ACZ, 2YVJ, 2ZON, 1T9G, 2GC4, 2A1T
OXIDOREDUCTASE/PROTEIN BINDING	2F5Z
OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	2UXN
PHOSPHOTRANSFERASE	1GLA, 1KI6
PHOTOSYNTHESIS	1B33, 1B8D, 1EYX, 1F99, 1GH0, 1I7Y, 1IJD, 1IZL, 1JB0, 1K6L, 1L9B, 1L9J, 1Q90, 1QGW, 1S5L, 1VF5, 1W5C, 2BV8, 2E 74, 2JIY, 2JJ0, 2O01, 2VJH, 2VJT, 2VML, 2ZT9, 3DBJ
POLYMERASE	2C35
PROTEIN BINDING/TRANSFERASE	2A78, 2OV2
SERINE PROTEASE	1DY8, 2HNT
SERINE PROTEINASE	1DX5
TRANSERASE,TOXIN	1S5E

TRANSFERASE	1BUH, 1CF4, 1D8D, 1DCE, 1F3M, 1F51, 1F5Q, 1F80, 1FM0, 1GO3, 1H5R, 1IW7, 1JQJ, 1JR3, 1KA9, 1MU2, 1N4Q, 1N8Z, 1N95, 1O2F, 1OW7, 1P16, 1POI, 1Q95, 1S78, 1TN6, 1TQY, 1U54, 1VRA, 1VYW, 1W98, 1XPK, 1XXH, 1XXI, 1Y14, 1YNJ, 1Z7M, 1ZUN, 2A3I, 2B8K, 2B9I, 2BE7, 2BE9, 2BOV, 2BTW, 2C52, 2DBU, 2DRN, 2EG4, 2F49, 2F9I, 2FEW, 2FHJ, 2FTK, 2GHO, 2GOO, 2HHF, 2HWN, 2HY5, 2HYB, 2I2X, 2IDO, 2IFG, 2J0M, 2JGZ, 2NNW, 2NPT, 2O2V, 2ONL, 2OQ1, 2PA8, 2QIE, 2QM6, 2QR1, 2R5C, 2RF4, 2RF9, 2V1Y, 2V36, 2V4I, 2V55, 2V5Q, 2V8Q, 2VDU, 2VDW, 2VGO, 2VJM, 2WEL, 3A1G, 3BWN, 3C66, 3C72, 3CDK, 3CR3, 3D7U, 3DRA, 3E0J, 3E8C, 3EZB, 3FDS, 3FHI, 3FLO, 3GLH, 3GM1, 3GTU, 3H1C, 3HGK, 3HKZ, 3HPG, 1IW7, 1LTX, 1HVU
TRANSFERASE/HYDROLASE	2BCJ, 2CG5
OTHER	1OE9, 1BXR, 1AJS, 1BJO, 1NWD, 2BCX, 1CDL, 1PON, 1SY9, 2BBM, 1CFF, 1CKK, 1CKN, 2PCF, 1AY7, 1DHK, 1TOC, 1TCO, 1IBC, 1A4Y, 1AVZ, 1BGX, 1YCP, 1SPB, 1JSU, 1DAN, 1AW8, 2HZE, 1QFN, 3CFA, 1BPL, 2QAR, 2QB0, 1MF8, 2FHX, 1M63, 1ONK, 1F96, 2GMI, 2K2Q, 3C14, 1XFU, 1XFV, 1GPW, 2NV2, 1RYP, 1NDO, 1HMV, 1OCC, 1MMO, 2V1D, 5CSC, 1HBH, 1PRC, 1PSS, 1FPP, 1PMA, 2PE6, 2QHO, 1EGP, 2BKR, 1E 44, 1CAX

[0058] A sub-collection of the collection of protein secondary structures potentially involved in modulating enzymatic activity is a collection of protein secondary structures at the interface of two-chain inter-protein interactions that include kinases. A representative collection of secondary structures that are at an interface of a two-chain inter-protein interaction that includes a kinase is shown in Table 6 below. The specific amino acid interface residues comprising the helical structures at the interface of the two-chain inter-protein interaction are also shown in Table 6. These, along with other helical structures at an interface of a kinase, are also included in Table 2.

Table 6: Interface Residues of the Secondary Structure Inter-Protein Interaction for Representative Kinases

PDB CODE	PARTNER	CHAIN	NUMBER	RESIDUES	SEQ ID NO:
1BLX	B	A	104 to 112	DLTTYLDKV	22206
1BLX	A	B	5 to 19	VCVGDRLSGAR	22207
1BLX	A	B	44 to 48	TALNV	22208
1BLX	A	B	76 to 84	SPVHDAART	22209
1KDX	B	A	597 to 611	QDLRSHLVHKLVQAI	22210
1KDX	B	A	646 to 664	RDEYYHLLAEKIYKIQKEL	22211
1KDX	A	B	119 to 131	TDSQKRREILSRR	22212
1KDX	A	B	134 to 145	YRKILNDLSSDA	22213
1OW6	D	A	1011 to 1046	VIDSLQQEYKKQMLTAHALAVDAKN LLDQARLKM	22214
1OW6	A	D	2 to 13	TRELDELMASLS	22215
1OW6	F	C	949 to 975	EYVPMVKEVGLALRTLATVDETIPLP	22216
1OW6	F	C	981 to 1007	REIEMAQKLLNSDLGELINKMKLAQQY	22217

1OW6	C	F	2 to 12	TRELDELMASL	22218
1WMH	B	A	73 to 88	SQLELEEAFRLYE	22219
1WMH	A	B	38 to 51	GFQEFSRLLRAVHQIPG	22220
1YJ5	C	B	227 to 242	PAEVFKGKVEAVLEKL	22221
2A19	A	B	489 to 500	FETSKFFTDLRD	22222
2CH4	W	A	497 to 501	VSEVS	22223
2CH4	A	W	507 to 517	MDVVKNVVESL	22224
2CH4	B	Y	140 to 145	KIIEEI	22225
2EHB	D	A	33 to 46	EEVEALYELFKLS	22226
2EHB	D	A	58 to 65	EEFQLALF	22227
2EHB	D	A	74 to 83	FADRIFDVFD	22228
2EHB	D	A	93 to 102	GEFVRSLGVF	22229
2EHB	D	A	109 to 120	HEKVKFAFKLYD	22230
2EHB	D	A	130 to 143	EELKEMVALHES	22231
2EHB	D	A	150 to 164	DMIEVMVDKAFVQAD	22232
2EHB	D	A	174 to 183	DEWKDFVSLN	22233
2EHB	A	D	311 to 318	NAFEMITL	22234
2GIT	F	D	57 to 84	PEYWEGETRKVKAHSQTHARV DLGTLRGY	22235
2GIT	F	D	138 to 149	MAQTTKHKWEA	22236
2GIT	F	D	152 to 160	VAEQLRAYL	22237
2GIT	F	D	162 to 174	GTCVEWLRRYLEN	22238
2NPT	D	A	74 to 95	SDEEMKAMLSYYSTVMEQQVN	22239
2NPT	B	C	75 to 95	DEEMKAMLSYYSTVMEQQVN	22240

[0059] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating immune system function. Table 7 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating immune system function. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 7.

Table 7: Representative HIPP Interactions Involved in Immune Function

CLASSIFICATION	***PDB CODE***
ANTIBIOTIC/IMMUNE SYSTEM	1XKM
ANTIBODY	1BFO, 1CE1, 1HEZ, 1UWE, 1GHF, 1JTO
ANTITUMOR PROTEIN	1JM7, 1GH6, 1T2V
BLOOD CLOTTING	1I5K, 1J9C, 1JMO, 1JOU, 1JY2, 1LQ8, 1LWU, 1M1J, 1N73, 1N86, 1SDD, 1SQ0, 1U0N, 1XMN, 2A45, 2B5T, 2FFD, 2HOD, 2PUQ, 2VVC, 3BVH, 3GHG, 3H32, 2ODY, 2ADF
CATALYTIC ANTIBODY	15C8, 1KEL, 1YED
CIRCADIAN CLOCK PROTEIN	1SUY, 1U9I
COAGULATION FACTOR	1RFN, 1IXX, 1E0F
COMPLEX (ANTIBODY/PEPTIDE)	1SM3, 2HIP

COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN)	1OS0
COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)	1NFD
COMPLEX (OXIDOREDUCTASE/ANTIBODY)	1AR1
COMPLEX(ANTIBODY-ANTIGEN)	1BJ1, 1FBI, 1FCC, 2JEL, 1JHL, 3HFM
HISTOCOMPATIBILITY ANTIGEN I-AK	1IAK
HYDROLASE, BLOOD CLOTTING, TOXIN	2E3X
HYDROLASE, BLOOD CLOTTING	2H9E, 3ENS
HYDROLASE/IMMUNE SYSTEM	1T6V, 1ZV5, 1ZVY, 3D9A, 3G3A, 3G3B, 3H42
IMMUNE SYSTEM	1OQD, 1BM3, 1BX2, 1BZ7, 1C12, 1C5B, 1C5D, 1CL7, 1CT8, 1CU4, 1CZ8, 1D9K, 1DEE, 1DN0, 1DQQ, 1DZB, 1ED3, 1EFX, 1EJO, 1ETZ, 1F11, 1F3D, 1F3J, 1F4W, 1F90, 1FE8, 1FG9, 1FH5, 1FJ1, 1FL5, 1FN4, 1FNS, 1FSK, 1FYH, 1G0Y, 1H0T, 1HDM, 1HQ4, 1HQR, 1HYR, 1I1A, 1I3R, 1I7Z, 1IL1, 1IM9, 1J8H, 1JGL, 1JGV, 1JL4, 1JNH, 1JNL, 1JPS, 1K8I, 1KC5, 1KCG, 1KCS, 1KFA, 1KJ2, 1KN2, 1KTD, 1KTK, 1L0X, 1L7T, 1LK3, 1LO0, 1LO4, 1LP1, 1LP9, 1LQS, 1MEX, 1MHP, 1MI5, 1MUJ, 1MVF, 1MWA, 1N0X, 1NAK, 1NC2, 1ND0, 1NGW, 1NJ9, 1NL0, 1OEY, 1OQO, 1P4B, 1PG7, 1PZ5, 1Q1J, 1Q72, 1Q9O, 1Q9W, 1R24, 1RHH, 1RIH, 1RJL, 1RZ7, 1RZF, 1RZG, 1RZI, 1S3K, 1S9V, 1SEQ, 1T4K, 1T66, 1TZH, 1TZI, 1U3H, 1UM4, 1UWX, 1UYW, 1W72, 1XCQ, 1XCT, 1XGP, 1YMM, 1YNK, 1YNT, 1YPZ, 1YY8, 1Z92, 1ZA6, 1ZAN, 1ZGL, 2A9M, 2AAB, 2ADG, 2AGJ, 2AI0, 2AJ3, 2AJZ, 2AK4, 2AP2, 2AQ1, 2ARJ, 2BC4, 2BDN, 2BRR, 2CMR, 2D03, 2DQT, 2E7L, 2EH8, 2ESV, 2F54, 2FJF, 2FL5, 2FX8, 2G2R, 2G60, 2G75, 2G9H, 2GJZ, 2GSI, 2HFG, 2HH0, 2HWZ, 2I26, 2I26, 2IAM, 2IAN, 2ICE, 2ICW, 2IPK, 2IPU, 2J5L, 2NNA, 2NOJ, 2NTF, 2NX5, 2O5X, 2OI9, 2OJZ, 2OQJ, 2OSL, 2P24, 2PXY, 2Q6W, 2Q86, 2Q8A, 2QEJ, 2QKI, 2QR0, 2RD7, 2UYL, 2V17, 2V7H, 2V7N, 2VL5, 2VLJ, 2VLR, 2VOL, 2VQ1, 2VWE, 2VXU, 2VXV, 2VYR, 2W65, 2W80, 2W9E, 2WBJ, 2WII, 2WIN, 2Z4Q, 2Z7X, 2Z8V, 2Z91, 2ZCK, 2ZPK, 32C2, 3BKJ, 3BKY, 3BQU, 3BT2, 3BZ4, 3C8K, 3CDG, 3CFB, 3CFD, 3CFK, 3CLE, 3CMO, 3CUP, 3CVH, 3D0L, 3D5O, 3D69, 3DGG, 3DIF, 3DVG, 3DXA, 3E3Q, 3E8U, 3EFD, 3EYF, 3EYQ, 3FFC, 3G04, 3G6A, 3G6D, 3G6J, 3GIZ, 3GJF, 3HAE, 3HC0, 3HE6, 3HE7, 3HG1, 3HNS, 3HRZ, 3HS0, 3HUJ, 3I2C, 7CEI, 1UVQ, 3GKW, 2FD6, 2FHZ, 2FSE, 3H0T, 2H9G, 1IQD, 1UJ3, 1Z3G, 3EOA, 1V7N, 2ERJ, 3D85, 3DUH, 3EO1, 1CBV, 1KEG, 2FR4, 3FFD, 3F8U, 1HH9, 1YJD, 1ZA3, 1HXY, 1LO5, 3ETB, 3B2U, 3GKW, 2FD6, 2FHZ, 2FSE, 1D9K, 1I3R, 1ZGL, 2GJ7, 2VXQ, 2JTT, 1TH1, 3FCS, 3FCU, 2GOX, 1XL3, 1IGC, 1WEJ, 1FPT, 1FDL, 2VIR, 1BVK, 1IAI, 1A2Y, 1NSN, 1MPA, 2HRP, 1AHW, 2SEB, 1SEB, 1AQD, 1AO7, 1BD2, 1UCY, 1ACY, 1KXV, 3EIQ, 1RIW, 1TB6, 1IAO, 1SBS, 1QLE, 1J34, 1QO3, 1QO3, 1OVA, 2Q97, 1FRT, 1UCY
IMMUNE SYSTEM RECEPTOR	2BNQ
IMMUNE SYSTEM, HYDROLASE	1C08, 1H0D, 1RI8, 1RJC, 2DQF, 2ZNW, 3EBA
IMMUNE SYSTEM/VIRAL PROTEIN	2DD8, 2I9L, 2QHR, 3CSY, 1GHQ, 2GJ7
IMMUNOGLOBULIN	1A3L, 1A4J, 1A6T, 1AD0, 1AD9, 1AE6, 1AJ7, 1AXT, 1BAF, 1CIC, 1CLO, 1CLY, 1DBA, 1DFB, 1FAI, 1FOR, 1GGI, 1IBG, 1IGF, 1IGT, 1IND, 1MCP, 1MFB, 1MIM, 1NLD, 1PLG, 1PSK, 1TET, 1VGE, 1YUH, 2FBJ, 2FGW, 2GFB, 2PCP, 7FAB, 12E8
ISOMERASE	1CB7, 1E1C, 1W2W, 1XRS, 2HP0, 2PV2, 2ZBK,

	3FDZ
ISOMERASE/IMMUNE SYSTEM	3F8U
TOXIN/IMMUNE SYSTEM	2NTS
TRANSFERASE/ANTIBODY/DNA	1T03
TRANSFERASE/IMMUNE SYSTEM/DNA	3GRW

[0060] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating cell membrane proteins or receptor interactions. Table 8 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating cell membrane proteins or receptor interactions. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 8.

Table 8: Representative HIPP Interactions of Membrane Proteins and Receptors

CLASSIFICATION	***PDB CODE***
CELL RECEPTOR	2CDE, 2CDF, 2CDG
LECTIN	1LEN, 1LOC, 1LOF, 2B7Y
LIPID BINDING PROTEIN	2PO6
MEMBRANE PROTEIN	1C17, 1EF1, 1H2S, 1K4C, 1KIL, 1ORQ, 1ORS, 1QD6, 1R3I, 1RPQ, 2A0L, 2A79, 2BE6, 2EXW, 2F93, 2F95, 2H8P, 2J8S, 2K9J, 2NZ0, 2ONK, 2QAC, 2QI9, 2VT1, 3B5N, 3C4M, 3C5J, 3CHX, 3DVE, 3EFF, 3EHU, 1Q68, 2RMK, 2FKW, 3BXK, 3CSL
MEMBRANE PROTEIN, IMMUNE SYSTEM, TOXIN	2F2L
MEMBRANE PROTEIN, PROTEIN TRANSPORT	3BZL, 3C01, 3C03, 3DIN, 2R9R
MEMBRANE PROTEIN, TRANSFERASE	2FFF
MEMBRANE PROTEIN,PROTEIN BINDING	2ODG, 1P8D
MEMBRANE PROTEIN/CHAPERON	1XKP
MEMBRANE PROTEIN/HYDROLASE	1P8V, 3DHW
MEMBRANE PROTEIN/MEMBRANE TRANSPORT	3DIN
OXIDOREDUCTASE, MEMBRANE PROTEIN	1YEW
OXYGEN BINDING	2R1H, 2RAO
PROTEIN BINDING/PROTEIN TRANSPORT	1VF6, 1VG0, 1VG9
RECEPTOR	2BYP, 2UZ6
RECEPTOR/GLYCOPROTEIN	2V5P
SUGAR BINDING PROTEIN	1GGP, 1LNU, 1PUM, 3C5Z, 3C60, 3C6L, 1NMU
OTHER	2PRG, 1A6A, 2SIV, 1GZL, 2IY1, 2J9D, 1RSO, 2HLF, 2FYL

[0061] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating other protein binding or have an unknown function. Table 9 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain

inter-protein interaction that are potentially involved in modulating other protein binding or have an unknown function. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 9.

Table 9: Representative HIPP Interactions Involved in Other Protein Binding or Unknown Function

CLASSIFICATION	*PDB CODE*
BINDING PROTEIN	1QO0
BIOSYNTHETIC PROTEIN	1TO9, 1TYG, 2HTM, 2Z2L, 2ZC5, 1RF8, 2ZU0, 1ZM2
COMPLEX (BLOOD COAGULATION/PEPTIDE)	1MKW
COMPLEX (OXIDOREDUCTASE/TRANSFERASE)	1EBD
COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE)	1X11
DE NOVO PROTEIN	1KD8, 1KDD, 1XOF, 1ZSZ, 1BB1, 2OTK, 1SVX
IMMUNE SYSTEM	1OQD, 1BM3, 1BX2, 1BZ7, 1C12, 1C5B, 1C5D, 1CL7, 1CT8, 1CU4, 1CZ8, 1D9K, 1DEE, 1DN0, 1DQQ, 1DZB, 1ED3, 1EFX, 1EJO, 1ETZ, 1F11, 1F3D, 1F3J, 1F4W, 1F90, 1FE8, 1FG9, 1FH5, 1FJ1, 1FL5, 1FN4, 1FNS, 1FSK, 1FYH, 1G0Y, 1H0T, 1HDM, 1HQ4, 1HQR, 1HYR, 1I1A, 1I3R, 1I7Z, 1IL1, 1IM9, 1J8H, 1JGL, 1JGV, 1JL4, 1JNH, 1JNL, 1JPS, 1K8I, 1KC5, 1KCG, 1KCS, 1KFA, 1KJ2, 1KN2, 1KTD, 1KTK, 1L0X, 1L7T, 1LK3, 1LO0, 1LO4, 1LP1, 1LP9, 1LQS, 1MEX, 1MHP, 1MI5, 1MUJ, 1MVF, 1MWA, 1N0X, 1NAK, 1NC2, 1ND0, 1NGW, 1NJ9, 1NL0, 1OEY, 1OQO, 1P4B, 1PG7, 1PZ5, 1Q1J, 1Q72, 1Q9O, 1Q9W, 1R24, 1RHH, 1RIH, 1RJL, 1RZ7, 1RZF, 1RZG, 1RZI, 1S3K, 1S9V, 1SEQ, 1T4K, 1T66, 1TZH, 1TZI, 1U3H, 1UM4, 1UWX, 1UYW, 1W72, 1XCQ, 1XCT, 1XGP, 1YMM, 1YNK, 1YNT, 1YPZ, 1YY8, 1Z92, 1ZA6, 1ZAN, 1ZGL, 2A9M, 2AAB, 2ADG, 2AGJ, 2AI0, 2AJ3, 2AJZ, 2AK4, 2AP2, 2AQ1, 2ARJ, 2BC4, 2BDN, 2BRR, 2CMR, 2D03, 2DQT, 2E7L, 2EH8, 2ESV, 2F54, 2FJF, 2FL5, 2FX8, 2G2R, 2G60, 2G75, 2G9H, 2GJZ, 2GSI, 2HFG, 2HH0, 2HWZ, 2I26, 2I26, 2IAM, 2IAN, 2ICE, 2ICW, 2IPK, 2IPU, 2J5L, 2NNA, 2NOJ, 2NTF, 2NX5, 2O5X, 2OI9, 2OJZ, 2OQJ, 2OSL, 2P24, 2PXY, 2Q6W, 2Q86, 2Q8A, 2QEJ, 2QKI, 2QR0, 2RD7, 2UYL, 2V17, 2V7H, 2V7N, 2VL5, 2VLJ, 2VLR, 2VOL, 2VQ1, 2VWE, 2VXU, 2VXV, 2VYR, 2W65, 2W80, 2W9E, 2WBJ, 2WII, 2WIN, 2Z4Q, 2Z7X, 2Z8V, 2Z91, 2ZCK, 2ZPK, 32C2, 3BKJ, 3BKY, 3BQU, 3BT2, 3BZ4, 3C8K, 3CDG, 3CFB, 3CFD, 3CFK, 3CLE, 3CMO, 3CUP, 3CVH, 3D0L, 3D5O, 3D69, 3DGG, 3DIF, 3DVG, 3DXA, 3E3Q, 3E8U, 3EFD, 3EYF, 3EYQ, 3FFC, 3G04, 3G6A, 3G6D, 3G6J, 3GIZ, 3GJF, 3HAE, 3HC0, 3HE6, 3HE7, 3HG1, 3HNS, 3HRZ, 3HS0, 3HUJ, 3I2C, 7CEI, 1UVQ, 3GKW, 2FD6, 2FHZ, 2FSE, 3H0T, 2H9G, 1IQD, 1UJ3, 1Z3G, 3EOA, 1V7N, 2ERJ, 3D85, 3DUH, 3EO1, 1CBV, 1KEG, 2FR4, 3FFD, 3F8U, 1HH9, 1YJD, 1ZA3, 1HXY, 1LO5, 3ETB, 3B2U, 3GKW, 2FD6, 2FHZ, 2FSE, 1D9K, 1I3R, 1ZGL, 2GJ7, 2VXQ, 2JTT, 1TH1, 3FCS, 3FCU, 2GOX, 1XL3, 1IGC, 1WEJ, 1FPT, 1FDL, 2VIR, 1BVK, 1IAI, 1A2Y, 1NSN, 1MPA, 2HRP, 1AHW, 2SEB, 1SEB, 1AQD, 1AO7, 1BD2, 1UCY, 1ACY, 1KXV, 3EIQ, 1RIW, 1TB6, 1IAO, 1SBS, 1QLE,

	1J34, 1QO3, 1QO3, 1OVA, 2Q97, 1FRT, 1UCY
METAL BINDING PROTEIN	1MXE, 1PSB, 1XK4, 1Z6O, 2HQW, 2K2F, 2O60, 2OGX, 2ZFB, 3G43, 2H61, 2H0D, 1QS7, 1IQ5, 1IWQ, 2JU0, 1YR5, 1ZUZ, 2BEC, 2E 30, 2FOT, 2JJZ, 2W73
PEPTIDE BINDING PROTEIN	2IHS
PLANT PROTEIN	1DGR, 1DGW, 2DS2, 2Q3N
PROTEIN BINDING	1IZN, 1L0O, 1OQP, 1X2T, 1YFN, 1ZL8, 1ZW3, 2ASQ, 2B87, 2DEN, 2DZN, 2FYZ, 2HYE, 2I94, 2IJ0, 2K3S, 2K8B, 2O98, 2ODB, 2R1T, 2VDB, 2ZL1, 3B71, 3CK4, 3CRP, 3DA7, 3DXC, 3F1I, 3GMW, 1ZL8
TRANSFERASE/PROTEIN BINDING	1LTX, 2QLV
UNKNOWN FUNCTION	1J7D, 1TPX, 2UVP, 2UYN, 2VH3, 3FXD, 2JND, 1QLS, 3PRO, 2V8F, 3MON

[0062] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating protein synthesis or turnover. Table 10 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating protein synthesis or turnover. These two-chain inter-protein interactions include chaperone proteins, proteosomes, ribosomes, and the like. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 10.

Table 10: Representative HIPP Interactions Involved in Protein Folding and Turnover

CLASSIFICATION	***PDB CODE***
CHAPERONE	1DKD, 1FXK, 1HT1, 1JYO, 1L2W, 1LZW, 1PCQ, 1TTW, 1USV, 1WE3, 1XQS, 2C2V, 2CG9, 2D0O, 2JKI, 2K5B, 2UWJ, 2VGX, 2ZDI, 3CQX, 3D2E, 3GZ1
CHAPERONE, PROTEIN TRANSPORT	2GUZ
CHAPERONE, STRUCTURAL, MEMBRANE PROTEIN	3BUW, 1ZE3
CHAPERONE/CELL INVASION	2FM8
COMPLEX (HSP24/HSP70)	1DKG
COMPLEX OF TWO ELONGATION FACTORS	1EFU, 1AIP
HISTONE/CHAPERONE	3CFV
HYDROLASE/TRANSLATION	2VSO
PROTEASOME ACTIVATOR	1AVO
PROTEIN SYNTHESIS/TRANSFERASE	2A19
PROTEIN TURNOVER/PROTEIN TURNOVER	2DYM
RIBOSOME	1CE7, 1DD4, 1G1X, 1HR0, 1I94, 1IBL, 1JJ2, 1KQS, 1N34, 1PNS, 1Q86, 1QVF, 1S1H, 1T0K, 1VOQ, 1VQN, 1VQP, 1VS5, 1VS6, 1VSA, 1VSP, 1W2B, 1XMQ, 1YL3, 1YL4, 2B9M, 2D3O, 2E5L, 2GY9, 2GYA, 2HGI, 2HGJ, 2HGP, 2HGR, 2HHH, 2I2P, 2I2T, 2J01, 2J03, 2J28, 2J37, 2OM7, 2OTJ, 2QA4, 2QBE, 2QEX, 2QOU, 2QOW, 2QOY, 2QP0, 2V46, 2VHM, 2VHN, 2VHO, 2WDI, 2WH1, 2WH2, 2WH4, 2ZJQ, 3BBN, 3BBO, 3BO0, 3CMA, 3D5A, 3D5B, 3D5D, 3DEG, 3F1E, 3F1F, 3FIC, 3FIH, 3FIK, 3FIN, 3G4S
RIBOSOME INHIBITOR	3DD7

RIBOSOME INHIBITOR, HYDROLASE	IJCH
STRUCTURAL PROTEIN/CHAPERONE	1XOU
TRANSFERASE/RIBOSOMAL PROTEIN	3CJS, 3CJT
TRANSLATION	1EJH, 1F60, 1RK8, 1RY1, 1XB2, 2D1P, 2D74, 2GID, 2HDN, 2JGB, 2QMU, 2V8W, 3CW2, 3E1Y
TRANSLATION/IMMUNE SYSTEM	1SYX
TRANSLATION/RNA	2GJE, 2GO5
OTHER	2GGP, 3C7N, 1HX1, 1G3I, 1G4B, 1YYF, 2Z5C, 2JSS, 2PQ4, 2IO5, 2NVU, 2FIF, 2PMZ, 1WKW

[0063] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating RNA binding. Table 11 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating RNA binding. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 11.

Table 11: Representative HIPP Interactions Involved in RNA Binding

CLASSIFICATION	*PDB CODE*
HYDROLASE	1AOK, 1APY, 1AYY, 1B5F, 1CLV, 1CP9, 1E1H, 1E9Y, 1EJR, 1EUV, 1EZQ, 1FFU, 1FLC, 1FS0, 1FWA, 1FX0, 1FXW, 1G0U, 1GK0, 1HR8, 1HWM, 1ICF, 1ID5, 1IRU, 1IXR, 1IXS, 1JBU, 1JD2, 1JTG, 1K3B, 1KFU, 1KLI, 1N8O, 1N9G, 1NB3, 1NBF, 1NBW, 1NFU, 1NX0, 1OOK, 1OQS, 1OR0, 1OWS, 1OYV, 1P0S, 1PC8, 1Q5Q, 1Q5R, 1Q7L, 1QHH, 1R6O, 1RZO, 1S70, 1SCJ, 1SP4, 1T3M, 1V02, 1VZJ, 1W0Y, 1W1I, 1WPX, 1WYW, 1X3Z, 1XD3, 1XM4, 1XZP, 1Y75, 1YBQ, 1YM0, 1YU6, 1Z00, 2A1D, 2A7U, 2ADV, 2AYO, 2BFZ, 2BGN, 2BO9, 2BR2, 2C4F, 2CLY, 2CMY, 2CZV, 2D07, 2DD4, 2DFX, 2DOI, 2DXB, 2ES4, 2F43, 2F4O, 2FHH, 2GD4, 2GEZ, 2GJX, 2H4C, 2HD5, 2HLD, 2IAE, 2IBI, 2IOF, 2IUC, 2IZO, 2J0Q, 2J0S, 2J0T, 2J0U, 2J59, 2J5G, 2J7Q, 2J88, 2JE6, 2JEA, 2JET, 2JIZ, 2NGR, 2NP0, 2NYL, 2P2C, 2P3F, 2P9V, 2PV9, 2QE7, 2QKL, 2QKM, 2QL5, 2QOG, 2QY0, 2RD4, 2V7Q, 2VBL, 2VBN, 2VBO, 2VOY, 2VSK, 2WAX, 2WG8, 2WHP, 2WJV, 2Z2Y, 2ZAE, 2ZAL, 2ZCY, 2ZIV, 2ZIX, 2ZLE, 2ZU6, 3BGO, 3BN9, 3C5W, 3C91, 3D7W, 3DF0, 3DW8, 3E6P, 3EDQ, 3EDX, 3ESW, 3F6Z, 3F75, 3FKS, 3FSG, 3G9K, 3H4P, 3HKI, 3HKJ, 3I3T, 3UBP, 1AYY, 1IRU, 2HLD, 2VOY, 2ZCY, 2ZLE, 3C91
HYDROLASE/RNA	3DD2
HYDROLASE/RNA BINDING PROTEIN/RNA	2HYI, 3EX7
ISOMERASE/BIOSYNTHETIC PROTEIN/RNA	2HVY, 3HAX, 3HAY, 2EY4
ISOMERASE/RNA	2RFK, 3HJW, 3HJY
LIGASE/RNA	1EIY
LIGASE/RNA BINDING PROTEIN	2HRK, 2HSN
RIBOSOME	1CE7, 1DD4, 1G1X, 1HR0, 1I94, 1IBL, 1JJ2, 1KQS, 1N34, 1PNS, 1Q86, 1QVF, 1S1H, 1T0K, 1VOQ, 1VQN, 1VQP, 1VS5, 1VS6, 1VSA, 1VSP, 1W2B, 1XMQ, 1YL3, 1YL4, 2B9M, 2D3O, 2E5L, 2GY9, 2GYA, 2HGI, 2HGJ, 2HGP, 2HGR, 2HHH, 2I2P, 2I2T, 2J01, 2J03, 2J28, 2J37, 2OM7, 2OTJ, 2QA4,

	2QBE, 2QEX, 2QOU, 2QOW, 2QOY, 2QP0, 2V46, 2VHM, 2VHN, 2VHO, 2WDI, 2WH1, 2WH2, 2WH4, 2ZJQ, 3BBN, 3BBO, 3BO0, 3CMA, 3D5A, 3D5B, 3D5D, 3DEG, 3F1E, 3F1F, 3FIC, 3FIH, 3FIK, 3FIN, 3G4S
RNA BINDING PROTEIN	1D3B, 1JGN, 1JH4, 1JMT, 1N52, 1NT2, 1O0P, 1P27, 1Y96, 2BA0, 2BA1, 2DT7, 2F9D, 2FHO, 1UW4, 2J98, 2UY1, 2W2H
RNA BINDING PROTEIN/RNA	1A9N, 2OZB
STRUCTURAL PROTEIN/RNA	1YSH
TRANSFERASE/RNA	1HVU
OTHER	2APO, 2ZKR, 3CM8

[0064] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating cell signaling. Table 12 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating cell signaling. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 12.

Table 12: Representative HIPP Interactions Involved in Cell Signalling

CLASSIFICATION	***PDB CODE***
ALU RIBONUCLEOPROTEIN PARTICLE	1E8O
CELL CYCLE	1DOA, 1F47, 1GO4, 1I2M, 1N2D, 1N4M, 1OTR, 1R4M, 1SA0, 1XEW, 2AFF, 2CCI, 2DFK, 2DOQ, 2GGM, 2GV5, 2I3S, 2I3T, 2K2I, 2OBH, 2QYF, 2RAW, 2RAX, 2V4Z, 2VE7, 2W96, 3DAB, 3DAC, 3DBH, 3EAB, 3EUH, 3EUK, 3FDO, 3G03, 3G33, 3G65, 3GGR
CIRCADIAN CLOCK PROTEIN	1SUY, 1U9I
COMPLEX (GTP-BINDING/TRANSDUCER)	1GG2, 1GOT, 1TBG
COMPLEX (INHIBITOR PROTEIN/KINASE)	1BI8
COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)	1TCE
CYTOKINE	1ES7, 1I1R, 1ICE, 1PGR, 2K03, 2PSM, 2VXS, 2VXT, 3D87
CYTOKINE/CYTOKINE RECEPTOR	2Q7N, 2B5I, 2Z3R, 3BPL, 3BPN, 3BPO, 3DI2, 3G9V
CYTOKINE/RECEPTOR	1J7V, 2QJ9
CYTOKINE/SIGNALING PROTEIN	2O26, 3DGC, 3EJJ
G PROTEIN	1ZBD
HORMONE	1A7F, 1PID, 1VKT, 2K6T, 2K91, 2KBC, 2OM0, 3BDY, 3FUB, 7INS, 2FJH, 1M2Z
HORMONE RECEPTOR	2ZSH, 3HHR, 3D48
HORMONE(MUSCLE RELAXANT)	6RLX
HORMONE/GROWTH FACTOR	1BP3, 1BSX, 1K3M, 1KF9, 1M4U, 1PMX, 1RDT, 1T1K, 1XWD, 2ARP, 2GH0, 2H62, 2H67, 2H8B, 2NXX, 2OCF
HORMONE/GROWTH FACTOR RECEPTOR	1DKF, 1QTY, 1R1K, 1R20, 1XDK, 1Z5X, 1RV6
HORMONE/GROWTH FACTOR/HORMONE RECEPTOR	1F6F
HORMONE/GROWTH FACTOR/TRANSFERASE	2FDB
HORMONE/HORMONE RECEPTOR	3D48
HORMONE/SIGNALING PROTEIN	3C9A
HYDROLASE/PROTEIN-BINDING	1NU7, 1NU9, 1V5I, 1ZNV, 2G4D, 2PT7, 1UPT
INSULIN-LIKE BRAIN-SECRETORY	1BOM

PEPTIDE	
ION CHANNEL/RECEPTOR	1OED, 2BG9
ISOMERASE/SIGNALING PROTEIN	1X75
LIGASE/SIGNALING PROTEIN	2JMF
NERVE GROWTH FACTOR/TRKA COMPLEX	1WWW
PROTEIN BINDING/HORMONE/GROWTH FACTOR	2DSQ, 2DSR
PROTEIN-BINDING	1IZN, 1L0O, 1OQP, 1X2T, 1YFN, 1ZL8, 1ZW3, 2ASQ, 2B87, 2DEN, 2DZN, 2FYZ, 2HYE, 2I94, 2IJ0, 2K3S, 2K8B, 2O98, 2ODB, 2R1T, 2VDB, 2ZL1, 3B71, 3CK4, 3CRP, 3DA7, 3DXC, 3F1I, 3GMW
PROTEIN-BINDING/HYDROLASE	2IO1
SIGNALING PROTEIN	1B9X, 1CC0, 1CXZ, 1DEV, 1DS6, 1EMU, 1FQJ, 1G4U, 1G4Y, 1HE1, 1HV2, 1I4D, 1JDP, 1JJO, 1KI1, 1KJY, 1KMI, 1KZ7, 1LB1, 1MDU, 1MR1, 1NF3, 1OO0, 1OXK, 1P22, 1R5V, 1R5W, 1S1C, 1SHZ, 1T0J, 1U0S, 1U7F, 1U8T, 1WR1, 1XD2, 1Y3A, 1YOV, 1Z2C, 1ZC4, 2BAP, 2BBA, 2BWE, 2FHW, 2FU5, 2GCO, 2GTP, 2H7V, 2HJ9, 2IHB, 2IK8, 2JY6, 2K42, 2NTY, 2ODE, 2P1N, 2P6A, 2PBI, 2QQK, 2QQN, 2R4R, 2RIV, 2VRW, 2WG3, 2ZET, 3BH6, 3BJI, 3C7K, 3CX6, 3EG5, 3EDL, 3FAL, 3HO5, 1HL6, 3C59, 3F6Q, 3GNI, 2PL9, 1E0A, 2CNW, 1EAY, 1XCG, 2RGN, 1FOE, 2NZ8, 2IE3, 2NPP, 1T34, 2PK9, 2POP, 1P9M, 1PVH, 2D9Q, 3HH2, 3CF6, 1HH4, 1NIW, 1K5D, 2ZVN, 3GCG
SIGNALING PROTEIN / CELL ADHESION	3D1M
SIGNALING PROTEIN,MEMBRANE PROTEIN	1X86, 3BS5
SIGNALING PROTEIN,TRANSFERASE	1IB1, 2OZA, 2QME, 2ZFD, 2EHB
SIGNALING PROTEIN/APOPTOSIS	2FJU
SIGNALING PROTEIN/HORMONE	2QKH
SIGNALING PROTEIN/HYDROLASE	2QIY, 2W2X, 3DOE
SIGNALING PROTEIN/LIPOPROTEIN	2REX
SIGNALING PROTEIN/TRANSPORT PROTEIN	3BC1
TRANSFERASE/HORMONE	2E9W
TRANSFERASE/SIGNALING PROTEIN	2AUH, 3CZU, 3DGE, 3HEI
OTHER	1A0O, 1CM1, 1AM4, 1GUA, 1WQ1, 1B6C, 1BI7, 1EFN, 1AGR, 1TX4, 1F45, 1I9R, 3EVS, 1EM8, 1KV6, 1L8C, 1LQB, 1S4Z, 1YKE, 2CZY, 2QXV, 2VPD, 2VPE, 2VPG, 1IYJ, 1MIU, 1N0W, 1MJE, 1CQT, 1D3U, 2H1O, 1IK9, 1UEL, 1OW3, 3A1Q, 2FO1, 3BRW, 1CN4, 3B4V, 2WC0, 2JRI, 2ZNV, 1H59, 3H9R, 1O9U, 2IZX, 1NEX, 1CUL, 2DWZ, 3EQY, 3FMO, 3FMP, 1KPE, 2RD0

[0065] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating cell structure or cellular adhesion. Table 13 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating cell structure or cellular adhesion. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about

100% of the protein secondary structures that are present in the PDB entries identified in Table 13.

Table 13: Representative HIPP Interactions Involved in Cell Structure or Adhesion

CLASSIFICATION	*PDB CODE*
CELL ADHESION	1DOW, 1I7W, 1J19, 1JPW, 1KUP, 1L5G, 1OHZ, 1QZ7, 1SYQ, 1TYE, 1U6H, 2CCL, 2D10, 2EMT, 2OZ4, 2P28, 2VN5, 2VZD, 2VZG, 2VZI, 2YVC, 3H2U, 3H2V,
CELL ADHESION, STRUCTURAL PROTEIN	1RKE, 1YDI, 2GWW, 2IBF
CELL ADHESION/IMMUNE SYSTEM	2VDN, 2VDO
COMPLEX (SKELETAL MUSCLE/MUSCLE PROTEIN)	1A2X
CONTRACTILE PROTEIN	1C0G, 1DFK, 1DFL, 1I84, 1J1D, 1J1E, 1M8Q, 1MVW, 1O18, 1QVI, 1RGI, 1YAG, 1YTZ, 1YV0, 2AKA, 2EC6, 2EKV, 2OS8, 3DTP, 1DFK, 1I84, 1J1E, 1M8Q, 1MVW, 1O18, 2EC6, 3DTP, 3B63
CYTOSKELETAL PROTEIN	2BTO
HYDROLASE/STRUCTURAL PROTEIN	2B59, 2Z0E
MOTOR PROTEIN	2KIN, 2VAS, 3DCO, 3KIN, 3H4S, 2BKI
MUSCLE PROTEIN	1BR1, 1WDC, 2BL0
STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	2FF6, 2V51, 2V52
OTHER	1H1V, 1XWJ, 1HLU, 2IX7, 1KXP, 3B63, 2DFS, 2AUS, 1MTP, 2G38, 2OPL, 3H6P, 3HHL, 1H8B, 1LUJ, 1M1E, 1MDU, 1MK9, 1MWN, 1NPQ, 1OZS, 1T60, 1Y64, 1ZAV, 2A40, 2A4J, 2ACM, 2BTQ, 2G9J, 2H7D, 2HL5, 2PBD, 2PG1, 2WBE, 3BYH, 3CHW, 3CIP, 3CJB, 3DWL, 3EDL, 3F3P, 2FV4, 2KBR, 3F7P, 3CJC, 1SQK, 3DAW, 1CJF

[0066] In another embodiment of the present invention, the collection is a collection of protein secondary structures from toxins, viruses, or bacteria. Table 14 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are from toxins, viruses, or bacteria. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 14.

Table 14: Representative HIPP Interactions of Toxins, Viruses, and Bacteria

CLASSIFICATION	*PDB CODE*
ANTIBIOTIC RESISTANCE	1E3A
BACTERIAL CELL DIVISION INHIBITOR	1OFU
ENTEROTOXIN	1HTL, 1LT4, 1TII
PROTEIN BINDING/TOXIN	2O02
PROTEIN BINDING/VIRAL PROTEIN	2BL5
PROTEIN BINDING/VIRUS/DNA	1ZLA
TOXIN	1BCP, 1ECI, 1KVD, 1PTO, 1R4P, 1R4Q, 1SB2, 1SR4, 1WQ9, 1XTC, 1XTG, 2F2F, 2OZN, 2ZOE, 3BPQ, 3BX4, 1TZN, 1UEX, 1GZS, 1HC9, 3BUZ, 2KC8, 1PTO
TOXIN INHIBITOR/TOXIN	2A6Q
TOXIN/ANTITOXIN	3DBO, 3G5O, 3H87
TOXIN/PROTEIN BINDING	2NYD
TOXIN/TOXIN INHIBITOR	1TFO

TUBERCULOSIS	1WA8
VIRAL PROTEIN	1C8O, 1FAV, 1G2C, 1JEK, 1JMU, 1JSD, 1JSM, 1M93, 1QRJ, 1RD8, 1RU7, 1RUY, 1RUZ, 1SVF, 1T6O, 1TI8, 1ZV8, 2BEQ, 2BEZ, 2FK0, 2GOL, 2H1L, 2IBX, 2RFT, 3DNL, 3DS3, 3EPC, 3EPD, 3EPF, 3EYJ, 3EYM, 3GBM, 1JXP, 2NZ1, 2Z2T, 3HHZ, 3CL3
VIRAL PROTEIN, RECOMBINATION	2B4J, 3F9K
VIRAL PROTEIN, REPLICATION	2AHM
VIRAL PROTEIN/ TRANSLATION	1LJ2
VIRAL PROTEIN/APOPTOSIS	3BL2, 3DVU
VIRAL PROTEIN/IMMUNE SYSTEM	1A3R, 1AFV, 1EO8, 1F58, 1FRG, 1G9M, 1KEN, 1KG0, 1QFU, 1YYL, 1ZTX, 2B4C, 2NY7, 2QAD, 3BGF, 3FKU, 3GBN
VIRAL PROTEIN/NUCLEAR PROTEIN	2RHK
VIRAL PROTEIN/SIGNALING PROTEIN	3CL3
VIRUS	1AL0, 1B35, 1BBT, 1BEV, 1D4M, 1EAH, 1EV1, 1FMD, 1NY7, 1OOP, 1PIV, 1POV, 1R1A, 1RHI, 1TME, 1UF2, 1Z7S, 1Z8Y, 1ZBA, 2BTV, 2MEV, 2QQP, 2W0C, 3CJI, 3GZU, 1QGC, 1RVF
VIRUS/DNA	2BPA
VIRUS/RECEPTOR	1V9U, 1Z7Z, 2JIK
VIRUS/RNA	1BMV, 1F8V, 2BBV, 2Q26
OTHER	2GYK, 2PF4, 2PKG, 2AJF, 1YRT, 3DCG, 1N 0V

[0067] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating gene transcription. Table 15 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating gene transcription. These two-chain inter-protein interactions include transcriptional activators, repressors, or other components of the transcription machinery. A preferred collection according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 15.

Table 15: Representative HIPP Interactions Involved in Transcription

CLASSIFICATION	*PDB CODE*
IMMUNE SYSTEM	1OQD, 1BM3, 1BX2, 1BZ7, 1C12, 1C5B, 1C5D, 1CL7, 1CT8, 1CU4, 1CZ8, 1D9K, 1DEE, 1DN0, 1DQQ, 1DZB, 1ED3, 1EFX, 1EJO, 1ETZ, 1F11, 1F3D, 1F3J, 1F4W, 1F90, 1FE8, 1FG9, 1FH5, 1FJ1, 1FL5, 1FN4, 1FNS, 1FSK, 1FYH, 1G0Y, 1H0T, 1HDM, 1HQ4, 1HQR, 1HYR, 1I1A, 1I3R, 1I7Z, 1IL1, 1IM9, 1J8H, 1JGL, 1JGV, 1JL4, 1JNH, 1JNL, 1JPS, 1K8I, 1KC5, 1KCG, 1KCS, 1KFA, 1KJ2, 1KN2, 1KTD, 1KTK, 1L0X, 1L7T, 1LK3, 1LO0, 1LO4, 1LP1, 1LP9, 1LQS, 1MEX, 1MHP, 1MI5, 1MUJ, 1MVF, 1MWA, 1N0X, 1NAK, 1NC2, 1ND0, 1NGW, 1NJ9, 1NL0, 1OEY, 1OQO, 1P4B, 1PG7, 1PZ5, 1Q1J, 1Q72, 1Q9O, 1Q9W, 1R24, 1RHH, 1RIH, 1RJL, 1RZ7, 1RZF, 1RZG, 1RZI, 1S3K, 1S9V, 1SEQ, 1T4K, 1T66, 1TZH, 1TZI, 1U3H, 1UM4, 1UWX, 1UYW, 1W72, 1XCQ, 1XCT, 1XGP, 1YMM, 1YNK, 1YNT, 1YPZ, 1YY8, 1Z92, 1ZA6, 1ZAN, 1ZGL, 2A9M, 2AAB, 2ADG, 2AGJ, 2AI0, 2AJ3, 2AJZ, 2AK4, 2AP2, 2AQ1, 2ARJ, 2BC4, 2BDN, 2BRR, 2CMR, 2D03, 2DQT, 2E7L, 2EH8, 2ESV, 2F54, 2FJF, 2FL5,

	2FX8, 2G2R, 2G60, 2G75, 2G9H, 2GJZ, 2GSI, 2HFG, 2HH0, 2HWZ, 2I26, 2I26, 2IAM, 2IAN, 2ICE, 2ICW, 2IPK, 2IPU, 2J5L, 2NNA, 2NOJ, 2NTF, 2NX5, 2O5X, 2OI9, 2OJZ, 2OQJ, 2OSL, 2P24, 2PXY, 2Q6W, 2Q86, 2Q8A, 2QEJ, 2QKI, 2QR0, 2RD7, 2UYL, 2V17, 2V7H, 2V7N, 2VL5, 2VLJ, 2VLR, 2VOL, 2VQ1, 2VWE, 2VXU, 2VXV, 2VYR, 2W65, 2W80, 2W9E, 2WBJ, 2WII, 2WIN, 2Z4Q, 2Z7X, 2Z8V, 2Z91, 2ZCK, 2ZPK, 32C2, 3BKJ, 3BKY, 3BQU, 3BT2, 3BZ4, 3C8K, 3CDG, 3CFB, 3CFD, 3CFK, 3CLE, 3CMO, 3CUP, 3CVH, 3D0L, 3D5O, 3D69, 3DGG, 3DIF, 3DVG, 3DXA, 3E3Q, 3E8U, 3EFD, 3EYF, 3EYQ, 3FFC, 3G04, 3G6A, 3G6D, 3G6J, 3GIZ, 3GJF, 3HAE, 3HC0, 3HE6, 3HE7, 3HG1, 3HNS, 3HRZ, 3HS0, 3HUJ, 3I2C, 7CEI, 1UVQ, 3GKW, 2FD6, 2FHZ, 2FSE, 3H0T, 2H9G, 1IQD, 1UJ3, 1Z3G, 3EOA, 1V7N, 2ERJ, 3D85, 3DUH, 3EO1, 1CBV, 1KEG, 2FR4, 3FFD, 3F8U, 1HH9, 1YJD, 1ZA3, 1HXY, 1LO5, 3ETB, 3B2U, 3GKW, 2FD6, 2FHZ, 2FSE, 1D9K, 1I3R, 1ZGL, 2GJ7
TRANSCRIPTION	1CI6, 1E 50, 1F3U, 1F93, 1FM6, 1FMH, 1G1E, 1HQM, 1I3Q, 1K3Z, 1K74, 1K7L, 1KBH, 1KKQ, 1L3E, 1LKY, 1MK2, 1MZN, 1NIK, 1NRL, 1ONV, 1OR7, 1OVL, 1PD7, 1PZL, 1R2B, 1RP3, 1S5R, 1SB0, 1SV0, 1TFC, 1TIL, 1U2U, 1VCB, 1WCM, 1XLS, 1YOK, 1ZDT, 2ACL, 2AGH, 2BZW, 2D5R, 2DVQ, 2E3K, 2FEP, 2FMM, 2GL7, 2GPP, 2GPV, 2GS0, 2HZM, 2HZS, 2IZV, 2JBA, 2JF9, 2JFA, 2K7L, 2NNU, 2NPI, 2NS8, 2NZU, 2O9I, 2P7V, 2PHE, 2PHG, 2Q0O, 2RMS, 2RNR, 2V5H, 2VUS, 2WAQ, 2WB1, 2Z2S, 2ZNL, 3BLH, 3BP8, 3C0T, 3D24, 3D3C, 3DGP, 3DOM, 3E1K, 3F5C, 3FBI
TRANSCRIPTION ACTIVATOR/INHIBITOR	1H2M
TRANSCRIPTION REGULATION	1UTB, 1YUC, 2CPW
TRANSCRIPTION REGULATION COMPLEX	1BH8, 1KDX
TRANSCRIPTION REGULATOR	1B0N, 2KA4, 2KA6, 2P5T, 3BEJ, 3C8G
TRANSCRIPTION REPRESSION	1PK1
TRANSCRIPTION REPRESSOR,CELL CYCLE	3BIM
TRANSCRIPTION,TRANSCRIPTIONREGULATION	3ECH
TRANSCRIPTION,TRANSFERASE/DNA-RNA HYBRID	3ERC, 3GTM, 3HOU, 3HOY
TRANSCRIPTION/CELL CYCLE	2OVQ
TRANSCRIPTION/DNA	1A02, 1AWC, 1C9B, 1CF7, 1FOS, 1IHF, 1IO4, 1JFI, 1JFI, 1MDY, 1MNM, 1NGM, 1NH2, 1NKP, 1NLW, 1NVP, 1O4X, 1R0N, 1RIO, 1RM1, 1S9K, 1T2K, 1XS9, 1ZVV, 2F8X, 2HAN, 2QL2, 2R5Y, 3DZU
TRANSCRIPTION/PROTEIN BINDING/DNA	1TQE
TRANSCRIPTION/TBP-ASSOCIATED FACTORS	1H3O
TRANSCRIPTION/TRANSFERASE	1P4Q, 1XIU, 1ZOQ, 3GFK
TRANSCRIPTIONAL COACTIVATOR	1OJH
TRANSFERASE/TRANSCRIPTION	2JZB, 2K8F, 2WIU, 3BRT, 3BRV
OTHER	1TBA, 3HQR, 1SSE, 2AVU, 1L2I, 3EU7, 1ZHI, 1R8U, 3DCT, 1RZR, 2AJQ

[0068] In another embodiment of the present invention, the collection is a collection of protein secondary structures potentially involved in modulating cellular transport. Table 16 below is a list of PDB entries taken from Table 2 that contain secondary structures at the interface of a two-chain inter-protein interaction that are potentially involved in modulating cellular transport. A preferred collection

according to the present embodiment contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the protein secondary structures that are present in the PDB entries identified in Table 16.

Table 16: Representative HIPP Interactions Involved in Transport

CLASSIFICATION	*PDB CODE*
ENDOCYTOSIS	1W63, 2JKR, 2JXC, 2IV8, 2G3Q
ENDOCYTOSIS/EXOCYTOSIS	1JTH, 1L4A, 2EQB, 2G30, 2OCY, 2PJW, 2PJX, 3C98
EXOCYTOSIS	2CJS, 3HD7
HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	2G77
HYDROLASE/TRANSPORT PROTEIN	2R6G, 2ZXE, 3B8E
LIPID TRANSPORT/ ENDOCYTOSIS/ CHAPERONE	2FCW
METAL BINDING PROTEIN/TRANSPORT PROTEIN	2BEC, 2E30
METAL TRANSPORT	1EXB, 1SUV
METAL TRANSPORT, HYDROLASE	2PMS, 3CJK
METAL TRANSPORT,MEMBRANE PROTEIN	2A5T
OXIDOREDUCTASE/LIPID TRANSPORT	3EJB
OXIDOREDUCTASE/METAL TRANSPORT	1WX5, 1ZRT
OXYGEN STORAGE, OXYGEN TRANSPORT	2RI4, 3D4X, 3DHR, 3DHT, 3FS4, 1XQ5
OXYGEN STORAGE/TRANSPORT	1FHJ, 1FSX, 1GCV, 1HBR, 1HV4, 1JEB, 1JY7, 1V4U, 1V75, 1XQ5, 1Y8H, 1YHU, 2AA1, 2D2M, 2GTL
OXYGEN TRANSPORT	1A9W, 1CG5, 1FDH, 1HDS, 1OUU, 1QPW, 1SCT, 2W72, 3FH9, 3HRW
PROTEIN TRANSPORT	1J2J, 1NRJ, 1R4A, 1RE0, 1RH5, 1RJ9, 1TU3, 1UKV, 1W7P, 1X79, 1YHN, 1Z0J, 1Z0K, 2BSK, 2C5I, 2D3G, 2D7C, 2GZD, 2H4M, 2HV8, 2J9U, 2JDQ, 2JQ9, 2JQK, 2K3W, 2K8M, 2NUP, 2OT3, 2PM6, 2QTV, 2QTV, 2R17, 2RET, 2V6X, 2V8S, 2VDA, 2VGL, 2W83, 2W84, 2W85, 2ZME, 3CI0, 3CJH, 3CPH, 3CPJ, 3CQC, 3CQG, 3CUE, 3CUQ, 3DL8, 3DXR, 3EZJ, 3GJX, 1YD8, 1UKL, 2ZJS, 3CFI, 2C1M, 3DKN, 1M2O, 1WR6, 1WRD, 2FNJ, 2A5D
PROTEIN TRANSPORT, HYDROLASE	3BG0
PROTEIN TRANSPORT, MEMBRANE PROTEIN	3DEP
PROTEIN TRANSPORT,ANTIMICROBIAL PROTEIN	2HDI
PROTEIN TRANSPORT/EXCHANGE FACTOR	1R8Q
PROTEIN TRANSPORT/SPLICING	3BBP
TRANSPORT PROTEIN	2J3R, 2J3W, 1IA0, 1JN5, 1MO1, 1S6C, 1SFC, 1T3L, 1U5T, 1URQ, 1VYT, 1Y74, 1Y76, 2BH1, 2EFC, 2F66, 2I2R, 2NPS, 2OT8, 2P22, 2P4N, 2QMB, 2QNA, 3C3Q, 3CWZ, 3D31, 3D32, 3EA5, 3FH6
TRANSPORT PROTEIN/CHAPERONE	2P58
TRANSPORT PROTEIN/LIPOPROTEIN	2HQS
TRANSPORT PROTEIN/OXYGEN BINDING	3BCQ
TRANSPORT PROTEIN/SIGNALING PROTEIN	2NUU
OTHER	3FIE, 3BPS, 1KPS, 1DE4, 1KKL, 1LOT, 1UJW, 3BSZ, 2C0L

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[0069] Another aspect of the present invention relates to methods of screening therapeutic drug candidates to identify candidates that are potentially effective in modulating two-chain inter-protein interactions having a secondary structure at their interface. These methods involve selecting a protein secondary structure from among a collection of protein secondary structures described herein. In one embodiment, a therapeutic drug candidate is contacted with an agent that mimics the protein secondary structure (*i.e.*, secondary structure mimetic). The drug candidate and mimetic agent are contacted under conditions effective for the therapeutic drug candidate to bind to the agent and binding between the therapeutic drug candidate and the agent is detected. Detecting binding between the therapeutic drug candidate and the agent indicates that the therapeutic drug candidate is potentially effective in modulating a two-chain inter-protein interaction having the protein secondary structure at its interface.

[0070] In another embodiment, a therapeutic drug candidate that mimics the protein secondary structure is provided. The therapeutic drug candidate is contacted with at least one protein (or a fragment thereof) involved in a two-chain inter-protein interaction having the protein secondary structure at its interface under conditions effective for the therapeutic drug candidate to bind to the at least one protein (or fragment), and binding between the therapeutic drug candidate and the at least one protein (or fragment) is detected. Detecting binding between the therapeutic drug candidate and the at least one protein (or fragment) indicates that the therapeutic drug candidate is potentially effective in modulating the two-chain inter-protein interaction.

[0071] Protein secondary structure mimics that are suitable for use as a drug candidate or as the target for a drug candidate in the above described methods of screening preferably comprise a molecular scaffold. Various molecular scaffolds of secondary structure are known in the art and can be modified in various ways to mimic the interaction interface residues, especially the hot-spot amino acid residues of the interaction, that have been identified using the methods of the present invention.

[0072] One type of molecular scaffold suitable for mimicking the identified secondary structures are protein surface scaffolds such as miniature protein motif scaffolds, which integrate the desired functionalities of a two-chain inter-protein interaction interface onto a stably folded structural peptide framework (Imperiali et

al., "Design Strategies for the Construction of Independently Folded Polypeptide Motifs," *Biopolymers* 47:23-29 (1998); Nygren et al., "Binding Proteins from Alternative Scaffolds," *J. Immunol. Methods* 290:3-28 (2004), which are hereby incorporated by reference in their entirety). Other suitable protein surface scaffolds include porphyrin and bipyridyl–metal complex scaffolds (Jain et al., "Protein Surface Recognition by Synthetic Recptors Based on Tetraphenylporphyrin Scaffold," *Org. Lett.* 2:1721-23 (2000); Takashima et al, "Ru(bpy)(3)-based Artificial Receptors Toward a Protein Surface: Selective Binding and Efficient Photoreduction of Cytochrome C," *Chem. Comm.* 2345-46 (1999), which are hereby incorporated by reference in their entirety), calixarene scaffolds (Blaskovich et al., "Design of GFB-111, A Platelet-Derived Growth Factor Binding Molecule with Antiangiogenic and Anticancer Activity Against Human Tumors in Mice," *Nat. Biotechnol.* 18:1065-70 (2000), which is hereby incorporated by reference in its entirety), naphthalene and quinoline-based scaffolds (Xu et al., "Evaluation of 'Credit Card' Libraries for Inhibition of HIV-1 gp41 Fusogenic Core Formation," *J. Comb. Chem.* 8:531-39 (2006), which is hereby incorporated by reference in its entirety), and cyclodextrins (Breslow et al., "Sequence Selective Binding of Peptides by Artificial Receptors in Aqueous Solution," *J. Am. Chem. Soc.* 120:3536-37 (1998), which is hereby incorporated by reference in its entirety).

[0073] A preferred class of agents for mimicking helical protein secondary structures include α-helix mimetic scaffolds. Suitable α-helical modular synthetic scaffolds include terphenyl derivatives (Figure 3; Orner et al., "Toward Proteomimetics: Terphenyl Derivative as Structural and Functional Mimics of Extended Regions of an α-Helix," *J. Am. Chem. Soc.* 123:5382-83 (2001), which is hereby incorporated by reference in its entirety), trispyridylamide derivatives (Ernst et al., "Design and Application of an α-Helix-Mimetic Scaffold Based on an Oligoamide-Foldamer Strategy: Antagonism of the Bak BH3/Bcl-xL Complex," *Angew. Chem. Int. Ed.* 42:535-39 (2003), which is hereby incorporated by reference in its entirety), terephthalamide derivatives (Yin et al., "Terephthalamide Derivatives as Mimetics of Helical Peptides: Disruption of the Bcl-x(L)/Bak Interaction," *J. Am. Chem. Soc.* 127:5463-68 (2005), which is hereby incorporated by reference in its entirety), terpyridine derivatives (Davis et al., "Synthesis of a 2,3′;6′3″-terpyridine

Scaffold as an α-Helix Mimetic," *Org. Lett.* 7:5405-08 (2005), which is hereby incorporated by reference in its entirety), and bisimidazole derivatives (VanCompernolle et al., "Small Molecule Inhibition of Hepatitis C Virus E2 Binding to CD81," *Virology* 314:371-80 (2003), which is hereby incorporated by reference in its entirety). Other α-helical mimetics include β-peptides and peptoids (both shown in Figure 3), constrained helices, and small molecule mimetics (*e.g.*, 1,4-benzodiazepine-2,5-diones, 3-hydroxymethylindole, and polycyclic ethers) (reviewed in Herschberger et al., "Scaffolds for Blocking Protein–Protein Interactions," *Curr. Top. Med. Chem.* 7:928-42 (2007), which is hereby incorporated by reference in its entirety) and side-chain cross-linked α-helices (Figure 3). In a preferred embodiment, the α-helical mimetic is a hydrogen-bond surrogate ("HBS") backbone cross-linked α-helix described in U.S. Patent No.7,202,332 to Arora et al., which is hereby incorporated by reference in its entirety.

[0074] β-Strand and β-turn secondary structure mimetic scaffolds are also suitable for mimicking the secondary structures that are at an interface of a two-chain inter-protein interaction. β-strand mimetics, which are typically designed to modulate protein–protease interactions, include the crosslinked β-strand mimetic scaffolds (*see e.g.*, Zutshi et al., "Targeting the Dimerization Interface of HIV-1 Protease: Inhibition with Cross-Linked Interfacial Peptides," *J. Am. Chem. Soc.* 119:4841-45 (1997), which is hereby incorporated by reference in its entirety) and peptidomimetic β-strand mimetic scaffolds. The peptidomimetic β-strand mimetics may contain various ring systems, including six-membered piperidine rings, pyridine rings, and pyrrolinone rings; cyclic urea complexes; or azacyclohexenone units incorporated into the peptide backbones (reviewed in Herschberger et al., "Scaffolds for Blocking Protein–protein Interactions," *Curr. Top. Med. Chem.* 7:928-42 (2007), which is hereby incorporated by reference in its entirety). Suitable β-turn mimetic scaffolds include β-D-glucose scaffolds (Hirschmann et al., "Nonpeptidal Peptidomimetics with a Beta-Glucose Scaffolding—A Partial Somatostatin Agonist Bearing a Close Structural Relationship to a Potent, Selective Substance-P Antagonist," *J. Am. Chem. Soc.* 114:9217-18 (1992), which is hereby incorporated by reference in its entirety), constrained structural mimetics to mimic type I β-turns (Etzkorn et al., "Cyclic Hexapeptides and Chimeric Peptides as Mimics of Tendamistat," *J. Am. Chem. Soc.* 116:10412-25

(1994), which is hereby incorporated by reference in its entirety), and conformationally constrained cyclic scaffolds (Virgilio et al., "Simultaneous Solid-Phase Synthesis of Beta-Turn Mimetics Incorporating Side Chain Functionality," *J. Am. Chem. Soc.* 116:11580-81 (1994); Maliartchouk et al., "A Designed Peptidomimetic Agonistic Ligand of TrkA Nerve Growth Factor Receptors," *Mol. Pharmacol.* 57:385-91 (2000); Ulysse et al., "A Light Activated β-Turn Scaffold Within a Somatostatin Analog: NMR Structure and Biological Activity," *Chem. Biol. Drug Des.* 67:127-36 (2006), which are hereby incorporated by reference in their entirety). The non-peptidic oligomers described in U.S. Patent Publication No. 20070105917 to Arora et al., which is hereby incorporated by reference in its entirety, are also suitable secondary structure mimetics that can be used in accordance with this aspect of the present invention.

[0075] Suitable screening assays for identifying potentially therapeutic drug candidates can be *in silico*, *in vitro*, or *ex vivo* based assays.

[0076] *In silico* or virtual screening assays are particularly useful for evaluating the binding between a secondary structure mimetic and a drug candidate for the identification of a protein binding pocket. A number of web-based programs and databases, such as Molsoft, exist to facilitate *in silico* screening and are suitable for use in accordance with this aspect of the invention. Villoutreix et al., "Free Resources to Assist Structure-Based Virtual Ligand Screening Experiments," *Curr. Protein Pept. Sci* 8(4):381-411 (2007), which is hereby incorporated by reference in its entirety, provides over 350 URLs to various free web-based applications and services for *in silico* screening.

[0077] In another embodiment of the present invention, the screening assay is an *in vitro* screening assay designed to detect a binding interaction between two potential binding partners. A number of *in vitro* screening assay formats are commercially available, for example AlphaScreen™ from Perkin Elmer®, that are particularly suitable for carrying out this aspect of the present invention. AlphaScreen is a bead-based chemistry, where members of the binding interaction (*e.g.*, the secondary structure mimetic agent and therapeutic drug candidate, or the secondary structure mimetic drug candidate and protein involved in the two-chain inter-protein interaction) are bound to donor and acceptor beads, respectively. Binding between

the members of the potential interaction brings the donor and acceptor beads in close proximity, facilitating energy transfer and light production that is detected at defined excitation/emission spectra.

[0078] An alternative *in vitro* screening assay format is a solid-phase assay, where one member of the potential binding interaction (*e.g.*, the secondary structure mimetic agent) is attached to a solid support and the other member of the binding interaction (*e.g.*, the drug candidate) contains a detectable label. Suitable detectable labels include fluorescent molecules, enzymes, prosthetic groups, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions.

[0079] Surface plasmon resonance (SPR)-based biomolecular interaction analysis is an alternative *in vitro* screening strategy suitable for detection of a binding interaction between a therapeutic drug candidate and a secondary structure mimetic agent (or between a secondary structure mimetic therapeutic drug candidate and a protein involved in a two-chain inter-protein interaction). In this assay format, one member of the binding interaction is immobilized on a biosensor chip. A microfluidic system injects an analyte solution containing the other interacting molecule over the sensor surface. Binding of the two members is qualitatively assessed in real-time using SPR-biosensors that visualize and measure the binding interaction based on the change in mass concentration that occurs on the sensor chip surface during the binding and dissociation process.

[0080] In another embodiment of the present invention, the screening assay is an *ex vivo* screening assay designed to detect (or, more preferably, validate) a binding interaction between the two members of the potential interaction. For example, an *ex vivo* assay where live cells expressing both proteins of a two-chain inter-protein interaction having the secondary structure at their interface are contacted with the therapeutic drug candidate (*e.g.*, a secondary structure mimetic). The ability of the drug candidate to modulate the two-chain inter-protein interaction is detected by assaying a downstream biological function of the two-chain inter-protein interaction. Suitable endpoints to measure will depend on the protein interaction being examined,

but may include, for example, gene transcription, kinase activity, DNA binding, enzyme activity, or other cell signaling activities.

[0081] In another embodiment of the present invention, the screening assay is an *in vivo* screening assay designed to detect, or more preferably, validate a binding interaction between the two members of the potential two-chain inter-protein interaction. For example, an *in vivo* assay may involve treating an animal that expresses both proteins of a two-chain inter-protein interaction having a secondary structure at their interface with a therapeutic drug candidate (e.g. a secondary structure mimetic). The ability of the drug candidate to modulate the two-chain inter-protein interaction is detected by assaying a downstream biological function of the two-chain inter-protein interaction in the animal. Suitable endpoints to measure will depend on the protein interaction being examined, but may include, for example, gene transcription, kinase activity, DNA binding, enzyme activity, or other cell signaling activities.

EXAMPLES

Example 1 — Identification of Helical Interfaces in Protein–Protein Interactions

[0082] The methodology utilized to identify helical interfaces in protein–protein interactions is outlined in Figure 4. Protein structures containing more than one protein entity were obtained from the Protein Data Bank (PDB) using the advanced search function available on the website and stored in a parent PDB file. A Perl script to construct individual PDB files for each interacting protein chain within the parent PDB file was developed. This script reads a PDB file, identifies atoms from different chains that interaction with each other, then creates a new formatted PDB file with those two chains. This process is repeated until all interacting chains have a new PDB file. If the parent PDB file contains more than one structure, only the first structure is considered.

[0083] A second Perl script to identify protein partner chains between separate entities was developed. This script reads a PDB file, identifies chains that belong to separate entities within the PDB file, and creates a list of the PDB code and partnering chains that are part of the separate entities. This enables the identification of those helix interfaces that are between separate protein entities, *i.e.*, inter-protein

interactions, as opposed to helical interfaces between chains in a single protein, *i.e.*, intra-protein interactions.

[0084] Having identified the inter-protein interactions, modifications to Rosetta© computational tools, written in C++ programming language, were utilized to identify helical interfaces between interacting protein chains. Rosetta© contains separate programs that identify interface residues and assigns secondary structure to a protein backbone. The computer program code developed here links these two routines to find protein chains with interface residues that lie within a helix. A helical segment was defined as one that contains at least four contiguous residues with ϕ and φ angles that are characteristic of the α-helix ($\varphi = -57° \pm 50°$, $\phi = -47° \pm 50°$). Often, protein–protein interfaces are defined according to geometrically continuous patches of residues on the surface of a protein that exclude solvent by binding to another chain. This definition might include some residues that are not really involved in the interaction or exclude some residues that play a key role in the interaction. Therefore, a distance threshold between residues of different chains was used.

[0085] An interface residue is defined as (i) a residue that has at least one atom within a 5 Å radius of an atom belonging to a binding partner in the protein complex, or (ii) a residue that becomes significantly buried upon complex formation, as measured by the density of C_β atoms within a sphere with a radius of 5 Å around the C_β atom of the residue of interest.

[0086] The length of each helix involved in helical interface protein–protein interactions was calculated using a C++ program.

[0087] The PDB structures involved in helical interface protein–protein interactions were classified according to molecular function. The categories were derived from those listed in the 'Advanced Search' option on the PDB website.

[0088] The PDB contains more than 55,000 structures (Berman et al., "The Protein Data Bank," *Nucleic Acids Res.* 28:235-242 (2000), which is hereby incorporated by reference in its entirety). Approximately 80% of these structures contain a single protein entity and 4% contain no protein entities. The remaining 16%, or about 8,678 structures, contain more than two separate protein entities and form the dataset for evaluation of helical interfaces in protein–protein interactions

("HIPP interactions") (Figure 5A). A computer analysis of this dataset revealed that 13% contained HIPP interactions. These complexes may also contain other secondary motifs, but the current study focuses solely on the helical portions.

[0089] In an initial analysis, a dataset of 7,066 HIPP interactions were identified. This dataset is disclosed in U.S. Provisional Patent Application Serial No. 61/166,211 and Jochim et al., "Assessment of Helical Interfaces in Protein–Protein Interactions," *Mol. Biosyst.* 5(9):924–6 (2009), which are hereby incorporated by reference in their entirety. The identified 7,066 HIPP complexes contain considerable redundancy in sequence and structure owing to the redundancy in the PDB. Structures with greater than 95% sequence similarity were removed with the CD-HIT algorithm (Li et al., "Clustering of Highly Homologous Sequences to Reduce the Size of Large Protein Databases," *Bioinformatics* 17:282-283 (2001), which is hereby incorporated by reference in its entirety) to obtain a better understanding of the types of complexes involved in HIPP interactions. This screen provided a non-redundant dataset of 1,658 HIPP interactions for analysis, which is disclosed in U.S. Provisional Patent Application Serial No. 61/166,211 and Jochim et al., "Assessment of Helical Interfaces in Protein–Protein Interactions," *Mol. Biosyst.* 5(9):924–6 (2009), which are hereby incorporated by reference in their entirety.

[0090] The CD-HIT algorithm used to remove the redundant interactions searches the sequence information of each chain of an interaction from the PDB FASTA file. Using this algorithm, however, redundant two-chain and single chain interactions were removed. Therefore, to ensure that only redundant two-chain interactions were removed (rather than redundant single chains), the chain identifier was removed from the FASTA file of the PDB entries in the dataset of 7,066 interactions and then the CD-HIT algorithm search was reexecuted, so that the entire amino acid sequence of the protein–protein complex is searched rather than just the individual protein chains. Using this approach, a non-redundant dataset of 2,561 HIPP interactions for analysis was identified, which is shown in Table 2 above. The helical two-chain inter-protein interactions of the non-redundant dataset are identified by their PDB code and function of the protein complex. In addition, the partner chains, helix size, number of hot-spot residues, and helix amino acid sequence are also identified. The helical inter-protein interactions are ranked by $\Delta\Delta G_{SUM}$

(Kcal/mol), which represents the sum of binding free energy for all hot spot residues in each helix. The $\Delta\Delta G_{AVE}$ (Kcal/mol), representing the sum of binding free energy for all hot spot residues in each helix divided by the number of hot spot residues in that helix, is also provided for each helical inter-protein interaction. The binding free energy values can be used to identify inter-protein interactions that can be easily targeted by helix mimetics or small molecule inhibitors. For example, inter-protein interactions having energy values of 3.0 kcal/mol and higher can be targeted by either helix mimetics or small molecule inhibitors. Inter-protein interactions having energy values in the range of 1.5–2.0 kcal/mol are more difficult to target with small molecules; however, these interactions can be targeted by helix mimetics.

[0091] The hot-spot residues of the helical two-chain inter-protein interactions of Table 2 were also identified and are show in Table 17 below. Hot spot residues within each interaction are identified by the PDB code of the protein complex, partner chain, residue number, and amino acid residue. The $\Delta\Delta G$ (Kcal/mol) for each hot spot residue is also provided. There were 43,397 hot-spot residues identified in the 2,561 HIPP interactions.

PDB CODE	PARTNER CHAINS	CHAIN	RESIDUE NUMBER	RESIDUE	ΔΔG (kcal/mol)	HELIX START RESIDUE #	HELIX END RESIDUE #
12 E8	L H	L	123	E	1.0	122	127
12 E8	L H	L	124	Q	2.0	122	127
12 E8	M P	M	124	Q	1.9	122	126
15C8	L H	L	124	Q	1.2	122	127
1A02	F J	F	172	L	2.4	141	192
1A02	F J	F	173	E	1.1	141	192
1A02	F J	F	179	L	1.7	141	192
1A02	F J	F	182	E	1.1	141	192
1A02	F J	F	183	I	1.8	141	192
1A02	F J	F	186	L	1.8	141	192
1A02	F J	J	290	L	1.3	268	317
1A02	F J	J	293	K	1.7	268	317
1A02	F J	J	297	L	1.8	268	317
1A02	F J	J	304	L	1.3	268	317
1A02	F J	J	311	L	1.8	268	317
1A02	F J	J	312	R	1.1	268	317
1A02	F J	J	315	V	1.4	268	317
1A02	N J	J	289	R	2.6	268	317
1A0H	A B	A	309	E	2.4	309	318
1A0H	A B	A	311	E	1.6	309	318
1A0H	A B	A	312	L	3.0	309	318
1A0H	A B	A	316	Y	1.8	309	318
1A0H	A B	B	568	K	1.0	567	575
1A0H	A B	B	569	W	1.0	567	575
1A0H	A B	B	574	I	1.2	567	575
1A0H	D E	D	316	Y	2.3	309	318
1A0H	D E	E	443	K	1.6	443	450
1A0H	D E	E	494	K	1.4	490	497
1A0H	D E	E	568	K	2.2	567	575
1A0H	D E	E	574	I	1.0	567	575
1A0O	A B	A	122	K	2.0	113	126
1A0O	A B	A	125	E	2.0	113	126
1A0O	C D	C	95	I	1.0	92	102
1A0O	C D	C	96	I	1.0	92	102
1A0O	C D	D	211	V	1.1	205	216
1A0O	C D	D	214	F	3.3	205	216
1A0O	E F	E	122	K	1.1	113	127
1A0O	E F	F	182	L	1.0	171	183
1A0O	G H	G	122	K	1.0	113	127
1A0O	G H	H	178	E	1.0	171	183
1A2K	B C	C	78	G	138.7	77	81
1A2X	A B	A	102	F	1.8	92	103
1A2X	A B	A	118	I	1.0	112	119
1A2X	A B	B	13	R	1.0	5	32
1A2X	A B	B	17	L	2.0	5	32
1A2X	A B	B	21	M	2.3	5	32
1A2X	A B	B	22	L	1.4	5	32
1A2X	A B	B	24	I	1.1	5	32
1A2Y	A C	C	121	Q	3.0	120	124
1A3L	L H	L	124	Q	1.1	122	127
1A3R	L H	L	124	Q	1.9	122	127
1A4J	A B	A	129	Q	1.6	127	132
1A4J	L H	L	129	Q	2.1	127	132
1A4Y	A B	B	32	R	1.7	23	34
1A4Y	D E	D	443	E	1.9	440	453
1A4Y	D E	E	5	R	1.9	5	13
1A4Y	D E	E	8	H	2.0	5	13
1A4Y	D E	E	32	R	1.2	23	33

1A6A	A B	A	48	F	3.1	46	52
1A6A	A B	A	70	L	3.0	56	77
1A6A	B C	B	74	R	2.1	74	89
1A6A	B C	B	78	Y	1.5	74	89
1A6A	B C	B	81	H	1.8	74	89
1A6A	B C	B	82	N	1.4	74	89
1A6A	B C	B	85	V	1.0	74	89
1A6T	A B	A	123	E	1.3	122	127
1A7F	A B	A	13	L	1.0	13	18
1A81	A H	A	129	R	1.3	120	135
1A93	A B	A	13	L	1.2	6	34
1A93	A B	A	17	E	1.2	6	34
1A93	A B	A	21	R	1.7	6	34
1A93	A B	B	10	N	2.3	6	34
1A93	A B	B	13	H	1.9	6	34
1A93	A B	B	17	I	1.7	6	34
1A93	A B	B	20	L	2.0	6	34
1A9N	A B	B	28	R	1.8	23	34
1A9N	A B	B	31	Y	2.1	23	34
1A9N	C D	D	28	R	1.9	23	34
1A9N	C D	D	31	Y	2.1	23	34
1A9N	C D	D	33	L	1.0	23	34
1A9W	A E	A	31	R	3.5	21	36
1A9W	A E	A	103	H	1.3	95	113
1A9W	A E	A	122	H	1.3	119	137
1A9W	A E	E	34	V	1.5	20	35
1A9W	A F	A	95	P	1.4	95	113
1A9W	A F	F	37	W	2.1	36	42
1A9W	A F	F	102	N	1.5	100	119
1A9W	C E	C	95	P	1.4	95	113
1A9W	C E	E	37	W	2.0	36	42
1A9W	C E	E	102	N	1.0	100	119
1A9W	C F	C	31	R	2.2	21	36
1A9W	C F	C	119	P	2.8	119	137
1A9W	C F	C	122	H	1.5	119	137
1A9W	C F	F	30	R	2.9	20	35
1A9W	C F	F	34	V	1.6	20	35
1A9W	C F	F	112	I	1.1	100	119
1ABR	A B	A	170	Y	2.2	169	181
1ACY	L H	L	123	E	1.0	122	127
1ACY	L H	L	124	Q	1.4	122	127
1AD0	A B	A	123	Q	1.3	121	127
1AD0	C D	C	123	Q	1.5	121	127
1AD9	L H	L	123	Q	1.1	121	125
1AE6	L H	L	122	E	1.1	121	126
1AE6	L H	H	100	Y	1.2	97	100
1AFV	A H	A	79	E	4.6	63	83
1AFV	A H	A	82	R	1.7	63	83
1AFV	A L	A	81	D	1.6	63	83
1AFV	A L	A	82	R	1.0	63	83
1AFV	A L	A	101	G	14.6	101	106
1AFV	A L	A	102	S	4.2	101	106
1AFV	B K	B	82	R	1.0	63	83
1AFV	B M	B	81	D	1.6	63	83
1AFV	B M	B	82	R	2.2	63	83
1AFV	B M	B	101	G	10.1	101	106
1AFV	B M	B	102	S	2.9	101	106
1AGR	A E	A	207	E	1.8	205	214
1AGR	A E	A	210	K	1.9	205	214
1AGR	A E	A	213	H	1.0	205	214

1AGR	A E	E	87	E	1.4	86	101
1AGR	A E	E	134	R	1.2	131	141
1AGR	A E	E	159	L	1.9	150	163
1AGR	D H	D	207	E	1.9	205	214
1AGR	D H	D	209	K	1.0	205	214
1AGR	D H	D	210	K	2.6	205	214
1AGR	D H	D	213	H	1.0	205	214
1AGR	D H	H	87	E	2.1	86	100
1AGR	D H	H	88	N	1.2	86	100
1AGR	D H	H	159	L	1.3	150	163
1AGR	D H	H	167	R	2.1	164	169
1AHJ	A B	A	24	W	2.0	19	33
1AHJ	A B	A	26	L	2.9	19	33
1AHJ	A B	A	30	L	2.2	19	33
1AHJ	A B	A	40	Y	1.5	40	52
1AHJ	A B	A	44	W	2.4	40	52
1AHJ	A B	A	45	K	2.3	40	52
1AHJ	A B	A	48	F	2.1	40	52
1AHJ	A B	A	118	W	1.5	118	122
1AHJ	A B	A	131	F	2.3	131	140
1AHJ	A B	A	134	R	1.8	131	140
1AHJ	A B	A	138	V	1.3	131	140
1AHJ	A B	A	139	R	2.1	131	140
1AHJ	A B	A	142	R	1.0	141	149
1AHJ	A B	A	194	D	2.5	193	198
1AHJ	A B	B	35	L	2.7	31	48
1AHJ	A B	B	37	Y	3.1	31	48
1AHJ	A B	B	39	L	2.3	31	48
1AHJ	A B	B	41	F	2.8	31	48
1AHJ	A B	B	47	L	1.4	31	48
1AHJ	A B	B	67	Y	1.5	64	70
1AHJ	A B	B	72	Y	2.1	72	88
1AHJ	A B	B	75	R	1.2	72	88
1AHJ	A B	B	95	L	1.1	92	100
1AHJ	C D	C	19	V	2.2	19	33
1AHJ	C D	C	22	R	3.0	19	33
1AHJ	C D	C	24	W	1.4	19	33
1AHJ	C D	C	26	L	2.9	19	33
1AHJ	C D	C	30	L	2.0	19	33
1AHJ	C D	C	40	Y	1.6	40	52
1AHJ	C D	C	44	W	3.5	40	52
1AHJ	C D	C	45	K	1.9	40	52
1AHJ	C D	C	48	F	2.0	40	52
1AHJ	C D	C	118	W	1.8	118	122
1AHJ	C D	C	131	F	2.4	131	140
1AHJ	C D	C	138	V	1.2	131	140
1AHJ	C D	C	139	R	1.9	131	140
1AHJ	C D	C	142	R	3.0	141	149
1AHJ	C D	C	147	E	1.3	141	149
1AHJ	C D	C	194	D	1.3	193	198
1AHJ	C D	D	32	W	2.1	31	48
1AHJ	C D	D	34	H	1.0	31	48
1AHJ	C D	D	35	L	2.7	31	48
1AHJ	C D	D	37	Y	2.3	31	48
1AHJ	C D	D	39	L	2.2	31	48
1AHJ	C D	D	41	F	3.0	31	48
1AHJ	C D	D	47	L	1.4	31	48
1AHJ	C D	D	72	Y	4.7	72	87
1AHJ	C D	D	74	E	2.0	72	87
1AHJ	C D	D	95	L	1.2	92	100

1AHJ	E F	E	22	R	1.0	19	33
1AHJ	E F	E	24	W	2.3	19	33
1AHJ	E F	E	26	L	3.1	19	33
1AHJ	E F	E	30	L	2.4	19	33
1AHJ	E F	E	40	Y	1.2	40	52
1AHJ	E F	E	44	W	3.6	40	52
1AHJ	E F	E	45	K	1.9	40	52
1AHJ	E F	E	48	F	4.3	40	52
1AHJ	E F	E	118	W	1.5	118	122
1AHJ	E F	E	131	F	2.3	131	140
1AHJ	E F	E	139	R	1.8	131	140
1AHJ	E F	E	142	R	1.8	141	149
1AHJ	E F	E	147	E	1.1	141	149
1AHJ	E F	E	194	D	1.1	193	198
1AHJ	E F	F	32	W	1.8	31	48
1AHJ	E F	F	34	H	1.0	31	48
1AHJ	E F	F	35	L	3.2	31	48
1AHJ	E F	F	37	Y	2.8	31	48
1AHJ	E F	F	39	L	2.2	31	48
1AHJ	E F	F	41	F	3.0	31	48
1AHJ	E F	F	47	L	1.4	31	48
1AHJ	E F	F	72	Y	2.1	72	87
1AHJ	E F	F	77	V	1.4	72	87
1AHJ	E F	F	95	L	1.3	92	100
1AHJ	G H	G	24	W	2.3	19	33
1AHJ	G H	G	26	L	4.6	19	33
1AHJ	G H	G	30	L	3.2	19	33
1AHJ	G H	G	40	Y	1.9	40	52
1AHJ	G H	G	44	W	3.9	40	52
1AHJ	G H	G	45	K	2.4	40	52
1AHJ	G H	G	48	F	1.9	40	52
1AHJ	G H	G	118	W	1.7	118	122
1AHJ	G H	G	131	F	2.4	131	140
1AHJ	G H	G	133	Y	1.3	131	140
1AHJ	G H	G	134	R	1.8	131	140
1AHJ	G H	G	138	V	1.4	131	140
1AHJ	G H	G	139	R	2.7	131	140
1AHJ	G H	G	142	R	1.4	141	149
1AHJ	G H	G	144	V	1.1	141	149
1AHJ	G H	G	147	E	1.1	141	149
1AHJ	G H	G	194	D	2.8	193	198
1AHJ	G H	H	35	L	2.7	35	48
1AHJ	G H	H	37	Y	2.4	35	48
1AHJ	G H	H	39	L	2.3	35	48
1AHJ	G H	H	41	F	3.2	35	48
1AHJ	G H	H	47	L	1.4	35	48
1AHJ	G H	H	67	Y	2.1	64	70
1AHJ	G H	H	72	Y	1.6	72	87
1AHJ	G H	H	95	L	1.2	92	100
1AHW	A F	F	60	T	2.2	60	66
1AIP	A C	A	119	H	1.0	114	127
1AIP	A C	A	146	L	1.6	145	161
1AIP	A C	C	18	M	2.7	18	28
1AIP	A C	C	19	M	1.4	18	28
1AIP	A C	C	22	K	1.3	18	28
1AIP	A C	C	81	D	1.7	81	86
1AIP	A C	C	82	F	4.7	81	86
1AIP	A C	C	180	I	2.6	169	181
1AIP	B C	C	98	M	1.3	87	104
1AIP	E C	C	145	G	138.5	136	155

1AIP	E H	H	102	M	1.7	87	104
1AIP	F H	F	146	L	1.2	145	161
1AIP	F H	F	150	V	3.6	145	161
1AIP	F H	H	18	M	2.0	18	28
1AIP	F H	H	19	M	1.2	18	28
1AIP	F H	H	22	K	2.1	18	28
1AIP	F H	H	82	F	4.3	81	86
1AIP	F H	H	180	I	2.8	169	181
1AJ7	L H	L	123	E	1.0	122	127
1AJ7	L H	L	124	Q	1.4	122	127
1AJS	A B	A	18	F	2.7	16	26
1AJS	A B	A	113	R	1.7	108	122
1AJS	A B	A	118	F	1.0	108	122
1AJS	A B	A	145	G	5.1	141	151
1AJS	A B	A	146	V	1.4	141	151
1AJS	A B	A	283	V	1.1	277	293
1AJS	A B	A	286	Q	1.0	277	293
1AJS	A B	B	57	E	1.5	51	62
1AJS	A B	B	113	R	1.5	108	122
1AJS	A B	B	145	G	10.8	143	151
1AJS	A B	B	282	R	1.1	277	293
1AJS	A B	B	283	V	1.1	277	293
1AJS	A B	B	292	R	1.3	277	293
1AKH	A B	A	84	F	4.3	79	92
1AKH	A B	A	98	K	4.4	97	108
1AKH	A B	A	99	E	4.7	97	108
1AKH	A B	A	102	E	1.6	97	108
1AKH	A B	B	196	L	2.1	194	202
1AKH	A B	B	199	L	1.1	194	202
1AL0	F B	F	134	Y	1.8	121	135
1ALL	A B	A	5	V	1.1	4	15
1ALL	A B	A	6	T	1.9	4	15
1ALL	A B	A	9	I	4.9	4	15
1ALL	A B	A	24	L	1.1	21	33
1ALL	A B	A	30	F	1.0	21	33
1ALL	A B	A	34	G	73.3	34	47
1ALL	A B	A	89	D	4.2	78	102
1ALL	A B	A	93	R	3.1	78	102
1ALL	A B	A	97	Y	2.9	78	102
1ALL	A B	A	100	V	1.1	78	102
1ALL	A B	B	5	I	2.8	4	15
1ALL	A B	B	9	I	2.4	4	15
1ALL	A B	B	31	F	2.7	21	33
1ALL	A B	B	34	G	58.7	34	47
1ALL	A B	B	38	V	1.2	34	47
1ALL	A B	B	93	R	2.3	78	102
1ALL	A B	B	97	Y	3.7	78	102
1ALL	A B	B	101	A	1.8	78	102
1ALL	A B	B	106	I	2.0	105	113
1AM4	A D	A	198	V	1.0	198	204
1AM4	A D	D	566	R	1.3	565	570
1AM4	A E	E	674	L	7.3	672	676
1AM4	B E	B	193	T	1.0	192	197
1AM4	B E	B	198	V	1.0	198	204
1AM4	C F	F	566	R	1.0	565	570
1AO7	A D	A	65	R	1.9	57	85
1AOI	A B	A	50	E	1.5	45	57
1AOI	A B	A	51	I	2.1	45	57
1AOI	A B	A	54	Y	1.7	45	57
1AOI	A B	A	67	F	1.6	64	79

1AOI	A B	A	70	L	2.0	64	79
1AOI	A B	A	74	I	2.2	64	79
1AOI	A B	A	78	F	2.5	64	79
1AOI	A B	A	92	L	1.9	86	114
1AOI	A B	A	97	E	1.3	86	114
1AOI	A B	A	99	Y	1.7	86	114
1AOI	A B	A	100	L	2.1	86	114
1AOI	A B	A	101	V	1.4	86	114
1AOI	A B	A	104	F	3.2	86	114
1AOI	A B	A	121	P	1.2	121	132
1AOI	A B	A	124	I	1.3	121	132
1AOI	A B	B	36	R	1.2	31	41
1AOI	A B	B	37	L	2.5	31	41
1AOI	A B	B	39	R	2.1	31	41
1AOI	A B	B	40	R	4.3	31	41
1AOI	A B	B	50	I	2.1	50	76
1AOI	A B	B	58	L	2.4	50	76
1AOI	A B	B	61	F	2.3	50	76
1AOI	A B	B	62	L	2.3	50	76
1AOI	A B	B	66	I	2.1	50	76
1AOI	A B	B	70	V	1.6	50	76
1AOI	A B	B	86	V	1.9	83	94
1AOI	A G	A	48	L	1.0	45	57
1AOI	A G	A	51	I	1.2	45	57
1AOI	A G	A	55	Q	1.0	45	57
1AOI	A G	A	112	I	1.1	86	114
1AOI	B D	B	74	E	2.3	50	76
1AOI	B D	B	75	H	1.3	50	76
1AOI	B D	B	88	Y	2.1	83	94
1AOI	B D	D	80	Y	2.8	53	81
1AOI	B D	D	89	R	2.0	88	99
1AOI	B D	D	96	R	2.3	88	99
1AOI	B H	H	65	D	1.0	53	81
1AOI	B H	H	68	E	2.0	53	81
1AOI	C D	C	46	G	2.3	45	73
1AOI	C D	C	49	V	1.8	45	73
1AOI	C D	C	50	Y	3.4	45	73
1AOI	C D	C	51	L	1.0	45	73
1AOI	C D	C	54	V	1.5	45	73
1AOI	C D	C	55	L	2.0	45	73
1AOI	C D	C	58	L	1.5	45	73
1AOI	C D	C	63	L	2.3	45	73
1AOI	C D	C	67	G	33.5	45	73
1AOI	C D	C	96	L	1.7	91	97
1AOI	C D	D	37	Y	1.7	35	46
1AOI	C D	D	41	V	1.4	35	46
1AOI	C D	D	45	V	2.0	35	46
1AOI	C D	D	58	I	1.2	53	81
1AOI	C D	D	67	F	2.2	53	81
1AOI	C D	D	75	S	1.0	53	81
1AOI	C D	D	91	I	1.6	88	99
1AOI	C D	D	111	G	193.7	102	120
1AOI	C D	D	115	V	1.4	102	120
1AOI	C D	D	118	Y	3.3	102	120
1AOI	E C	E	48	L	1.2	45	57
1AOI	E C	E	112	I	1.2	86	114
1AOI	E F	E	50	E	1.1	45	57
1AOI	E F	E	51	I	1.8	45	57
1AOI	E F	E	54	Y	1.1	45	57
1AOI	E F	E	70	L	1.6	64	77

1AOI	E F	E	73	E	2.0	64	77
1AOI	E F	E	74	I	2.3	64	77
1AOI	E F	E	92	L	1.4	86	114
1AOI	E F	E	99	Y	3.0	86	114
1AOI	E F	E	100	L	1.5	86	114
1AOI	E F	E	101	V	1.6	86	114
1AOI	E F	E	104	F	3.0	86	114
1AOI	E F	E	121	P	3.0	121	132
1AOI	E F	F	36	R	1.8	31	41
1AOI	E F	F	37	L	2.5	31	41
1AOI	E F	F	39	R	1.9	31	41
1AOI	E F	F	40	R	4.2	31	41
1AOI	E F	F	50	I	2.3	50	76
1AOI	E F	F	58	L	1.0	50	76
1AOI	E F	F	61	F	3.5	50	76
1AOI	E F	F	62	L	1.5	50	76
1AOI	E F	F	66	I	2.9	50	76
1AOI	E F	F	70	V	1.2	50	76
1AOI	E F	F	86	V	1.6	83	93
1AOI	F H	F	72	Y	1.8	50	76
1AOI	F H	F	75	H	2.7	50	76
1AOI	F H	F	88	Y	2.3	83	93
1AOI	F H	H	77	L	1.2	53	81
1AOI	F H	H	80	Y	3.1	53	81
1AOI	F H	H	96	R	2.2	88	99
1AOI	F H	H	97	L	1.8	88	99
1AOI	G H	G	20	R	1.2	17	22
1AOI	G H	G	29	R	1.4	27	36
1AOI	G H	G	49	V	1.6	45	73
1AOI	G H	G	50	Y	2.0	45	73
1AOI	G H	G	51	L	1.4	45	73
1AOI	G H	G	54	V	1.6	45	73
1AOI	G H	G	55	L	1.8	45	73
1AOI	G H	G	57	Y	2.8	45	73
1AOI	G H	G	58	L	1.8	45	73
1AOI	G H	G	63	L	2.9	45	73
1AOI	G H	G	67	G	40.9	45	73
1AOI	G H	G	80	P	1.3	80	88
1AOI	G H	G	83	L	1.0	80	88
1AOI	G H	G	92	E	1.5	91	97
1AOI	G H	G	93	L	1.0	91	97
1AOI	G H	G	96	L	1.1	91	97
1AOI	G H	H	37	Y	1.8	35	46
1AOI	G H	H	41	V	1.4	35	46
1AOI	G H	H	42	L	1.3	35	46
1AOI	G H	H	58	I	1.8	53	81
1AOI	G H	H	59	M	1.8	53	81
1AOI	G H	H	62	F	1.0	53	81
1AOI	G H	H	63	V	1.0	53	81
1AOI	G H	H	67	F	1.2	53	81
1AOI	G H	H	70	I	1.0	53	81
1AOI	G H	H	75	S	1.0	53	81
1AOI	G H	H	91	I	1.3	88	99
1AOI	G H	H	111	G	86.7	102	120
1AOI	G H	H	118	Y	1.9	102	120
1AOK	A B	A	2	L	3.3	2	14
1AOK	A B	A	3	F	3.4	2	14
1AOK	A B	A	6	G	3.6	2	14
1AOK	A B	B	2	L	1.5	2	14
1AOK	A B	B	3	F	1.6	2	14

1AOK	A B	B	9	I	1.7	2	14
1AOK	A B	B	20	W	3.1	18	22
1AON	C Q	C	234	L	1.1	234	244
1AON	D R	D	234	L	1.2	234	244
1AON	G U	G	234	L	1.0	234	244
1AON	G U	G	265	N	1.4	256	268
1APY	A B	A	21	W	4.5	14	26
1APY	A B	A	34	V	1.7	30	45
1APY	A B	A	37	G	63.0	30	45
1APY	A B	A	135	W	2.4	126	138
1APY	C B	B	238	D	1.3	237	243
1APY	C B	B	241	M	1.0	237	243
1APY	C D	C	21	W	7.6	14	26
1APY	C D	C	34	V	2.0	30	44
1APY	C D	C	37	G	56.3	30	44
1APY	C D	C	131	L	1.0	126	138
1APY	C D	C	135	W	2.1	126	138
1AQD	A B	A	70	L	1.8	56	77
1AQD	A B	A	76	R	2.3	56	77
1AQD	A B	B	57	D	1.6	55	63
1AQD	D E	D	66	D	2.9	56	77
1AQD	D E	D	70	L	1.6	56	77
1AQD	D E	D	76	R	2.0	56	77
1AQD	D E	E	57	D	1.0	55	64
1AQD	G H	G	47	E	2.1	46	50
1AQD	G H	G	48	F	2.5	46	50
1AQD	G H	G	70	L	1.9	56	77
1AQD	G H	G	76	R	2.6	56	77
1AQD	G H	H	57	D	1.5	55	64
1AR1	A B	A	84	G	182.5	84	101
1AR1	A B	A	356	F	2.5	348	364
1AR1	A B	A	357	S	6.3	348	364
1AR1	A B	A	359	I	7.9	348	364
1AR1	A B	A	360	A	6.3	348	364
1AR1	A B	A	362	M	1.8	348	364
1AR1	A B	A	388	V	1.2	371	395
1AR1	A B	A	397	P	1.3	396	403
1AR1	A B	A	398	L	1.8	396	403
1AR1	A B	A	402	Y	1.3	396	403
1AR1	A B	A	465	F	1.7	442	469
1AR1	A B	A	485	W	1.8	483	513
1AR1	A B	B	34	L	1.4	26	59
1AR1	A B	B	49	V	5.8	26	59
1AR1	A B	B	53	L	9.4	26	59
1AR1	A B	B	77	I	6.2	76	81
1AR1	A B	B	78	E	6.4	76	81
1AR1	A B	B	82	T	5.5	82	104
1AR1	A B	B	100	L	1.6	82	104
1AR1	A B	B	103	S	2.0	82	104
1AR1	B D	B	29	H	2.5	26	59
1AVF	P A	P	13	I	1.7	13	20
1AVF	P A	P	14	R	1.2	13	20
1AVF	Q J	Q	13	I	3.5	13	20
1AVF	Q J	Q	16	T	1.6	13	20
1AVO	A B	A	29	L	1.2	8	30
1AVO	A B	A	33	F	1.2	31	45
1AVO	A B	A	36	K	3.0	31	45
1AVO	A B	A	37	I	1.7	31	45
1AVO	A B	A	40	L	1.1	31	45
1AVO	A B	A	43	F	1.4	31	45

1AVO	A B	A	44	L	2.1	31	45
1AVO	A B	B	117	L	1.6	108	139
1AVO	A B	B	120	E	1.6	108	139
1AVO	A B	B	123	D	1.2	108	139
1AVO	A B	B	134	W	1.8	108	139
1AVO	A B	B	202	H	1.6	195	233
1AVO	A B	B	209	Y	3.1	195	233
1AVO	A B	B	216	V	1.3	195	233
1AVO	A B	B	220	R	2.1	195	233
1AVO	A B	B	223	Y	2.5	195	233
1AVO	A N	N	234	F	1.3	234	239
1AVO	C D	C	21	L	2.5	8	45
1AVO	C D	C	36	K	2.4	8	45
1AVO	C D	C	37	I	1.4	8	45
1AVO	C D	C	40	L	1.5	8	45
1AVO	C D	C	44	L	2.3	8	45
1AVO	C D	D	109	K	1.3	108	139
1AVO	C D	D	113	L	1.0	108	139
1AVO	C D	D	120	E	1.5	108	139
1AVO	C D	D	134	W	2.1	108	139
1AVO	C D	D	202	H	1.4	195	233
1AVO	C D	D	209	Y	2.7	195	233
1AVO	C D	D	216	V	1.3	195	233
1AVO	C D	D	220	R	2.4	195	233
1AVO	E D	D	234	F	1.2	234	239
1AVO	E F	E	29	L	1.3	8	45
1AVO	E F	E	32	Y	4.0	8	45
1AVO	E F	E	33	F	2.7	8	45
1AVO	E F	E	36	K	6.9	8	45
1AVO	E F	E	37	I	1.6	8	45
1AVO	E F	E	40	L	1.2	8	45
1AVO	E F	E	44	L	2.2	8	45
1AVO	E F	F	109	K	3.9	108	139
1AVO	E F	F	120	E	1.6	108	139
1AVO	E F	F	123	D	1.1	108	139
1AVO	E F	F	134	W	1.4	108	139
1AVO	E F	F	202	H	1.5	195	233
1AVO	E F	F	206	E	2.7	195	233
1AVO	E F	F	209	Y	2.6	195	233
1AVO	E F	F	210	R	2.7	195	233
1AVO	E F	F	220	R	2.4	195	233
1AVO	E F	F	223	Y	3.7	195	233
1AVO	G H	G	21	L	2.5	8	45
1AVO	G H	G	33	F	3.0	8	45
1AVO	G H	G	36	K	3.0	8	45
1AVO	G H	G	37	I	1.6	8	45
1AVO	G H	G	40	L	1.4	8	45
1AVO	G H	G	44	L	2.4	8	45
1AVO	G H	H	109	K	1.5	108	139
1AVO	G H	H	113	L	1.4	108	139
1AVO	G H	H	120	E	1.7	108	139
1AVO	G H	H	123	D	1.1	108	139
1AVO	G H	H	134	W	1.7	108	139
1AVO	G H	H	202	H	1.5	195	233
1AVO	G H	H	209	Y	1.9	195	233
1AVO	G H	H	216	V	1.4	195	233
1AVO	G H	H	220	R	2.6	195	233
1AVO	G H	H	223	Y	3.1	195	233
1AVO	I J	I	32	Y	2.4	8	45
1AVO	I J	I	33	F	2.9	8	45

1AVO	I J	I	36	K	3.0	8	45
1AVO	I J	I	37	I	1.6	8	45
1AVO	I J	I	40	L	3.0	8	45
1AVO	I J	I	43	F	1.8	8	45
1AVO	I J	I	44	L	4.0	8	45
1AVO	I J	J	109	K	1.6	108	139
1AVO	I J	J	113	L	1.2	108	139
1AVO	I J	J	116	R	1.9	108	139
1AVO	I J	J	117	L	2.0	108	139
1AVO	I J	J	120	E	1.5	108	139
1AVO	I J	J	123	D	1.2	108	139
1AVO	I J	J	134	W	1.5	108	139
1AVO	I J	J	198	R	1.1	195	233
1AVO	I J	J	202	H	1.5	195	233
1AVO	I J	J	209	Y	3.6	195	233
1AVO	I J	J	212	I	1.8	195	233
1AVO	I J	J	216	V	2.6	195	233
1AVO	I J	J	220	R	2.7	195	233
1AVO	I J	J	223	Y	4.0	195	233
1AVO	I J	J	227	Y	1.4	195	233
1AVO	K J	J	234	F	1.1	234	239
1AVO	K L	K	17	F	1.5	8	45
1AVO	K L	K	21	L	1.9	8	45
1AVO	K L	K	29	L	1.3	8	45
1AVO	K L	K	36	K	2.4	8	45
1AVO	K L	K	37	I	1.6	8	45
1AVO	K L	K	40	L	2.1	8	45
1AVO	K L	K	43	F	1.3	8	45
1AVO	K L	K	44	L	2.1	8	45
1AVO	K L	L	113	L	1.1	108	139
1AVO	K L	L	120	E	1.4	108	139
1AVO	K L	L	123	D	1.1	108	139
1AVO	K L	L	134	W	2.9	108	139
1AVO	K L	L	209	Y	2.3	195	233
1AVO	K L	L	212	I	1.3	195	233
1AVO	K L	L	216	V	1.9	195	233
1AVO	K L	L	220	R	1.9	195	233
1AVO	M N	M	21	L	2.3	8	45
1AVO	M N	M	29	L	1.0	8	45
1AVO	M N	M	32	Y	3.8	8	45
1AVO	M N	M	33	F	3.3	8	45
1AVO	M N	M	36	K	2.9	8	45
1AVO	M N	M	37	I	1.2	8	45
1AVO	M N	M	40	L	1.5	8	45
1AVO	M N	M	44	L	2.2	8	45
1AVO	M N	N	120	E	1.5	108	139
1AVO	M N	N	123	D	1.1	108	139
1AVO	M N	N	134	W	2.0	108	139
1AVO	M N	N	202	H	1.4	195	233
1AVO	M N	N	209	Y	3.0	195	233
1AVO	M N	N	216	V	1.0	195	233
1AVO	M N	N	220	R	2.7	195	233
1AVO	M N	N	223	Y	3.2	195	233
1AVZ	B C	B	90	F	1.3	81	95
1AW8	A B	B	95	D	1.4	95	100
1AW8	B E	E	77	H	1.5	74	78
1AWC	A B	A	323	W	1.4	322	331
1AWC	A B	A	324	Q	1.5	322	331
1AWC	A B	A	333	K	1.0	333	339
1AWC	A B	A	414	L	1.1	411	429

1AWC	A B	A	417	L	1.0	411	429
1AWC	A B	B	110	W	2.1	107	114
1AWC	A B	B	113	E	1.6	107	114
1AWC	A B	B	143	I	1.7	140	147
1AXC	C D	D	150	F	2.4	147	151
1AXC	E F	F	147	M	3.1	147	151
1AXC	E F	F	150	F	2.5	147	151
1AXT	L H	L	124	Q	1.2	122	127
1AY7	A B	B	35	D	1.5	34	42
1AY7	A B	B	39	D	2.9	34	42
1AYY	A B	A	14	G	7.9	12	27
1AYY	A B	A	22	W	3.3	12	27
1AYY	A B	A	25	L	1.0	12	27
1AYY	A B	A	35	V	1.8	31	45
1AYY	A B	A	38	G	59.9	31	45
1AYY	A B	A	39	V	1.7	31	45
1AYY	A B	A	43	E	1.5	31	45
1AYY	A B	A	135	W	2.9	126	139
1AYY	A D	A	108	G	330.6	107	116
1AYY	A D	A	112	F	1.3	107	116
1AYY	A D	D	242	I	1.7	228	246
1AYY	C B	C	108	G	115.5	107	116
1AYY	C D	C	14	G	3.0	12	27
1AYY	C D	C	18	N	11.0	12	27
1AYY	C D	C	22	W	14.3	12	27
1AYY	C D	C	35	V	1.7	31	45
1AYY	C D	C	38	G	38.4	31	45
1AYY	C D	C	39	V	1.7	31	45
1AYY	C D	C	43	E	1.0	31	45
1AYY	C D	C	89	I	1.2	88	98
1AYY	C D	C	135	W	3.5	126	138
1AZZ	A C	A	57	H	2.1	56	61
1AZZ	A C	A	172	Y	1.2	165	174
1AZZ	B C	B	237	W	1.5	235	243
1AZZ	B D	B	172	Y	1.3	165	174
1B0N	A B	A	60	T	1.0	58	62
1B0N	A B	A	78	W	5.2	76	87
1B0N	A B	A	81	L	1.1	76	87
1B0N	A B	A	82	V	1.9	76	87
1B0N	A B	A	83	R	3.4	76	87
1B0N	A B	A	86	M	1.8	76	87
1B0N	A B	A	92	K	2.0	92	108
1B0N	A B	A	95	F	4.4	92	108
1B0N	A B	A	98	F	4.3	92	108
1B0N	A B	A	99	L	7.5	92	108
1B0N	A B	B	14	E	2.3	13	25
1B0N	A B	B	15	W	5.1	13	25
1B0N	A B	B	19	M	1.8	13	25
1B0N	A B	B	21	E	1.5	13	25
1B0N	A B	B	23	K	2.1	13	25
1B0N	A B	B	32	I	1.1	29	39
1B0N	A B	B	35	Y	2.6	29	39
1B0N	A B	B	36	L	2.2	29	39
1B27	B E	E	36	D	1.5	35	43
1B27	B E	E	40	D	4.8	35	43
1B33	A B	A	3	V	1.0	2	13
1B33	A B	A	7	I	2.5	2	13
1B33	A B	A	22	L	2.1	19	31
1B33	A B	A	26	K	1.3	19	31
1B33	A B	A	36	L	2.0	32	45

1B33	A B	A	85	D	1.3	74	98
1B33	A B	A	89	R	3.8	74	98
1B33	A B	A	93	Y	2.2	74	98
1B33	A B	A	96	V	1.0	74	98
1B33	A B	B	5	I	1.2	4	15
1B33	A B	B	9	I	2.2	4	15
1B33	A B	B	13	D	1.5	4	15
1B33	A B	B	24	L	1.5	21	33
1B33	A B	B	30	Y	1.2	21	33
1B33	A B	B	31	F	1.7	21	33
1B33	A B	B	34	G	73.7	34	47
1B33	A B	B	38	V	1.1	34	47
1B33	A B	B	90	R	3.1	75	99
1B33	A B	B	94	Y	3.1	75	99
1B33	A B	B	97	L	2.1	75	99
1B33	A I	A	26	K	1.2	19	31
1B33	A I	I	54	E	1.1	48	61
1B33	C B	B	76	R	1.5	75	99
1B33	C B	B	78	Y	1.1	75	99
1B33	C D	C	7	I	2.6	2	13
1B33	C D	C	22	L	1.9	19	31
1B33	C D	C	26	K	1.1	19	31
1B33	C D	C	28	F	1.1	19	31
1B33	C D	C	32	G	100.6	32	45
1B33	C D	C	36	L	2.1	32	45
1B33	C D	C	85	D	1.1	74	98
1B33	C D	C	89	R	3.4	74	98
1B33	C D	C	93	Y	2.1	74	98
1B33	C D	C	96	V	1.4	74	98
1B33	C D	D	5	I	1.2	4	16
1B33	C D	D	9	I	1.9	4	16
1B33	C D	D	13	D	1.4	4	16
1B33	C D	D	31	F	3.3	21	33
1B33	C D	D	34	G	188.6	34	47
1B33	C D	D	38	V	2.0	34	47
1B33	C D	D	90	R	2.4	75	99
1B33	C D	D	94	Y	2.4	75	99
1B33	C D	D	97	L	1.4	75	99
1B33	D N	D	115	T	1.0	112	120
1B33	D N	D	119	L	1.4	112	120
1B33	D N	N	36	W	1.3	35	46
1B33	E D	D	78	Y	1.4	75	99
1B33	E F	E	3	V	1.0	2	13
1B33	E F	E	7	I	2.8	2	13
1B33	E F	E	11	D	1.2	2	13
1B33	E F	E	22	L	1.8	19	31
1B33	E F	E	26	K	1.7	19	31
1B33	E F	E	28	F	1.3	19	31
1B33	E F	E	29	V	1.1	19	31
1B33	E F	E	32	G	54.4	32	45
1B33	E F	E	36	L	1.9	32	45
1B33	E F	E	85	D	6.9	74	98
1B33	E F	E	89	R	3.3	74	98
1B33	E F	E	93	Y	3.7	74	98
1B33	E F	E	96	V	1.2	74	98
1B33	E F	F	5	I	1.5	4	16
1B33	E F	F	9	I	2.4	4	16
1B33	E F	F	30	Y	1.2	21	47
1B33	E F	F	31	F	3.4	21	47
1B33	E F	F	34	G	128.6	21	47

1B33	E F	F	38	V	1.5	21	47
1B33	E F	F	90	R	4.4	75	99
1B33	E F	F	91	Y	1.2	75	99
1B33	E F	F	94	Y	5.1	75	99
1B33	E N	E	105	E	1.0	101	107
1B33	E N	E	106	I	1.0	101	107
1B33	H I	H	4	T	1.6	2	13
1B33	H I	H	7	I	3.0	2	13
1B33	H I	H	22	L	1.5	19	31
1B33	H I	H	32	G	63.4	32	45
1B33	H I	H	36	L	2.1	32	45
1B33	H I	H	89	R	2.4	74	98
1B33	H I	H	93	Y	3.3	74	98
1B33	H I	H	96	V	1.1	74	98
1B33	H I	I	5	I	1.1	4	16
1B33	H I	I	9	I	2.3	4	16
1B33	H I	I	28	K	1.1	21	33
1B33	H I	I	31	F	3.0	21	33
1B33	H I	I	34	G	32.1	34	47
1B33	H I	I	38	V	1.0	34	47
1B33	H I	I	90	R	3.2	75	99
1B33	H I	I	94	Y	3.1	75	99
1B33	H I	I	97	L	1.5	75	99
1B33	H M	M	78	Y	1.8	75	99
1B33	I O	O	22	L	1.7	22	26
1B33	J I	I	78	Y	1.2	75	99
1B33	J K	J	7	I	1.2	2	13
1B33	J K	J	11	D	1.7	2	13
1B33	J K	J	28	F	1.0	19	31
1B33	J K	J	29	V	1.0	19	31
1B33	J K	J	32	G	58.2	32	45
1B33	J K	J	36	L	1.8	32	45
1B33	J K	J	89	R	2.6	74	98
1B33	J K	J	93	Y	3.5	74	98
1B33	J K	K	9	I	1.7	4	16
1B33	J K	K	13	D	1.0	4	16
1B33	J K	K	31	F	2.6	21	33
1B33	J K	K	34	G	153.2	34	47
1B33	J K	K	90	R	2.7	75	99
1B33	J K	K	94	Y	2.7	75	99
1B33	K O	K	115	T	1.5	112	120
1B33	K O	K	119	L	1.6	112	120
1B33	K O	O	36	W	1.0	36	47
1B33	K O	O	44	Q	1.0	36	47
1B33	L K	K	78	Y	1.3	75	99
1B33	L M	L	4	T	1.0	2	13
1B33	L M	L	7	I	3.2	2	13
1B33	L M	L	26	K	1.1	19	31
1B33	L M	L	32	G	103.9	32	45
1B33	L M	L	36	L	2.3	32	45
1B33	L M	L	85	D	1.1	74	98
1B33	L M	L	89	R	3.4	74	98
1B33	L M	L	93	Y	3.1	74	98
1B33	L M	L	96	V	1.2	74	98
1B33	L M	M	5	I	1.6	4	15
1B33	L M	M	9	I	2.3	4	15
1B33	L M	M	27	L	1.0	21	33
1B33	L M	M	31	F	3.6	21	33
1B33	L M	M	34	G	96.9	34	47
1B33	L M	M	38	V	1.0	34	47

1B33	L M	M	90	R	2.7	75	99
1B33	L M	M	94	Y	3.1	75	99
1B33	L M	M	97	L	1.6	75	99
1B33	L O	L	105	E	1.5	101	107
1B35	A B	A	10	R	1.8	10	14
1B35	A B	B	156	R	2.7	154	161
1B35	A B	B	159	L	1.2	154	161
1B35	A B	B	160	I	1.2	154	161
1B35	A B	B	166	G	4.4	164	170
1B35	A B	B	169	G	1.4	164	170
1B35	A C	A	34	Q	1.1	32	39
1B35	A C	A	38	I	2.0	32	39
1B35	A C	A	45	I	1.6	45	49
1B35	A C	A	46	R	1.4	45	49
1B35	A C	A	47	Q	1.4	45	49
1B35	A C	A	48	L	1.0	45	49
1B35	A C	A	90	Q	2.1	90	96
1B35	A C	A	94	Y	1.1	90	96
1B35	A C	C	56	L	1.5	56	61
1B35	A C	C	106	H	2.0	106	112
1B35	B C	B	164	L	1.1	164	170
1B35	B C	B	168	S	1.1	164	170
1B4U	A B	A	13	Y	2.2	10	19
1B4U	A B	A	17	F	1.6	10	19
1B4U	A B	A	35	Y	1.5	35	44
1B4U	A B	A	39	Q	1.4	35	44
1B4U	A B	A	42	M	1.3	35	44
1B4U	A B	A	50	R	2.1	47	56
1B4U	A B	A	89	V	1.0	89	99
1B4U	A B	A	91	F	1.8	89	99
1B4U	A B	A	103	F	1.2	103	110
1B4U	A B	A	122	M	1.3	115	124
1B4U	A B	B	229	H	1.7	229	236
1B4U	A B	B	230	I	1.6	229	236
1B4U	A B	B	233	L	1.4	229	236
1B4U	A D	A	10	V	1.0	10	19
1B4U	A D	A	11	H	1.1	10	19
1B4U	A D	A	13	Y	1.3	10	19
1B4U	A D	D	104	W	1.5	100	113
1B4U	A D	D	105	H	1.1	100	113
1B4U	A D	D	112	L	1.6	100	113
1B4U	C B	C	10	V	1.1	10	18
1B4U	C B	C	13	Y	1.3	10	18
1B4U	C B	C	32	R	1.0	28	34
1B4U	C B	B	104	W	1.3	100	113
1B4U	C B	B	105	H	1.2	100	113
1B4U	C B	B	112	L	1.9	100	113
1B4U	C D	C	13	Y	2.1	10	18
1B4U	C D	C	17	F	1.9	10	18
1B4U	C D	C	35	Y	1.2	35	44
1B4U	C D	C	39	Q	1.3	35	44
1B4U	C D	C	50	R	2.2	47	56
1B4U	C D	C	90	Y	1.5	89	99
1B4U	C D	C	91	F	1.6	89	99
1B4U	C D	C	103	F	1.1	103	110
1B4U	C D	C	118	Y	1.8	115	124
1B4U	C D	C	122	M	1.4	115	124
1B4U	C D	D	229	H	1.5	229	236
1B4U	C D	D	230	I	1.1	229	236
1B4U	C D	D	233	L	1.1	229	236

1B4U	C D	D	234	R	1.2	229	236
1B5F	A B	A	228	V	1.6	225	235
1B5F	A B	A	231	I	2.4	225	235
1B5F	C D	C	138	Y	1.0	136	143
1B5F	C D	C	228	V	1.9	225	235
1B5F	C D	C	231	I	2.2	225	235
1B6C	A B	B	195	L	2.5	195	204
1B6C	A B	B	196	L	2.0	195	204
1B6C	A B	B	199	R	1.9	195	204
1B6C	A B	B	203	R	1.1	195	204
1B6C	A B	B	242	W	1.8	239	252
1B6C	A B	B	243	F	1.8	239	252
1B6C	C D	D	195	L	1.0	195	204
1B6C	C D	D	196	L	1.5	195	204
1B6C	C D	D	243	F	2.3	239	252
1B6C	C H	H	291	Y	1.1	288	295
1B6C	E B	B	291	Y	1.7	288	295
1B6C	E F	F	195	L	1.3	195	204
1B6C	E F	F	196	L	2.4	195	204
1B6C	E F	F	199	R	1.5	195	204
1B6C	E F	F	243	F	2.4	239	252
1B6C	G H	H	195	L	2.4	195	204
1B6C	G H	H	196	L	1.9	195	204
1B6C	G H	H	199	R	1.9	195	204
1B6C	G H	H	203	R	1.0	195	204
1B6C	G H	H	243	F	1.0	239	252
1B8D	A B	A	5	I	1.2	4	15
1B8D	A B	A	6	T	1.4	4	15
1B8D	A B	A	9	I	1.8	4	15
1B8D	A B	A	24	L	1.5	21	47
1B8D	A B	A	31	I	1.1	21	47
1B8D	A B	A	48	H	1.2	48	63
1B8D	A B	A	87	D	1.1	76	100
1B8D	A B	A	91	R	3.5	76	100
1B8D	A B	A	94	N	2.2	76	100
1B8D	A B	A	95	Y	4.8	76	100
1B8D	A B	A	98	V	1.5	76	100
1B8D	A B	A	99	V	1.8	76	100
1B8D	A B	A	108	W	1.8	103	111
1B8D	A B	B	9	V	2.1	4	15
1B8D	A B	B	13	D	1.4	4	15
1B8D	A B	B	31	I	1.4	22	33
1B8D	A B	B	34	G	92.2	34	47
1B8D	A B	B	38	L	1.7	34	47
1B8D	A B	B	91	R	2.3	76	100
1B8D	A B	B	95	Y	3.7	76	100
1B8D	A B	B	98	L	1.3	76	100
1B8D	A L	A	157	D	2.0	146	163
1B8D	K B	K	157	D	2.0	146	163
1B8D	K L	K	5	I	1.3	4	15
1B8D	K L	K	6	T	2.2	4	15
1B8D	K L	K	9	I	2.7	4	15
1B8D	K L	K	10	S	1.0	4	15
1B8D	K L	K	24	L	2.0	21	47
1B8D	K L	K	31	I	1.1	21	47
1B8D	K L	K	48	H	1.2	48	63
1B8D	K L	K	91	R	3.0	76	100
1B8D	K L	K	94	N	2.6	76	100
1B8D	K L	K	95	Y	3.8	76	100
1B8D	K L	K	98	V	2.2	76	100

1B8D	K L	K	99	V	1.6	76	100
1B8D	K L	K	108	W	1.9	103	111
1B8D	K L	L	9	V	1.7	4	15
1B8D	K L	L	13	D	1.3	4	15
1B8D	K L	L	28	K	1.0	22	33
1B8D	K L	L	31	I	1.5	22	33
1B8D	K L	L	34	G	11.3	34	47
1B8D	K L	L	38	L	1.9	34	47
1B8D	K L	L	91	R	3.1	76	100
1B8D	K L	L	95	Y	2.4	76	100
1B8D	K L	L	98	L	1.4	76	100
1B8D	K L	L	104	V	1.3	103	108
1B9X	A B	A	7	L	1.1	4	25
1B9X	A B	A	15	K	1.6	4	25
1B9X	A B	A	18	I	1.2	4	25
1B9X	A B	A	30	L	1.4	30	34
1B9X	A B	B	522	L	1.9	511	527
1B9X	A B	B	540	F	3.8	533	546
1B9X	A B	B	543	Y	2.4	533	546
1B9X	A B	B	544	V	1.0	533	546
1B9X	A C	C	22	P	1.4	22	34
1B9X	A C	C	25	V	2.3	22	34
1B9X	A C	C	28	D	2.1	22	34
1B9X	A C	C	29	W	1.2	22	34
1B9X	A C	C	101	M	2.0	38	106
1BAF	L H	L	124	Q	1.3	122	127
1BB1	A B	A	3	I	1.4	2	34
1BB1	A B	A	17	I	1.0	2	34
1BB1	A B	A	31	I	1.9	2	34
1BB1	A B	B	6	I	1.8	2	34
1BB1	A C	A	6	I	1.3	2	34
1BB1	A C	A	27	I	1.3	2	34
1BB1	A C	A	30	Y	1.5	2	34
1BB1	A C	C	17	I	2.0	3	34
1BB1	A C	C	21	K	1.2	3	34
1BB1	A C	C	31	I	1.7	3	34
1BB1	B C	B	3	I	1.5	2	34
1BB1	B C	C	6	I	1.4	3	34
1BB1	B C	C	13	I	1.4	3	34
1BB1	B C	C	20	I	1.3	3	34
1BB1	B C	C	27	I	1.5	3	34
1BCC	A B	A	80	E	1.7	72	82
1BCC	A B	B	363	K	1.7	355	371
1BCC	A B	B	370	M	1.3	355	371
1BCC	A C	A	436	R	1.2	434	439
1BCC	A G	A	434	Y	1.7	434	439
1BCC	C D	C	71	C	11.4	62	74
1BCC	C D	C	224	Y	3.5	221	247
1BCC	C D	C	227	F	2.4	221	247
1BCC	C D	C	231	L	2.2	221	247
1BCC	C D	C	245	L	2.2	221	247
1BCC	C D	C	246	F	2.0	221	247
1BCC	C D	D	205	G	7.3	199	233
1BCC	C D	D	208	M	2.0	199	233
1BCC	C D	D	219	V	2.1	199	233
1BCC	C D	D	222	M	1.3	199	233
1BCC	C D	D	223	K	1.0	199	233
1BCC	C D	D	227	W	3.9	199	233
1BCC	C D	D	230	L	1.7	199	233
1BCC	C E	C	51	L	1.1	34	54

1BCC	C E	E	58	F	1.2	25	59
1BCC	D F	F	60	F	2.3	52	71
1BCC	D F	F	64	R	1.7	52	71
1BCC	D F	F	67	D	1.1	52	71
1BCC	D H	D	184	K	5.9	179	195
1BCC	D H	H	17	L	1.2	16	25
1BCC	D H	H	44	V	1.7	28	45
1BCC	D H	H	59	F	3.8	55	77
1BCC	D H	H	74	F	7.2	55	77
1BCC	D J	D	23	H	1.6	23	35
1BCC	D J	D	203	R	1.1	199	233
1BCC	D J	D	206	L	1.3	199	233
1BCC	D J	D	207	K	1.9	199	233
1BCC	D J	J	35	F	2.1	24	46
1BCC	D J	J	43	Y	1.1	24	46
1BCC	D J	J	52	W	3.4	52	60
1BCC	E G	E	33	K	1.0	25	59
1BCC	E J	E	34	G	11.6	25	59
1BCC	E J	E	49	Y	2.5	25	59
1BCC	E J	E	52	K	1.0	25	59
1BCC	E J	J	10	Y	2.0	5	14
1BCC	E J	J	27	G	27.2	24	46
1BCC	E J	J	31	F	2.0	24	46
1BCC	E J	J	32	E	1.7	24	46
1BCC	G H	H	56	E	1.7	55	77
1BCC	G H	H	60	D	1.1	55	77
1BCP	A D	A	229	E	2.7	228	233
1BCP	A E	A	69	Q	1.3	57	77
1BCP	A E	A	76	R	1.1	57	77
1BCP	B D	B	146	Y	1.2	146	158
1BCP	B D	D	63	P	33.7	63	74
1BCP	B D	D	66	V	1.1	63	74
1BCP	B F	B	148	R	2.2	146	158
1BCP	B F	B	152	M	1.0	146	158
1BCP	C E	C	146	Y	2.1	146	158
1BCP	C E	C	150	R	1.1	146	158
1BCP	C E	C	154	Y	1.7	146	158
1BCP	C E	C	157	Y	2.0	146	158
1BCP	C E	E	63	P	20.0	63	75
1BCP	C E	E	64	M	1.5	63	75
1BCP	C E	E	66	V	1.4	63	75
1BCP	C E	E	67	M	1.5	63	75
1BCP	E F	E	69	R	1.4	63	75
1BCP	E F	E	72	F	1.3	63	75
1BCP	E F	F	52	W	2.1	51	66
1BCP	E F	F	55	T	1.4	51	66
1BCP	E F	F	59	F	1.0	51	66
1BCP	G J	G	229	E	1.1	228	233
1BCP	G K	G	69	Q	1.3	57	77
1BCP	G K	G	76	R	1.1	57	77
1BCP	H J	H	157	Y	1.0	146	158
1BCP	H J	J	63	P	27.8	63	74
1BCP	H J	J	66	V	1.0	63	74
1BCP	H L	H	147	S	1.1	146	158
1BCP	H L	H	151	K	1.6	146	158
1BCP	H L	H	152	M	1.4	146	158
1BCP	H L	L	54	D	1.6	51	66
1BCP	H L	L	64	Y	1.8	51	66
1BCP	I J	I	152	L	1.0	146	159
1BCP	I K	I	146	Y	2.2	146	159

1BCP	I K	I	150	R	1.1	146	159
1BCP	I K	I	154	Y	1.7	146	159
1BCP	I K	I	158	M	1.1	146	159
1BCP	I K	K	63	P	9.3	63	75
1BCP	I K	K	66	V	1.3	63	75
1BCP	I K	K	67	M	2.1	63	75
1BCP	I K	K	70	A	1.0	63	75
1BCP	I K	K	71	V	1.2	63	75
1BCP	I K	K	74	Q	1.2	63	75
1BCP	K L	K	72	F	1.2	63	75
1BCP	K L	L	52	W	2.4	51	66
1BCP	K L	L	55	T	1.2	51	66
1BCP	K L	L	59	F	1.9	51	66
1BCR	A B	A	60	Y	1.2	58	64
1BCR	A B	A	150	H	1.3	149	163
1BCR	A B	A	183	H	1.5	181	194
1BCR	A B	A	184	D	1.8	181	194
1BCR	A B	A	187	G	263.0	181	194
1BCR	A B	A	191	F	2.7	181	194
1BCR	A B	A	192	W	1.9	181	194
1BCR	A B	B	274	Y	4.6	271	279
1BCR	A B	B	275	S	1.9	271	279
1BCR	A B	B	278	Y	2.3	271	279
1BCR	A B	B	288	L	1.5	282	289
1BCR	A B	B	348	Y	1.2	343	362
1BCR	A B	B	402	H	1.1	399	403
1BCR	A B	B	408	L	1.6	404	417
1BCR	A B	B	411	F	1.1	404	417
1BCR	A B	B	414	F	3.3	404	417
1BCR	A B	B	415	L	1.6	404	417
1BD2	A D	A	62	G	2.5	57	86
1BD2	A D	A	65	R	2.4	57	86
1BDJ	A B	B	750	E	1.3	744	758
1BDJ	A B	B	754	E	2.8	744	758
1BDJ	A B	B	761	H	1.4	759	774
1BFO	A B	A	124	Q	1.6	122	126
1BFO	C D	C	124	Q	1.9	122	126
1BFO	E F	E	123	E	1.0	122	126
1BFO	E F	E	124	Q	1.6	122	126
1BFO	G H	G	124	Q	1.1	122	126
1BGX	L H	L	123	E	2.2	122	128
1BGX	L H	L	127	S	1.5	122	128
1BGX	T L	T	475	F	1.4	453	477
1BGX	T L	T	487	R	2.0	487	494
1BGX	T L	T	489	Q	1.2	487	494
1BGY	A B	A	80	E	2.7	74	83
1BGY	A B	B	83	F	1.3	82	92
1BGY	A B	B	87	R	1.8	82	92
1BGY	A C	A	436	R	1.4	434	439
1BGY	A I	A	130	E	1.0	124	143
1BGY	B R	B	83	F	2.7	82	92
1BGY	B R	B	135	W	1.7	134	141
1BGY	B R	R	96	E	1.0	89	108
1BGY	B R	R	107	W	1.3	89	108
1BGY	C D	C	77	W	3.1	76	104
1BGY	C D	C	223	Y	4.6	220	246
1BGY	C D	C	230	L	2.5	220	246
1BGY	C D	D	205	G	35.8	198	233
1BGY	C D	D	216	L	1.0	198	233
1BGY	C D	D	226	K	4.1	198	233

1BGY	C D	D	227	W	8.2	198	233
1BGY	C D	D	229	V	1.4	198	233
1BGY	C D	D	230	L	2.3	198	233
1BGY	C E	E	58	F	2.5	30	64
1BGY	C F	C	319	P	1.4	319	340
1BGY	C F	C	376	L	1.5	345	377
1BGY	C F	F	26	F	2.0	25	30
1BGY	C F	F	29	L	3.0	25	30
1BGY	C F	F	62	I	1.1	52	71
1BGY	C F	F	66	L	1.1	52	71
1BGY	C G	C	333	L	1.0	319	340
1BGY	C G	C	337	W	3.9	319	340
1BGY	C G	C	347	Y	1.4	345	377
1BGY	C G	G	52	F	2.9	44	72
1BGY	C G	G	55	F	2.1	44	72
1BGY	C G	G	59	Y	1.2	44	72
1BGY	C G	G	62	G	43.1	44	72
1BGY	C G	G	66	F	2.4	44	72
1BGY	D E	D	215	L	1.5	198	233
1BGY	D E	D	218	L	1.0	198	233
1BGY	D E	D	225	H	1.3	198	233
1BGY	D E	E	39	V	1.8	30	64
1BGY	D E	E	46	G	1.3	30	64
1BGY	D F	F	60	F	1.3	52	71
1BGY	D G	D	224	R	6.6	198	233
1BGY	D G	D	225	H	1.3	198	233
1BGY	D H	H	40	C	2.4	34	47
1BGY	D H	H	41	D	2.2	34	47
1BGY	D H	H	54	C	4.1	54	59
1BGY	D H	H	55	T	5.8	54	59
1BGY	D H	H	56	E	2.3	54	59
1BGY	D H	H	58	L	2.5	54	59
1BGY	D J	D	203	R	2.1	198	233
1BGY	D J	D	206	L	1.6	198	233
1BGY	D J	D	207	K	1.7	198	233
1BGY	D J	D	210	L	1.9	198	233
1BGY	D J	D	214	L	1.2	198	233
1BGY	D J	J	35	F	3.2	17	47
1BGY	D J	J	36	D	1.0	17	47
1BGY	D J	J	40	D	1.0	17	47
1BGY	D J	J	43	Y	2.4	17	47
1BGY	D J	J	44	E	1.7	17	47
1BGY	E J	E	30	E	1.7	30	64
1BGY	E J	E	34	G	45.8	30	64
1BGY	E J	E	49	Y	1.7	30	64
1BGY	E J	E	52	K	1.1	30	64
1BGY	E J	J	20	F	1.4	17	47
1BGY	E J	J	31	F	1.2	17	47
1BGY	E J	J	32	E	1.4	17	47
1BGY	J K	J	22	L	1.5	17	47
1BGY	J K	K	23	L	1.9	16	36
1BGY	M N	M	80	E	1.4	74	83
1BGY	M O	M	436	R	1.3	434	439
1BGY	M U	M	140	E	1.4	124	143
1BGY	N F	N	83	F	2.2	82	92
1BGY	N F	F	104	R	1.1	89	108
1BGY	N F	F	107	W	1.1	89	108
1BGY	N U	N	156	Q	2.5	155	168
1BGY	O P	O	67	T	2.9	63	70
1BGY	O P	O	77	W	1.1	76	101

1BGY	O P	O	223	Y	2.4	220	243
1BGY	O P	O	224	Y	1.0	220	243
1BGY	O P	O	233	L	1.3	220	243
1BGY	O P	O	241	L	2.1	220	243
1BGY	O P	P	200	H	1.7	198	233
1BGY	O P	P	205	G	55.1	198	233
1BGY	O P	P	208	M	1.8	198	233
1BGY	O P	P	216	L	1.0	198	233
1BGY	O P	P	219	V	1.0	198	233
1BGY	O P	P	227	W	3.5	198	233
1BGY	O Q	Q	57	Q	1.0	30	64
1BGY	O Q	Q	58	F	1.7	30	64
1BGY	O R	O	376	L	7.3	345	378
1BGY	O R	R	26	F	2.0	25	30
1BGY	O R	R	62	I	2.9	52	71
1BGY	O R	R	66	L	1.4	52	71
1BGY	O S	O	326	W	2.0	319	340
1BGY	O S	O	337	W	3.8	319	340
1BGY	O S	O	347	Y	1.7	345	378
1BGY	O S	S	52	F	1.3	44	72
1BGY	O S	S	55	F	1.4	44	72
1BGY	O S	S	59	Y	1.6	44	72
1BGY	O S	S	62	G	48.6	44	72
1BGY	O S	S	66	F	2.6	44	72
1BGY	P Q	P	211	M	1.1	198	233
1BGY	P Q	P	215	L	1.5	198	233
1BGY	P Q	Q	39	V	1.1	30	64
1BGY	P Q	Q	46	G	1.2	30	64
1BGY	P R	R	60	F	1.7	52	71
1BGY	P R	R	70	M	1.2	52	71
1BGY	P S	P	224	R	6.5	198	233
1BGY	P S	P	225	H	1.3	198	233
1BGY	P T	T	40	C	1.5	35	47
1BGY	P T	T	41	D	1.5	35	47
1BGY	P T	T	55	T	7.8	54	75
1BGY	P T	T	56	E	1.7	54	75
1BGY	P V	P	203	R	1.6	198	233
1BGY	P V	V	35	F	1.6	17	47
1BGY	P V	V	43	Y	2.2	17	47
1BGY	Q V	Q	30	E	1.3	30	64
1BGY	Q V	Q	34	G	74.8	30	64
1BGY	Q V	Q	49	Y	1.1	30	64
1BGY	Q V	V	20	F	1.5	17	47
1BGY	Q V	V	31	F	1.3	17	47
1BGY	V W	V	22	L	1.3	17	47
1BGY	V W	W	23	L	1.9	16	36
1BH8	A B	A	57	L	1.2	51	75
1BH8	A B	A	61	V	1.0	51	75
1BH8	A B	A	64	F	3.0	51	75
1BH8	A B	A	65	I	1.4	51	75
1BH8	A B	A	73	M	1.0	51	75
1BH8	A B	B	120	R	1.4	115	127
1BH8	A B	B	137	L	1.4	131	139
1BH8	A B	B	154	M	1.1	148	176
1BH8	A B	B	159	K	1.0	148	176
1BH8	A B	B	161	F	4.5	148	176
1BH8	A B	B	162	V	1.7	148	176
1BH8	A B	B	163	G	5.6	148	176
1BH8	A B	B	166	V	1.5	148	176
1BI4	A B	A	102	L	1.9	94	106

1BI4	A B	A	181	F	1.1	172	186
1BI4	A B	A	184	N	1.3	172	186
1BI4	A B	A	185	H	1.9	172	186
1BI4	A B	A	201	V	1.2	196	208
1BI4	A B	B	181	F	1.9	172	185
1BI4	A B	B	184	N	1.2	172	185
1BI4	A B	B	208	I	1.4	196	209
1BI7	A B	B	18	T	1.1	14	22
1BI8	A B	B	21	V	1.3	21	30
1BI8	A B	B	54	T	1.2	54	63
1BI8	A B	B	88	D	1.2	87	96
1BI8	C D	D	21	V	1.3	21	30
1BI8	C D	D	54	T	1.2	54	63
1BI8	C D	D	88	D	1.2	87	96
1BIQ	A B	A	37	E	1.4	34	46
1BIQ	A B	A	40	I	1.0	34	46
1BIQ	A B	A	41	E	1.8	34	46
1BIQ	A B	A	85	S	1.1	67	97
1BIQ	A B	A	86	I	1.2	67	97
1BIQ	A B	A	89	R	5.6	67	97
1BIQ	A B	A	105	E	1.5	102	128
1BIQ	A B	A	106	T	1.8	102	128
1BIQ	A B	A	110	T	1.2	102	128
1BIQ	A B	A	113	F	3.1	102	128
1BIQ	A B	A	120	R	1.8	102	128
1BIQ	A B	A	137	F	1.9	133	143
1BIQ	A B	A	141	V	1.3	133	143
1BIQ	A B	A	158	D	3.2	153	171
1BIQ	A B	A	166	Y	1.4	153	171
1BIQ	A B	A	169	L	2.6	153	171
1BIQ	A B	B	82	L	1.3	67	98
1BIQ	A B	B	86	I	1.0	67	98
1BIQ	A B	B	89	R	4.4	67	98
1BIQ	A B	B	105	E	2.7	102	128
1BIQ	A B	B	113	F	2.5	102	128
1BIQ	A B	B	120	R	2.3	102	128
1BIQ	A B	B	123	T	2.2	102	128
1BIQ	A B	B	127	R	1.8	102	128
1BIQ	A B	B	137	F	2.0	133	142
1BIQ	A B	B	158	D	2.6	153	171
1BIQ	A B	B	161	I	1.0	153	171
1BIQ	A B	B	166	Y	1.2	153	171
1BIQ	A B	B	169	L	2.9	153	171
1BJ1	J K	J	124	Q	1.3	122	127
1BJ1	L H	L	124	Q	1.5	122	128
1BJO	A B	A	23	Q	1.9	16	25
1BJO	A B	A	78	G	2.0	76	87
1BJO	A B	A	109	E	1.1	101	113
1BJO	A B	A	244	F	1.4	243	259
1BJO	A B	B	19	L	1.8	16	25
1BJO	A B	B	77	R	1.1	76	87
1BJO	A B	B	78	G	2.0	76	87
1BJO	A B	B	109	E	2.5	101	113
1BJO	A B	B	244	F	1.4	243	259
1BM3	L H	L	123	E	1.6	122	127
1BM3	L H	L	124	Q	1.3	122	127
1BOM	A B	B	19	C	1.0	16	23
1BP3	A B	A	18	H	1.0	6	35
1BP3	A B	A	25	F	2.9	6	35
1BP3	A B	A	64	R	1.1	64	68

1BP3	A B	A	164	Y	2.7	155	185
1BP3	A B	A	167	R	1.9	155	185
1BP3	A B	A	172	K	1.2	155	185
1BP3	A B	A	174	E	1.0	155	185
1BP3	A B	A	183	R	1.1	155	185
1BPL	A B	A	80	K	1.4	80	93
1BPL	A B	A	87	I	1.6	80	93
1BPL	A B	A	91	H	1.3	80	93
1BPL	A B	B	211	E	1.0	206	223
1BPL	A B	B	212	I	1.3	206	223
1BPL	A B	B	215	W	3.5	206	223
1BPL	A B	B	218	W	5.1	206	223
1BPL	A B	B	219	Y	4.4	206	223
1BPL	A B	B	222	E	1.8	206	223
1BPL	A B	B	363	Y	4.4	363	367
1BPL	A B	B	385	E	1.3	381	393
1BPL	A B	B	391	R	1.7	381	393
1BR1	A B	A	796	I	1.4	793	813
1BR1	A B	A	799	F	2.6	793	813
1BR1	A B	A	802	Q	1.2	793	813
1BR1	A B	B	88	Y	2.0	85	93
1BR1	A B	B	91	G	14.0	85	93
1BR1	A B	B	112	L	1.6	106	113
1BR1	A B	B	122	E	1.1	121	129
1BR1	A B	B	125	E	1.9	121	129
1BR1	A B	B	126	Q	1.0	121	129
1BR1	A H	H	85	F	1.8	85	93
1BR1	A H	H	145	R	4.2	140	150
1BR1	C D	C	729	E	1.9	727	731
1BR1	C D	C	796	I	1.4	793	813
1BR1	C D	C	799	F	2.6	793	813
1BR1	C D	C	802	Q	1.2	793	813
1BR1	C D	C	807	L	1.1	793	813
1BR1	C D	C	812	F	1.6	793	813
1BR1	C D	D	88	Y	1.0	85	93
1BR1	C D	D	91	G	15.5	85	93
1BR1	C D	D	125	E	1.1	121	129
1BR1	E F	E	796	I	1.4	793	813
1BR1	E F	E	799	F	2.5	793	813
1BR1	E F	E	804	R	2.0	793	813
1BR1	E F	E	807	L	1.6	793	813
1BR1	E F	E	812	F	1.1	793	813
1BR1	E F	F	88	Y	1.1	85	93
1BR1	E F	F	91	G	15.6	85	93
1BR1	E F	F	125	E	1.2	121	129
1BR1	G H	G	729	E	1.0	727	731
1BR1	G H	G	796	I	1.4	793	813
1BR1	G H	G	799	F	2.6	793	813
1BR1	G H	G	807	L	1.6	793	813
1BR1	G H	G	812	F	2.3	793	813
1BR1	G H	H	88	Y	1.1	85	93
1BR1	G H	H	91	G	33.0	85	93
1BR1	G H	H	125	E	1.2	121	129
1BSX	A X	A	454	L	1.0	453	460
1BSX	A X	X	689	I	1.4	689	694
1BSX	A X	X	690	L	1.8	689	694
1BSX	A X	X	693	L	1.4	689	694
1BSX	B Y	B	454	L	1.0	453	460
1BSX	B Y	Y	689	I	1.4	689	694
1BSX	B Y	Y	690	L	1.8	689	694

1BSX	B Y	Y	693	L	1.4	689	694
1BTH	J K	J	14	E	1.8	14	14
1BTH	J K	J	14	E	1.5	14	14
1BTH	J K	J	14	L	2.0	14	14
1BTH	J K	J	14	Y	1.6	14	14
1BTH	L H	L	14	E	1.1	14	14
1BUH	A B	A	209	I	2.2	208	219
1BUH	A B	A	210	D	1.3	208	219
1BUH	A B	A	213	F	1.2	208	219
1BVK	A C	C	121	Q	1.8	120	125
1BVK	D F	F	121	Q	1.5	120	125
1BVK	D F	F	124	I	1.6	120	125
1BVY	A F	A	100	H	1.4	94	106
1BVY	A F	A	309	K	1.0	305	310
1BVY	A F	F	494	E	1.4	492	507
1BVY	A F	F	609	F	1.0	609	628
1BVY	A F	F	610	E	1.7	609	628
1BX2	A B	A	48	F	1.6	46	50
1BX2	A B	A	70	L	1.7	56	78
1BX2	A C	A	58	G	47.5	56	78
1BX2	A C	A	65	V	1.0	56	78
1BX2	A C	A	66	D	1.4	56	78
1BX2	A C	A	68	A	1.2	56	78
1BX2	A C	A	72	I	1.2	56	78
1BX2	A C	A	76	R	1.0	56	78
1BX2	B C	B	78	Y	1.5	66	89
1BX2	B C	B	81	H	1.4	66	89
1BX2	B C	B	82	N	1.1	66	89
1BX2	B C	B	85	V	1.2	66	89
1BX2	D E	D	48	F	1.6	46	50
1BX2	D E	D	70	L	1.9	56	78
1BX2	D E	D	76	R	1.0	56	78
1BX2	D E	E	53	L	1.1	52	64
1BX2	D E	E	57	D	1.1	52	64
1BX2	D F	D	58	G	139.4	56	78
1BX2	D F	D	65	V	1.2	56	78
1BX2	E F	E	78	Y	1.9	65	86
1BX2	E F	E	81	H	1.9	65	86
1BX2	E F	E	82	N	1.4	65	86
1BX2	E F	E	85	V	1.5	65	86
1BXL	A B	A	126	V	3.3	119	131
1BXL	A B	A	129	E	1.0	119	131
1BXN	A I	A	222	L	1.1	217	236
1BXN	A I	A	423	R	12.4	415	436
1BXN	A I	A	427	E	1.4	415	436
1BXN	A I	A	434	N	1.0	415	436
1BXN	A I	A	453	W	1.9	439	454
1BXN	A I	I	21	K	1.1	16	29
1BXN	A I	I	25	Y	1.0	16	29
1BXN	A L	A	186	R	1.0	185	198
1BXN	A L	A	189	G	292.4	185	198
1BXN	A L	A	190	R	1.0	185	198
1BXN	A L	A	193	Y	1.0	185	198
1BXN	C I	C	186	R	1.1	185	198
1BXN	C I	C	189	G	259.7	185	198
1BXN	C J	C	222	L	1.0	217	236
1BXN	C J	C	427	E	1.4	415	436
1BXN	C J	C	431	L	1.3	415	436
1BXN	C J	C	453	W	2.0	439	454
1BXN	C J	J	21	K	1.2	16	29

1BXN	C J	J	25	Y	1.0	16	29
1BXN	E J	E	189	G	260.1	185	198
1BXN	E J	E	190	R	1.2	185	198
1BXN	E J	E	193	Y	1.4	185	198
1BXN	E K	E	222	L	1.2	217	236
1BXN	E K	E	427	E	1.0	415	436
1BXN	E K	E	431	L	1.6	415	436
1BXN	E K	E	453	W	2.0	439	454
1BXN	E K	K	21	K	1.5	16	29
1BXN	E K	K	25	Y	1.3	16	29
1BXN	G K	G	186	R	1.9	185	198
1BXN	G K	G	189	G	267.2	185	198
1BXN	G K	G	190	R	2.0	185	198
1BXN	G K	G	193	Y	1.8	185	198
1BXN	G L	G	222	L	1.1	217	236
1BXN	G L	G	427	E	1.4	415	436
1BXN	G L	G	434	N	1.1	415	436
1BXN	G L	G	453	W	2.1	439	454
1BXN	G L	L	21	K	1.1	16	29
1BXN	G L	L	25	Y	1.0	16	29
1BXR	A B	A	265	R	2.0	258	276
1BXR	A B	A	461	W	1.5	460	480
1BXR	A B	A	464	V	1.2	460	480
1BXR	A B	B	115	T	1.2	115	125
1BXR	A B	B	116	R	3.4	115	125
1BXR	A B	B	117	K	1.9	115	125
1BXR	C D	C	260	E	1.6	258	276
1BXR	C D	C	461	W	1.1	460	480
1BXR	C D	C	464	V	1.4	460	480
1BXR	C D	D	115	T	1.2	115	126
1BXR	C D	D	116	R	2.0	115	126
1BXR	C D	D	120	R	1.4	115	126
1BXR	C D	D	123	R	2.5	115	126
1BXR	E F	E	258	D	1.0	258	276
1BXR	E F	E	259	K	1.5	258	276
1BXR	E F	E	265	R	2.1	258	276
1BXR	E F	E	461	W	1.9	460	480
1BXR	E F	F	115	T	1.1	115	125
1BXR	E F	F	116	R	3.2	115	125
1BXR	E F	F	117	K	1.1	115	125
1BXR	E F	F	120	R	1.2	115	125
1BXR	E F	F	362	D	2.4	362	380
1BXR	G H	G	260	E	1.6	258	276
1BXR	G H	G	265	R	2.0	258	276
1BXR	G H	G	461	W	4.4	460	480
1BXR	G H	G	464	V	1.3	460	480
1BXR	G H	H	115	T	1.1	115	126
1BXR	G H	H	116	R	21.7	115	126
1BXR	G H	H	117	K	1.0	115	126
1BXR	G H	H	120	R	1.0	115	126
1BXR	G H	H	123	R	1.1	115	126
1BZ7	A B	A	124	Q	2.0	123	127
1C08	B C	C	63	W	1.1	60	64
1C08	B C	C	97	K	4.8	89	99
1C0G	S A	S	73	Q	2.0	73	90
1C0G	S A	S	77	G	9.7	73	90
1C0G	S A	S	81	I	2.4	73	90
1C0G	S A	S	82	F	1.7	73	90
1C0G	S A	S	84	V	1.3	73	90
1C0G	S A	A	143	Y	1.4	137	145

1C0G	S A	A	345	I	2.9	338	349
1C12	A B	A	124	Q	1.1	122	128
1C17	L M	L	76	F	1.2	46	79
1C4Z	A D	A	694	Y	1.4	687	697
1C4Z	A D	D	9	K	1.1	8	12
1C5B	L H	L	124	Q	1.7	122	127
1C5D	A B	A	122	E	1.1	121	126
1C5D	L H	L	122	E	1.3	121	127
1C8O	A B	A	4	F	1.8	2	11
1C8O	A B	A	20	P	1.0	20	34
1C9B	A B	A	177	F	1.6	177	183
1C9B	A B	A	192	G	1.8	188	202
1C9B	E F	E	177	F	1.6	177	183
1C9B	E F	E	192	G	3.5	188	202
1C9B	I J	I	177	F	1.1	177	183
1C9B	I J	I	192	G	3.2	188	202
1C9B	M N	M	177	F	1.1	177	183
1C9B	M N	M	192	G	1.8	188	202
1C9B	M N	M	250	P	1.6	250	264
1C9B	Q R	Q	177	F	1.5	177	183
1C9B	Q R	Q	192	G	2.9	188	202
1C9B	Q R	R	271	E	1.3	270	277
1CA0	B C	C	237	W	1.3	235	243
1CA0	B C	C	238	V	1.2	235	243
1CA0	B C	C	241	T	2.8	235	243
1CA0	B C	C	242	L	1.2	235	243
1CA0	G H	H	234	L	1.2	234	245
1CA0	G H	H	235	V	1.1	234	245
1CA0	G H	H	237	W	5.4	234	245
1CA0	G H	H	238	V	1.1	234	245
1CA0	G H	H	242	L	2.3	234	245
1CAX	A D	A	196	E	1.0	192	199
1CAX	A D	D	412	N	1.2	403	413
1CAX	C F	C	199	Y	3.0	192	200
1CAX	C F	C	206	I	1.1	203	209
1CAX	C F	F	405	E	8.6	404	413
1CAX	C F	F	408	E	8.3	404	413
1CAX	C F	F	409	L	2.2	404	413
1CAX	C F	F	410	L	8.1	404	413
1CAX	E B	E	194	F	1.2	192	200
1CAX	E B	E	199	Y	1.0	192	200
1CAX	E B	B	394	V	1.7	392	397
1CAX	E B	B	409	L	1.0	404	411
1CAX	E F	F	275	Q	3.1	274	280
1CAX	E F	F	276	L	1.2	274	280
1CB7	A B	A	18	V	1.4	17	31
1CB7	A B	A	22	I	1.6	17	31
1CB7	A B	A	68	E	1.8	67	72
1CB7	A B	A	69	I	1.1	67	72
1CB7	A B	A	70	D	1.5	67	72
1CB7	A B	A	107	R	1.1	101	112
1CB7	A B	B	98	Y	1.3	97	101
1CB7	A B	B	471	F	1.2	463	475
1CB7	C D	C	18	V	1.3	17	30
1CB7	C D	C	22	I	1.6	17	30
1CB7	C D	C	69	I	1.3	67	72
1CB7	C D	D	110	G	2.6	104	118
1CB7	C D	D	471	F	1.2	463	475
1CBV	L H	L	128	E	1.1	127	131
1CBW	B C	C	241	T	1.2	231	243

1CC0	A E	A	71	P	99.9	67	75
1CC0	A E	A	105	H	1.4	89	107
1CC0	A E	A	106	F	1.2	89	107
1CC0	C F	C	71	P	79.7	67	75
1CC1	S L	S	56	M	1.3	55	68
1CC1	S L	L	53	I	1.7	50	55
1CC1	S L	L	61	D	1.9	59	68
1CC1	S L	L	172	R	1.5	151	182
1CC1	S L	L	173	R	1.2	151	182
1CC1	S L	L	176	H	1.2	151	182
1CC1	S L	L	177	E	1.4	151	182
1CC1	S L	L	181	M	1.1	151	182
1CC1	S L	L	483	G	7.9	480	490
1CC1	S L	L	487	R	1.5	480	490
1CDL	A E	A	12	F	1.9	6	20
1CDL	A E	A	14	E	1.0	6	20
1CDL	A E	A	19	F	1.6	6	20
1CDL	A E	A	51	M	1.0	45	55
1CDL	A E	A	68	F	1.1	65	74
1CDL	A E	A	71	M	1.0	65	74
1CDL	A E	A	72	M	2.1	65	74
1CDL	A E	A	84	E	1.6	78	93
1CDL	A E	A	85	I	1.3	78	93
1CDL	A E	A	92	F	1.5	78	93
1CDL	A E	A	105	L	2.4	102	112
1CDL	A E	A	124	M	1.8	118	129
1CDL	A E	A	125	I	1.0	118	129
1CDL	A E	A	141	F	2.5	138	146
1CDL	A E	E	798	R	2.1	798	814
1CDL	A E	E	799	K	2.2	798	814
1CDL	A E	E	800	W	7.1	798	814
1CDL	A E	E	805	H	2.3	798	814
1CDL	A E	E	807	V	2.1	798	814
1CDL	A E	E	808	R	2.1	798	814
1CDL	A E	E	810	I	1.2	798	814
1CDL	A E	E	812	R	1.3	798	814
1CDL	A E	E	813	L	1.4	798	814
1CDL	B F	B	7	E	1.2	6	20
1CDL	B F	B	12	F	1.8	6	20
1CDL	B F	B	92	F	1.9	78	93
1CDL	B F	B	105	L	1.3	102	112
1CDL	B F	B	124	M	2.2	118	129
1CDL	B F	B	141	F	1.0	138	146
1CDL	B F	B	144	M	2.3	138	146
1CDL	B F	F	798	R	1.6	798	814
1CDL	B F	F	799	K	1.8	798	814
1CDL	B F	F	800	W	7.0	798	814
1CDL	B F	F	801	Q	1.1	798	814
1CDL	B F	F	804	G	18.9	798	814
1CDL	B F	F	807	V	2.1	798	814
1CDL	B F	F	813	L	1.6	798	814
1CDL	C G	C	14	E	1.0	6	20
1CDL	C G	C	72	M	1.2	65	74
1CDL	C G	C	92	F	1.0	78	93
1CDL	C G	C	105	L	1.1	102	113
1CDL	C G	C	124	M	1.5	118	129
1CDL	C G	C	141	F	1.1	138	145
1CDL	C G	G	798	R	1.4	797	813
1CDL	C G	G	799	K	1.0	797	813
1CDL	C G	G	800	W	5.1	797	813

1CDL	C G	G	804	G	11.1	797	813
1CDL	C G	G	805	H	1.6	797	813
1CDL	D G	D	47	E	3.0	45	56
1CDL	D G	G	798	R	2.5	797	813
1CDL	D G	G	802	K	1.0	797	813
1CDL	D H	D	11	E	1.4	6	20
1CDL	D H	D	12	F	1.2	6	20
1CDL	D H	D	14	E	1.9	6	20
1CDL	D H	D	68	F	1.5	65	73
1CDL	D H	D	71	M	1.5	65	73
1CDL	D H	D	72	M	1.0	65	73
1CDL	D H	D	109	M	1.4	102	113
1CDL	D H	D	141	F	1.1	138	144
1CDL	D H	H	799	K	1.6	799	815
1CDL	D H	H	800	W	3.5	799	815
1CDL	D H	H	801	Q	1.0	799	815
1CDL	D H	H	802	K	1.1	799	815
1CDL	D H	H	805	H	3.3	799	815
1CDL	D H	H	807	V	1.7	799	815
1CDL	D H	H	810	I	1.2	799	815
1CDL	D H	H	812	R	1.4	799	815
1CDL	D H	H	813	L	1.4	799	815
1CE1	L H	L	124	Q	1.3	122	128
1CE7	A B	A	169	W	1.2	165	177
1CF4	A B	A	173	I	3.2	166	178
1CF7	A B	A	67	G	6.4	55	69
1CF7	A B	B	72	R	1.3	71	86
1CFF	A B	A	105	L	1.2	103	113
1CFF	A B	A	109	M	2.5	103	113
1CFF	A B	A	120	E	1.8	118	129
1CFF	A B	A	124	M	1.0	118	129
1CFF	A B	A	127	E	2.0	118	129
1CFF	A B	A	141	F	1.1	138	147
1CFF	A B	A	145	M	1.1	138	147
1CFF	A B	B	9	F	3.5	9	18
1CFF	A B	B	11	G	74.8	9	18
1CG5	A B	A	31	R	3.4	21	36
1CG5	A B	A	35	L	3.1	21	36
1CG5	A B	A	108	V	1.1	96	114
1CG5	A B	A	122	H	2.4	119	137
1CG5	A B	B	30	R	4.0	20	35
1CG5	A B	B	34	V	1.6	20	35
1CG5	A B	B	107	V	1.2	95	114
1CG5	A B	B	111	L	1.2	95	114
1CG5	A B	B	122	H	2.3	119	139
1CG5	A B	B	126	Y	1.4	119	139
1CGI	E I	E	172	W	1.4	165	173
1CGI	E I	I	36	V	2.3	34	44
1CHO	F G	G	235	V	1.6	235	245
1CHO	F G	G	237	W	4.6	235	245
1CHO	F G	G	238	V	1.4	235	245
1CHO	F G	G	241	T	1.1	235	245
1CHO	F G	G	242	L	2.4	235	245
1CI6	A B	A	320	L	1.0	287	341
1CI6	A B	A	327	L	1.5	287	341
1CI6	A B	A	330	E	1.0	287	341
1CI6	A B	A	331	I	2.2	287	341
1CI6	A B	A	334	L	3.0	287	341
1CI6	A B	A	335	K	1.5	287	341
1CI6	A B	A	337	L	1.2	287	341

1CI6	A B	A	338	I	1.7	287	341
1CI6	A B	B	257	L	2.3	240	283
1CI6	A B	B	261	N	1.5	240	283
1CI6	A B	B	264	L	2.2	240	283
1CI6	A B	B	268	V	1.5	240	283
1CI6	A B	B	271	L	1.4	240	283
1CI6	A B	B	275	L	1.8	240	283
1CI6	A B	B	278	L	3.3	240	283
1CI6	A B	B	279	R	1.1	240	283
1CI6	A B	B	282	F	2.7	240	283
1CIC	A B	A	123	E	1.3	122	127
1CIC	A B	A	124	Q	2.3	122	127
1CIC	C D	C	123	E	1.2	122	128
1CIC	C D	C	124	Q	1.6	122	128
1CJF	A C	A	3	W	3.8	3	11
1CJF	A C	A	6	Y	3.1	3	11
1CJF	A C	A	133	H	2.4	120	137
1CJF	B C	B	136	R	1.0	120	137
1CKK	A B	A	51	M	1.0	45	56
1CKK	A B	A	71	M	1.3	71	76
1CKK	A B	B	7	W	3.5	7	17
1CKK	A B	B	14	K	1.6	7	17
1CKN	A B	B	204	K	1.3	196	207
1CL7	L H	L	124	Q	1.3	122	128
1CLO	L H	L	124	Q	1.5	122	127
1CLV	A I	A	245	F	2.0	245	255
1CLY	L H	L	124	Q	1.0	122	128
1CM1	A B	A	7	E	1.7	6	20
1CM1	A B	A	11	E	2.4	6	20
1CM1	A B	A	19	F	2.3	6	20
1CM1	A B	A	72	M	1.0	65	74
1CM1	A B	A	92	F	2.6	84	93
1CM1	A B	A	127	E	1.0	118	129
1CM1	A B	A	141	F	1.4	138	146
1CM1	A B	A	145	M	1.5	138	146
1CM1	A B	B	296	R	1.1	295	310
1CM1	A B	B	298	K	1.1	295	310
1CM1	A B	B	299	L	1.8	295	310
1CM1	A B	B	300	K	1.9	295	310
1CM1	A B	B	301	G	31.8	295	310
1CM1	A B	B	303	I	2.0	295	310
1CM1	A B	B	304	L	1.8	295	310
1CM1	A B	B	308	L	1.6	295	310
1CN4	A C	C	103	R	1.1	89	113
1CN4	B C	C	150	R	1.2	138	151
1CP9	A B	A	25	L	2.4	22	37
1CP9	A B	A	26	F	2.3	22	37
1CP9	A B	A	28	G	81.0	22	37
1CP9	A B	A	29	Y	5.0	22	37
1CP9	A B	A	36	D	1.8	22	37
1CP9	A B	A	39	F	1.0	38	48
1CP9	A B	A	47	S	1.5	38	48
1CP9	A B	A	61	I	2.3	61	70
1CP9	A B	A	65	K	1.0	61	70
1CP9	A B	A	68	R	1.0	61	70
1CP9	A B	A	87	E	1.1	85	108
1CP9	A B	A	90	I	1.1	85	108
1CP9	A B	A	91	L	1.4	85	108
1CP9	A B	A	94	Y	2.0	85	108
1CP9	A B	A	115	K	1.9	115	120

1CP9	A B	A	119	D	1.3	115	120
1CP9	A B	A	151	I	2.5	150	164
1CP9	A B	A	153	N	3.0	150	164
1CP9	A B	A	172	F	2.4	166	177
1CP9	A B	A	173	F	1.1	166	177
1CP9	A B	A	175	Q	2.8	166	177
1CP9	A B	B	148	L	3.0	147	159
1CP9	A B	B	152	M	3.0	147	159
1CP9	A B	B	367	F	2.8	367	371
1CP9	A B	B	370	W	1.4	367	371
1CP9	A B	B	395	L	1.2	391	402
1CPC	A B	A	9	V	1.9	4	15
1CPC	A B	A	24	I	1.0	21	47
1CPC	A B	A	31	F	1.5	21	47
1CPC	A B	A	38	L	1.0	21	47
1CPC	A B	A	93	R	3.0	78	101
1CPC	A B	A	97	Y	4.1	78	101
1CPC	A B	A	100	V	1.4	78	101
1CPC	A B	B	5	F	1.3	4	15
1CPC	A B	B	24	I	1.1	21	33
1CPC	A B	B	93	R	1.3	78	102
1CPC	A B	B	97	Y	2.6	78	102
1CPC	A B	B	100	F	4.5	78	102
1CPC	K L	K	5	L	1.4	4	15
1CPC	K L	K	6	T	1.8	4	15
1CPC	K L	K	9	V	2.1	4	15
1CPC	K L	K	24	I	1.3	21	47
1CPC	K L	K	31	F	1.7	21	47
1CPC	K L	K	38	L	1.0	21	47
1CPC	K L	K	93	R	2.7	78	102
1CPC	K L	K	97	Y	4.8	78	102
1CPC	K L	K	100	V	1.2	78	102
1CPC	K L	L	5	F	1.6	4	15
1CPC	K L	L	9	V	1.9	4	15
1CPC	K L	L	13	D	1.0	4	15
1CPC	K L	L	31	V	1.3	21	33
1CPC	K L	L	34	G	36.4	34	47
1CPC	K L	L	93	R	2.0	78	102
1CPC	K L	L	97	Y	3.1	78	102
1CPC	K L	L	100	F	4.8	78	102
1CPC	K L	L	106	V	1.1	105	123
1CQ4	A B	A	39	I	1.2	36	43
1CQT	A I	I	312	V	1.2	312	319
1CQT	B J	J	813	K	1.0	812	816
1CSE	E I	E	104	Y	1.0	104	117
1CSE	E I	E	107	I	1.6	104	117
1CT8	A B	A	124	Q	1.5	122	127
1CT8	C D	C	124	Q	1.6	122	127
1CU4	L H	L	124	Q	2.3	122	126
1CUL	A B	A	413	V	1.9	409	430
1CUL	A B	A	424	D	2.6	409	430
1CUL	A B	B	912	L	2.3	909	927
1CUL	A B	B	913	R	2.6	909	927
1CUL	A B	B	916	N	1.0	909	927
1CUL	A B	B	917	E	2.1	909	927
1CUL	A B	B	919	I	1.0	909	927
1CUL	A B	B	923	D	2.0	909	927
1CUL	B C	B	914	L	1.4	909	927
1CUL	B C	B	917	E	1.4	909	927
1CUL	B C	B	989	H	2.0	967	990

1CXZ	A B	B	43	R	1.0	29	67
1CXZ	A B	B	78	R	2.2	71	97
1CXZ	A B	B	88	H	1.1	71	97
1CZ8	L H	L	124	Q	1.3	122	127
1D2Z	A B	A	90	W	1.0	82	94
1D2Z	A B	A	93	Q	1.7	82	94
1D2Z	A B	B	146	D	1.4	142	153
1D2Z	C B	C	48	H	1.7	39	53
1D2Z	C B	C	52	L	1.3	39	53
1D2Z	C B	C	112	N	1.6	111	117
1D2Z	C B	C	115	R	2.4	111	117
1D2Z	C B	B	38	D	1.9	38	50
1D2Z	C D	C	90	W	1.1	82	94
1D2Z	C D	C	93	Q	1.8	82	94
1D2Z	C D	C	107	K	2.4	98	108
1D2Z	C D	D	146	D	1.1	142	154
1D3B	A B	A	6	P	1.5	6	13
1D3B	C D	C	6	P	1.7	6	14
1D3B	C D	C	10	L	1.4	6	14
1D3B	E F	E	6	P	2.0	6	14
1D3B	G H	G	6	P	2.1	6	14
1D3B	I J	I	6	P	1.9	6	14
1D3B	K L	K	6	P	2.1	6	13
1D3U	A B	B	1164	R	1.2	1151	1166
1D3U	A B	B	1191	R	1.0	1183	1197
1D8D	A B	A	96	F	1.7	94	110
1D8D	A B	A	131	Y	3.8	131	144
1D8D	A B	A	132	T	1.1	131	144
1D8D	A B	A	166	Y	1.2	166	180
1D8D	A B	A	170	H	2.2	166	180
1D8D	A B	A	200	Y	5.2	200	213
1D8D	A B	A	234	N	3.2	234	246
1D8D	A B	A	235	S	2.9	234	246
1D8D	A B	A	237	W	1.9	234	246
1D8D	A B	A	238	N	1.6	234	246
1D8D	A B	A	241	H	1.1	234	246
1D8D	A B	A	274	E	1.6	274	288
1D8D	A B	A	275	S	1.9	274	288
1D8D	A B	A	282	G	68.3	274	288
1D8D	A B	A	355	Y	2.3	353	366
1D8D	A B	A	358	Y	2.8	353	366
1D8D	A B	B	44	T	1.3	43	65
1D8D	A B	B	100	R	2.4	100	114
1D8D	A B	B	129	F	1.0	120	134
1D8D	A B	B	251	Y	1.3	249	262
1D8D	A B	B	271	K	1.0	270	281
1D8D	A B	B	280	R	1.4	270	281
1D9K	B C	C	61	Q	1.4	56	77
1D9K	C D	C	70	L	1.9	56	77
1D9K	C D	C	73	L	1.6	56	77
1D9K	C P	C	68	H	1.4	56	77
1D9K	D P	D	60	Y	1.2	55	63
1D9K	D P	D	61	W	1.2	55	63
1D9K	E H	H	70	R	1.3	68	84
1D9K	G H	G	70	L	1.5	56	77
1D9K	G H	G	76	R	1.5	56	77
1D9K	H Q	H	56	P	46.3	52	58
1D9K	H Q	H	60	Y	5.1	59	63
1DAN	L H	H	128	F	1.5	126	129
1DAN	L H	H	129	T	1.2	126	129

1DAN	T U	U	102	P	2.8	102	106
1DAN	T U	U	103	Y	1.1	102	106
1DBA	L H	L	124	Q	1.2	122	126
1DCE	A B	A	28	Y	1.0	22	41
1DCE	A B	A	64	T	1.5	63	78
1DCE	A B	A	67	N	1.5	63	78
1DCE	A B	A	111	H	2.4	107	118
1DCE	A B	A	115	W	1.2	107	118
1DCE	A B	A	143	F	1.3	143	156
1DCE	A B	A	178	Y	3.2	178	193
1DCE	A B	A	179	S	1.0	178	193
1DCE	A B	A	182	H	2.3	178	193
1DCE	A B	A	230	F	2.6	226	237
1DCE	A B	A	234	W	1.7	226	237
1DCE	A B	A	421	Y	1.4	419	441
1DCE	A B	A	424	D	3.1	419	441
1DCE	A B	B	213	D	1.2	212	221
1DCE	A B	B	217	W	4.0	212	221
1DCE	A B	B	218	W	1.8	212	221
1DCE	A B	B	290	H	3.0	288	301
1DCE	C D	C	36	F	1.1	22	41
1DCE	C D	C	64	T	1.5	63	78
1DCE	C D	C	67	N	1.1	63	78
1DCE	C D	C	143	F	2.6	143	156
1DCE	C D	C	147	D	1.3	143	156
1DCE	C D	C	178	Y	4.5	178	192
1DCE	C D	C	179	S	1.0	178	192
1DCE	C D	C	182	H	6.4	178	192
1DCE	C D	C	230	F	2.9	226	236
1DCE	C D	C	233	R	1.2	226	236
1DCE	C D	C	234	W	2.1	226	236
1DCE	C D	C	421	Y	2.3	419	441
1DCE	C D	C	424	D	2.3	419	441
1DCE	C D	D	217	W	3.7	212	221
1DCE	C D	D	290	H	2.7	288	301
1DD4	A C	A	3	I	2.0	3	11
1DD4	A C	A	6	I	2.7	3	11
1DD4	A C	A	10	I	1.5	3	11
1DD4	A C	A	21	L	1.8	15	29
1DD4	A C	C	3	I	2.2	2	12
1DD4	A C	C	6	I	1.3	2	12
1DD4	A C	C	7	I	1.7	2	12
1DD4	A C	C	10	I	1.3	2	12
1DD4	A C	C	25	L	1.7	18	29
1DD4	A D	A	87	E	1.4	85	93
1DD4	A D	A	91	L	1.2	85	93
1DD4	B C	B	91	L	1.3	85	93
1DD4	B C	C	5	E	1.1	2	12
1DD4	B D	B	3	I	2.0	3	11
1DD4	B D	B	6	I	2.2	3	11
1DD4	B D	B	10	I	1.4	3	11
1DD4	B D	B	21	L	1.9	15	30
1DD4	B D	B	24	K	1.0	15	30
1DD4	B D	B	25	L	1.2	15	30
1DD4	B D	B	28	K	1.0	15	30
1DD4	B D	D	3	I	1.8	2	13
1DD4	B D	D	4	D	1.2	2	13
1DD4	B D	D	6	I	2.3	2	13
1DD4	B D	D	7	I	2.6	2	13
1DD4	B D	D	10	I	1.6	2	13

1DD4	B D	D	21	L	1.5	15	29
1DD4	B D	D	25	L	1.9	15	29
1DE4	A C	A	78	V	1.7	59	86
1DE4	A C	A	146	E	2.0	140	151
1DE4	A C	A	150	H	1.7	140	151
1DE4	A C	C	619	L	3.4	611	628
1DE4	A C	C	629	R	1.3	629	635
1DE4	A C	C	641	W	2.2	640	662
1DE4	A C	C	643	Y	2.3	640	662
1DE4	A C	C	644	S	1.0	640	662
1DE4	D F	D	63	L	1.2	59	86
1DE4	D F	D	78	V	1.7	59	86
1DE4	D F	D	81	W	3.1	59	86
1DE4	D F	D	85	E	1.0	59	86
1DE4	D F	D	150	H	2.8	140	151
1DE4	D F	D	156	Q	1.1	152	177
1DE4	D F	F	619	L	4.1	612	628
1DE4	D F	F	641	W	1.9	640	662
1DE4	G I	G	74	H	1.9	59	86
1DE4	G I	G	77	T	2.8	59	86
1DE4	G I	G	78	V	4.2	59	86
1DE4	G I	G	81	W	1.7	59	86
1DE4	G I	G	146	E	1.6	140	151
1DE4	G I	G	150	H	2.3	140	151
1DE4	G I	I	616	S	1.1	612	628
1DE4	G I	I	640	Q	1.5	640	662
1DE4	G I	I	641	W	2.3	640	662
1DE4	G I	I	643	Y	2.1	640	662
1DE4	G I	I	644	S	1.0	640	662
1DE4	G I	I	650	F	2.7	640	662
1DEE	A B	A	124	Q	1.1	122	127
1DEE	C D	C	1123	E	1.3	1122	1127
1DEE	C D	C	1124	Q	1.5	1122	1127
1DEE	D G	G	1824	Q	1.9	1822	1835
1DEE	D G	G	1827	G	31.7	1822	1835
1DEE	D G	G	1845	E	1.8	1839	1853
1DEE	E F	E	2124	Q	1.4	2122	2127
1DEE	F H	H	2824	Q	1.5	2822	2835
1DEE	F H	H	2827	G	11.0	2822	2835
1DEE	F H	H	2828	F	1.4	2822	2835
1DEE	F H	H	2831	S	1.1	2822	2835
1DEE	F H	H	2834	D	1.4	2822	2835
1DEV	A B	B	680	Y	4.3	677	681
1DEV	A B	B	686	P	1.0	686	691
1DEV	A B	B	689	Q	1.0	686	691
1DFB	L H	L	122	Q	1.3	120	125
1DFK	A Y	A	804	Q	1.0	802	814
1DFK	A Y	A	808	L	1.5	802	814
1DFK	A Y	A	810	V	1.2	802	814
1DFK	A Y	A	815	I	1.4	815	823
1DFK	A Y	A	816	R	1.1	815	823
1DFK	A Y	A	817	K	55.8	815	823
1DFK	A Y	A	818	W	56.7	815	823
1DFK	A Y	A	829	L	1.5	825	834
1DFK	A Y	A	833	V	1.0	825	834
1DFK	A Y	Y	59	M	1.9	53	62
1DFK	A Y	Y	72	F	101.8	70	78
1DFK	A Y	Y	76	F	115.5	70	78
1DFK	A Y	Y	89	I	1.1	86	94
1DFK	A Z	A	782	I	2.1	766	797

1DFK	A Z	A	789	I	2.5	766	797
1DFK	A Z	A	791	G	23.2	766	797
1DFK	A Z	A	796	K	2.0	766	797
1DFK	A Z	Z	17	L	1.7	5	22
1DFK	A Z	Z	110	L	3.1	103	113
1DFK	A Z	Z	124	E	1.2	119	129
1DFK	A Z	Z	149	M	1.7	141	151
1DFK	Y Z	Z	20	F	1.1	5	22
1DFL	A Y	A	807	G	1.1	802	814
1DFL	A Y	A	808	L	1.5	802	814
1DFL	A Y	A	810	V	1.1	802	814
1DFL	A Y	A	815	I	1.4	815	823
1DFL	A Y	A	816	R	1.1	815	823
1DFL	A Y	A	818	W	1.8	815	823
1DFL	A Y	A	829	L	1.6	826	834
1DFL	A Y	A	830	Y	1.2	826	834
1DFL	A Y	A	833	V	1.0	826	834
1DFL	A Y	Y	59	M	2.1	53	62
1DFL	A Z	A	781	I	1.8	766	797
1DFL	A Z	A	782	I	2.1	766	797
1DFL	A Z	A	789	I	2.0	766	797
1DFL	A Z	A	793	L	2.9	766	797
1DFL	A Z	A	796	K	2.0	766	797
1DFL	A Z	Z	17	L	1.9	5	22
1DFL	A Z	Z	110	L	3.1	103	113
1DFL	A Z	Z	124	E	1.2	119	129
1DFL	A Z	Z	148	V	1.6	141	151
1DFL	A Z	Z	149	M	2.7	141	151
1DFL	B W	B	807	G	1.1	802	814
1DFL	B W	B	808	L	1.5	802	814
1DFL	B W	B	815	I	1.4	815	823
1DFL	B W	B	816	R	1.1	815	823
1DFL	B W	B	818	W	1.8	815	823
1DFL	B W	B	821	L	1.2	815	823
1DFL	B W	B	829	L	1.6	826	834
1DFL	B W	B	830	Y	1.2	826	834
1DFL	B W	W	59	M	2.1	53	62
1DFL	B X	B	781	I	1.8	766	797
1DFL	B X	B	782	I	2.1	766	797
1DFL	B X	B	789	I	2.0	766	797
1DFL	B X	B	793	L	2.9	766	797
1DFL	B X	B	796	K	2.0	766	797
1DFL	B X	B	809	S	1.8	802	814
1DFL	B X	X	21	W	4.2	5	22
1DFL	B X	X	110	L	3.1	103	113
1DFL	B X	X	124	E	2.5	119	129
1DFL	B X	X	148	V	1.6	141	151
1DFL	B X	X	149	M	2.6	141	151
1DFL	W X	X	20	F	1.2	5	22
1DGH	A B	A	12	M	1.1	11	19
1DGH	A B	A	15	W	3.9	11	19
1DGH	A B	A	16	K	1.5	11	19
1DGH	A B	A	59	D	2.0	55	66
1DGH	A B	A	63	H	2.5	55	66
1DGH	A B	A	326	F	2.0	325	331
1DGH	A B	A	363	R	1.4	349	367
1DGH	A B	A	366	L	1.3	349	367
1DGH	A B	B	15	W	3.7	11	18
1DGH	A B	B	16	K	1.5	11	18
1DGH	A B	B	60	E	1.7	55	66

1DGH	A B	B	62	A	2.7	55	66
1DGH	A B	B	326	F	2.3	325	331
1DGH	A D	A	163	S	1.0	161	169
1DGH	A D	A	184	D	1.4	179	189
1DGH	A D	A	188	L	1.0	179	189
1DGH	A D	A	360	D	1.1	349	367
1DGH	A D	A	363	R	1.4	349	367
1DGH	A D	A	364	H	1.4	349	367
1DGH	A D	D	163	S	1.0	161	169
1DGH	A D	D	184	D	2.0	179	189
1DGH	A D	D	188	L	1.0	179	189
1DGH	A D	D	360	D	1.2	349	367
1DGH	A D	D	363	R	1.2	349	367
1DGH	A D	D	364	H	1.3	349	367
1DGH	A D	D	474	I	1.1	472	486
1DGH	C B	C	163	S	1.1	161	169
1DGH	C B	C	184	D	1.2	179	189
1DGH	C B	C	188	L	1.0	179	189
1DGH	C B	C	360	D	1.0	349	367
1DGH	C B	C	363	R	1.2	349	367
1DGH	C B	B	163	S	1.1	161	169
1DGH	C B	B	184	D	1.0	179	189
1DGH	C B	B	188	L	1.0	179	189
1DGH	C B	B	360	D	1.1	349	367
1DGH	C D	C	12	M	1.1	11	19
1DGH	C D	C	15	W	4.0	11	19
1DGH	C D	C	16	K	1.8	11	19
1DGH	C D	C	59	D	1.8	55	66
1DGH	C D	C	326	F	2.4	325	331
1DGH	C D	C	355	L	1.4	349	367
1DGH	C D	C	363	R	1.4	349	367
1DGH	C D	D	12	M	1.2	11	18
1DGH	C D	D	15	W	4.0	11	18
1DGH	C D	D	16	K	1.4	11	18
1DGH	C D	D	326	F	1.7	325	331
1DGR	A V	A	194	F	2.6	192	200
1DGR	A W	A	199	Y	2.5	192	200
1DGR	A W	A	209	T	2.0	203	210
1DGR	A W	W	394	V	1.7	392	399
1DGR	A W	W	397	L	1.2	392	399
1DGR	A W	W	405	E	1.2	403	410
1DGR	A W	W	409	L	1.6	403	410
1DGR	A X	X	276	L	1.0	274	279
1DGR	B M	B	209	T	1.4	203	210
1DGR	B M	M	394	V	1.6	392	399
1DGR	B M	M	397	L	1.2	392	399
1DGR	B M	M	409	L	1.8	403	410
1DGR	B N	B	194	F	2.2	192	199
1DGR	B V	V	276	L	1.1	274	279
1DGR	C N	N	276	L	1.2	274	280
1DGR	C N	N	279	L	3.1	274	280
1DGR	C X	C	194	F	2.2	192	200
1DGR	C Y	C	199	Y	2.4	192	200
1DGR	C Y	Y	394	V	1.8	392	399
1DGR	C Y	Y	397	L	1.2	392	399
1DGR	C Y	Y	409	L	1.4	403	410
1DGW	A X	X	276	L	1.4	274	280
1DGW	A X	X	279	L	3.3	274	280
1DHK	A B	A	256	F	1.7	256	268
1DII	A C	C	617	H	1.4	607	620

1DII	B D	D	617	H	1.5	607	620
1DIO	A B	A	304	G	9.9	303	309
1DIO	A B	B	115	F	1.0	113	123
1DIO	A B	B	194	P	1.6	192	196
1DIO	A B	B	197	Q	1.8	197	210
1DIO	A B	B	202	I	1.1	197	210
1DIO	A B	B	204	H	1.2	197	210
1DIO	A B	B	205	I	1.1	197	210
1DIO	A G	A	210	K	1.0	205	214
1DIO	A G	A	240	W	2.6	239	252
1DIO	A G	A	243	G	1.0	239	252
1DIO	A G	A	244	F	4.3	239	252
1DIO	A G	A	471	L	1.4	470	480
1DIO	A G	A	490	L	8.2	483	496
1DIO	A G	G	45	L	1.4	45	49
1DIO	A G	G	69	V	1.5	66	72
1DIO	A G	G	86	L	1.1	83	96
1DIO	A G	G	89	Q	1.6	83	96
1DIO	A G	G	100	R	1.4	99	114
1DIO	A G	G	101	L	2.2	99	114
1DIO	A G	G	105	F	1.9	99	114
1DIO	A G	G	107	R	1.6	99	114
1DIO	A G	G	111	L	1.3	99	114
1DIO	A G	G	116	D	1.4	116	126
1DIO	A G	G	120	L	1.7	116	126
1DIO	A G	G	123	Y	2.5	116	126
1DIO	A G	G	155	F	1.7	150	166
1DIO	A G	G	158	E	1.2	150	166
1DIO	A G	G	162	L	1.0	150	166
1DIO	A G	G	163	Y	1.2	150	166
1DIO	L E	L	304	G	12.0	303	309
1DIO	L E	E	115	F	1.2	113	123
1DIO	L E	E	194	P	1.8	192	210
1DIO	L E	E	197	Q	2.6	192	210
1DIO	L E	E	202	I	1.2	192	210
1DIO	L E	E	204	H	1.0	192	210
1DIO	L E	E	205	I	1.3	192	210
1DIO	L M	L	64	H	1.4	61	71
1DIO	L M	L	210	K	1.2	205	214
1DIO	L M	L	213	M	1.8	205	214
1DIO	L M	L	229	E	2.2	229	235
1DIO	L M	L	233	T	2.3	229	235
1DIO	L M	L	240	W	1.6	239	252
1DIO	L M	L	243	G	29.0	239	252
1DIO	L M	L	244	F	4.1	239	252
1DIO	L M	L	474	V	5.0	470	481
1DIO	L M	L	490	L	5.4	483	499
1DIO	L M	L	494	K	1.3	483	499
1DIO	L M	M	66	L	4.5	66	71
1DIO	L M	M	101	L	1.4	99	111
1DIO	L M	M	105	F	1.3	99	111
1DIO	L M	M	120	L	1.3	116	126
1DIO	L M	M	123	Y	3.3	116	126
1DIO	L M	M	124	N	1.1	116	126
1DIO	L M	M	155	F	2.7	150	166
1DIO	L M	M	162	L	1.1	150	166
1DIO	L M	M	163	Y	2.0	150	166
1DKD	C G	C	230	I	1.0	230	244
1DKD	C G	C	234	L	1.8	230	244
1DKF	A B	A	395	E	1.7	391	413

1DKF	A B	A	402	Y	3.5	391	413
1DKF	A B	A	422	K	1.4	419	425
1DKF	A B	A	428	P	1.5	426	440
1DKF	A B	B	353	E	1.0	345	367
1DKF	A B	B	356	L	1.0	345	367
1DKF	A B	B	376	K	1.4	371	379
1DKF	A B	B	378	L	1.1	371	379
1DKG	A D	A	82	K	1.3	66	83
1DKG	A D	D	257	L	1.3	256	273
1DKG	A D	D	268	K	1.0	256	273
1DML	A B	B	1206	L	1.0	1201	1209
1DML	A B	B	1227	L	1.2	1220	1235
1DML	A B	B	1231	F	5.3	1220	1235
1DML	A B	B	1234	L	2.7	1220	1235
1DML	A F	F	1225	R	2.0	1220	1234
1DML	A F	F	1232	D	1.8	1220	1234
1DML	C D	D	1206	L	1.3	1201	1209
1DML	C D	D	1231	F	5.2	1220	1235
1DML	C D	D	1234	L	2.4	1220	1235
1DML	E F	F	1206	L	1.2	1201	1209
1DML	E F	F	1226	M	1.1	1220	1234
1DML	E F	F	1227	L	1.3	1220	1234
1DML	E F	F	1231	F	2.5	1220	1234
1DML	G H	H	1206	L	1.2	1201	1209
1DML	G H	H	1224	R	1.0	1220	1234
1DML	G H	H	1226	M	1.3	1220	1234
1DML	G H	H	1227	L	1.4	1220	1234
1DML	G H	H	1228	H	1.3	1220	1234
1DML	G H	H	1229	R	1.1	1220	1234
1DML	G H	H	1231	F	4.2	1220	1234
1DML	G H	H	1232	D	1.7	1220	1234
1DN0	C D	C	125	Q	1.1	123	128
1DOA	A B	A	66	R	2.8	65	69
1DOA	A B	A	67	L	2.2	65	69
1DOA	A B	A	68	R	1.0	65	69
1DOA	A B	A	103	H	2.1	87	105
1DOA	A B	A	104	H	1.3	87	105
1DOA	A B	B	38	I	1.2	35	40
1DOA	A B	B	51	Y	2.8	46	57
1DOA	A B	B	55	L	1.7	46	57
1DOW	A B	A	61	L	1.2	58	83
1DOW	A B	A	65	V	1.4	58	83
1DOW	A B	A	72	F	2.8	58	83
1DOW	A B	A	111	F	1.0	106	114
1DOW	A B	A	132	L	1.5	126	143
1DOW	A B	A	146	D	1.2	146	166
1DOW	A B	B	125	L	2.6	121	130
1DOW	A B	B	133	K	1.3	133	142
1DOW	A B	B	136	V	1.2	133	142
1DOW	A B	B	139	L	2.3	133	142
1DP5	A B	B	8	V	2.9	3	31
1DP5	A B	B	11	I	1.5	3	31
1DP5	A B	B	12	F	2.8	3	31
1DP5	A B	B	19	L	1.6	3	31
1DP5	A B	B	21	G	20.2	3	31
1DP5	A B	B	22	D	2.0	3	31
1DP5	A B	B	25	V	1.0	3	31
1DP5	A B	B	26	V	1.9	3	31
1DP5	A B	B	30	F	2.3	3	31
1DPJ	A B	B	8	V	2.3	4	31

1DPJ	A B	B	10	E	1.5	4	31
1DPJ	A B	B	11	I	1.5	4	31
1DPJ	A B	B	12	F	2.7	4	31
1DPJ	A B	B	18	K	1.3	4	31
1DPJ	A B	B	19	L	1.8	4	31
1DPJ	A B	B	21	G	24.4	4	31
1DPJ	A B	B	22	D	2.1	4	31
1DPJ	A B	B	25	V	1.0	4	31
1DPJ	A B	B	26	V	1.4	4	31
1DPJ	A B	B	30	F	2.0	4	31
1DQQ	A B	A	124	Q	1.7	122	127
1DQQ	C D	C	124	Q	1.4	122	127
1DS6	A B	A	66	R	1.6	65	69
1DS6	A B	A	67	L	3.3	65	69
1DS6	A B	A	103	H	2.1	87	105
1DS6	A B	B	35	L	2.8	32	38
1DS6	A B	B	45	L	1.9	43	54
1DS6	A B	B	48	Y	2.5	43	54
1DS6	A B	B	49	K	1.4	43	54
1DS6	A B	B	52	L	1.5	43	54
1DS6	A B	B	53	L	1.3	43	54
1DTD	A B	B	41	P	1.1	41	47
1DTD	A B	B	42	W	2.9	41	47
1DWL	A B	B	12	G	36.9	11	15
1DX5	A M	A	14	E	2.1	14	14
1DX5	A M	A	14	E	2.0	14	14
1DX5	A M	A	14	L	1.0	14	14
1DX5	A M	A	14	Y	3.6	14	14
1DX5	A M	M	242	I	1.3	235	245
1DX5	A O	O	126	R	1.0	126	130
1DX5	A O	O	235	K	1.1	235	245
1DX5	B M	M	235	K	1.1	235	245
1DX5	B N	B	14	E	1.9	14	14
1DX5	B N	B	14	E	2.2	14	14
1DX5	B N	B	14	L	1.5	14	14
1DX5	B N	B	14	Y	3.6	14	14
1DX5	B N	N	242	I	1.1	235	245
1DX5	C N	N	126	R	1.1	126	130
1DX5	C O	C	14	E	2.7	14	14
1DX5	C O	C	14	E	2.0	14	14
1DX5	C O	C	14	L	1.2	14	14
1DX5	C O	C	14	Y	3.7	14	14
1DX5	C O	O	238	I	1.3	235	245
1DX5	C O	O	242	I	1.6	235	245
1DX5	D P	D	14	E	2.4	14	14
1DX5	D P	D	14	E	1.9	14	14
1DX5	D P	D	14	Y	3.4	14	14
1DX5	D P	P	235	K	1.0	235	245
1DX5	D P	P	239	Q	1.1	235	245
1DX5	M I	I	428	E	2.0	426	430
1DX5	M I	I	429	N	2.2	426	430
1DX5	O K	K	428	E	1.3	426	430
1DX5	O K	K	429	N	3.4	426	430
1DX5	P L	L	429	N	2.1	426	430
1DY8	A C	A	20	S	1.2	13	23
1DZB	B Y	Y	112	R	1.0	109	114
1E 08	A D	A	112	Y	5.2	108	113
1E 08	A D	A	147	F	2.9	146	165
1E 08	A D	A	151	V	1.0	146	165
1E 08	A D	A	154	W	2.5	146	165

1E 08	A D	A	210	L	1.2	203	219
1E 08	A D	A	214	Y	3.7	203	219
1E 08	A D	A	309	F	1.6	302	312
1E 08	A D	D	42	Y	3.0	39	55
1E 08	A D	D	47	I	1.6	39	55
1E 08	A D	D	49	G	97.4	39	55
1E 08	A D	D	67	Q	3.7	66	74
1E 08	A D	D	68	V	1.0	66	74
1E 08	A D	D	71	L	2.6	66	74
1E 08	A D	D	72	Y	1.1	66	74
1E 08	A E	E	12	G	395.9	11	15
1E 44	B A	B	2	F	5.4	2	7
1E 44	B A	B	5	Y	2.6	2	7
1E 44	B A	B	6	G	76.2	2	7
1E 50	A B	B	17	F	1.0	16	20
1E0A	A B	A	169	F	2.0	165	178
1E0A	A B	B	107	L	1.1	101	108
1E0F	A D	A	14	E	1.0	14	14
1E0F	A D	A	14	Y	2.9	14	14
1E1C	A B	A	24	R	1.1	21	33
1E1C	A B	A	294	F	1.1	294	316
1E1C	A B	A	295	F	2.1	294	316
1E1C	A B	A	310	K	1.4	294	316
1E1C	A B	A	342	Y	1.8	341	359
1E1C	A B	A	346	V	1.4	341	359
1E1C	A B	A	347	R	3.3	341	359
1E1C	A B	A	350	I	1.1	341	359
1E1C	A B	A	378	F	2.2	377	395
1E1C	A B	A	408	Y	1.2	407	430
1E1C	A B	A	421	W	1.3	407	430
1E1C	A B	B	23	L	2.2	23	27
1E1C	A B	B	26	D	1.1	23	27
1E1C	A B	B	35	W	1.7	32	44
1E1C	A B	B	291	F	2.6	290	311
1E1C	A B	B	306	R	2.3	290	311
1E1C	A B	B	310	V	1.1	290	311
1E1C	A B	B	337	Y	2.1	336	353
1E1C	A B	B	348	F	3.5	336	353
1E1C	A B	B	374	F	1.3	373	391
1E1C	A B	B	381	N	1.0	373	391
1E1C	A B	B	385	V	1.8	373	391
1E1C	A B	B	386	L	1.2	373	391
1E1C	A B	B	389	E	4.1	373	391
1E1C	A B	B	403	Y	2.5	403	426
1E1C	A B	B	404	Y	1.3	403	426
1E1C	A B	B	417	W	4.7	403	426
1E1C	A B	B	424	E	1.5	403	426
1E1C	C D	C	24	R	1.3	21	33
1E1C	C D	C	294	F	1.4	294	315
1E1C	C D	C	295	F	1.9	294	315
1E1C	C D	C	310	K	1.9	294	315
1E1C	C D	C	313	H	1.0	294	315
1E1C	C D	C	342	Y	1.8	341	359
1E1C	C D	C	346	V	1.4	341	359
1E1C	C D	C	347	R	3.5	341	359
1E1C	C D	C	353	M	1.7	341	359
1E1C	C D	C	378	F	2.0	377	395
1E1C	C D	C	389	F	3.4	377	395
1E1C	C D	C	393	E	3.2	377	395
1E1C	C D	C	408	Y	1.9	407	430

1E1C	C D	C	418	R	1.5	407	430
1E1C	C D	D	23	L	1.9	23	27
1E1C	C D	D	26	D	1.3	23	27
1E1C	C D	D	35	W	3.3	32	45
1E1C	C D	D	38	E	1.0	32	45
1E1C	C D	D	291	F	2.2	290	311
1E1C	C D	D	302	E	3.4	290	311
1E1C	C D	D	303	A	2.9	290	311
1E1C	C D	D	306	R	3.1	290	311
1E1C	C D	D	307	I	3.4	290	311
1E1C	C D	D	309	E	2.9	290	311
1E1C	C D	D	310	V	4.2	290	311
1E1C	C D	D	337	Y	2.3	336	354
1E1C	C D	D	341	L	1.3	336	354
1E1C	C D	D	342	R	3.0	336	354
1E1C	C D	D	345	I	1.0	336	354
1E1C	C D	D	348	F	2.6	336	354
1E1C	C D	D	374	F	1.4	373	391
1E1C	C D	D	385	V	1.5	373	391
1E1C	C D	D	389	E	1.9	373	391
1E1C	C D	D	403	Y	2.9	403	426
1E1C	C D	D	410	R	4.6	403	426
1E1C	C D	D	413	A	2.9	403	426
1E1C	C D	D	414	D	2.8	403	426
1E1C	C D	D	417	W	4.1	403	426
1E1C	C D	D	420	F	4.1	403	426
1E1C	C D	D	421	Q	3.4	403	426
1E1C	C D	D	424	E	1.4	403	426
1E1H	A B	A	92	K	2.8	80	100
1E1H	A B	A	96	R	2.9	80	100
1E1H	A B	A	102	L	3.5	101	113
1E1H	A B	A	103	G	1.3	101	113
1E1H	A B	A	106	L	1.1	101	113
1E1H	A B	A	109	S	1.2	101	113
1E1H	A B	A	216	P	1.7	216	232
1E1H	A B	A	222	H	1.0	216	232
1E1H	A B	A	225	I	2.6	216	232
1E1H	A B	A	226	H	3.1	216	232
1E1H	A B	A	229	H	1.3	216	232
1E1H	A B	B	259	F	1.9	259	266
1E1H	A B	B	260	E	2.0	259	266
1E1H	A B	B	261	E	2.2	259	266
1E1H	A B	B	263	R	2.2	259	266
1E1H	A B	B	265	F	4.5	259	266
1E1H	A B	B	281	F	3.8	275	299
1E1H	A B	B	285	Y	2.5	275	299
1E1H	A B	B	288	K	1.0	275	299
1E1H	A B	B	292	V	1.4	275	299
1E1H	A B	B	296	L	1.0	275	299
1E1H	A B	B	316	F	2.3	309	320
1E1H	A B	B	319	K	2.8	309	320
1E1H	A B	B	344	L	4.3	334	348
1E1H	A B	B	347	I	2.4	334	348
1E1H	A B	B	353	F	4.2	350	358
1E1H	A B	B	356	F	2.6	350	358
1E1H	A B	B	357	F	3.8	350	358
1E1H	C D	C	92	K	2.1	80	100
1E1H	C D	C	96	R	2.7	80	100
1E1H	C D	C	102	L	3.4	101	113
1E1H	C D	C	106	L	1.1	101	113

1E1H	C D	C	109	S	1.0	101	113
1E1H	C D	C	216	P	1.4	216	232
1E1H	C D	C	218	V	1.2	216	232
1E1H	C D	C	222	H	1.2	216	232
1E1H	C D	C	226	H	2.1	216	232
1E1H	C D	C	229	H	2.2	216	232
1E1H	C D	D	259	F	1.9	259	266
1E1H	C D	D	260	E	2.8	259	266
1E1H	C D	D	261	E	1.1	259	266
1E1H	C D	D	281	F	2.4	275	299
1E1H	C D	D	285	Y	2.4	275	299
1E1H	C D	D	288	K	1.0	275	299
1E1H	C D	D	292	V	1.2	275	299
1E1H	C D	D	296	L	1.0	275	299
1E1H	C D	D	316	F	3.9	309	320
1E1H	C D	D	319	K	2.5	309	320
1E1H	C D	D	344	L	1.2	334	348
1E1H	C D	D	353	F	4.4	350	358
1E1H	C D	D	356	F	2.7	350	358
1E1H	C D	D	357	F	3.8	350	358
1E3A	A B	A	25	W	3.5	24	39
1E3A	A B	A	27	L	3.0	24	39
1E3A	A B	A	28	F	1.9	24	39
1E3A	A B	A	29	Y	1.2	24	39
1E3A	A B	A	31	Y	6.1	24	39
1E3A	A B	A	33	Y	2.3	24	39
1E3A	A B	A	38	D	1.7	24	39
1E3A	A B	A	41	F	1.0	40	51
1E3A	A B	A	42	Q	3.3	40	51
1E3A	A B	A	63	V	1.1	63	72
1E3A	A B	A	65	F	1.8	63	72
1E3A	A B	A	70	R	2.9	63	72
1E3A	A B	A	81	Q	1.9	75	84
1E3A	A B	A	89	D	1.1	87	108
1E3A	A B	A	92	I	1.2	87	108
1E3A	A B	A	96	Y	1.7	87	108
1E3A	A B	A	117	K	1.5	117	122
1E3A	A B	A	138	F	4.7	131	146
1E3A	A B	A	141	T	1.0	131	146
1E3A	A B	A	152	E	3.2	152	166
1E3A	A B	A	153	I	2.1	152	166
1E3A	A B	A	154	D	1.7	152	166
1E3A	A B	A	155	N	2.6	152	166
1E3A	A B	A	158	L	2.3	152	166
1E3A	A B	A	177	Q	2.8	168	179
1E3A	A B	A	178	L	1.5	168	179
1E3A	A B	A	208	T	2.0	207	212
1E3A	A B	A	249	F	2.1	238	252
1E3A	A B	B	410	E	1.2	410	422
1E3A	A B	B	411	V	1.8	410	422
1E3A	A B	B	414	L	1.7	410	422
1E3A	A B	B	415	L	1.3	410	422
1E3A	A B	B	417	W	1.6	410	422
1E3A	A B	B	419	H	1.3	410	422
1E3A	A B	B	658	I	1.0	654	665
1E3D	A B	A	33	D	17.1	32	40
1E3D	A B	A	37	L	1.1	32	40
1E3D	A B	A	57	E	3.1	54	65
1E3D	A B	A	211	R	1.9	208	212
1E3D	A B	B	54	I	1.9	51	56

1E3D	A B	B	62	D	1.1	60	69
1E3D	A B	B	167	F	1.0	154	171
1E3D	A B	B	207	R	1.0	192	220
1E3D	A B	B	209	Q	1.5	192	220
1E3D	A B	B	214	K	1.0	192	220
1E3D	C D	C	22	E	2.1	19	26
1E3D	C D	C	33	D	5.4	32	40
1E3D	C D	D	62	D	1.3	60	69
1E3D	C D	D	121	L	3.3	96	127
1E3D	C D	D	124	L	5.2	96	127
1E3D	C D	D	167	F	1.0	154	171
1E3D	C D	D	210	V	1.2	192	220
1E3D	C D	D	214	K	1.1	192	220
1E6E	A B	A	60	N	1.2	60	71
1E6E	A B	A	211	R	2.6	207	215
1E6E	A B	A	244	R	2.1	240	255
1E6E	A B	A	370	R	1.2	367	371
1E6E	A B	A	384	F	1.7	376	396
1E6E	A B	B	72	D	1.0	72	80
1E6E	A B	B	76	D	2.2	72	80
1E6E	A B	B	79	D	2.1	72	80
1E6E	C D	C	211	R	2.5	207	215
1E6E	C D	C	384	F	1.6	376	396
1E6E	C D	D	76	D	1.7	72	80
1E6V	A B	B	355	G	10.7	352	363
1E6V	A B	B	359	G	359.5	352	363
1E6V	A B	B	362	F	2.0	352	363
1E6V	A C	A	370	M	1.4	370	391
1E6V	A C	A	374	K	1.3	370	391
1E6V	A C	A	382	L	2.0	370	391
1E6V	A C	A	385	L	1.0	370	391
1E6V	A C	A	389	E	1.7	370	391
1E6V	A C	A	396	E	3.2	392	398
1E6V	A C	A	401	G	25.1	401	421
1E6V	A C	A	432	L	1.4	423	441
1E6V	A C	A	435	I	1.3	423	441
1E6V	A C	A	436	L	1.1	423	441
1E6V	A C	A	439	E	2.2	423	441
1E6V	A C	A	440	G	1.9	423	441
1E6V	A C	C	19	R	1.4	14	24
1E6V	A C	C	103	Y	1.2	102	113
1E6V	A C	C	107	R	1.3	102	113
1E6V	A C	C	235	L	1.0	232	251
1E6V	A C	C	238	V	1.2	232	251
1E6V	A C	C	239	Q	1.9	232	251
1E6V	A C	C	242	H	2.6	232	251
1E6V	A C	C	243	E	1.6	232	251
1E6V	A C	C	246	T	2.4	232	251
1E6V	A C	C	249	G	165.3	232	251
1E6V	A C	C	250	Y	1.4	232	251
1E6V	A E	A	256	F	3.0	249	262
1E6V	A E	A	288	V	9.6	286	291
1E6V	A E	E	137	M	1.0	128	145
1E6V	B C	B	234	F	1.0	234	247
1E6V	B C	B	267	G	169.9	266	280
1E6V	B C	B	318	N	1.2	300	323
1E6V	B C	B	320	G	10.3	300	323
1E6V	B C	B	334	Y	2.1	328	341
1E6V	B C	B	338	L	1.6	328	341
1E6V	B C	C	73	L	1.6	69	74

1E6V	B C	C	110	M	1.3	102	113
1E6V	B C	C	111	W	3.0	102	113
1E6V	B C	C	234	L	4.1	232	251
1E6V	B C	C	241	I	1.0	232	251
1E6V	B C	C	244	L	1.1	232	251
1E6V	B F	F	250	Y	1.6	232	251
1E6V	D B	D	256	F	3.0	249	262
1E6V	D B	D	499	H	1.0	487	503
1E6V	D B	B	137	M	1.2	128	145
1E6V	D E	E	359	G	359.4	352	363
1E6V	D E	E	362	F	2.0	352	363
1E6V	D F	D	370	M	1.4	370	391
1E6V	D F	D	374	K	1.3	370	391
1E6V	D F	D	382	L	2.1	370	391
1E6V	D F	D	389	E	1.0	370	391
1E6V	D F	D	390	R	2.4	370	391
1E6V	D F	D	393	A	1.2	392	398
1E6V	D F	D	396	E	3.0	392	398
1E6V	D F	D	401	G	24.8	401	421
1E6V	D F	D	432	L	1.4	423	441
1E6V	D F	D	435	I	1.3	423	441
1E6V	D F	D	436	L	1.1	423	441
1E6V	D F	D	439	E	2.2	423	441
1E6V	D F	D	440	G	1.9	423	441
1E6V	D F	F	19	R	1.4	14	24
1E6V	D F	F	103	Y	1.2	102	113
1E6V	D F	F	107	R	1.3	102	113
1E6V	D F	F	235	L	1.0	232	251
1E6V	D F	F	238	V	1.2	232	251
1E6V	D F	F	239	Q	1.6	232	251
1E6V	D F	F	242	H	2.6	232	251
1E6V	D F	F	243	E	1.6	232	251
1E6V	D F	F	246	T	2.4	232	251
1E6V	D F	F	249	G	165.6	232	251
1E6V	D F	F	250	Y	1.4	232	251
1E6V	E C	C	250	Y	1.6	232	251
1E6V	E F	E	234	F	1.0	234	247
1E6V	E F	E	267	G	169.9	266	280
1E6V	E F	E	318	N	1.2	300	323
1E6V	E F	E	320	G	10.1	300	323
1E6V	E F	E	334	Y	2.1	328	341
1E6V	E F	E	338	L	1.6	328	341
1E6V	E F	F	73	L	1.6	69	74
1E6V	E F	F	110	M	1.3	102	113
1E6V	E F	F	111	W	3.0	102	113
1E6V	E F	F	241	I	1.0	232	251
1E6V	E F	F	244	L	1.1	232	251
1E6Y	A B	B	2352	G	44.1	2349	2360
1E6Y	A B	B	2356	G	261.6	2349	2360
1E6Y	A B	B	2359	F	1.4	2349	2360
1E6Y	A C	A	1387	L	1.4	1387	1408
1E6Y	A C	A	1391	K	3.4	1387	1408
1E6Y	A C	A	1395	T	1.4	1387	1408
1E6Y	A C	A	1399	L	1.0	1387	1408
1E6Y	A C	A	1403	E	1.0	1387	1408
1E6Y	A C	A	1406	E	2.5	1387	1408
1E6Y	A C	A	1412	L	2.1	1409	1415
1E6Y	A C	A	1413	E	4.1	1409	1415
1E6Y	A C	A	1418	G	146.4	1418	1438
1E6Y	A C	A	1449	L	1.9	1440	1458

1E6Y	A C	A	1452	Y	1.0	1440	1458
1E6Y	A C	A	1453	L	1.1	1440	1458
1E6Y	A C	A	1456	E	1.4	1440	1458
1E6Y	A C	C	3018	R	1.9	3013	3023
1E6Y	A C	C	3100	Y	1.1	3099	3110
1E6Y	A C	C	3104	Y	1.0	3099	3110
1E6Y	A C	C	3233	V	1.5	3227	3246
1E6Y	A C	C	3234	H	2.8	3227	3246
1E6Y	A C	C	3237	F	4.7	3227	3246
1E6Y	A C	C	3238	D	1.8	3227	3246
1E6Y	A C	C	3240	R	1.4	3227	3246
1E6Y	A C	C	3244	G	252.1	3227	3246
1E6Y	A C	C	3245	F	1.3	3227	3246
1E6Y	A E	A	1246	G	5.4	1234	1253
1E6Y	A E	A	1267	F	2.6	1260	1272
1E6Y	A E	A	1270	K	1.1	1260	1272
1E6Y	A E	A	1445	S	1.2	1440	1458
1E6Y	A E	E	5154	K	2.2	5150	5159
1E6Y	A E	E	5158	W	1.1	5150	5159
1E6Y	B C	B	2230	F	1.7	2229	2243
1E6Y	B C	B	2233	H	1.1	2229	2243
1E6Y	B C	B	2263	G	165.0	2262	2276
1E6Y	B C	B	2267	E	1.1	2262	2276
1E6Y	B C	B	2297	V	2.7	2297	2320
1E6Y	B C	B	2298	P	1.1	2297	2320
1E6Y	B C	B	2315	N	1.9	2297	2320
1E6Y	B C	B	2317	G	24.9	2297	2320
1E6Y	B C	B	2331	Y	2.0	2322	2341
1E6Y	B C	B	2334	D	1.5	2322	2341
1E6Y	B C	B	2335	I	2.4	2322	2341
1E6Y	B C	B	2339	E	3.1	2322	2341
1E6Y	B C	C	3068	R	1.9	3066	3071
1E6Y	B C	C	3104	Y	2.3	3099	3110
1E6Y	B C	C	3108	I	1.8	3099	3110
1E6Y	B C	C	3228	E	1.2	3227	3246
1E6Y	B C	C	3232	W	3.0	3227	3246
1E6Y	B C	C	3235	R	1.9	3227	3246
1E6Y	B C	C	3236	I	1.6	3227	3246
1E6Y	B C	C	3240	R	2.0	3227	3246
1E6Y	B C	C	3243	F	2.5	3227	3246
1E6Y	B F	F	6245	F	2.1	6227	6246
1E6Y	D B	D	4246	G	7.2	4234	4253
1E6Y	D B	D	4267	F	2.4	4260	4272
1E6Y	D B	D	4445	S	1.2	4440	4458
1E6Y	D B	B	2140	M	1.2	2125	2143
1E6Y	D B	B	2154	K	2.1	2150	2159
1E6Y	D B	B	2158	W	1.0	2150	2159
1E6Y	D C	D	4134	L	1.9	4123	4135
1E6Y	D E	D	4455	K	1.2	4440	4458
1E6Y	D E	E	5334	D	1.2	5322	5341
1E6Y	D E	E	5352	G	34.5	5349	5360
1E6Y	D E	E	5356	G	276.1	5349	5360
1E6Y	D E	E	5359	F	1.3	5349	5360
1E6Y	D F	D	4387	L	1.5	4387	4408
1E6Y	D F	D	4391	K	3.0	4387	4408
1E6Y	D F	D	4395	T	1.4	4387	4408
1E6Y	D F	D	4399	L	2.0	4387	4408
1E6Y	D F	D	4403	E	1.8	4387	4408
1E6Y	D F	D	4406	E	1.4	4387	4408
1E6Y	D F	D	4412	L	1.7	4409	4415

1E6Y	D F	D	4413	E	3.9	4409	4415
1E6Y	D F	D	4418	G	89.6	4418	4438
1E6Y	D F	D	4449	L	1.9	4440	4458
1E6Y	D F	D	4452	Y	1.0	4440	4458
1E6Y	D F	D	4453	L	1.3	4440	4458
1E6Y	D F	D	4456	E	1.3	4440	4458
1E6Y	D F	F	6018	R	2.1	6013	6023
1E6Y	D F	F	6230	V	1.8	6227	6246
1E6Y	D F	F	6233	V	1.6	6227	6246
1E6Y	D F	F	6234	H	2.3	6227	6246
1E6Y	D F	F	6237	F	4.6	6227	6246
1E6Y	D F	F	6238	D	1.5	6227	6246
1E6Y	D F	F	6240	R	1.2	6227	6246
1E6Y	D F	F	6244	G	255.6	6227	6246
1E6Y	D F	F	6245	F	1.2	6227	6246
1E6Y	E C	C	3245	F	2.0	3227	3246
1E6Y	E F	E	5230	F	1.0	5229	5243
1E6Y	E F	E	5263	G	147.0	5262	5276
1E6Y	E F	E	5267	E	1.3	5262	5276
1E6Y	E F	E	5297	V	2.0	5297	5319
1E6Y	E F	E	5315	N	1.9	5297	5319
1E6Y	E F	E	5317	G	41.3	5297	5319
1E6Y	E F	E	5331	Y	1.9	5322	5341
1E6Y	E F	E	5334	D	1.5	5322	5341
1E6Y	E F	E	5335	I	2.4	5322	5341
1E6Y	E F	E	5339	E	3.1	5322	5341
1E6Y	E F	F	6104	Y	1.7	6099	6109
1E6Y	E F	F	6108	I	1.7	6099	6109
1E6Y	E F	F	6228	E	1.2	6227	6246
1E6Y	E F	F	6232	W	3.0	6227	6246
1E6Y	E F	F	6235	R	1.9	6227	6246
1E6Y	E F	F	6236	I	1.6	6227	6246
1E6Y	E F	F	6240	R	1.9	6227	6246
1E6Y	E F	F	6243	F	2.7	6227	6246
1E7P	A B	A	98	R	1.6	96	103
1E7P	A B	A	158	H	1.0	156	172
1E7P	A B	A	166	N	2.5	156	172
1E7P	A B	A	169	L	1.0	156	172
1E7P	A B	A	347	E	1.1	346	354
1E7P	A B	A	352	F	1.5	346	354
1E7P	A B	B	44	R	1.0	36	48
1E7P	A B	B	116	Q	1.0	113	118
1E7P	B C	B	162	G	5.8	162	167
1E7P	B C	B	166	M	1.5	162	167
1E7P	B C	B	193	E	1.2	192	199
1E7P	B C	B	196	Y	2.0	192	199
1E7P	B C	B	197	E	2.9	192	199
1E7P	B C	B	216	D	1.3	213	217
1E7P	B C	B	236	V	1.4	224	237
1E7P	B C	C	21	R	2.0	21	27
1E7P	B C	C	111	F	1.1	105	119
1E7P	B C	C	114	H	1.4	105	119
1E7P	B C	C	118	M	1.0	105	119
1E7P	B C	C	206	R	1.8	203	217
1E7P	B F	F	6	I	1.7	5	12
1E7P	B F	F	7	L	2.0	5	12
1E7P	B F	F	10	Y	2.9	5	12
1E7P	D E	D	98	R	1.6	96	103
1E7P	D E	D	158	H	1.0	156	172
1E7P	D E	D	169	L	1.0	156	172

1E7P	D E	D	347	E	1.1	346	353
1E7P	D E	D	352	F	1.8	346	353
1E7P	D E	D	464	F	2.1	463	478
1E7P	D E	E	37	F	1.2	36	48
1E7P	D E	E	44	R	1.1	36	48
1E7P	D E	E	116	Q	1.0	113	118
1E7P	E C	C	6	I	1.7	5	12
1E7P	E C	C	7	L	1.8	5	12
1E7P	E C	C	10	Y	2.9	5	12
1E7P	E F	E	162	G	5.8	162	167
1E7P	E F	E	166	M	1.5	162	167
1E7P	E F	E	193	E	1.2	192	199
1E7P	E F	E	196	Y	2.3	192	199
1E7P	E F	E	197	E	2.9	192	199
1E7P	E F	E	215	H	4.6	213	217
1E7P	E F	E	216	D	1.3	213	217
1E7P	E F	E	225	Q	3.6	224	237
1E7P	E F	E	236	V	1.4	224	237
1E7P	E F	F	21	R	2.4	21	27
1E7P	E F	F	111	F	1.1	105	119
1E7P	E F	F	114	H	1.4	105	119
1E7P	E F	F	118	M	1.0	105	119
1E7P	E F	F	122	D	4.4	121	136
1E7P	E F	F	193	K	3.4	168	195
1E7P	E F	F	206	R	1.9	203	217
1E7P	G H	G	158	H	1.0	156	172
1E7P	G H	G	169	L	1.0	156	172
1E7P	G H	G	347	E	1.1	346	354
1E7P	G H	G	352	F	1.7	346	354
1E7P	G H	G	464	F	2.1	463	478
1E7P	G H	H	37	F	1.0	36	48
1E7P	G H	H	44	R	1.0	36	48
1E7P	G H	H	116	Q	1.0	113	118
1E7P	H I	H	162	G	5.9	162	167
1E7P	H I	H	166	M	1.5	162	167
1E7P	H I	H	193	E	1.2	192	199
1E7P	H I	H	196	Y	3.7	192	199
1E7P	H I	H	197	E	2.9	192	199
1E7P	H I	H	216	D	1.3	213	217
1E7P	H I	H	236	V	1.4	224	237
1E7P	H I	I	21	R	2.0	21	27
1E7P	H I	I	111	F	1.1	105	119
1E7P	H I	I	114	H	1.4	105	119
1E7P	H I	I	118	M	1.0	105	119
1E7P	H I	I	206	R	1.8	203	217
1E7P	H L	L	6	I	1.7	5	12
1E7P	H L	L	7	L	2.4	5	12
1E7P	H L	L	10	Y	2.7	5	12
1E7P	J K	J	158	H	1.0	156	172
1E7P	J K	J	169	L	1.0	156	172
1E7P	J K	J	347	E	1.1	346	354
1E7P	J K	J	352	F	1.8	346	354
1E7P	J K	J	464	F	2.1	463	478
1E7P	J K	K	37	F	1.1	36	48
1E7P	J K	K	44	R	1.0	36	48
1E7P	J K	K	116	Q	1.0	113	118
1E7P	K I	I	6	I	1.5	5	12
1E7P	K I	I	7	L	2.1	5	12
1E7P	K I	I	10	Y	2.6	5	12
1E7P	K L	K	162	G	5.7	162	167

1E7P	K L	K	166	M	1.5	162	167
1E7P	K L	K	193	E	1.2	192	199
1E7P	K L	K	196	Y	2.0	192	199
1E7P	K L	K	197	E	2.9	192	199
1E7P	K L	K	216	D	1.3	213	217
1E7P	K L	K	236	V	1.4	224	237
1E7P	K L	L	21	R	2.4	21	27
1E7P	K L	L	111	F	1.1	105	119
1E7P	K L	L	114	H	1.4	105	119
1E7P	K L	L	118	M	1.0	105	119
1E7P	K L	L	206	R	1.8	203	217
1E8O	A B	A	58	D	1.8	56	74
1E8O	A B	A	59	V	3.1	56	74
1E8O	A B	A	70	M	1.6	56	74
1E8O	A B	A	73	M	1.1	56	74
1E8O	C D	C	63	E	1.6	59	75
1E8O	C D	C	70	M	2.3	59	75
1E8O	C D	C	73	M	1.2	59	75
1E8O	C D	D	80	Q	1.0	76	91
1E8O	C D	D	88	R	1.0	76	91
1E9Y	A B	A	13	L	1.6	5	15
1E9Y	A B	A	77	M	1.4	74	78
1E9Y	A B	B	7	K	5.3	6	11
1E9Y	A B	B	9	Y	1.3	6	11
1E9Y	A B	B	10	V	4.9	6	11
1EAY	A C	A	96	I	1.3	92	101
1EAY	A C	A	122	K	1.4	113	128
1EAY	A C	A	125	E	1.3	113	128
1EAY	A C	A	126	K	1.4	113	128
1EAY	A C	C	171	E	1.2	171	183
1EAY	A C	C	182	L	1.1	171	183
1EAY	B D	B	96	I	1.0	92	102
1EAY	B D	D	182	L	1.1	171	183
1EAY	B D	D	211	V	1.0	205	213
1EBD	A C	A	437	E	1.9	436	442
1EBD	A C	C	137	K	1.3	133	142
1EBD	B C	C	140	R	1.4	133	142
1EBD	B C	C	141	E	1.5	133	142
1ECI	A B	A	7	I	1.2	5	21
1ECI	A B	A	11	V	1.0	5	21
1ECI	A B	A	18	W	2.5	5	21
1ECI	A B	B	5	V	1.0	3	19
1ECI	A B	B	9	I	1.9	3	19
1ECI	A B	B	13	L	1.2	3	19
1ECI	A B	B	16	M	1.8	3	19
1ED3	A C	A	66	I	1.6	57	85
1ED3	A C	A	73	I	1.3	57	85
1ED3	A C	A	77	D	3.6	57	85
1ED3	A C	A	143	T	1.1	138	150
1ED3	A C	A	147	W	2.1	138	150
1ED3	A C	A	152	Y	3.2	152	162
1ED3	A C	A	156	L	1.0	152	162
1ED3	A C	A	167	W	2.1	163	175
1ED3	D F	D	66	I	1.6	57	85
1ED3	D F	D	70	W	2.3	57	85
1ED3	D F	D	77	D	2.1	57	85
1ED3	D F	D	147	W	2.1	138	150
1ED3	D F	D	152	Y	2.5	152	162
1EER	A B	A	48	F	1.4	48	52
1EER	A C	A	11	V	1.0	9	26

1EER	A C	A	14	R	1.2	9	26
1EER	A C	A	103	R	2.9	89	113
1EER	A C	A	108	L	1.2	89	113
1EF1	A C	A	124	L	2.2	119	135
1EF1	A C	A	160	Q	1.5	155	161
1EF1	A C	A	175	W	3.4	165	179
1EF1	A C	A	193	K	1.3	184	198
1EF1	A C	A	197	D	1.4	184	198
1EF1	A C	C	511	E	1.7	511	515
1EF1	A C	C	522	L	1.1	516	531
1EF1	A C	C	525	L	1.7	516	531
1EF1	A C	C	528	E	1.0	516	531
1EF1	A C	C	529	L	2.0	516	531
1EF1	A C	C	562	I	1.0	555	563
1EF1	A C	C	570	R	1.8	567	576
1EF1	A C	C	571	I	2.0	567	576
1EF1	A C	C	574	F	2.7	567	576
1EF1	B D	B	120	E	1.0	119	135
1EF1	B D	B	124	L	2.0	119	135
1EF1	B D	B	160	Q	1.1	155	161
1EF1	B D	B	175	W	4.2	165	179
1EF1	B D	B	197	D	1.7	184	198
1EF1	B D	D	522	L	1.3	516	533
1EF1	B D	D	525	L	2.6	516	533
1EF1	B D	D	528	E	1.3	516	533
1EF1	B D	D	529	L	2.2	516	533
1EF1	B D	D	556	Y	1.5	555	562
1EF1	B D	D	558	T	1.0	555	562
1EF1	B D	D	570	R	3.4	567	576
1EFN	A B	B	90	F	1.6	81	94
1EFN	C D	D	90	F	1.4	81	95
1EFP	A B	A	262	I	1.0	262	267
1EFP	A B	B	98	P	1.1	98	112
1EFP	A B	B	99	L	1.1	98	112
1EFP	A B	B	134	M	1.1	130	140
1EFP	A B	B	239	V	1.9	239	244
1EFP	A B	B	242	L	2.0	239	244
1EFP	C D	C	300	V	1.3	297	307
1EFP	C D	C	304	L	1.1	297	307
1EFP	C D	D	99	L	1.1	98	112
1EFP	C D	D	133	Q	1.4	130	140
1EFP	C D	D	239	V	2.2	239	244
1EFP	C D	D	242	L	2.1	239	244
1EFU	A B	A	28	T	1.1	24	39
1EFU	A B	A	84	H	1.1	84	93
1EFU	A B	B	19	M	1.4	19	29
1EFU	A B	B	81	F	5.1	80	84
1EFU	A B	B	82	V	1.2	80	84
1EFU	A B	B	170	M	1.3	162	175
1EFU	A B	B	271	F	3.8	271	279
1EFU	A B	B	275	V	1.6	271	279
1EFU	C D	C	118	H	3.7	115	125
1EFU	C D	C	148	L	1.3	143	160
1EFU	C D	D	20	M	1.8	19	29
1EFU	C D	D	80	D	3.0	80	85
1EFU	C D	D	81	F	5.4	80	85
1EFU	C D	D	271	F	4.4	271	279
1EFU	C D	D	275	V	3.4	271	279
1EFU	C D	D	278	M	1.0	271	279
1EFX	A D	A	146	K	1.2	138	150

1EGP	A B	A	25	F	1.0	18	29
1EIY	A B	A	108	R	1.0	102	117
1EIY	A B	A	232	H	2.6	230	243
1EIY	A B	A	234	K	1.3	230	243
1EIY	A B	A	235	G	178.3	230	243
1EIY	A B	B	344	R	1.4	340	348
1EIY	A B	B	458	D	1.0	456	461
1EJH	A E	A	69	V	1.6	69	78
1EJH	A E	A	73	W	3.5	69	78
1EJH	A E	A	135	L	1.5	125	139
1EJH	A E	E	626	R	1.4	626	632
1EJH	A E	E	629	L	2.7	626	632
1EJH	A E	E	630	L	1.1	626	632
1EJH	B F	B	69	V	1.7	69	78
1EJH	B F	B	70	E	1.3	69	78
1EJH	B F	B	73	W	2.6	69	78
1EJH	B F	F	628	F	1.1	626	632
1EJH	B F	F	629	L	2.1	626	632
1EJH	C G	C	69	V	1.8	69	79
1EJH	C G	C	73	W	2.7	69	79
1EJH	C G	C	135	L	1.0	122	139
1EJH	C G	G	626	R	1.1	626	633
1EJH	C G	G	629	L	2.2	626	633
1EJH	C G	G	632	F	1.3	626	633
1EJM	E B	B	549	E	1.5	548	555
1EJO	L H	L	2127	E	1.3	2126	2131
1EJO	L H	L	2128	Q	1.5	2126	2131
1EJR	C A	A	3006	R	1.8	3005	3027
1EJR	C A	A	3009	D	1.5	3005	3027
1EJR	C A	A	3010	K	2.0	3005	3027
1EJR	C A	A	3012	L	1.7	3005	3027
1EJR	C A	A	3013	L	3.3	3005	3027
1EJR	C A	A	3032	Y	1.1	3032	3050
1EJR	C A	A	3033	P	1.1	3032	3050
1EJR	C A	A	3076	M	1.1	3073	3077
1EJR	C B	C	1006	R	2.0	1006	1013
1EJR	C B	C	1009	Y	1.4	1006	1013
1EM8	A B	A	33	W	2.0	20	35
1EM8	A B	A	57	W	2.9	46	59
1EM8	A B	B	53	L	1.3	52	61
1EM8	A B	B	118	R	1.6	115	128
1EM8	A B	B	122	W	5.4	115	128
1EM8	A B	B	129	E	1.6	129	133
1EM8	C D	C	33	W	2.3	20	35
1EM8	C D	D	56	D	1.0	52	61
1EM8	C D	D	59	R	1.1	52	61
1EM8	C D	D	118	R	1.4	115	128
1EM8	C D	D	122	W	4.8	115	128
1EM8	C D	D	129	E	1.7	129	133
1EMU	A B	A	156	F	1.0	149	163
1EMU	A B	A	160	G	15.9	149	163
1EMU	A B	B	2039	L	1.4	2037	2047
1EMU	A B	B	2040	L	2.4	2037	2047
1EO2	A B	B	327	S	1.3	325	329
1EO8	A B	B	48	I	1.2	38	56
1EO8	A B	B	85	E	1.9	76	126
1EO8	A B	B	89	I	1.7	76	126
1EO8	A B	B	92	W	1.5	76	126
1EO8	A B	B	100	V	2.7	76	126
1EO8	A B	B	104	N	2.4	76	126

1EO8	A B	B	115	M	1.0	76	126
1EP3	A B	A	36	Y	1.0	31	37
1EP3	A B	A	274	F	1.9	271	276
1EP3	A B	B	250	E	1.3	248	252
1EPT	A C	C	242	I	1.7	235	243
1EQZ	A B	A	29	R	1.8	27	37
1EQZ	A B	A	46	G	1.0	45	73
1EQZ	A B	A	49	V	1.8	45	73
1EQZ	A B	A	50	Y	4.0	45	73
1EQZ	A B	A	51	L	2.2	45	73
1EQZ	A B	A	54	V	1.5	45	73
1EQZ	A B	A	55	L	2.3	45	73
1EQZ	A B	A	57	Y	2.3	45	73
1EQZ	A B	A	58	L	1.9	45	73
1EQZ	A B	A	63	L	1.2	45	73
1EQZ	A B	A	67	G	262.5	45	73
1EQZ	A B	A	80	P	1.3	80	89
1EQZ	A B	A	83	L	1.6	80	89
1EQZ	A B	A	96	L	2.1	91	97
1EQZ	A B	B	40	Y	2.3	38	49
1EQZ	A B	B	44	V	1.4	38	49
1EQZ	A B	B	61	I	1.9	56	84
1EQZ	A B	B	62	M	1.0	56	84
1EQZ	A B	B	65	F	1.2	56	84
1EQZ	A B	B	69	I	1.1	56	84
1EQZ	A B	B	70	F	3.4	56	84
1EQZ	A B	B	73	I	1.2	56	84
1EQZ	A B	B	94	I	2.0	91	102
1EQZ	A B	B	109	H	1.0	105	123
1EQZ	A B	B	114	G	149.0	105	123
1EQZ	A B	B	118	V	1.2	105	123
1EQZ	A B	B	121	Y	2.7	105	123
1EQZ	A G	G	48	L	1.0	45	55
1EQZ	A G	G	94	E	1.2	86	114
1EQZ	A G	G	112	I	1.2	86	114
1EQZ	B D	B	99	R	1.8	91	102
1EQZ	B D	B	100	L	1.5	91	102
1EQZ	C D	C	51	I	1.3	45	55
1EQZ	C D	C	67	F	1.3	64	79
1EQZ	C D	C	70	L	2.1	64	79
1EQZ	C D	C	74	I	2.3	64	79
1EQZ	C D	C	78	F	3.0	64	79
1EQZ	C D	C	87	S	1.0	86	114
1EQZ	C D	C	92	L	2.2	86	114
1EQZ	C D	C	97	E	1.6	86	114
1EQZ	C D	C	99	Y	2.3	86	114
1EQZ	C D	C	100	L	1.7	86	114
1EQZ	C D	C	101	V	1.6	86	114
1EQZ	C D	C	104	F	3.0	86	114
1EQZ	C D	C	121	P	1.5	121	132
1EQZ	C D	C	124	I	1.5	121	132
1EQZ	C D	D	36	R	2.0	31	41
1EQZ	C D	D	37	L	2.1	31	41
1EQZ	C D	D	39	R	2.0	31	41
1EQZ	C D	D	40	R	3.5	31	41
1EQZ	C D	D	50	I	2.4	48	76
1EQZ	C D	D	57	V	1.0	48	76
1EQZ	C D	D	58	L	1.2	48	76
1EQZ	C D	D	61	F	3.4	48	76
1EQZ	C D	D	62	L	2.3	48	76

1EQZ	C D	D	66	I	3.0	48	76
1EQZ	C D	D	70	V	1.5	48	76
1EQZ	C D	D	86	V	1.8	83	93
1EQZ	E F	E	29	R	1.6	27	37
1EQZ	E F	E	33	L	2.2	27	37
1EQZ	E F	E	49	V	1.8	45	73
1EQZ	E F	E	50	Y	4.1	45	73
1EQZ	E F	E	54	V	1.5	45	73
1EQZ	E F	E	55	L	3.6	45	73
1EQZ	E F	E	57	Y	2.2	45	73
1EQZ	E F	E	58	L	2.3	45	73
1EQZ	E F	E	63	L	2.4	45	73
1EQZ	E F	E	80	P	1.2	80	89
1EQZ	E F	E	83	L	1.5	80	89
1EQZ	E F	E	93	L	1.3	91	97
1EQZ	E F	F	40	Y	2.8	38	49
1EQZ	E F	F	44	V	1.5	38	49
1EQZ	E F	F	45	L	1.0	38	49
1EQZ	E F	F	48	V	1.0	38	49
1EQZ	E F	F	61	I	2.0	56	84
1EQZ	E F	F	62	M	1.7	56	84
1EQZ	E F	F	65	F	2.4	56	84
1EQZ	E F	F	66	V	1.1	56	84
1EQZ	E F	F	70	F	1.4	56	84
1EQZ	E F	F	94	I	2.1	91	102
1EQZ	E F	F	106	L	1.8	104	123
1EQZ	E F	F	114	G	77.0	104	123
1EQZ	E F	F	118	V	1.2	104	123
1EQZ	E F	F	121	Y	1.8	104	123
1EQZ	F H	F	76	E	2.4	56	84
1EQZ	F H	F	83	Y	2.5	56	84
1EQZ	F H	F	100	L	2.4	91	102
1EQZ	F H	H	68	D	1.6	50	76
1EQZ	F H	H	72	Y	1.4	50	76
1EQZ	F H	H	88	Y	1.9	83	93
1EQZ	F H	H	92	R	2.1	83	93
1EQZ	G H	G	51	I	1.8	45	55
1EQZ	G H	G	54	Y	1.0	45	55
1EQZ	G H	G	67	F	1.5	64	79
1EQZ	G H	G	70	L	2.1	64	79
1EQZ	G H	G	73	E	1.1	64	79
1EQZ	G H	G	74	I	2.2	64	79
1EQZ	G H	G	78	F	2.5	64	79
1EQZ	G H	G	92	L	1.6	86	114
1EQZ	G H	G	99	Y	2.0	86	114
1EQZ	G H	G	100	L	1.7	86	114
1EQZ	G H	G	101	V	1.7	86	114
1EQZ	G H	G	104	F	3.3	86	114
1EQZ	G H	G	121	P	1.4	121	131
1EQZ	G H	G	124	I	1.3	121	131
1EQZ	G H	H	36	R	2.2	31	41
1EQZ	G H	H	37	L	3.3	31	41
1EQZ	G H	H	39	R	1.7	31	41
1EQZ	G H	H	40	R	2.7	31	41
1EQZ	G H	H	58	L	1.0	50	76
1EQZ	G H	H	61	F	2.0	50	76
1EQZ	G H	H	62	L	1.8	50	76
1EQZ	G H	H	66	I	2.9	50	76
1EQZ	G H	H	67	R	1.3	50	76
1EQZ	G H	H	70	V	1.2	50	76

1EQZ	G H	H	86	V	1.5	83	93
1ES7	A D	D	785	F	3.3	783	789
1ES7	A D	D	788	K	1.6	783	789
1ES7	C B	B	285	F	2.6	283	289
1ES7	C B	B	288	K	1.6	283	289
1ES7	C D	D	786	Q	1.4	783	789
1ETZ	A B	A	127	E	1.3	125	130
1ETZ	A H	A	186	R	1.2	185	190
1ETZ	L B	L	186	R	1.0	185	189
1ETZ	L H	L	127	E	1.0	125	130
1EUC	A B	A	111	D	1.4	109	121
1EUC	A B	A	113	V	2.6	109	121
1EUC	A B	A	116	K	1.3	109	121
1EUC	A B	A	117	H	2.4	109	121
1EUC	A B	A	168	E	2.1	163	176
1EUC	A B	B	274	G	32.2	273	286
1EUC	A B	B	275	L	1.7	273	286
1EUC	A B	B	277	M	2.0	273	286
1EUC	A B	B	281	D	4.5	273	286
1EUV	A B	A	438	R	1.9	437	443
1EUV	A B	A	451	D	4.6	451	464
1EUV	A B	A	455	E	2.3	451	464
1EUV	A B	A	474	F	3.3	473	482
1EUV	A B	A	477	T	1.8	473	482
1EXB	A E	A	203	R	1.2	192	205
1EXB	A E	A	235	K	1.3	222	236
1EYS	C M	C	204	L	1.1	204	221
1EYS	C M	C	248	W	2.5	243	260
1EYS	C M	M	191	R	1.6	178	192
1EYS	C M	M	294	Y	1.9	293	300
1EYS	L H	L	218	E	1.1	217	228
1EYS	L H	H	248	L	1.2	233	249
1EYS	L M	L	111	R	1.4	92	120
1EYS	L M	L	115	I	1.6	92	120
1EYS	L M	L	119	L	2.1	92	120
1EYS	L M	L	124	H	3.5	124	130
1EYS	L M	L	162	L	1.0	158	170
1EYS	L M	L	188	F	1.2	179	207
1EYS	L M	L	195	L	2.8	179	207
1EYS	L M	L	199	G	1.5	179	207
1EYS	L M	L	203	L	2.5	179	207
1EYS	L M	L	219	H	1.3	217	228
1EYS	L M	L	222	T	1.6	217	228
1EYS	L M	L	241	G	453.6	234	259
1EYS	L M	L	242	L	1.9	234	259
1EYS	L M	M	87	K	2.0	83	88
1EYS	L M	M	131	R	3.0	112	139
1EYS	L M	M	135	R	4.5	112	139
1EYS	L M	M	136	A	1.7	112	139
1EYS	L M	M	137	E	1.7	112	139
1EYS	L M	M	144	H	1.6	144	160
1EYS	L M	M	179	F	3.0	178	192
1EYS	L M	M	208	L	1.6	199	224
1EYS	L M	M	215	F	3.5	199	224
1EYS	L M	M	219	G	3.6	199	224
1EYS	L M	M	223	L	2.1	199	224
1EYS	L M	M	234	I	1.0	233	239
1EYS	L M	M	249	L	2.1	243	255
1EYS	L M	M	250	F	2.2	243	255
1EYS	L M	M	252	R	1.1	243	255

1EYS	L M	M	253	W	4.7	243	255
1EYS	L M	M	266	R	1.2	261	274
1EYS	M H	M	203	L	1.0	199	224
1EYS	M H	M	235	D	1.8	233	239
1EYS	M H	M	245	E	1.5	243	255
1EYS	M H	M	267	W	3.7	261	274
1EYS	M H	M	270	W	1.7	261	274
1EYS	M H	H	26	L	2.1	11	35
1EYS	M H	H	27	I	1.5	11	35
1EYS	M H	H	30	L	2.5	11	35
1EYS	M H	H	31	R	1.1	11	35
1EYS	M H	H	34	D	2.0	11	35
1EYS	M H	H	233	L	4.9	233	249
1EYS	M H	H	237	D	1.9	233	249
1EYX	A B	A	9	I	2.4	4	15
1EYX	A B	A	24	L	1.7	21	47
1EYX	A B	A	31	I	1.2	21	47
1EYX	A B	A	38	L	1.6	21	47
1EYX	A B	A	48	H	1.3	48	63
1EYX	A B	A	87	D	1.1	76	100
1EYX	A B	A	91	R	1.7	76	100
1EYX	A B	A	98	V	1.3	76	100
1EYX	A B	A	108	W	1.1	103	111
1EYX	A B	B	24	L	1.6	21	33
1EYX	A B	B	34	G	3.7	34	47
1EYX	A B	B	38	L	2.1	34	47
1EYX	A B	B	91	R	2.0	76	100
1EYX	A B	B	95	Y	2.0	76	100
1EYX	A B	B	98	L	1.9	76	100
1EYX	K L	K	9	I	2.9	4	15
1EYX	K L	K	24	L	1.1	21	47
1EYX	K L	K	31	I	1.0	21	47
1EYX	K L	K	38	L	1.2	21	47
1EYX	K L	K	48	H	1.2	48	63
1EYX	K L	K	91	R	2.0	76	100
1EYX	K L	K	94	N	1.4	76	100
1EYX	K L	K	95	Y	3.2	76	100
1EYX	K L	K	98	V	1.7	76	100
1EYX	K L	K	108	W	1.2	103	111
1EYX	K L	L	13	D	1.0	4	15
1EYX	K L	L	34	G	2.4	34	45
1EYX	K L	L	38	L	1.0	34	45
1EYX	K L	L	87	E	1.1	76	100
1EYX	K L	L	91	R	2.2	76	100
1EYX	K L	L	95	Y	2.2	76	100
1EYX	K L	L	98	L	2.7	76	100
1EZQ	A B	A	127	W	4.7	125	131
1EZX	A B	A	27	T	1.1	27	45
1EZX	A B	A	54	P	1.3	54	67
1F11	A B	A	124	Q	1.2	122	127
1F2U	A B	A	36	K	4.6	36	48
1F2U	A B	A	37	S	1.4	36	48
1F2U	A B	B	801	G	11.1	794	812
1F2U	A B	B	805	R	3.1	794	812
1F2U	A D	D	795	G	32.3	794	812
1F2U	C B	B	795	G	63.5	794	812
1F2U	C D	C	36	K	2.2	36	48
1F2U	C D	C	40	L	1.2	36	48
1F2U	C D	C	136	I	1.2	129	137
1F2U	C D	D	801	G	21.3	794	812

1F34	A B	B	115	E	1.2	98	119
1F3D	J K	J	124	Q	1.5	122	126
1F3D	L H	L	124	Q	1.7	122	127
1F3J	A P	A	68	H	1.3	56	77
1F3J	B P	B	60	Y	2.3	55	89
1F3J	B P	B	70	R	1.1	55	89
1F3J	B P	B	79	C	2.3	55	89
1F3J	B P	B	81	H	1.1	55	89
1F3J	B P	B	82	N	2.1	55	89
1F3J	D E	D	73	L	1.8	56	77
1F3J	D E	E	53	L	1.5	52	88
1F3J	D E	E	86	E	1.2	52	88
1F3J	E Q	E	60	Y	1.1	52	88
1F3J	E Q	E	67	Y	1.5	52	88
1F3J	E Q	E	70	R	1.4	52	88
1F3J	E Q	E	81	H	1.7	52	88
1F3J	E Q	E	82	N	1.9	52	88
1F3M	A C	A	130	F	3.2	121	136
1F3M	A C	C	315	E	1.7	309	319
1F3M	A C	C	470	L	2.5	469	480
1F3M	A C	C	473	L	1.0	469	480
1F3M	A C	C	474	Y	1.9	469	480
1F3M	B D	B	116	E	2.7	114	120
1F3M	B D	B	130	F	2.4	121	132
1F3M	B D	D	471	R	2.3	469	480
1F3U	A B	A	31	W	2.6	25	33
1F3U	C D	C	31	W	2.8	25	33
1F3U	E F	E	31	W	2.5	25	34
1F3U	G H	G	31	W	2.8	25	33
1F3V	A B	A	150	E	1.2	150	163
1F45	A B	B	34	R	1.1	21	36
1F45	A B	B	60	V	1.4	59	63
1F45	A B	B	181	R	2.1	132	196
1F45	A B	B	182	I	1.1	132	196
1F45	A B	B	185	V	2.6	132	196
1F45	A B	B	189	R	2.4	132	196
1F45	A B	B	193	Y	1.7	132	196
1F47	B A	A	8	I	2.4	8	16
1F47	B A	A	11	F	2.1	8	16
1F4W	L H	L	127	E	1.1	125	130
1F51	A E	A	30	H	1.1	15	45
1F51	A E	A	33	M	1.0	15	45
1F51	A E	A	37	Q	1.8	15	45
1F51	A E	A	40	K	1.2	15	45
1F51	A E	A	41	G	6.2	15	45
1F51	A E	E	1214	G	3.9	1213	1224
1F51	A E	E	1215	I	1.7	1213	1224
1F51	B E	B	263	K	1.0	249	270
1F51	B F	B	241	G	1.4	216	245
1F51	C G	C	440	K	1.3	416	446
1F51	C G	C	441	G	2.9	416	446
1F51	D H	D	630	H	3.4	620	642
1F51	D H	D	634	N	2.6	620	642
1F51	D H	D	638	L	1.4	620	642
1F51	D H	D	640	K	1.5	620	642
1F51	D H	D	641	G	11.4	620	642
1F51	D H	H	1414	G	1.2	1413	1423
1F51	D H	H	1415	I	1.2	1413	1423
1F51	D H	H	1418	L	1.4	1413	1423
1F58	L H	L	124	Q	1.0	122	127

1F5Q	A B	A	49	I	1.4	46	58
1F5Q	A B	A	50	R	2.8	46	58
1F5Q	A B	A	56	K	1.2	46	58
1F5Q	A B	B	19	D	2.4	17	36
1F5Q	A B	B	26	R	1.1	17	36
1F5Q	C B	B	201	H	1.7	192	205
1F5Q	C B	B	230	H	1.7	226	242
1F5Q	C D	C	49	I	1.3	46	58
1F5Q	C D	C	50	R	1.3	46	58
1F5Q	C D	D	19	D	1.0	17	36
1F5Q	C D	D	23	M	2.5	17	36
1F5Q	C D	D	104	K	2.0	91	107
1F5Q	C D	D	155	Y	2.2	149	160
1F60	A B	A	20	K	1.4	20	31
1F60	A B	A	64	K	1.0	56	70
1F60	A B	A	68	E	2.3	56	70
1F66	A B	A	450	E	1.3	445	455
1F66	A B	A	451	I	1.8	445	455
1F66	A B	A	454	Y	1.2	445	455
1F66	A B	A	470	L	2.2	464	479
1F66	A B	A	474	I	2.1	464	479
1F66	A B	A	478	F	2.2	464	479
1F66	A B	A	497	E	1.1	486	514
1F66	A B	A	499	Y	2.5	486	514
1F66	A B	A	500	L	1.8	486	514
1F66	A B	A	501	V	1.6	486	514
1F66	A B	A	504	F	3.0	486	514
1F66	A B	A	521	P	1.4	521	532
1F66	A B	A	524	I	1.4	521	532
1F66	A B	B	36	R	1.9	31	41
1F66	A B	B	37	L	2.2	31	41
1F66	A B	B	39	R	3.2	31	41
1F66	A B	B	40	R	4.1	31	41
1F66	A B	B	50	I	2.1	48	76
1F66	A B	B	61	F	3.2	48	76
1F66	A B	B	62	L	1.3	48	76
1F66	A B	B	66	I	2.6	48	76
1F66	A B	B	70	V	1.4	48	76
1F66	A G	A	508	N	1.2	486	514
1F66	A G	A	512	I	1.1	486	514
1F66	B D	B	88	Y	1.2	83	93
1F66	B D	D	1280	Y	2.4	1253	1281
1F66	B D	D	1296	R	1.5	1288	1299
1F66	C D	C	822	R	1.0	819	823
1F66	C D	C	831	R	2.1	829	838
1F66	C D	C	852	V	1.7	850	875
1F66	C D	C	853	Y	3.0	850	875
1F66	C D	C	858	L	2.0	850	875
1F66	C D	C	860	Y	1.9	850	875
1F66	C D	C	861	L	1.4	850	875
1F66	C D	C	866	L	1.8	850	875
1F66	C D	C	870	G	270.3	850	875
1F66	C D	C	883	P	1.1	883	893
1F66	C D	C	886	L	1.4	883	893
1F66	C D	C	899	L	1.2	894	900
1F66	C D	D	1241	V	1.8	1235	1246
1F66	C D	D	1258	I	1.9	1253	1281
1F66	C D	D	1259	M	1.6	1253	1281
1F66	C D	D	1262	F	2.5	1253	1281
1F66	C D	D	1267	F	1.7	1253	1281

1F66	C D	D	1291	I	1.4	1288	1299
1F66	C D	D	1303	L	1.6	1302	1322
1F66	C D	D	1311	G	114.5	1302	1322
1F66	C D	D	1318	Y	4.1	1302	1322
1F66	E C	E	648	L	1.2	645	656
1F66	E C	E	655	Q	1.0	645	656
1F66	E C	E	712	I	1.2	686	714
1F66	E F	E	651	I	1.7	645	656
1F66	E F	E	654	Y	1.3	645	656
1F66	E F	E	667	F	1.1	664	677
1F66	E F	E	670	L	2.2	664	677
1F66	E F	E	673	E	1.1	664	677
1F66	E F	E	674	I	2.1	664	677
1F66	E F	E	699	Y	2.8	686	714
1F66	E F	E	700	L	1.3	686	714
1F66	E F	E	701	V	1.5	686	714
1F66	E F	E	704	F	3.2	686	714
1F66	E F	E	721	P	1.4	721	732
1F66	E F	E	724	I	1.5	721	732
1F66	E F	F	236	R	2.2	231	241
1F66	E F	F	237	L	2.4	231	241
1F66	E F	F	239	R	1.8	231	241
1F66	E F	F	240	R	2.9	231	241
1F66	E F	F	253	E	1.1	248	276
1F66	E F	F	257	V	1.4	248	276
1F66	E F	F	258	L	1.8	248	276
1F66	E F	F	261	F	3.4	248	276
1F66	E F	F	262	L	1.1	248	276
1F66	E F	F	266	I	2.8	248	276
1F66	E F	F	286	V	1.1	283	293
1F66	F D	F	291	K	1.4	283	293
1F66	F H	F	272	Y	2.8	248	276
1F66	F H	F	275	H	2.4	248	276
1F66	F H	F	288	Y	1.3	283	293
1F66	F H	H	1473	E	1.4	1453	1481
1F66	F H	H	1477	L	1.0	1453	1481
1F66	F H	H	1480	Y	1.9	1453	1481
1F66	F H	H	1497	L	1.7	1488	1499
1F66	G H	G	1022	R	1.1	1019	1023
1F66	G H	G	1031	R	2.0	1029	1038
1F66	G H	G	1032	I	1.0	1029	1038
1F66	G H	G	1052	V	1.6	1050	1075
1F66	G H	G	1053	Y	3.5	1050	1075
1F66	G H	G	1058	L	2.2	1050	1075
1F66	G H	G	1060	Y	2.9	1050	1075
1F66	G H	G	1061	L	1.7	1050	1075
1F66	G H	G	1066	L	2.0	1050	1075
1F66	G H	G	1083	P	1.0	1083	1093
1F66	G H	G	1086	L	1.4	1083	1093
1F66	G H	G	1099	L	1.3	1094	1100
1F66	G H	H	1437	Y	1.7	1435	1446
1F66	G H	H	1438	V	1.0	1435	1446
1F66	G H	H	1441	V	1.8	1435	1446
1F66	G H	H	1458	I	1.9	1453	1481
1F66	G H	H	1459	M	1.8	1453	1481
1F66	G H	H	1462	F	2.3	1453	1481
1F66	G H	H	1463	V	1.0	1453	1481
1F66	G H	H	1467	F	3.1	1453	1481
1F66	G H	H	1491	I	1.4	1488	1499
1F66	G H	H	1511	G	70.6	1502	1520

1F66	G H	H	1515	V	1.2	1502	1520
1F66	G H	H	1518	Y	3.1	1502	1520
1F6F	A B	A	71	K	1.7	71	77
1F6F	A B	A	177	H	1.7	162	195
1F6F	A B	A	178	R	4.6	162	195
1F6F	A B	A	181	S	1.5	162	195
1F6F	A B	A	182	K	1.2	162	195
1F6F	A C	A	24	R	2.9	18	45
1F6F	A C	A	131	G	3.7	113	140
1F6M	B D	D	96	K	1.2	96	107
1F6M	B D	D	97	G	2.3	96	107
1F6M	F H	F	141	F	1.1	136	142
1F6M	F H	H	96	K	1.3	96	107
1F80	A E	A	14	R	1.9	12	17
1F80	A E	A	21	R	1.7	21	30
1F80	A E	A	24	R	2.4	21	30
1F80	A E	A	25	F	1.2	21	30
1F80	A E	A	28	R	3.9	21	30
1F80	A E	A	54	F	1.2	43	65
1F80	A E	E	40	V	1.8	38	50
1F80	A E	E	41	E	1.1	38	50
1F80	A E	E	44	M	1.6	38	50
1F80	A E	E	45	E	2.4	38	50
1F80	A E	E	47	E	2.6	38	50
1F80	A E	E	56	D	1.8	56	62
1F80	A E	E	60	E	1.2	56	62
1F80	B D	B	14	R	1.3	12	22
1F80	B D	B	21	R	1.0	12	22
1F80	B D	B	28	R	2.1	25	30
1F80	B D	B	54	F	1.0	43	65
1F80	B D	D	56	D	1.0	56	62
1F80	C F	C	25	F	1.1	22	30
1F80	C F	C	28	R	1.8	22	30
1F80	C F	C	54	F	1.5	43	65
1F80	C F	F	43	V	1.2	38	50
1F8V	A D	A	339	P	1.4	339	350
1F8V	A D	A	348	L	1.7	339	350
1F8V	A D	D	364	F	3.6	363	375
1F8V	A D	D	365	W	4.4	363	375
1F8V	A D	D	368	V	1.5	363	375
1F8V	B D	B	339	P	1.0	339	350
1F90	L H	L	123	E	1.0	122	127
1F93	A E	A	55	L	1.1	52	61
1F93	A E	E	12	L	1.0	7	19
1F93	A F	A	48	G	22.0	43	49
1F93	A F	A	52	R	1.0	52	61
1F93	A F	F	8	L	1.1	7	19
1F93	A F	F	11	E	1.0	7	19
1F93	B E	B	48	G	6.1	43	49
1F93	B E	E	8	L	1.0	7	19
1F93	B E	E	12	L	1.1	7	19
1F93	B F	B	55	L	1.4	52	61
1F93	C G	C	48	G	6.8	43	49
1F93	C G	G	8	L	1.0	7	19
1F93	C H	C	55	L	1.2	52	61
1F93	C H	H	8	L	1.3	7	19
1F93	D G	D	55	L	1.0	52	61
1F93	D H	D	48	G	111.0	43	49
1F93	D H	D	52	R	1.9	52	61
1F93	D H	H	8	L	2.5	7	19

1F93	D H	H	11	E	1.3	7	19
1F96	B C	B	35	E	1.1	35	51
1F99	A B	A	9	I	2.7	4	15
1F99	A B	A	24	L	1.1	21	47
1F99	A B	A	31	Y	1.4	21	47
1F99	A B	A	38	L	1.9	21	47
1F99	A B	A	93	R	1.3	78	101
1F99	A B	A	97	Y	4.2	78	101
1F99	A B	A	100	V	1.1	78	101
1F99	A B	A	106	P	1.9	105	113
1F99	A B	B	9	V	4.0	4	15
1F99	A B	B	10	A	1.8	4	15
1F99	A B	B	24	I	1.3	21	33
1F99	A B	B	31	V	1.0	21	33
1F99	A B	B	38	L	2.0	34	46
1F99	A L	A	118	I	1.2	115	122
1F99	A L	L	83	L	1.1	76	100
1F99	K L	K	6	T	1.4	4	15
1F99	K L	K	9	I	2.0	4	15
1F99	K L	K	24	L	1.2	21	47
1F99	K L	K	27	V	1.1	21	47
1F99	K L	K	31	Y	1.4	21	47
1F99	K L	K	38	L	1.2	21	47
1F99	K L	K	93	R	1.7	78	102
1F99	K L	K	97	Y	4.8	78	102
1F99	K L	K	100	V	1.3	78	102
1F99	K L	K	101	V	1.0	78	102
1F99	K L	L	9	V	3.1	4	16
1F99	K L	L	31	V	1.0	21	33
1F99	K L	L	34	G	12.3	34	47
1F99	K L	L	38	L	1.6	34	47
1F99	K L	L	41	V	1.4	34	47
1F99	K L	L	44	I	2.6	34	47
1F99	K L	L	91	R	1.2	76	100
1F99	K L	L	95	Y	2.2	76	100
1F99	K L	L	98	I	3.3	76	100
1F99	K N	K	117	E	1.3	115	122
1F99	K N	N	83	L	1.1	76	100
1F99	M N	M	5	L	3.8	4	15
1F99	M N	M	6	T	1.3	4	15
1F99	M N	M	9	I	5.9	4	15
1F99	M N	M	12	A	2.9	4	15
1F99	M N	M	24	L	4.1	21	47
1F99	M N	M	27	V	4.9	21	47
1F99	M N	M	31	Y	1.5	21	47
1F99	M N	M	38	L	1.1	21	47
1F99	M N	M	42	K	1.2	21	47
1F99	M N	M	93	R	2.8	78	101
1F99	M N	M	97	Y	4.7	78	101
1F99	M N	N	9	V	2.0	4	15
1F99	M N	N	24	I	1.2	21	33
1F99	M N	N	28	L	1.0	21	33
1F99	M N	N	31	V	1.1	21	33
1F99	M N	N	34	G	10.9	34	47
1F99	M N	N	38	L	4.9	34	47
1F99	M N	N	41	V	1.5	34	47
1F99	M N	N	44	I	3.4	34	47
1F99	M N	N	45	T	4.2	34	47
1F99	M N	N	91	R	4.7	76	100
1F99	M N	N	94	S	3.1	76	100

1F99	M N	N	95	Y	4.2	76	100
1F9E	A B	A	189	L	1.2	182	196
1F9E	A B	B	350	I	1.7	348	362
1F9E	A B	B	353	L	1.5	348	362
1F9E	A B	B	357	L	1.1	348	362
1F9E	C D	C	189	L	1.3	182	196
1F9E	C D	D	350	I	1.7	348	362
1F9E	C D	D	353	L	1.6	348	362
1F9E	C D	D	357	L	1.1	348	362
1F9E	E F	E	189	L	1.3	182	196
1F9E	E F	F	350	I	1.0	348	362
1F9E	E F	F	353	L	1.6	348	362
1F9E	E F	F	357	L	1.1	348	362
1F9E	G H	G	189	L	1.3	182	196
1F9E	G H	H	350	I	1.3	348	362
1F9E	G H	H	353	L	1.4	348	362
1F9E	I J	I	189	L	1.3	182	196
1F9E	I J	J	353	L	1.5	348	362
1F9E	I J	J	357	L	1.1	348	362
1F9E	K J	J	375	Y	1.2	366	381
1F9E	K L	K	189	L	1.3	182	196
1F9E	K L	L	353	L	1.6	348	362
1F9E	K L	L	357	L	1.1	348	362
1FAI	L H	L	124	Q	1.3	122	127
1FAV	A C	C	131	I	1.2	128	138
1FAV	A C	C	135	I	1.4	128	138
1FBI	H X	X	97	K	1.6	89	100
1FBI	P Q	P	123	E	1.1	122	128
1FBV	A C	A	369	E	1.3	365	373
1FBV	A C	A	408	W	2.9	402	411
1FBV	A C	C	1006	R	1.0	1006	1017
1FBV	A C	C	1008	M	1.1	1006	1017
1FBV	A C	C	1009	K	2.5	1006	1017
1FBV	A C	C	1012	E	1.4	1006	1017
1FBV	A C	C	1015	R	2.0	1006	1017
1FBV	A C	C	1016	K	2.4	1006	1017
1FCC	A C	C	28	K	7.6	26	37
1FCC	B D	D	34	A	6.6	26	37
1FCD	A C	A	306	Y	1.9	305	324
1FCD	A C	A	383	R	2.0	378	396
1FCD	A C	A	387	Y	3.7	378	396
1FCD	A C	A	390	S	1.7	378	396
1FCD	A C	A	394	N	2.4	378	396
1FCD	A C	C	6	M	1.6	4	10
1FCD	A C	C	13	G	2.4	11	15
1FCD	A C	C	14	C	2.4	11	15
1FCD	A C	C	59	K	1.0	52	60
1FCD	A C	C	131	Y	2.0	126	138
1FCD	A C	C	135	D	1.2	126	138
1FCD	B D	B	306	Y	2.0	305	322
1FCD	B D	B	379	W	3.2	378	400
1FCD	B D	B	383	R	2.1	378	400
1FCD	B D	B	387	Y	1.3	378	400
1FCD	B D	B	390	S	2.3	378	400
1FCD	B D	B	394	N	1.4	378	400
1FCD	B D	D	6	M	1.9	4	10
1FCD	B D	D	13	G	168.0	11	15
1FCD	B D	D	52	T	5.0	52	59
1FCD	B D	D	128	Y	4.4	126	138
1FCD	B D	D	131	Y	1.9	126	138

1FDH	A G	A	31	R	3.0	21	36
1FDH	A G	A	103	H	3.0	95	111
1FDH	A G	A	107	V	1.2	95	111
1FDH	A G	A	122	H	1.5	119	139
1FDH	A G	G	26	E	2.2	20	35
1FDH	A G	G	34	V	1.5	20	35
1FDH	A G	G	108	N	2.9	101	118
1FDH	A G	G	112	T	2.6	101	118
1FDH	A G	G	124	P	1.4	124	142
1FDH	A G	G	131	Q	2.7	124	142
1FDH	A H	A	97	N	1.2	95	111
1FDH	B G	B	97	N	1.2	95	111
1FDH	B H	B	31	R	3.2	21	36
1FDH	B H	B	103	H	3.0	95	111
1FDH	B H	B	107	V	1.2	95	111
1FDH	B H	H	26	E	2.3	20	35
1FDH	B H	H	34	V	1.5	20	35
1FDH	B H	H	112	T	2.6	101	118
1FDH	B H	H	124	P	1.3	124	142
1FDH	B H	H	131	Q	2.7	124	142
1FDL	L H	L	124	Q	1.1	122	128
1FDL	L Y	Y	121	Q	1.1	120	124
1FE8	B I	B	990	H	1.0	988	997
1FE8	C J	C	990	H	1.4	988	997
1FE8	C J	C	993	S	3.3	988	997
1FE8	C J	C	994	L	1.1	988	997
1FE8	H L	L	123	E	1.7	122	127
1FE8	H L	L	124	Q	1.0	122	127
1FE8	I M	M	124	Q	1.4	122	127
1FE8	J N	N	124	Q	1.3	122	126
1FFT	A B	A	357	I	1.1	356	369
1FFT	A B	A	367	L	1.2	356	369
1FFT	A B	A	368	F	1.6	356	369
1FFT	A B	B	45	L	1.1	42	52
1FFT	A B	B	64	G	1.4	62	66
1FFT	A C	A	206	I	1.1	187	213
1FFT	A C	A	240	I	1.0	229	241
1FFT	A C	A	245	I	1.7	242	259
1FFT	A C	C	31	I	1.6	29	34
1FFT	F G	F	353	M	1.0	342	355
1FFT	F G	F	364	F	1.5	356	369
1FFT	F G	F	368	F	3.5	356	369
1FFT	F G	F	408	F	1.4	404	411
1FFT	F G	F	410	L	1.1	404	411
1FFT	F G	G	64	G	4.5	62	66
1FFT	F H	F	206	I	1.4	187	213
1FFT	F H	F	210	V	2.0	187	213
1FFU	B C	B	124	Y	1.7	123	133
1FFU	B C	B	790	Y	2.4	789	799
1FFU	B C	B	793	W	2.5	789	799
1FFU	B C	B	794	K	1.3	789	799
1FFU	B C	C	265	D	1.2	264	285
1FFU	B C	C	266	Y	4.4	264	285
1FFU	B C	C	270	M	1.2	264	285
1FFU	D E	D	27	H	1.5	25	33
1FFU	D E	D	30	R	1.9	25	33
1FFU	D E	D	90	Q	1.6	88	96
1FFU	D E	D	94	Y	1.7	88	96
1FFU	D E	D	103	F	3.7	103	119
1FFU	D E	D	128	R	2.7	124	131

1FFU	D E	D	142	Q	2.2	142	156
1FFU	D E	E	30	F	1.3	25	31
1FFU	D E	E	124	Y	5.1	123	133
1FFU	D E	E	128	D	1.5	123	133
1FFU	D E	E	298	R	2.5	298	305
1FFU	D E	E	687	M	1.1	686	707
1FFU	D E	E	691	G	2.3	686	707
1FFU	D E	E	694	H	2.9	686	707
1FFU	D E	E	695	G	144.9	686	707
1FFU	D E	E	699	E	1.2	686	707
1FFU	D F	F	38	L	1.6	36	43
1FFU	D F	F	42	K	1.4	36	43
1FFU	D F	F	80	D	1.0	78	83
1FFU	D F	F	105	Q	2.4	104	108
1FFU	E F	E	124	Y	1.6	123	133
1FFU	E F	E	131	E	1.0	123	133
1FFU	E F	E	790	Y	1.9	789	799
1FFU	E F	E	793	W	1.5	789	799
1FFU	E F	E	794	K	2.4	789	799
1FFU	E F	F	266	Y	4.0	264	285
1FFU	E F	F	270	M	1.0	264	285
1FG9	A C	A	9	E	1.8	3	15
1FG9	A C	A	12	K	1.5	3	15
1FG9	A D	A	111	H	2.2	103	112
1FG9	B C	B	111	H	2.0	103	112
1FG9	B D	B	9	E	2.0	3	16
1FG9	B D	D	106	R	1.7	104	108
1FH5	L H	L	125	Q	1.4	123	129
1FHJ	A B	A	31	R	2.7	21	36
1FHJ	A B	A	122	H	2.2	119	137
1FHJ	A B	B	30	R	3.3	20	35
1FHJ	A B	B	34	V	1.1	20	35
1FHJ	A D	A	95	P	1.6	95	113
1FHJ	A D	D	37	W	3.4	36	42
1FHJ	A D	D	102	N	1.5	100	119
1FHJ	C B	C	95	P	1.7	95	113
1FHJ	C B	B	37	W	3.5	36	42
1FHJ	C B	B	102	N	1.5	100	119
1FHJ	C D	C	31	R	2.7	21	36
1FHJ	C D	C	122	H	2.5	119	137
1FHJ	C D	D	30	R	3.2	20	35
1FHJ	C D	D	34	V	1.0	20	35
1FHJ	C D	D	116	H	1.0	100	119
1FIQ	A B	B	265	G	2.0	263	271
1FIQ	A B	B	266	I	1.2	263	271
1FIQ	A B	B	341	Q	1.6	340	346
1FIQ	A C	A	31	R	1.9	26	34
1FIQ	A C	A	32	R	1.0	26	34
1FIQ	A C	A	115	F	3.1	115	131
1FIQ	A C	A	157	L	1.1	154	160
1FIQ	A C	C	1197	G	125.2	1188	1209
1FIQ	A C	C	1204	G	3.3	1188	1209
1FIQ	B C	B	514	S	1.2	505	528
1FIQ	B C	B	517	F	3.0	505	528
1FIQ	B C	C	677	H	1.0	675	684
1FJ1	A B	A	123	E	1.5	122	128
1FJ1	A B	A	124	Q	1.4	122	128
1FJ1	C D	C	124	Q	1.6	122	128
1FL5	L H	L	124	Q	1.5	122	127
1FLC	A B	B	56	K	1.3	43	66

1FLC	A B	B	82	L	2.2	82	124
1FLC	A B	B	85	E	4.8	82	124
1FLC	A B	B	93	L	1.3	82	124
1FLC	A B	B	104	V	1.5	82	124
1FLC	A B	B	105	G	5.2	82	124
1FLC	A B	B	111	L	1.2	82	124
1FLC	A F	F	47	K	1.1	43	66
1FLC	A F	F	51	D	7.9	43	66
1FLC	C B	B	47	K	1.0	43	66
1FLC	C D	D	52	I	1.9	43	66
1FLC	C D	D	56	K	2.0	43	66
1FLC	C D	D	59	I	1.2	43	66
1FLC	C D	D	63	I	1.5	43	66
1FLC	C D	D	85	E	1.9	82	124
1FLC	C D	D	96	L	1.1	82	124
1FLC	C D	D	104	V	2.1	82	124
1FLC	C D	D	105	G	31.5	82	124
1FLC	E D	D	47	K	1.0	43	66
1FLC	E F	F	56	K	1.3	43	66
1FLC	E F	F	63	I	1.3	43	66
1FLC	E F	F	85	E	1.8	82	124
1FLC	E F	F	93	L	1.1	82	124
1FLC	E F	F	104	V	2.1	82	124
1FLC	E F	F	105	G	91.6	82	124
1FM0	D E	E	58	M	2.1	58	74
1FM6	A D	A	394	E	1.8	386	408
1FM6	A D	A	397	Y	3.1	386	408
1FM6	A D	A	401	E	1.2	386	408
1FM6	A D	A	423	P	4.9	421	437
1FM6	A D	A	426	R	1.1	421	437
1FM6	A D	D	414	L	1.0	403	425
1FM6	A D	D	434	K	2.4	431	460
1FM6	A D	D	436	L	1.1	431	460
1FM6	D E	E	689	I	1.2	688	697
1FM6	D E	E	690	L	1.8	688	697
1FM6	D E	E	693	L	1.4	688	697
1FM6	D E	E	694	L	1.1	688	697
1FM6	U V	U	280	V	1.0	266	286
1FM6	U V	U	294	L	1.4	294	317
1FM6	U V	U	450	F	2.0	449	454
1FM6	U V	U	453	E	1.6	449	454
1FM6	U V	V	632	I	3.2	631	639
1FM6	U V	V	636	L	1.2	631	639
1FM6	U V	V	637	L	2.0	631	639
1FM6	U X	U	394	E	1.2	386	408
1FM6	U X	U	397	Y	3.0	386	408
1FM6	U X	U	417	K	1.2	414	420
1FM6	U X	U	419	L	2.0	414	420
1FM6	U X	U	422	L	1.1	421	443
1FM6	U X	U	423	P	1.1	421	443
1FM6	U X	X	434	K	2.0	431	460
1FM6	U X	X	436	L	1.2	431	460
1FM6	U X	X	437	Q	1.0	431	460
1FM6	X Y	X	315	V	2.5	311	333
1FM6	X Y	Y	690	L	1.7	688	696
1FM6	X Y	Y	693	L	1.2	688	696
1FM6	X Y	Y	694	L	2.5	688	696
1FMH	A B	A	8	E	1.1	2	31
1FMH	A B	A	15	E	1.4	2	31
1FMH	A B	A	23	V	1.0	2	31

1FMH	A B	A	26	L	1.8	2	31
1FMH	A B	A	30	C	17.5	2	31
1FMH	A B	B	5	L	1.6	2	30
1FMH	A B	B	22	K	1.2	2	30
1FMH	A B	B	23	V	1.3	2	30
1FMH	A B	B	26	L	1.8	2	30
1FN4	A B	A	120	E	1.1	119	123
1FN4	A B	A	121	Q	3.2	119	123
1FNS	H A	A	635	V	1.0	634	644
1FNS	H A	A	636	R	1.7	634	644
1FNS	L A	A	636	R	2.1	634	644
1FNS	L H	L	124	Q	1.8	122	127
1FNT	a b	a	51	D	1.7	49	69
1FNT	a b	b	96	R	2.3	81	98
1FNT	A B	A	126	Q	1.2	114	132
1FNT	A B	A	129	T	2.5	114	132
1FNT	A G	A	30	Y	2.5	26	39
1FNT	A H	A	106	Y	4.0	87	108
1FNT	A I	I	66	H	1.4	49	71
1FNT	B C	C	24	Y	2.2	21	30
1FNT	B I	I	65	L	1.5	49	71
1FNT	C D	D	22	Y	2.0	18	30
1FNT	C D	D	29	R	1.1	18	30
1FNT	C i	C	26	L	1.3	21	30
1FNT	C J	C	100	K	1.0	81	102
1FNT	C J	J	64	L	1.1	48	69
1FNT	D E	E	26	Y	3.5	22	29
1FNT	D K	D	98	L	1.4	83	99
1FNT	D K	K	65	L	1.5	49	71
1FNT	D K	K	68	I	1.4	49	71
1FNT	D K	K	69	R	1.1	49	71
1FNT	D L	L	69	R	1.1	50	71
1FNT	D L	L	70	E	1.5	50	71
1FNT	E F	F	24	Y	2.2	20	32
1FNT	E L	E	97	V	1.5	82	103
1FNT	E L	E	101	L	1.1	82	103
1FNT	E L	L	65	L	1.4	50	71
1FNT	E L	L	68	L	1.3	50	71
1FNT	E M	M	66	Y	1.9	63	69
1FNT	E M	M	82	R	1.6	77	91
1FNT	E M	M	86	H	1.2	77	91
1FNT	F g	F	31	Q	1.1	20	32
1FNT	F G	G	25	Y	2.1	21	33
1FNT	F M	M	64	K	1.3	63	69
1FNT	F M	M	68	F	1.8	63	69
1FNT	F N	F	98	V	1.2	78	100
1FNT	F N	F	99	F	1.1	78	100
1FNT	F N	N	83	Y	1.3	81	97
1FNT	F N	N	87	Y	1.0	81	97
1FNT	G e	G	24	E	1.7	21	33
1FNT	G H	G	98	F	2.8	81	102
1FNT	G N	G	92	R	1.5	81	102
1FNT	G N	G	99	K	1.6	81	102
1FNT	G N	N	60	K	1.9	49	68
1FNT	G N	N	61	D	2.6	49	68
1FNT	H b	b	138	F	1.0	138	148
1FNT	H I	H	57	D	1.0	49	68
1FNT	I a	a	140	F	1.1	136	146
1FNT	I a	a	173	K	1.2	168	185
1FNT	I b	b	145	P	1.0	138	148

1FNT	I J	J	87	Y	1.0	75	89
1FNT	I J	J	156	E	1.2	151	168
1FNT	J a	J	139	G	96.9	134	145
1FNT	J a	J	140	M	1.1	134	145
1FNT	J a	J	142	E	1.6	134	145
1FNT	J a	J	167	D	1.2	151	168
1FNT	J a	a	142	D	1.4	136	146
1FNT	J K	J	52	T	3.5	48	69
1FNT	J K	J	53	T	3.8	48	69
1FNT	J K	K	84	R	3.0	76	92
1FNT	J K	K	137	F	1.9	134	147
1FNT	J Z	Z	166	H	1.2	150	168
1FNT	J Z	Z	198	W	1.8	193	205
1FNT	K L	K	50	G	222.0	49	71
1FNT	K L	K	57	E	1.0	49	71
1FNT	K Z	K	144	D	3.1	134	147
1FNT	K Z	Z	135	F	1.8	133	144
1FNT	K Z	Z	167	R	2.4	150	168
1FNT	L M	L	51	D	1.3	50	71
1FNT	L M	L	54	F	1.1	50	71
1FNT	L M	L	195	E	1.0	193	205
1FNT	L M	M	89	Y	3.8	77	91
1FNT	M N	M	51	D	1.8	49	62
1FNT	M N	N	96	R	2.7	81	97
1FNT	O k	O	32	F	1.4	26	39
1FNT	O P	O	126	Q	1.1	114	132
1FNT	O P	O	130	Q	2.3	114	132
1FNT	O P	O	131	R	1.7	114	132
1FNT	O P	P	23	Y	7.9	20	25
1FNT	O P	P	121	A	1.6	107	123
1FNT	O U	O	30	Y	2.5	26	39
1FNT	O U	O	92	N	1.3	87	108
1FNT	O V	O	106	Y	3.9	87	108
1FNT	O V	V	64	E	1.3	49	68
1FNT	O W	W	66	H	1.3	49	71
1FNT	P Q	Q	24	Y	2.3	21	30
1FNT	P W	P	94	H	1.1	79	96
1FNT	P W	W	65	L	1.6	49	71
1FNT	Q p	Q	26	L	1.8	21	30
1FNT	Q R	R	22	Y	2.2	18	30
1FNT	Q R	R	29	R	1.1	18	30
1FNT	Q X	X	60	Y	1.0	48	69
1FNT	Q X	X	64	L	1.0	48	69
1FNT	Q Y	Q	98	Y	1.4	81	102
1FNT	Q Y	Y	66	Y	1.2	49	71
1FNT	Q Y	Y	69	R	1.7	49	71
1FNT	Q Y	Y	85	Q	1.0	76	92
1FNT	R S	S	26	Y	3.5	22	29
1FNT	R Y	R	98	L	1.4	83	99
1FNT	R Y	Y	65	L	1.4	49	71
1FNT	R Y	Y	69	R	1.0	49	71
1FNT	S a	a	66	Y	1.1	49	69
1FNT	S a	a	82	R	1.8	77	91
1FNT	S a	a	86	H	1.3	77	91
1FNT	S T	T	24	Y	2.0	20	32
1FNT	S Z	S	101	L	1.0	82	103
1FNT	S Z	Z	65	L	1.3	50	71
1FNT	S Z	Z	68	L	1.3	50	71
1FNT	T a	T	89	R	1.1	78	100
1FNT	T a	a	65	W	1.2	49	69

1FNT	T a	a	68	F	1.1	49	69
1FNT	T b	b	83	Y	1.7	81	98
1FNT	T b	b	87	Y	5.0	81	98
1FNT	T n	T	31	Q	1.2	20	32
1FNT	T U	T	110	H	1.2	105	112
1FNT	T U	U	25	Y	2.2	21	33
1FNT	U b	U	92	R	1.7	81	102
1FNT	U b	U	99	K	1.1	81	102
1FNT	U b	b	61	D	1.5	49	68
1FNT	V N	V	190	P	1.0	190	196
1FNT	V N	N	138	F	1.2	138	148
1FNT	V N	N	142	M	1.4	138	148
1FNT	V W	V	57	D	1.1	49	68
1FNT	V W	W	132	L	1.0	131	139
1FNT	W M	M	140	F	1.0	136	146
1FNT	W M	M	173	K	1.6	168	185
1FNT	W N	W	132	L	1.3	131	139
1FNT	W N	N	146	L	1.1	138	148
1FNT	W N	N	175	V	1.0	162	179
1FNT	W X	X	144	L	1.0	134	145
1FNT	W X	X	160	Q	1.3	151	168
1FNT	X L	L	166	H	1.3	150	168
1FNT	X L	L	194	G	1.1	193	205
1FNT	X L	L	198	W	1.1	193	205
1FNT	X M	X	139	G	173.7	134	145
1FNT	X Y	Y	137	F	1.8	134	147
1FNT	Y L	L	135	F	2.1	133	144
1FNT	Y L	L	137	Y	1.4	133	144
1FNT	Y Z	Y	50	G	187.1	49	71
1FNT	Y Z	Y	57	E	1.2	49	71
1FNT	Z a	Z	54	F	2.6	50	71
1FNT	Z a	Z	195	E	1.2	193	205
1FNT	Z a	a	89	Y	4.0	77	91
1FOE	A B	A	1184	S	1.4	1182	1186
1FOE	A B	A	1187	I	1.7	1187	1194
1FOE	A B	A	1192	R	9.1	1187	1194
1FOE	A B	A	1199	L	1.5	1195	1206
1FOE	A B	B	66	R	2.1	65	69
1FOE	A B	B	67	L	1.5	65	69
1FOE	A D	D	94	R	1.0	87	105
1FOE	A D	D	99	P	3.4	87	105
1FOE	A D	D	100	E	1.3	87	105
1FOE	C D	C	1184	S	1.3	1182	1186
1FOE	C D	C	1187	I	1.2	1187	1194
1FOE	C D	C	1190	I	3.6	1187	1194
1FOE	C D	C	1191	Q	3.8	1187	1194
1FOE	C D	C	1195	K	4.4	1195	1206
1FOE	C D	C	1198	L	5.0	1195	1206
1FOE	C D	C	1199	L	1.2	1195	1206
1FOE	C D	C	1228	A	4.1	1226	1233
1FOE	C D	C	1231	I	3.7	1226	1233
1FOE	C D	C	1232	N	4.1	1226	1233
1FOE	C D	D	66	R	2.1	65	69
1FOE	C D	D	67	L	1.9	65	69
1FOE	E F	E	1149	H	1.3	1122	1157
1FOE	E F	E	1184	S	1.4	1182	1186
1FOE	E F	E	1187	I	2.6	1187	1194
1FOE	E F	E	1191	Q	9.1	1187	1194
1FOE	E F	E	1198	L	1.0	1195	1206
1FOE	E F	E	1199	L	1.0	1195	1206

1FOE	E F	F	66	R	2.1	65	69
1FOE	E F	F	67	L	1.1	65	69
1FOE	G H	G	1184	S	1.0	1182	1186
1FOE	G H	G	1187	I	1.6	1187	1194
1FOE	G H	G	1192	R	6.0	1187	1194
1FOE	G H	G	1198	L	1.0	1195	1206
1FOE	G H	G	1232	N	6.7	1226	1233
1FOE	G H	H	65	D	1.6	65	69
1FOE	G H	H	66	R	1.8	65	69
1FOE	G H	H	67	L	1.9	65	69
1FOR	L H	L	123	Q	1.2	121	127
1FOS	E F	E	166	Q	1.2	140	197
1FOS	E F	E	172	L	1.2	140	197
1FOS	E F	E	173	E	1.0	140	197
1FOS	E F	E	176	K	1.0	140	197
1FOS	E F	E	179	L	1.2	140	197
1FOS	E F	E	183	I	1.6	140	197
1FOS	E F	E	186	L	1.6	140	197
1FOS	E F	F	289	L	1.7	267	322
1FOS	E F	F	292	K	1.6	267	322
1FOS	E F	F	303	L	1.0	267	322
1FOS	E F	F	310	L	2.3	267	322
1FOS	E F	F	317	L	3.3	267	322
1FOS	E F	F	321	V	1.7	267	322
1FPP	B A	B	129	F	1.3	120	134
1FPP	B A	B	271	K	1.3	270	279
1FPP	B A	A	96	F	3.9	94	109
1FPP	B A	A	131	Y	1.8	131	144
1FPP	B A	A	167	Q	1.3	166	179
1FPP	B A	A	170	H	1.5	166	179
1FPP	B A	A	200	Y	3.5	200	213
1FPP	B A	A	238	N	1.9	234	246
1FPP	B A	A	241	H	1.1	234	246
1FPP	B A	A	282	G	70.5	274	283
1FPP	B A	A	355	Y	2.3	353	367
1FPP	B A	A	358	Y	2.6	353	367
1FPT	L H	L	49	Y	1.3	49	53
1FQ1	A B	A	183	I	1.7	183	190
1FQ1	A B	A	186	Y	2.5	183	190
1FQ1	A B	B	209	I	1.3	208	219
1FQ1	A B	B	213	F	1.0	208	219
1FQJ	A B	A	203	E	1.1	201	210
1FQJ	A B	A	206	K	3.5	201	210
1FQJ	A B	A	209	H	1.3	201	210
1FQJ	A B	B	367	G	2.4	367	379
1FQJ	A B	B	395	L	1.0	386	406
1FQJ	A B	B	397	K	1.4	386	406
1FQJ	A C	A	204	R	1.7	201	210
1FQJ	A C	A	207	W	1.1	201	210
1FQJ	A C	A	208	I	2.9	201	210
1FQJ	A C	A	244	K	1.0	238	251
1FQJ	A C	A	248	S	1.0	238	251
1FQJ	A C	C	69	P	1.0	69	73
1FQJ	A C	C	70	W	3.7	69	73
1FQJ	A C	C	78	L	2.1	78	84
1FQJ	A C	C	81	L	1.5	78	84
1FQJ	D E	E	367	G	1.5	367	377
1FQJ	D E	E	395	L	1.4	386	407
1FQJ	D E	E	397	K	1.2	386	407
1FQV	A B	A	133	S	2.1	126	134

1FQV	A B	A	137	K	1.9	137	144
1FQV	A B	A	138	R	1.2	137	144
1FQV	A B	A	139	W	2.5	137	144
1FQV	A B	A	140	Y	2.5	137	144
1FQV	A B	B	135	I	1.5	132	139
1FQV	A B	B	136	R	1.4	132	139
1FQV	A B	B	149	E	1.6	147	156
1FQV	A B	B	153	V	1.0	147	156
1FQV	A F	F	64	H	1.6	52	65
1FQV	A F	F	88	W	1.0	87	93
1FQV	C D	C	120	I	1.7	114	123
1FQV	C D	C	139	W	1.2	137	144
1FQV	C D	C	140	Y	1.7	137	144
1FQV	C D	D	123	V	1.1	113	128
1FQV	C D	D	127	I	1.1	113	128
1FQV	C D	D	135	I	1.2	132	139
1FQV	E F	E	120	I	1.5	114	123
1FQV	E F	E	127	P	3.4	126	134
1FQV	E F	E	131	K	2.8	126	134
1FQV	E F	E	133	S	3.8	126	134
1FQV	E F	E	139	W	1.4	137	143
1FQV	E F	E	140	Y	3.5	137	143
1FQV	E F	E	166	R	3.5	161	169
1FQV	E F	F	101	F	1.1	97	110
1FQV	E F	F	123	V	1.0	113	128
1FQV	E F	F	135	I	1.1	132	139
1FQV	E F	F	136	R	1.2	132	139
1FQV	E F	F	153	V	3.2	147	156
1FQV	G H	G	120	I	1.8	114	123
1FQV	G H	G	140	Y	1.0	137	144
1FQV	G H	H	101	F	1.7	97	110
1FQV	G H	H	135	I	2.1	132	139
1FQV	G H	H	136	R	1.5	132	139
1FQV	G H	H	153	V	1.1	147	156
1FQV	I J	I	120	I	1.6	114	123
1FQV	I J	I	137	K	2.3	137	144
1FQV	I J	I	139	W	1.7	137	144
1FQV	I J	I	140	Y	1.1	137	144
1FQV	I J	I	167	L	1.0	161	172
1FQV	I J	J	101	F	1.7	97	110
1FQV	I J	J	104	I	2.0	97	110
1FQV	I J	J	127	I	1.3	113	128
1FQV	I J	J	135	I	1.2	132	139
1FQV	I J	J	136	R	1.4	132	139
1FQV	I J	J	153	V	1.1	147	157
1FQV	K L	K	120	I	1.0	114	123
1FQV	K L	K	131	K	1.4	126	134
1FQV	K L	K	137	K	1.6	137	144
1FQV	K L	K	139	W	1.2	137	144
1FQV	K L	K	140	Y	1.4	137	144
1FQV	K L	L	101	F	5.0	97	110
1FQV	K L	L	127	I	1.6	113	128
1FQV	K L	L	135	I	1.0	132	139
1FQV	K L	L	136	R	1.1	132	139
1FQV	M N	M	120	I	2.1	114	123
1FQV	M N	M	137	K	2.3	137	143
1FQV	M N	M	139	W	1.5	137	143
1FQV	M N	M	140	Y	1.2	137	143
1FQV	M N	N	135	I	1.3	132	139
1FQV	M N	N	136	R	1.5	132	139

1FQV	M N	N	153	V	1.1	147	157
1FQV	O L	L	64	H	1.0	52	65
1FQV	O P	O	120	I	2.2	114	123
1FQV	O P	O	139	W	2.0	137	144
1FQV	O P	P	104	I	2.0	97	110
1FQV	O P	P	123	V	1.0	113	128
1FQV	O P	P	135	I	1.4	132	139
1FRG	L H	L	130	Q	1.1	128	133
1FRT	A C	A	134	P	17.9	134	145
1FS0	E G	E	91	E	1.1	87	104
1FS0	E G	E	93	R	1.0	87	104
1FS0	E G	E	98	K	1.7	87	104
1FS0	E G	E	128	L	1.1	114	133
1FS0	E G	G	45	Y	3.2	20	58
1FS0	E G	G	52	V	1.1	20	58
1FS0	E G	G	93	I	1.0	91	109
1FS0	E G	G	104	K	1.1	91	109
1FS0	E G	G	150	I	1.0	146	162
1FS0	E G	G	151	G	24.8	146	162
1FS0	E G	G	154	K	1.1	146	162
1FS0	E G	G	155	V	1.2	146	162
1FS0	E G	G	215	L	1.7	212	248
1FS0	E G	G	225	E	2.0	212	248
1FS0	E G	G	229	Y	1.2	212	248
1FS1	A B	A	116	L	1.4	114	122
1FS1	A B	A	120	I	1.7	114	122
1FS1	A B	A	139	W	1.4	137	144
1FS1	A B	B	104	I	1.6	97	111
1FS1	A B	B	127	I	1.9	113	128
1FS1	A B	B	135	I	1.0	132	139
1FS1	C D	C	120	I	2.1	114	123
1FS1	C D	C	139	W	1.2	137	144
1FS1	C D	D	105	L	1.2	97	110
1FS1	C D	D	132	P	1.2	132	139
1FS1	C D	D	135	I	1.1	132	139
1FS2	A B	A	120	I	1.9	114	124
1FS2	A B	A	137	K	1.2	137	144
1FS2	A B	A	139	W	1.4	137	144
1FS2	A B	B	101	F	4.4	97	111
1FS2	A B	B	105	L	1.1	97	111
1FS2	A B	B	123	V	1.0	113	128
1FS2	A B	B	127	I	1.5	113	128
1FS2	A B	B	135	I	1.3	132	139
1FS2	A B	B	136	R	1.3	132	139
1FS2	A D	A	211	H	3.0	207	215
1FS2	A D	A	232	D	1.9	232	239
1FS2	A D	A	233	P	9.1	232	239
1FS2	A D	A	237	T	1.5	232	239
1FS2	A D	A	262	T	1.9	257	267
1FS2	C B	C	211	H	1.4	207	215
1FS2	C D	C	120	I	1.7	114	124
1FS2	C D	C	139	W	2.0	137	144
1FS2	C D	D	101	F	4.2	97	111
1FS2	C D	D	105	L	1.0	97	111
1FS2	C D	D	127	I	1.6	113	128
1FS2	C D	D	135	I	1.4	132	139
1FS2	C D	D	136	R	1.4	132	139
1FSK	H I	H	124	Q	1.1	122	126
1FSX	A B	A	31	R	2.7	21	36
1FSX	A B	A	107	V	1.7	95	113

1FSX	A B	A	122	H	2.5	119	137
1FSX	A B	B	230	R	3.2	220	235
1FSX	A B	B	234	V	1.2	220	235
1FSX	A B	B	312	V	2.3	300	319
1FSX	A B	B	316	R	4.6	300	319
1FSX	A B	B	324	P	1.3	324	344
1FSX	A D	A	95	P	1.7	95	113
1FSX	A D	D	637	W	2.7	636	642
1FSX	A D	D	702	N	1.6	700	719
1FSX	C B	C	495	P	2.0	495	513
1FSX	C B	B	302	N	1.2	300	319
1FSX	C D	C	431	R	2.9	421	436
1FSX	C D	C	434	L	1.5	421	436
1FSX	C D	C	507	V	2.8	495	513
1FSX	C D	C	522	H	2.6	519	537
1FSX	C D	D	630	R	3.7	620	635
1FSX	C D	D	634	V	1.2	620	635
1FSX	C D	D	712	V	1.3	700	719
1FSX	C D	D	716	R	1.7	700	719
1FSX	C D	D	724	P	1.2	724	744
1FWA	A C	A	13	L	1.8	5	27
1FWA	B C	C	9	Y	2.0	6	13
1FX0	A B	A	204	S	1.1	203	212
1FX0	A B	A	276	L	1.6	264	278
1FX0	A B	A	455	R	1.1	453	463
1FXK	A C	C	123	M	1.1	90	137
1FXK	B C	B	37	E	1.3	35	48
1FXK	B C	B	44	E	1.1	35	48
1FXK	B C	B	45	L	1.0	35	48
1FXT	A B	A	114	Q	1.3	102	115
1FXW	A F	A	198	R	1.1	198	215
1FXW	A F	F	30	R	1.0	23	37
1FYH	A B	A	21	D	1.0	20	24
1FYH	A B	A	311	H	2.5	303	312
1FYH	A B	A	315	Q	1.1	313	319
1FYH	D B	D	202	G	37.1	202	215
1FYH	D E	D	311	H	3.1	303	312
1FYH	D E	D	314	I	1.3	313	319
1FYH	D E	D	315	Q	1.0	313	319
1FYZ	A C	A	27	E	1.0	25	31
1FYZ	A C	A	28	V	1.7	25	31
1FYZ	A C	A	65	K	2.7	64	84
1FYZ	A C	A	67	Y	1.9	64	84
1FYZ	A C	A	97	P	1.2	97	128
1FYZ	A C	A	115	Y	2.4	97	128
1FYZ	A C	A	122	G	47.2	97	128
1FYZ	A C	A	123	M	2.9	97	128
1FYZ	A C	A	125	W	5.4	97	128
1FYZ	A C	A	142	L	2.2	131	161
1FYZ	A C	A	145	I	1.3	131	161
1FYZ	A C	A	146	R	1.0	131	161
1FYZ	A C	A	149	H	3.5	131	161
1FYZ	A C	A	156	Y	1.3	131	161
1FYZ	A C	A	172	R	3.2	171	178
1FYZ	A C	A	181	W	1.5	179	188
1FYZ	A C	A	185	K	1.5	179	188
1FYZ	A C	A	186	R	1.6	179	188
1FYZ	A C	A	190	D	3.1	189	193
1FYZ	A C	C	16	M	1.5	14	23
1FYZ	A C	C	20	I	2.3	14	23

1FYZ	A C	C	52	L	2.4	48	54
1FYZ	A C	C	53	T	1.0	48	54
1FYZ	A C	C	110	V	1.1	106	130
1FYZ	A C	C	111	K	1.2	106	130
1FYZ	A C	C	113	K	1.5	106	130
1FYZ	A C	C	117	W	4.7	106	130
1FYZ	A C	C	128	S	1.2	106	130
1FYZ	A C	C	153	L	1.0	138	163
1FYZ	A C	C	154	F	1.3	138	163
1FYZ	A C	C	157	Y	3.7	138	163
1FYZ	A C	C	158	G	51.9	138	163
1FYZ	A C	C	161	N	1.2	138	163
1FYZ	A C	C	176	R	1.5	173	203
1FYZ	A C	C	184	F	4.1	173	203
1FYZ	A C	C	188	D	1.5	173	203
1FYZ	A C	C	191	Q	1.3	173	203
1FYZ	A C	C	195	L	1.1	173	203
1FYZ	A C	C	199	F	1.4	173	203
1FYZ	A C	C	202	K	1.1	173	203
1FYZ	A C	C	215	K	1.1	212	220
1FYZ	A C	C	232	E	1.5	225	237
1FYZ	A C	C	235	W	3.0	225	237
1FYZ	A E	A	266	Y	2.3	261	293
1FYZ	A E	A	272	N	1.0	261	293
1FYZ	A E	A	452	W	1.7	451	460
1FYZ	A E	A	454	E	2.1	451	460
1FYZ	A E	A	455	R	5.5	451	460
1FYZ	A E	A	458	L	2.7	451	460
1FYZ	A E	E	136	G	9.5	125	144
1FYZ	A E	E	140	M	2.1	125	144
1FYZ	A E	E	143	R	1.4	125	144
1FYZ	A E	E	152	L	1.3	152	160
1FYZ	A E	E	155	L	1.6	152	160
1FYZ	A E	E	156	R	2.4	152	160
1FYZ	A E	E	159	R	2.7	152	160
1FYZ	B C	C	366	D	1.1	349	371
1FYZ	B D	B	27	E	1.6	25	31
1FYZ	B D	B	28	V	1.5	25	31
1FYZ	B D	B	65	K	1.9	64	84
1FYZ	B D	B	67	Y	2.1	64	84
1FYZ	B D	B	97	P	1.3	97	128
1FYZ	B D	B	115	Y	2.3	97	128
1FYZ	B D	B	122	G	21.7	97	128
1FYZ	B D	B	125	W	5.5	97	128
1FYZ	B D	B	142	L	2.5	131	161
1FYZ	B D	B	145	I	1.2	131	161
1FYZ	B D	B	146	R	1.8	131	161
1FYZ	B D	B	149	H	3.5	131	161
1FYZ	B D	B	153	Y	1.5	131	161
1FYZ	B D	B	156	Y	1.4	131	161
1FYZ	B D	B	172	R	3.3	171	178
1FYZ	B D	B	181	W	1.0	179	188
1FYZ	B D	B	185	K	1.2	179	188
1FYZ	B D	B	186	R	1.6	179	188
1FYZ	B D	B	190	D	1.9	189	194
1FYZ	B D	D	16	M	1.4	14	24
1FYZ	B D	D	20	I	2.4	14	24
1FYZ	B D	D	52	L	2.8	48	54
1FYZ	B D	D	53	T	1.0	48	54
1FYZ	B D	D	110	V	1.2	106	130

1FYZ	B D	D	111	K	1.0	106	130
1FYZ	B D	D	113	K	1.5	106	130
1FYZ	B D	D	117	W	4.1	106	130
1FYZ	B D	D	153	L	1.2	138	170
1FYZ	B D	D	154	F	1.1	138	170
1FYZ	B D	D	157	Y	2.4	138	170
1FYZ	B D	D	158	G	83.2	138	170
1FYZ	B D	D	176	R	1.0	173	203
1FYZ	B D	D	184	F	4.2	173	203
1FYZ	B D	D	192	M	1.7	173	203
1FYZ	B D	D	194	Q	1.0	173	203
1FYZ	B D	D	195	L	3.0	173	203
1FYZ	B D	D	199	F	1.2	173	203
1FYZ	B D	D	202	K	1.4	173	203
1FYZ	B D	D	215	K	1.1	212	220
1FYZ	B D	D	235	W	1.5	225	236
1FYZ	B F	B	266	Y	2.7	261	293
1FYZ	B F	B	269	T	1.4	261	293
1FYZ	B F	B	272	N	1.7	261	293
1FYZ	B F	B	452	W	1.9	451	460
1FYZ	B F	B	455	R	1.3	451	460
1FYZ	B F	B	456	M	1.2	451	460
1FYZ	B F	B	457	W	1.8	451	460
1FYZ	B F	B	458	L	4.3	451	460
1FYZ	B F	B	459	A	1.8	451	460
1FYZ	B F	F	136	G	3.6	125	144
1FYZ	B F	F	152	L	1.5	152	160
1FYZ	B F	F	155	L	1.6	152	160
1FYZ	B F	F	156	R	2.3	152	160
1FYZ	C E	C	243	E	2.1	241	250
1FYZ	C E	C	312	Y	2.1	310	324
1FYZ	C E	C	318	R	2.1	310	324
1FYZ	C E	C	319	N	1.3	310	324
1FYZ	C E	C	320	W	1.9	310	324
1FYZ	C E	C	322	G	1.4	310	324
1FYZ	C E	E	12	R	1.9	10	21
1FYZ	C E	E	61	E	2.3	53	72
1FYZ	C E	E	74	E	1.9	74	79
1FYZ	C E	E	77	F	3.2	74	79
1FYZ	C E	E	78	R	1.2	74	79
1FYZ	C E	E	111	H	1.4	104	118
1FYZ	C E	E	115	R	4.1	104	118
1FYZ	C E	E	125	V	1.5	125	144
1FYZ	C E	E	126	N	4.0	125	144
1FYZ	C E	E	139	L	1.6	125	144
1FYZ	C E	E	143	R	1.2	125	144
1FYZ	D F	D	312	Y	2.3	310	337
1FYZ	D F	F	12	R	1.2	10	21
1FYZ	D F	F	61	E	1.5	52	72
1FYZ	D F	F	77	F	1.3	74	79
1FYZ	D F	F	125	V	1.4	125	144
1FYZ	D F	F	126	N	2.1	125	144
1G0U	A B	A	121	Q	1.8	109	124
1G0U	A B	B	26	Y	3.0	22	33
1G0U	A B	B	84	D	1.3	82	104
1G0U	A B	B	86	E	1.0	82	104
1G0U	A B	B	87	I	1.1	82	104
1G0U	A G	A	23	Q	1.0	22	33
1G0U	A G	A	26	Y	3.0	22	33
1G0U	A G	A	83	P	1.6	82	99

1G0U	A G	A	84	D	1.3	82	99
1G0U	A G	A	86	R	1.3	82	99
1G0U	A G	A	90	D	3.5	82	99
1G0U	A G	G	114	K	1.3	109	126
1G0U	A G	G	121	Q	2.8	109	126
1G0U	A G	G	179	F	1.1	169	179
1G0U	A H	H	65	L	1.1	49	70
1G0U	A H	H	68	L	1.0	49	70
1G0U	B C	B	118	D	1.7	109	126
1G0U	B C	B	121	Q	1.7	109	126
1G0U	B C	B	125	Q	1.2	109	126
1G0U	B C	C	23	Q	1.1	22	34
1G0U	B C	C	26	Y	3.5	22	34
1G0U	B C	C	84	D	1.4	82	103
1G0U	B C	C	86	R	2.8	82	103
1G0U	B I	B	97	Q	1.3	82	104
1G0U	B I	I	61	Y	1.6	49	71
1G0U	B I	I	64	N	1.2	49	71
1G0U	B I	I	65	L	1.5	49	71
1G0U	B I	I	68	L	1.1	49	71
1G0U	B J	B	103	Y	3.2	82	104
1G0U	B J	J	66	Y	1.4	49	71
1G0U	C D	D	26	Y	3.4	22	33
1G0U	C J	C	93	R	1.1	82	103
1G0U	C J	J	65	L	1.7	49	71
1G0U	D E	E	26	Y	2.5	22	33
1G0U	D K	D	93	R	1.0	82	103
1G0U	D K	D	101	L	1.2	82	103
1G0U	D K	K	65	L	1.1	49	70
1G0U	D K	K	68	L	1.3	49	70
1G0U	D L	D	102	Y	1.3	82	103
1G0U	D L	L	66	Y	2.3	49	69
1G0U	D L	L	81	R	1.6	76	90
1G0U	D L	L	85	H	1.2	76	90
1G0U	E F	E	114	H	1.2	109	123
1G0U	E F	E	121	Q	3.8	109	123
1G0U	E F	F	26	Y	3.5	22	33
1G0U	E F	F	84	D	1.3	82	103
1G0U	E F	F	86	R	1.0	82	103
1G0U	E L	E	93	R	1.8	82	103
1G0U	E L	L	65	W	1.6	49	69
1G0U	E L	L	68	F	1.8	49	69
1G0U	F G	F	121	Q	1.0	109	123
1G0U	F G	G	23	Q	1.8	22	34
1G0U	F G	G	26	Y	2.0	22	34
1G0U	F G	G	84	D	1.1	82	104
1G0U	F N	F	99	F	1.2	82	103
1G0U	F N	N	66	Y	1.6	49	70
1G0U	G H	G	110	D	2.2	109	126
1G0U	G H	G	111	V	1.6	109	126
1G0U	G H	G	114	K	1.3	109	126
1G0U	G N	G	93	K	1.6	82	104
1G0U	G N	G	101	Y	2.1	82	104
1G0U	G N	N	61	Y	1.9	49	70
1G0U	H I	H	51	D	4.0	49	70
1G0U	H I	I	88	Y	1.8	76	90
1G0U	H I	I	135	F	1.7	131	142
1G0U	H I	I	139	E	2.0	131	142
1G0U	H I	I	152	F	2.7	148	165
1G0U	H I	I	153	E	3.7	148	165

1G0U	H N	H	88	F	1.9	76	90
1G0U	H N	N	53	Q	1.6	49	70
1G0U	H Z	H	164	W	1.4	148	165
1G0U	H Z	Z	133	L	1.2	131	143
1G0U	H Z	Z	157	D	1.5	148	165
1G0U	H Z	Z	164	E	1.6	148	165
1G0U	I J	I	57	E	1.7	49	71
1G0U	I J	J	84	R	2.3	76	90
1G0U	I J	J	132	F	1.7	129	142
1G0U	I Y	Y	164	H	1.6	148	166
1G0U	I Y	Y	196	F	1.0	192	204
1G0U	I Y	Y	197	W	1.8	192	204
1G0U	I Z	I	136	G	107.8	131	142
1G0U	I Z	I	137	M	2.0	131	142
1G0U	I Z	I	139	E	1.4	131	142
1G0U	I Z	I	157	Q	1.2	148	165
1G0U	I Z	I	164	D	1.1	148	165
1G0U	I Z	Z	136	P	1.4	131	143
1G0U	J K	J	50	G	49.7	49	71
1G0U	J K	J	57	E	1.1	49	71
1G0U	J K	K	88	Y	1.6	76	90
1G0U	J Y	J	139	D	1.1	129	142
1G0U	J Y	J	140	H	1.1	129	142
1G0U	J Y	J	165	R	2.4	148	166
1G0U	J Y	Y	136	G	3.3	131	141
1G0U	K L	K	51	D	3.4	49	70
1G0U	K L	K	53	Q	2.7	49	70
1G0U	K L	K	54	F	3.3	49	70
1G0U	K L	K	55	W	1.7	49	70
1G0U	K L	L	88	Y	5.9	76	90
1G0U	L M	L	51	D	1.5	49	69
1G0U	L M	M	88	Y	2.5	76	92
1G0U	M N	M	53	Q	1.9	49	68
1G0U	O P	O	121	Q	1.7	109	126
1G0U	O P	O	125	Q	1.3	109	126
1G0U	O P	P	23	Q	1.3	22	33
1G0U	O P	P	26	Y	2.0	22	33
1G0U	O U	O	26	Y	3.2	22	34
1G0U	O V	O	97	H	1.2	82	99
1G0U	O V	V	65	L	1.3	49	70
1G0U	P Q	P	118	D	1.8	109	126
1G0U	P Q	P	121	Q	1.4	109	126
1G0U	P Q	P	125	Q	1.1	109	126
1G0U	P Q	Q	86	R	3.1	82	103
1G0U	P W	P	93	R	1.7	82	104
1G0U	P W	P	97	Q	1.6	82	104
1G0U	P W	W	61	Y	1.6	49	70
1G0U	P W	W	64	N	1.4	49	70
1G0U	P W	W	65	L	1.4	49	70
1G0U	P W	W	68	L	1.7	49	70
1G0U	P X	P	103	Y	1.2	82	104
1G0U	Q R	Q	121	Q	1.2	109	123
1G0U	Q R	R	26	Y	2.5	22	33
1G0U	Q R	R	84	D	1.0	82	103
1G0U	Q X	Q	101	L	1.0	82	103
1G0U	Q X	X	58	Y	1.1	49	70
1G0U	Q X	X	65	L	1.5	49	70
1G0U	R S	S	26	Y	3.2	22	33
1G0U	R Y	R	101	L	1.3	82	103
1G0U	R Z	R	102	Y	1.4	82	103

1G0U	R Z	Z	85	H	1.2	76	90
1G0U	S T	S	121	Q	3.2	109	123
1G0U	S T	T	23	Q	1.4	22	33
1G0U	S T	T	26	Y	3.3	22	33
1G0U	S Z	S	93	R	1.9	82	103
1G0U	S Z	Z	64	K	1.2	49	69
1G0U	S Z	Z	65	W	2.1	49	69
1G0U	S Z	Z	68	F	2.2	49	69
1G0U	T U	T	121	Q	1.2	109	123
1G0U	T U	T	173	K	1.0	169	180
1G0U	T U	U	23	Q	2.6	22	34
1G0U	T U	U	26	Y	3.0	22	34
1G0U	T U	U	83	P	2.7	82	103
1G0U	V L	V	164	W	1.2	148	165
1G0U	V L	L	133	L	1.2	131	143
1G0U	V L	L	150	E	1.3	148	165
1G0U	V L	L	154	L	1.0	148	165
1G0U	V L	L	157	D	2.0	148	165
1G0U	V L	L	161	S	1.8	148	165
1G0U	V M	V	132	L	1.5	131	139
1G0U	V M	M	133	M	1.4	129	141
1G0U	V M	M	137	L	1.5	129	141
1G0U	V M	M	161	V	1.3	148	166
1G0U	V W	V	51	D	3.6	49	70
1G0U	V W	W	88	Y	2.0	76	90
1G0U	V W	W	153	E	4.0	148	165
1G0U	W K	K	164	H	1.4	148	166
1G0U	W K	K	197	W	1.7	192	204
1G0U	W L	W	136	G	76.1	131	142
1G0U	W L	W	139	E	1.8	131	142
1G0U	W L	L	136	P	2.1	131	143
1G0U	W L	L	140	N	1.8	131	143
1G0U	W L	L	141	Q	1.4	131	143
1G0U	W X	W	57	E	1.5	49	70
1G0U	X K	K	136	G	3.6	131	141
1G0U	X Y	X	50	G	72.5	49	70
1G0U	X Y	X	54	Q	1.4	49	70
1G0U	X Y	X	57	E	1.2	49	70
1G0U	X Y	Y	88	Y	1.8	76	90
1G0U	Y Z	Y	51	D	3.5	49	70
1G0U	Y Z	Y	53	Q	2.7	49	70
1G0U	Y Z	Y	54	F	3.1	49	70
1G0U	Y Z	Y	55	W	1.5	49	70
1G0U	Y Z	Z	84	Q	1.0	76	90
1G0U	Y Z	Z	88	Y	8.1	76	90
1G0Y	R I	I	9	S	1.3	6	12
1G1E	A B	A	9	I	1.7	9	21
1G1E	A B	A	13	L	1.1	9	21
1G1E	A B	B	332	L	1.2	322	346
1G1X	F B	B	4	K	1.5	4	14
1G1X	F B	B	5	E	1.3	4	14
1G1X	F H	H	65	I	1.0	65	76
1G20	A B	A	23	K	1.3	22	30
1G20	A B	A	86	V	1.5	86	92
1G20	A B	A	87	G	11.6	86	92
1G20	A B	A	90	Q	1.6	86	92
1G20	A B	A	91	Y	2.6	86	92
1G20	A B	A	123	I	2.1	120	126
1G20	A B	A	134	L	1.3	128	142
1G20	A B	A	137	E	2.5	128	142

1G20	A B	A	141	L	1.5	128	142
1G20	A B	A	158	L	1.2	154	160
1G20	A B	A	240	I	1.7	240	245
1G20	A B	A	334	E	1.8	332	347
1G20	A B	A	341	K	1.4	332	347
1G20	A B	A	407	Y	1.0	406	417
1G20	A B	B	20	Y	2.8	18	33
1G20	A B	B	23	M	1.1	18	33
1G20	A B	B	31	F	3.2	18	33
1G20	A B	B	52	Y	2.7	50	57
1G20	A B	B	93	Q	1.2	93	108
1G20	A B	B	94	G	158.1	93	108
1G20	A B	B	98	Y	2.6	93	108
1G20	A B	B	102	Y	1.5	93	108
1G20	A B	B	133	D	1.3	128	142
1G20	A B	B	157	V	1.8	153	158
1G20	A B	B	428	W	2.5	427	434
1G20	A D	A	466	T	1.3	453	468
1G20	A D	D	330	M	1.3	322	337
1G20	A D	D	359	H	2.2	359	363
1G20	A D	D	360	T	1.2	359	363
1G20	A E	A	157	G	3.1	154	160
1G20	A E	E	100	R	2.8	98	112
1G20	A E	E	103	I	1.2	98	112
1G20	A F	A	124	V	1.7	120	126
1G20	A F	A	125	F	2.8	120	126
1G20	A F	F	101	G	2.7	98	112
1G20	B E	B	124	V	2.4	120	126
1G20	B E	B	125	F	2.0	120	126
1G20	B E	E	101	G	3.9	98	112
1G20	C B	C	466	T	1.5	453	468
1G20	C B	B	330	M	1.3	322	337
1G20	C B	B	352	V	1.0	342	358
1G20	C B	B	359	H	2.2	359	363
1G20	C B	B	360	T	1.1	359	363
1G20	C D	C	23	K	1.4	22	30
1G20	C D	C	86	V	1.6	86	92
1G20	C D	C	87	G	8.9	86	92
1G20	C D	C	91	Y	2.7	86	92
1G20	C D	C	123	I	1.6	120	126
1G20	C D	C	133	K	1.0	128	142
1G20	C D	C	137	E	2.4	128	142
1G20	C D	C	141	L	2.5	128	142
1G20	C D	C	158	L	1.2	154	160
1G20	C D	C	236	W	2.8	234	239
1G20	C D	C	240	I	1.7	240	245
1G20	C D	C	261	E	1.3	259	264
1G20	C D	C	334	E	1.4	332	347
1G20	C D	C	341	K	1.2	332	347
1G20	C D	C	407	Y	1.5	406	417
1G20	C D	C	429	F	3.8	427	434
1G20	C D	C	430	I	1.2	427	434
1G20	C D	C	454	D	2.0	453	468
1G20	C D	D	20	Y	3.1	18	31
1G20	C D	D	23	M	1.6	18	31
1G20	C D	D	24	L	1.6	18	31
1G20	C D	D	43	V	1.2	37	47
1G20	C D	D	52	Y	2.0	50	57
1G20	C D	D	93	Q	2.0	93	108
1G20	C D	D	94	G	131.1	93	108

1G20	C D	D	98	Y	2.7	93	108
1G20	C D	D	133	D	1.6	128	143
1G20	C D	D	142	Y	2.5	128	143
1G20	C D	D	157	V	1.3	153	158
1G20	C D	D	428	W	1.9	427	437
1G20	C D	D	450	F	1.0	449	459
1G20	C G	C	157	G	1.9	154	160
1G20	C G	C	158	L	1.2	154	160
1G20	C G	G	100	R	1.8	98	113
1G20	C H	C	120	E	2.3	120	126
1G20	C H	C	123	I	2.8	120	126
1G20	C H	C	124	V	2.3	120	126
1G20	C H	C	125	F	2.4	120	126
1G20	C H	H	58	M	1.4	57	64
1G20	C H	H	100	R	2.1	98	112
1G20	C H	H	101	G	1.4	98	112
1G20	D G	D	120	E	7.5	120	125
1G20	D G	D	121	D	6.8	120	125
1G20	D G	D	124	V	9.1	120	125
1G20	D G	G	59	E	7.6	57	64
1G20	D G	G	62	A	7.3	57	64
1G20	D G	G	101	G	11.1	98	113
1G20	D H	D	156	E	1.8	153	158
1G20	D H	D	300	K	1.1	299	310
1G20	D H	H	100	R	1.8	98	112
1G2C	A B	A	184	G	4.3	163	207
1G2C	A B	A	195	L	1.1	163	207
1G2C	A B	A	198	Y	2.5	163	207
1G2C	A B	B	488	F	1.5	485	514
1G2C	A B	B	495	V	1.6	485	514
1G2C	A B	B	498	K	1.1	485	514
1G2C	A B	B	505	F	1.2	485	514
1G2C	A D	A	196	K	2.4	163	207
1G2C	A D	D	488	F	3.4	486	515
1G2C	A D	D	492	I	1.5	486	515
1G2C	A D	D	499	I	1.3	486	515
1G2C	A D	D	513	L	1.4	486	515
1G2C	C D	C	184	G	5.8	161	207
1G2C	C D	C	198	Y	1.9	161	207
1G2C	C D	D	495	V	1.5	486	515
1G2C	C D	D	505	F	2.9	486	515
1G2C	C F	C	196	K	3.5	161	207
1G2C	C F	C	204	L	1.3	161	207
1G2C	C F	F	488	F	4.0	485	515
1G2C	C F	F	489	D	1.2	485	515
1G2C	C F	F	499	I	1.7	485	515
1G2C	C F	F	506	I	1.1	485	515
1G2C	C F	F	513	L	1.3	485	515
1G2C	E B	E	168	K	1.1	161	207
1G2C	E B	E	172	L	1.0	161	207
1G2C	E B	E	178	V	1.6	161	207
1G2C	E B	E	196	K	3.2	161	207
1G2C	E B	E	204	L	1.8	161	207
1G2C	E B	B	488	F	4.3	485	514
1G2C	E B	B	489	D	1.5	485	514
1G2C	E B	B	492	I	1.6	485	514
1G2C	E B	B	499	I	1.7	485	514
1G2C	E B	B	503	L	1.1	485	514
1G2C	E B	B	506	I	1.6	485	514
1G2C	E B	B	513	L	1.6	485	514

1G2C	E F	E	195	L	1.0	161	207
1G2C	E F	E	198	Y	2.4	161	207
1G2C	E F	F	488	F	2.2	485	515
1G2C	E F	F	495	V	1.3	485	515
1G2C	E F	F	505	F	2.1	485	515
1G2C	E F	F	508	K	1.0	485	515
1G2C	G H	G	184	G	9.8	161	207
1G2C	G H	G	195	L	1.0	161	207
1G2C	G H	G	198	Y	2.4	161	207
1G2C	G H	H	488	F	1.0	485	514
1G2C	G H	H	495	V	1.7	485	514
1G2C	G H	H	505	F	2.4	485	514
1G2C	G J	G	175	N	1.0	161	207
1G2C	G J	G	196	K	4.7	161	207
1G2C	G J	G	204	L	1.5	161	207
1G2C	G J	J	488	F	3.9	485	515
1G2C	G J	J	489	D	1.2	485	515
1G2C	G J	J	492	I	1.3	485	515
1G2C	G J	J	513	L	1.6	485	515
1G2C	I J	I	184	G	5.4	163	207
1G2C	I J	I	195	L	1.0	163	207
1G2C	I J	I	198	Y	1.1	163	207
1G2C	I J	J	488	F	1.6	485	515
1G2C	I J	J	495	V	1.0	485	515
1G2C	I J	J	498	K	1.0	485	515
1G2C	I J	J	505	F	3.1	485	515
1G2C	I L	I	196	K	3.2	163	207
1G2C	I L	I	204	L	1.3	163	207
1G2C	I L	L	488	F	3.7	485	514
1G2C	I L	L	489	D	1.0	485	514
1G2C	I L	L	492	I	1.4	485	514
1G2C	I L	L	499	I	1.4	485	514
1G2C	I L	L	506	I	1.2	485	514
1G2C	I L	L	513	L	1.6	485	514
1G2C	M N	M	184	G	2.9	161	206
1G2C	M N	M	191	K	1.4	161	206
1G2C	M N	M	194	D	1.5	161	206
1G2C	M N	M	195	L	1.2	161	206
1G2C	M N	M	198	Y	1.3	161	206
1G2C	M N	N	488	F	2.0	485	514
1G2C	M N	N	495	V	1.1	485	514
1G2C	M N	N	505	F	2.4	485	514
1G2C	M P	M	175	N	1.1	161	206
1G2C	M P	M	196	K	3.0	161	206
1G2C	M P	M	204	L	1.3	161	206
1G2C	M P	P	488	F	3.5	485	514
1G2C	M P	P	492	I	1.6	485	514
1G2C	M P	P	499	I	1.2	485	514
1G2C	O P	O	184	G	1.7	159	207
1G2C	O P	P	498	K	1.0	485	514
1G2C	O P	P	505	F	2.4	485	514
1G2C	O R	O	172	L	1.0	159	207
1G2C	O R	O	196	K	3.6	159	207
1G2C	O R	O	204	L	1.1	159	207
1G2C	O R	R	488	F	4.4	485	516
1G2C	O R	R	489	D	1.3	485	516
1G2C	O R	R	492	I	1.5	485	516
1G2C	O R	R	499	I	1.5	485	516
1G2C	O R	R	506	I	1.3	485	516
1G2C	O R	R	513	L	1.7	485	516

1G2C	Q R	Q	184	G	1.8	161	207
1G2C	Q R	Q	191	K	1.7	161	207
1G2C	Q R	Q	194	D	1.4	161	207
1G2C	Q R	Q	198	Y	2.8	161	207
1G2C	Q R	R	488	F	1.8	485	516
1G2C	Q R	R	495	V	1.1	485	516
1G2C	Q R	R	498	K	1.4	485	516
1G2C	Q R	R	505	F	2.6	485	516
1G2C	Q R	R	512	L	1.0	485	516
1G2C	S T	S	184	G	6.8	160	207
1G2C	S T	S	195	L	2.9	160	207
1G2C	S T	S	198	Y	1.7	160	207
1G2C	S T	S	202	Q	2.3	160	207
1G2C	S T	S	203	L	2.5	160	207
1G2C	S T	T	488	F	1.8	485	516
1G2C	S T	T	495	V	1.5	485	516
1G2C	S T	T	505	F	1.9	485	516
1G2C	S V	S	196	K	3.0	160	207
1G2C	S V	S	204	L	1.2	160	207
1G2C	S V	V	488	F	3.6	485	514
1G2C	S V	V	489	D	1.2	485	514
1G2C	S V	V	492	I	1.3	485	514
1G2C	S V	V	506	I	1.2	485	514
1G2C	S V	V	513	L	1.8	485	514
1G2C	U V	U	163	E	2.0	161	208
1G2C	U V	U	194	D	2.3	161	208
1G2C	U V	U	195	L	1.3	161	208
1G2C	U V	U	198	Y	2.3	161	208
1G2C	U V	V	495	V	1.1	485	514
1G2C	U V	V	501	Q	1.0	485	514
1G2C	U V	V	505	F	3.9	485	514
1G2C	U V	V	513	L	1.1	485	514
1G2C	U X	U	175	N	1.1	161	208
1G2C	U X	U	196	K	3.4	161	208
1G2C	U X	X	488	F	4.3	485	515
1G2C	U X	X	489	D	1.2	485	515
1G2C	U X	X	492	I	1.3	485	515
1G2C	U X	X	499	I	1.3	485	515
1G2C	U X	X	506	I	1.5	485	515
1G2C	U X	X	513	L	1.6	485	515
1G2C	W T	W	168	K	1.2	161	207
1G2C	W T	W	178	V	1.6	161	207
1G2C	W T	W	196	K	2.9	161	207
1G2C	W T	W	204	L	1.5	161	207
1G2C	W T	T	488	F	3.9	485	516
1G2C	W T	T	489	D	1.0	485	516
1G2C	W T	T	492	I	1.2	485	516
1G2C	W T	T	499	I	1.5	485	516
1G2C	W T	T	513	L	1.4	485	516
1G2C	W X	W	166	K	1.0	161	207
1G2C	W X	W	184	G	16.2	161	207
1G2C	W X	W	194	D	1.7	161	207
1G2C	W X	W	195	L	2.5	161	207
1G2C	W X	X	488	F	1.0	485	515
1G2C	W X	X	495	V	1.2	485	515
1G2C	W X	X	498	K	1.3	485	515
1G2C	W X	X	505	F	1.1	485	515
1G3I	A H	H	54	F	3.1	50	67
1G3I	B H	H	76	V	1.0	71	83
1G3I	B I	I	54	F	1.7	50	67

1G3I	C I	I	73	K	1.1	71	81
1G3I	C I	I	76	V	1.1	71	81
1G3I	C J	J	54	F	1.4	50	67
1G3I	D J	J	76	V	1.4	71	81
1G3I	D J	J	80	K	1.0	71	81
1G3I	D K	K	54	F	1.8	50	67
1G3I	E K	K	72	L	2.7	71	83
1G3I	E K	K	76	V	1.2	71	83
1G3I	E L	L	54	F	2.4	50	67
1G3I	F G	G	54	F	2.9	50	67
1G3I	F G	G	57	F	1.6	50	67
1G3I	S M	M	73	K	1.0	71	83
1G3I	S R	R	54	F	3.5	51	63
1G3I	T M	M	54	F	4.0	51	63
1G3I	T N	N	73	K	1.0	71	83
1G3I	U N	N	54	F	2.1	51	66
1G3I	U O	O	73	K	1.0	71	83
1G3I	V P	P	72	L	1.0	71	83
1G3I	W Q	Q	73	K	1.1	71	83
1G3I	X Q	Q	54	F	1.4	51	63
1G3I	X R	R	73	K	1.1	71	83
1G3N	A B	B	11	S	1.3	7	15
1G3N	A B	B	50	P	1.4	50	59
1G3N	A B	B	76	D	2.6	73	80
1G3N	A C	A	59	I	1.5	56	72
1G3N	A C	A	67	H	1.6	56	72
1G3N	A C	A	71	F	2.0	56	72
1G3N	A C	C	102	L	1.1	93	109
1G3N	A C	C	107	L	1.3	93	109
1G3N	A C	C	128	R	1.1	128	142
1G3N	E F	E	107	T	2.0	105	110
1G3N	E F	F	76	D	1.4	73	81
1G3N	E G	E	67	H	1.2	56	72
1G3N	E G	E	71	F	1.9	56	72
1G3N	E G	G	28	I	1.3	17	29
1G3N	E G	G	103	V	1.0	93	109
1G3N	E G	G	107	L	1.5	93	109
1G3N	E G	G	115	T	1.0	115	121
1G3N	E G	G	128	R	1.8	128	142
1G3N	E G	G	132	I	2.0	128	142
1G3N	E G	G	136	K	1.6	128	142
1G4B	F M	M	62	R	1.9	51	66
1G4B	L O	O	58	E	1.3	51	66
1G4B	L O	O	61	E	1.3	51	66
1G4U	S R	S	178	G	1.1	168	188
1G4U	S R	S	209	R	1.1	207	220
1G4U	S R	S	214	N	1.1	207	220
1G4U	S R	S	255	E	5.3	253	260
1G4Y	B R	B	473	L	1.1	446	490
1G4Y	B R	B	476	Q	1.4	446	490
1G4Y	B R	B	483	L	1.5	446	490
1G4Y	B R	R	36	M	1.0	29	39
1G4Y	B R	R	47	E	2.4	45	55
1G4Y	B R	R	51	M	1.4	45	55
1G5J	A B	A	129	Q	4.5	122	135
1G5J	A B	A	130	V	1.2	122	135
1G5J	A B	A	133	E	1.1	122	135
1G5J	A B	B	309	G	8.1	306	320
1G5J	A B	B	313	R	1.0	306	320
1G5J	A B	B	319	F	3.6	306	320

1G72	A B	B	36	E	1.4	34	38
1G72	A B	B	37	L	1.3	34	38
1G72	A B	B	40	Q	2.0	39	57
1G72	A B	B	41	E	1.1	39	57
1G72	A B	B	47	M	1.3	39	57
1G72	A B	B	48	D	2.3	39	57
1G72	A B	B	50	R	2.1	39	57
1G72	A B	B	51	N	2.3	39	57
1G72	A B	B	55	I	1.1	39	57
1G72	C D	D	36	E	1.3	34	38
1G72	C D	D	37	L	1.4	34	38
1G72	C D	D	40	Q	1.8	39	57
1G72	C D	D	41	E	1.2	39	57
1G72	C D	D	47	M	1.2	39	57
1G72	C D	D	48	D	2.2	39	57
1G72	C D	D	50	R	1.2	39	57
1G72	C D	D	51	N	2.4	39	57
1G72	C D	D	54	R	1.2	39	57
1G72	C D	D	55	I	1.1	39	57
1G73	A C	A	92	H	5.3	72	119
1G73	A C	A	95	Y	2.8	72	119
1G73	A C	A	96	L	1.3	72	119
1G73	A C	A	99	E	3.8	72	119
1G73	A C	C	270	F	1.6	265	272
1G73	A D	D	323	W	2.7	316	324
1G73	B C	C	323	W	2.9	316	324
1G73	B D	B	96	L	1.0	72	119
1G73	B D	B	99	E	2.2	72	119
1G73	B D	B	103	M	1.5	72	119
1G73	B D	D	270	F	1.6	265	272
1G8K	A B	A	103	G	7.9	100	104
1G8K	A B	A	236	Y	1.7	235	239
1G8K	A B	A	244	L	1.0	240	253
1G8K	A B	A	286	I	1.5	282	292
1G8K	C D	C	103	G	8.0	100	104
1G8K	C D	C	236	Y	1.7	235	239
1G8K	C D	C	286	I	1.6	282	292
1G8K	E F	E	103	G	7.1	100	104
1G8K	E F	E	236	Y	1.7	235	239
1G8K	E F	E	286	I	1.4	282	292
1G8K	G H	G	103	G	7.2	100	104
1G8K	G H	G	236	Y	1.4	235	239
1G8K	G H	G	286	I	1.5	282	292
1G8K	G H	G	722	R	1.9	717	723
1G9M	L H	L	126	Q	1.5	124	130
1GCV	A B	A	118	P	1.1	118	136
1GCV	A B	A	121	H	2.3	118	136
1GCV	A B	B	30	R	3.1	20	35
1GCV	A B	B	34	V	1.3	20	35
1GCV	A B	B	102	V	1.3	90	108
1GCV	A B	B	106	Y	2.3	90	108
1GCV	A B	B	118	G	11.7	114	134
1GCV	A D	A	38	G	79.7	37	43
1GCV	A D	A	42	Y	1.0	37	43
1GCV	A D	A	95	P	1.3	95	113
1GCV	A D	A	97	N	1.4	95	113
1GCV	A D	D	37	W	3.5	36	42
1GCV	A D	D	92	S	1.0	92	108
1GCV	C B	C	38	G	54.6	37	43
1GCV	C B	C	42	Y	1.5	37	43

1GCV	C B	C	95	P	1.4	95	113
1GCV	C B	C	97	N	1.5	95	113
1GCV	C D	C	31	R	2.8	21	36
1GCV	C D	C	34	V	2.3	21	36
1GCV	C D	C	121	H	1.6	118	136
1GCV	C D	D	30	R	3.2	20	35
1GCV	C D	D	34	V	1.3	20	35
1GCV	C D	D	102	V	1.3	92	108
1GCV	C D	D	106	Y	1.9	92	108
1GCV	C D	D	114	P	2.1	114	132
1GCV	C D	D	118	G	11.6	114	132
1GG2	A B	A	19	I	1.9	10	32
1GG2	A B	A	23	L	1.1	10	32
1GG2	B G	B	3	E	1.2	3	26
1GG2	B G	B	4	L	1.7	3	26
1GG2	B G	B	7	L	2.3	3	26
1GG2	B G	B	14	L	1.6	3	26
1GG2	B G	B	22	R	1.1	3	26
1GG2	B G	B	25	C	1.7	3	26
1GG2	B G	B	33	I	1.4	30	36
1GG2	B G	G	9	I	1.9	9	24
1GG2	B G	G	13	R	1.2	9	24
1GG2	B G	G	16	V	1.0	9	24
1GG2	B G	G	19	L	2.5	9	24
1GG2	B G	G	37	L	1.0	30	44
1GG2	B G	G	40	Y	2.1	30	44
1GGI	M J	M	124	Q	1.4	122	127
1GGP	A B	A	169	R	1.0	169	173
1GGP	A B	A	170	Y	3.3	169	173
1GH0	A B	A	5	L	1.2	4	15
1GH0	A B	A	6	T	1.4	4	15
1GH0	A B	A	9	V	2.1	4	15
1GH0	A B	A	24	I	1.3	21	47
1GH0	A B	A	31	F	2.5	21	47
1GH0	A B	A	38	L	1.7	21	47
1GH0	A B	A	42	K	1.2	21	47
1GH0	A B	A	93	R	2.7	78	102
1GH0	A B	A	97	Y	3.0	78	102
1GH0	A B	A	100	I	1.2	78	102
1GH0	A B	B	6	T	1.4	4	15
1GH0	A B	B	9	V	1.9	4	15
1GH0	A B	B	13	D	2.4	4	15
1GH0	A B	B	24	I	1.7	21	33
1GH0	A B	B	31	V	1.3	21	33
1GH0	A B	B	38	L	1.5	34	47
1GH0	A B	B	91	R	1.2	76	100
1GH0	A B	B	98	F	4.1	76	100
1GH0	C D	C	5	L	1.3	4	15
1GH0	C D	C	9	V	1.6	4	15
1GH0	C D	C	24	I	1.0	21	47
1GH0	C D	C	31	F	1.9	21	47
1GH0	C D	C	38	L	1.4	21	47
1GH0	C D	C	42	K	1.3	21	47
1GH0	C D	C	93	R	2.7	78	102
1GH0	C D	C	97	Y	3.0	78	102
1GH0	C D	C	100	I	1.6	78	102
1GH0	C D	C	110	Y	1.0	104	113
1GH0	C D	D	5	F	1.7	4	16
1GH0	C D	D	9	V	2.3	4	16
1GH0	C D	D	13	D	1.4	4	16

1GH0	C D	D	24	I	1.6	21	33
1GH0	C D	D	31	V	1.3	21	33
1GH0	C D	D	38	L	1.4	34	47
1GH0	C D	D	91	R	1.8	76	100
1GH0	C D	D	95	Y	3.2	76	100
1GH0	C D	D	98	F	3.6	76	100
1GH0	C F	C	117	E	1.3	115	122
1GH0	C F	F	83	L	1.2	76	100
1GH0	E B	E	109	E	1.1	105	113
1GH0	E B	B	77	R	1.1	76	100
1GH0	E B	B	83	L	1.3	76	100
1GH0	E F	E	5	L	1.5	4	15
1GH0	E F	E	6	T	1.3	4	15
1GH0	E F	E	9	V	2.0	4	15
1GH0	E F	E	24	I	1.1	21	47
1GH0	E F	E	30	R	1.3	21	47
1GH0	E F	E	31	F	2.0	21	47
1GH0	E F	E	38	L	2.0	21	47
1GH0	E F	E	42	K	1.1	21	47
1GH0	E F	E	93	R	1.8	78	102
1GH0	E F	E	97	Y	3.5	78	102
1GH0	E F	E	100	I	2.1	78	102
1GH0	E F	F	5	F	4.4	4	15
1GH0	E F	F	6	T	1.5	4	15
1GH0	E F	F	9	V	1.4	4	15
1GH0	E F	F	24	I	2.3	21	33
1GH0	E F	F	31	V	1.3	21	33
1GH0	E F	F	38	L	1.8	34	47
1GH0	E F	F	91	R	1.7	76	100
1GH0	E F	F	95	Y	3.0	76	100
1GH0	E F	F	98	F	4.3	76	100
1GH0	G F	G	159	N	1.8	145	162
1GH0	G H	G	5	L	2.1	4	15
1GH0	G H	G	6	T	1.3	4	15
1GH0	G H	G	9	V	1.1	4	15
1GH0	G H	G	13	D	1.0	4	15
1GH0	G H	G	24	I	1.0	21	47
1GH0	G H	G	31	F	1.3	21	47
1GH0	G H	G	38	L	1.6	21	47
1GH0	G H	G	42	K	1.2	21	47
1GH0	G H	G	93	R	1.7	78	102
1GH0	G H	G	97	Y	3.2	78	102
1GH0	G H	G	100	I	1.6	78	102
1GH0	G H	H	5	F	2.2	4	15
1GH0	G H	H	9	V	1.5	4	15
1GH0	G H	H	24	I	1.7	21	33
1GH0	G H	H	31	V	1.3	21	33
1GH0	G H	H	38	L	1.1	34	47
1GH0	G H	H	91	R	2.0	76	100
1GH0	G H	H	95	Y	4.6	76	100
1GH0	G H	H	98	F	4.3	76	100
1GH0	G J	J	83	L	1.2	76	100
1GH0	I J	I	5	L	1.0	4	15
1GH0	I J	I	9	V	2.3	4	15
1GH0	I J	I	24	I	1.1	21	47
1GH0	I J	I	31	F	1.5	21	47
1GH0	I J	I	38	L	1.4	21	47
1GH0	I J	I	42	K	1.6	21	47
1GH0	I J	I	93	R	2.4	78	102
1GH0	I J	I	97	Y	2.6	78	102

1GH0	I J	I	100	I	2.0	78	102
1GH0	I J	J	9	V	2.1	4	15
1GH0	I J	J	13	D	1.3	4	15
1GH0	I J	J	24	I	1.4	21	33
1GH0	I J	J	31	V	1.3	21	33
1GH0	I J	J	38	L	1.6	34	47
1GH0	I J	J	91	R	1.9	76	100
1GH0	I J	J	95	Y	3.4	76	100
1GH0	I J	J	98	F	4.0	76	100
1GH0	I L	L	83	L	1.3	76	100
1GH0	K B	K	158	I	1.4	145	161
1GH0	K B	K	159	N	1.5	145	161
1GH0	K B	B	48	A	1.4	48	63
1GH0	K B	B	49	S	1.1	48	63
1GH0	K H	K	118	I	1.3	115	122
1GH0	K H	H	83	L	1.3	76	100
1GH0	K L	K	5	L	1.1	4	15
1GH0	K L	K	9	V	2.1	4	15
1GH0	K L	K	24	I	1.2	21	47
1GH0	K L	K	31	F	2.1	21	47
1GH0	K L	K	38	L	1.6	21	47
1GH0	K L	K	42	K	1.8	21	47
1GH0	K L	K	93	R	2.6	78	102
1GH0	K L	K	97	Y	1.3	78	102
1GH0	K L	L	5	F	1.7	4	15
1GH0	K L	L	9	V	1.8	4	15
1GH0	K L	L	13	D	1.6	4	15
1GH0	K L	L	24	I	1.5	21	33
1GH0	K L	L	31	V	1.4	21	33
1GH0	K L	L	38	L	1.8	34	47
1GH0	K L	L	91	R	1.6	76	100
1GH0	K L	L	95	Y	3.5	76	100
1GH0	K L	L	98	F	4.4	76	100
1GH0	M N	M	5	L	1.1	4	15
1GH0	M N	M	6	T	1.2	4	15
1GH0	M N	M	9	V	1.9	4	15
1GH0	M N	M	24	I	1.1	21	47
1GH0	M N	M	38	L	1.9	21	47
1GH0	M N	M	42	K	1.7	21	47
1GH0	M N	M	93	R	3.0	78	102
1GH0	M N	M	97	Y	3.4	78	102
1GH0	M N	M	100	I	1.6	78	102
1GH0	M N	M	110	Y	2.0	104	113
1GH0	M N	N	9	V	1.6	4	11
1GH0	M N	N	24	I	1.7	21	33
1GH0	M N	N	38	L	1.6	34	47
1GH0	M N	N	91	R	2.0	76	100
1GH0	M N	N	95	Y	3.1	76	100
1GH0	M N	N	98	F	4.1	76	100
1GH0	M P	P	83	L	1.0	76	100
1GH0	O P	O	9	V	1.7	4	15
1GH0	O P	O	24	I	1.2	21	47
1GH0	O P	O	31	F	1.8	21	47
1GH0	O P	O	38	L	1.3	21	47
1GH0	O P	O	42	K	1.1	21	47
1GH0	O P	O	93	R	2.6	78	102
1GH0	O P	O	97	Y	5.1	78	102
1GH0	O P	O	100	I	1.5	78	102
1GH0	O P	P	5	F	1.6	4	15
1GH0	O P	P	9	V	1.6	4	15

1GH0	O P	P	13	D	1.7	4	15
1GH0	O P	P	24	I	1.9	21	33
1GH0	O P	P	31	V	1.4	21	33
1GH0	O P	P	38	L	1.6	34	47
1GH0	O P	P	91	R	1.9	76	100
1GH0	O P	P	95	Y	1.9	76	100
1GH0	O P	P	98	F	4.0	76	100
1GH0	O R	R	83	L	2.4	76	100
1GH0	O V	O	159	N	1.9	145	161
1GH0	O V	V	49	S	1.1	48	63
1GH0	Q N	N	83	L	1.1	76	100
1GH0	Q R	Q	5	L	1.1	4	15
1GH0	Q R	Q	6	T	1.4	4	15
1GH0	Q R	Q	9	V	2.0	4	15
1GH0	Q R	Q	23	E	1.2	21	47
1GH0	Q R	Q	24	I	1.1	21	47
1GH0	Q R	Q	31	F	3.5	21	47
1GH0	Q R	Q	38	L	1.4	21	47
1GH0	Q R	Q	42	K	1.3	21	47
1GH0	Q R	Q	93	R	2.6	78	102
1GH0	Q R	Q	97	Y	6.2	78	102
1GH0	Q R	Q	100	I	1.2	78	102
1GH0	Q R	R	5	F	1.4	4	15
1GH0	Q R	R	6	T	1.1	4	15
1GH0	Q R	R	9	V	1.3	4	15
1GH0	Q R	R	13	D	1.4	4	15
1GH0	Q R	R	31	V	1.2	21	33
1GH0	Q R	R	38	L	1.0	34	47
1GH0	Q R	R	91	R	3.1	76	100
1GH0	Q R	R	95	Y	3.3	76	100
1GH0	Q R	R	98	F	4.6	76	100
1GH0	Q T	Q	159	N	1.4	145	161
1GH0	S R	S	159	N	1.5	145	161
1GH0	S T	S	5	L	1.5	4	15
1GH0	S T	S	9	V	2.0	4	15
1GH0	S T	S	24	I	1.1	21	47
1GH0	S T	S	31	F	2.2	21	47
1GH0	S T	S	38	L	1.4	21	47
1GH0	S T	S	42	K	1.2	21	47
1GH0	S T	S	93	R	2.7	78	102
1GH0	S T	S	97	Y	4.4	78	102
1GH0	S T	S	100	I	1.5	78	102
1GH0	S T	S	110	Y	1.3	104	113
1GH0	S T	T	5	F	1.9	4	15
1GH0	S T	T	13	D	1.4	4	15
1GH0	S T	T	24	I	1.8	21	33
1GH0	S T	T	31	V	1.9	21	33
1GH0	S T	T	38	L	1.4	34	47
1GH0	S T	T	91	R	1.8	76	100
1GH0	S T	T	95	Y	3.5	76	100
1GH0	S T	T	98	F	4.2	76	100
1GH0	S V	V	83	L	1.2	76	100
1GH0	U P	U	159	N	2.2	145	161
1GH0	U P	P	49	S	1.5	48	63
1GH0	U V	U	9	V	1.8	4	15
1GH0	U V	U	24	I	1.4	21	47
1GH0	U V	U	31	F	1.9	21	47
1GH0	U V	U	38	L	1.5	21	47
1GH0	U V	U	42	K	1.3	21	47
1GH0	U V	U	93	R	2.4	78	102

1GH0	U V	U	97	Y	2.6	78	102
1GH0	U V	U	100	I	1.6	78	102
1GH0	U V	V	5	F	1.7	4	15
1GH0	U V	V	9	V	1.6	4	15
1GH0	U V	V	13	D	1.5	4	15
1GH0	U V	V	24	I	1.4	21	33
1GH0	U V	V	31	V	1.3	21	33
1GH0	U V	V	38	L	1.9	34	47
1GH0	U V	V	91	R	2.0	76	100
1GH0	U V	V	95	Y	1.7	76	100
1GH0	U V	V	98	F	4.6	76	100
1GH0	U X	X	83	L	1.0	76	100
1GH0	W N	W	159	N	2.3	145	161
1GH0	W T	W	117	E	1.3	115	122
1GH0	W T	T	83	L	1.5	76	100
1GH0	W X	W	5	L	1.1	4	15
1GH0	W X	W	6	T	1.0	4	15
1GH0	W X	W	9	V	2.2	4	15
1GH0	W X	W	24	I	1.2	21	47
1GH0	W X	W	31	F	2.4	21	47
1GH0	W X	W	38	L	1.9	21	47
1GH0	W X	W	42	K	1.2	21	47
1GH0	W X	W	93	R	2.2	78	102
1GH0	W X	W	97	Y	4.0	78	102
1GH0	W X	W	100	I	1.7	78	102
1GH0	W X	X	5	F	1.6	4	16
1GH0	W X	X	6	T	1.9	4	16
1GH0	W X	X	9	V	2.0	4	16
1GH0	W X	X	13	D	1.2	4	16
1GH0	W X	X	24	I	1.9	21	33
1GH0	W X	X	31	V	1.4	21	33
1GH0	W X	X	38	L	1.4	34	47
1GH0	W X	X	91	R	1.9	76	100
1GH0	W X	X	95	Y	1.3	76	100
1GH0	W X	X	98	F	3.9	76	100
1GH6	A B	A	100	E	1.8	91	102
1GH6	A B	B	721	F	1.5	721	731
1GH6	A B	B	725	V	1.5	721	731
1GH6	A B	B	753	I	2.6	752	764
1GH6	A B	B	756	Y	2.9	752	764
1GH6	A B	B	762	Q	1.3	752	764
1GH6	A B	B	765	K	1.8	765	770
1GHF	L H	L	123	E	1.0	122	126
1GHF	L H	L	124	Q	1.5	122	126
1GHQ	A B	A	112	K	1.9	104	118
1GHQ	A B	A	116	L	1.4	104	118
1GHQ	A B	A	117	E	1.1	104	118
1GK0	A B	A	40	F	1.6	36	51
1GK0	A B	A	41	Y	2.2	36	51
1GK0	A B	A	42	G	11.9	36	51
1GK0	A B	A	43	Y	2.0	36	51
1GK0	A B	A	47	Q	2.5	36	51
1GK0	A B	A	49	R	1.2	36	51
1GK0	A B	A	55	I	1.3	52	64
1GK0	A B	A	58	L	2.0	52	64
1GK0	A B	A	59	Y	1.6	52	64
1GK0	A B	A	75	E	1.9	75	84
1GK0	A B	A	79	V	1.3	75	84
1GK0	A B	A	80	W	1.2	75	84
1GK0	A B	A	93	W	4.4	86	96

1GK0	A B	A	101	F	3.8	99	119
1GK0	A B	A	108	F	4.0	99	119
1GK0	A B	A	157	T	2.2	154	159
1GK0	A B	B	508	V	1.3	505	512
1GK0	C D	C	37	P	3.1	36	51
1GK0	C D	C	40	F	1.7	36	51
1GK0	C D	C	41	Y	2.1	36	51
1GK0	C D	C	42	G	11.0	36	51
1GK0	C D	C	43	Y	1.6	36	51
1GK0	C D	C	47	Q	2.3	36	51
1GK0	C D	C	49	R	1.2	36	51
1GK0	C D	C	55	I	1.3	52	64
1GK0	C D	C	58	L	1.9	52	64
1GK0	C D	C	59	Y	1.6	52	64
1GK0	C D	C	75	E	2.6	75	84
1GK0	C D	C	80	W	1.2	75	84
1GK0	C D	C	93	W	4.6	86	96
1GK0	C D	C	101	F	3.8	99	119
1GK0	C D	C	108	F	3.9	99	119
1GK0	C D	C	157	T	2.2	154	159
1GK0	C D	D	154	F	1.0	151	155
1GK0	C D	D	508	V	1.4	505	512
1GLA	F G	F	40	V	1.7	39	43
1GLA	F G	G	474	I	1.7	474	478
1GLA	F G	G	479	R	1.9	479	494
1GLA	F G	G	481	Y	1.3	479	494
1GO3	E F	E	34	Y	3.0	22	35
1GO3	E F	E	180	K	1.1	173	184
1GO3	E F	F	21	M	1.1	14	27
1GO3	E F	F	24	R	2.7	14	27
1GO3	E F	F	34	Q	2.3	32	44
1GO3	E F	F	40	Y	3.3	32	44
1GO3	E F	F	71	K	1.8	66	76
1GO3	E F	F	82	D	1.5	80	87
1GO3	M N	M	34	Y	2.3	22	35
1GO3	M N	N	20	I	1.7	14	27
1GO3	M N	N	21	M	1.2	14	27
1GO3	M N	N	24	R	2.6	14	27
1GO3	M N	N	34	Q	2.4	32	44
1GO3	M N	N	40	Y	3.1	32	44
1GO3	M N	N	71	K	2.3	66	76
1GO4	E C	E	549	P	1.6	549	573
1GO4	E C	C	64	Y	2.3	59	78
1GO4	F B	F	549	P	1.4	549	578
1GO4	F B	B	64	Y	2.2	59	78
1GO4	G A	G	549	P	1.2	549	576
1GO4	G A	A	64	Y	2.2	59	78
1GO4	G B	G	492	L	2.8	487	521
1GO4	G B	G	496	E	1.7	487	521
1GOT	A B	A	15	L	2.4	7	28
1GOT	A B	A	19	L	1.4	7	28
1GOT	A B	A	206	K	2.8	204	211
1GOT	A B	A	209	H	1.1	204	211
1GOT	B G	B	7	L	2.8	3	25
1GOT	B G	B	14	L	1.1	3	25
1GOT	B G	B	15	K	1.8	3	25
1GOT	B G	B	18	I	9.0	3	25
1GOT	B G	B	30	L	1.4	30	34
1GOT	B G	B	33	I	1.2	30	34
1GOT	B G	G	18	E	1.1	11	27

1GOT	B G	G	21	Q	1.5	11	27
1GOT	B G	G	25	E	1.4	11	27
1GOT	B G	G	26	V	1.3	11	27
1GOT	B G	G	40	F	4.2	33	47
1GOT	B G	G	41	R	1.6	33	47
1GOT	B G	G	43	Y	3.2	33	47
1GOT	B G	G	44	V	1.3	33	47
1GOT	B G	G	52	P	4.9	52	56
1GOT	B G	G	53	L	2.4	52	56
1GOT	B G	G	54	V	1.1	52	56
1GPQ	A C	A	105	I	1.0	104	117
1GPQ	A D	A	120	E	1.3	118	122
1GPQ	A D	A	121	N	2.4	118	122
1GPQ	B C	B	121	N	1.9	118	122
1GPQ	B C	C	34	F	1.2	25	36
1GPQ	B D	B	105	I	1.1	104	117
1GPW	A B	B	18	R	2.8	13	24
1GPW	A D	A	108	E	1.1	103	109
1GPW	C D	D	18	R	1.8	14	26
1GPW	C D	D	184	K	1.6	184	197
1GPW	E F	F	18	R	1.0	14	24
1GUA	A B	A	21	V	1.4	16	25
1GX7	A D	A	112	Y	1.8	108	118
1GX7	A D	A	116	D	1.6	108	118
1GX7	A D	A	147	F	2.5	146	165
1GX7	A D	A	154	W	4.1	146	165
1GX7	A D	A	155	E	1.9	146	165
1GX7	A D	A	210	L	2.0	203	212
1GX7	A D	A	214	Y	2.1	213	219
1GX7	A D	D	40	K	1.3	39	56
1GX7	A D	D	42	Y	2.7	39	56
1GX7	A D	D	43	M	1.4	39	56
1GX7	A D	D	46	R	1.9	39	56
1GX7	A D	D	47	I	1.0	39	56
1GX7	A D	D	49	G	4.7	39	56
1GX7	A D	D	51	Y	5.0	39	56
1GX7	A D	D	68	V	2.9	66	74
1GX7	A D	D	71	L	2.6	66	74
1GX7	A D	D	72	Y	3.4	66	74
1GX7	A E	E	66	Y	1.0	65	71
1GXS	A B	A	70	G	21.1	68	77
1GXS	A B	A	126	D	1.6	126	144
1GXS	A B	A	170	Y	1.0	159	172
1GXS	A B	A	171	R	1.1	159	172
1GXS	A B	A	196	D	1.8	193	206
1GXS	A B	A	199	G	23.5	193	206
1GXS	A B	A	204	W	1.9	193	206
1GXS	A B	B	292	F	2.6	290	299
1GXS	A B	B	293	N	2.1	290	299
1GXS	A B	B	297	Y	6.5	290	299
1GXS	A B	B	298	L	1.3	290	299
1GXS	A B	B	307	L	1.1	301	308
1GXS	A B	B	326	I	2.7	324	329
1GXS	A B	B	327	F	4.1	324	329
1GXS	A B	B	328	D	1.3	324	329
1GXS	A B	B	343	E	1.6	338	347
1GXS	A B	B	344	L	2.0	338	347
1GXS	A B	B	425	F	1.6	421	434
1GXS	A B	B	428	F	3.8	421	434
1GXS	A B	B	431	F	4.2	421	434

1GXS	A B	B	432	L	2.1	421	434
1GXS	A D	A	205	W	2.1	193	206
1GXS	A D	A	212	D	1.2	212	223
1GXS	A D	D	368	R	1.7	364	373
1GXS	C B	C	205	W	4.6	193	206
1GXS	C B	C	244	E	1.1	232	246
1GXS	C B	B	368	R	2.2	364	375
1GXS	C D	C	70	G	3.3	68	77
1GXS	C D	C	126	D	1.3	126	144
1GXS	C D	C	196	D	1.5	193	206
1GXS	C D	C	199	G	53.0	193	206
1GXS	C D	C	202	E	1.3	193	206
1GXS	C D	C	204	W	1.7	193	206
1GXS	C D	D	292	F	2.4	290	299
1GXS	C D	D	297	Y	3.8	290	299
1GXS	C D	D	307	L	1.2	301	308
1GXS	C D	D	326	I	2.6	324	329
1GXS	C D	D	327	F	4.1	324	329
1GXS	C D	D	344	L	2.2	338	347
1GXS	C D	D	369	R	1.2	364	373
1GXS	C D	D	425	F	2.0	421	434
1GXS	C D	D	428	F	5.1	421	434
1GXS	C D	D	431	F	3.8	421	434
1GXS	C D	D	432	L	2.1	421	434
1GZL	A C	A	29	L	1.0	2	44
1GZL	A C	A	35	W	4.1	2	44
1GZL	A C	A	36	G	1.2	2	44
1GZL	A C	C	635	I	1.0	629	638
1GZL	B D	B	29	L	1.0	2	45
1GZL	B D	B	32	L	1.6	2	45
1GZL	B D	B	35	W	2.5	2	45
1GZL	B D	D	631	W	1.1	629	639
1GZL	B D	D	638	Y	2.0	629	639
1GZS	B A	B	106	Y	1.3	104	133
1GZS	B A	B	109	Q	1.2	104	133
1GZS	B A	B	124	D	2.6	104	133
1GZS	B A	A	65	D	1.0	65	73
1GZS	B A	A	66	R	1.2	65	73
1GZS	B A	A	67	L	2.0	65	73
1GZS	B A	A	70	L	1.6	65	73
1GZS	B C	B	226	L	1.6	221	237
1GZS	D C	D	106	Y	1.3	104	133
1GZS	D C	D	124	D	2.3	104	133
1GZS	D C	D	137	I	2.1	137	152
1GZS	D C	C	67	L	2.2	65	73
1GZS	D C	C	70	L	1.2	65	73
1H0D	A B	A	123	Q	1.6	121	126
1H0H	A B	A	211	D	2.4	200	212
1H0H	A B	A	225	R	2.8	225	229
1H0H	A B	A	871	P	1.1	871	877
1H0H	A B	A	872	W	4.5	871	877
1H0H	A B	B	16	G	35.0	16	25
1H0H	A B	B	19	V	1.6	16	25
1H0H	A B	B	143	R	2.6	141	145
1H0H	K L	K	211	D	2.1	200	212
1H0H	K L	K	225	R	2.7	225	229
1H0H	K L	K	871	P	1.1	871	877
1H0H	K L	K	872	W	4.5	871	877
1H0H	K L	L	16	G	35.3	16	25
1H0H	K L	L	19	V	1.7	16	25

1H0H	K L	L	23	Q	1.2	16	25
1H0H	K L	L	24	W	1.0	16	25
1H0H	K L	L	143	R	2.7	141	145
1H0T	A B	A	14	Y	2.6	4	18
1H0T	A B	B	13	G	70.8	6	18
1H1L	A B	A	85	V	1.6	85	91
1H1L	A B	A	86	G	78.6	85	91
1H1L	A B	A	89	Q	1.2	85	91
1H1L	A B	A	90	Y	3.1	85	91
1H1L	A B	A	122	I	1.5	119	124
1H1L	A B	A	132	K	1.0	127	141
1H1L	A B	A	136	E	2.6	127	141
1H1L	A B	A	139	L	1.0	127	141
1H1L	A B	A	140	L	2.3	127	141
1H1L	A B	A	238	I	1.5	232	243
1H1L	A B	A	332	Q	1.3	330	345
1H1L	A B	A	405	Y	1.2	404	415
1H1L	A B	A	423	I	1.1	423	433
1H1L	A B	A	427	Y	3.7	423	433
1H1L	A B	A	431	K	1.0	423	433
1H1L	A B	B	19	Y	1.1	17	29
1H1L	A B	B	22	L	3.0	17	29
1H1L	A B	B	41	V	1.2	35	46
1H1L	A B	B	50	Y	2.0	48	55
1H1L	A B	B	91	Q	2.2	91	106
1H1L	A B	B	92	G	272.1	91	106
1H1L	A B	B	96	Y	2.4	91	106
1H1L	A B	B	100	Y	2.0	91	106
1H1L	A B	B	139	L	3.0	126	140
1H1L	A B	B	155	V	1.6	151	157
1H1L	A B	B	424	W	2.6	423	434
1H1L	A B	B	446	F	1.1	445	455
1H1L	A D	A	464	T	1.4	451	466
1H1L	A D	D	326	M	1.1	318	333
1H1L	A D	D	344	R	2.0	338	354
1H1L	A D	D	352	L	2.2	338	354
1H1L	A D	D	355	H	1.8	355	359
1H1L	C B	C	464	T	1.5	451	466
1H1L	C B	B	326	M	1.3	318	333
1H1L	C B	B	344	R	2.1	338	354
1H1L	C B	B	352	L	2.2	338	354
1H1L	C B	B	355	H	2.3	355	359
1H1L	C B	B	356	T	1.0	355	359
1H1L	C D	C	85	V	1.5	85	91
1H1L	C D	C	86	G	41.0	85	91
1H1L	C D	C	89	Q	1.6	85	91
1H1L	C D	C	122	I	1.6	119	124
1H1L	C D	C	132	K	1.2	127	141
1H1L	C D	C	133	L	1.1	127	141
1H1L	C D	C	136	E	3.4	127	141
1H1L	C D	C	139	L	1.2	127	141
1H1L	C D	C	140	L	2.2	127	141
1H1L	C D	C	157	L	1.1	153	158
1H1L	C D	C	234	W	5.9	232	244
1H1L	C D	C	238	I	1.5	232	244
1H1L	C D	C	259	E	4.3	257	262
1H1L	C D	C	405	Y	2.8	404	415
1H1L	C D	C	427	Y	3.8	423	432
1H1L	C D	C	428	I	1.2	423	432
1H1L	C D	D	19	Y	1.7	17	29

1H1L	C D	D	26	K	4.1	17	29
1H1L	C D	D	38	V	1.1	35	45
1H1L	C D	D	41	V	1.3	35	45
1H1L	C D	D	50	Y	3.1	48	55
1H1L	C D	D	53	L	1.7	48	55
1H1L	C D	D	91	Q	1.7	91	106
1H1L	C D	D	92	G	198.9	91	106
1H1L	C D	D	118	E	1.2	118	124
1H1L	C D	D	139	L	3.8	126	141
1H1L	C D	D	140	Y	3.3	126	141
1H1L	C D	D	155	V	1.8	151	157
1H1L	C D	D	424	W	2.8	423	434
1H1L	C D	D	443	Y	1.0	442	455
1H1V	G A	G	481	I	1.5	473	490
1H1V	G A	G	482	L	1.0	473	490
1H1V	G A	A	143	Y	1.0	137	145
1H1V	G A	A	345	I	1.4	338	349
1H2A	S L	S	19	G	1.5	19	25
1H2A	S L	S	22	E	1.1	19	25
1H2A	S L	S	37	L	2.0	32	40
1H2A	S L	S	38	D	1.9	32	40
1H2A	S L	S	258	W	3.7	257	262
1H2A	S L	L	63	I	2.6	61	66
1H2A	S L	L	64	I	2.4	61	66
1H2A	S L	L	71	R	1.3	70	79
1H2A	S L	L	75	H	1.4	70	79
1H2A	S L	L	76	F	3.6	70	79
1H2A	S L	L	122	H	1.9	106	134
1H2A	S L	L	173	K	2.0	164	179
1H2A	S L	L	177	F	1.3	164	179
1H2A	S L	L	216	L	2.9	202	230
1H2A	S L	L	217	R	1.5	202	230
1H2A	S L	L	219	Q	2.7	202	230
1H2A	S L	L	224	R	1.1	202	230
1H2M	A S	A	162	F	2.1	156	164
1H2M	A S	A	163	L	1.3	156	164
1H2M	A S	A	167	W	2.0	167	177
1H2M	A S	S	818	L	2.1	816	822
1H2M	A S	S	819	L	2.4	816	822
1H2R	S L	S	22	E	1.4	19	26
1H2R	S L	S	37	L	1.0	32	40
1H2R	S L	S	258	W	3.5	257	261
1H2R	S L	S	259	D	2.1	257	261
1H2R	S L	L	64	I	2.1	61	66
1H2R	S L	L	71	R	1.3	70	79
1H2R	S L	L	72	D	1.4	70	79
1H2R	S L	L	75	H	2.1	70	79
1H2R	S L	L	76	F	3.2	70	79
1H2R	S L	L	177	F	1.2	164	179
1H2R	S L	L	216	L	2.9	202	230
1H2R	S L	L	217	R	1.2	202	230
1H2R	S L	L	219	Q	1.5	202	230
1H2R	S L	L	220	V	1.0	202	230
1H2R	S L	L	247	Y	1.8	247	251
1H2S	A B	A	170	L	1.1	154	181
1H2S	A B	A	173	I	1.3	154	181
1H2S	A B	A	191	T	1.2	190	223
1H2S	A B	A	196	L	2.8	190	223
1H2S	A B	B	36	F	1.5	25	51
1H2S	A B	B	43	E	1.2	25	51

1H2S	A B	B	69	I	2.3	53	82
1H2S	A B	B	73	I	1.8	53	82
1H2S	A B	B	76	G	5.8	53	82
1H3O	A B	A	879	R	1.6	873	886
1H3O	A B	A	880	I	1.0	873	886
1H3O	A B	A	883	I	1.2	873	886
1H3O	A B	A	896	V	1.5	896	917
1H3O	A B	A	899	Y	3.6	896	917
1H3O	A B	A	900	V	1.1	896	917
1H3O	A B	A	906	Q	1.1	896	917
1H3O	A B	A	907	R	1.0	896	917
1H3O	A B	A	908	L	1.7	896	917
1H3O	A B	A	912	V	1.4	896	917
1H3O	A B	B	66	L	2.6	60	71
1H3O	A B	B	70	V	1.5	60	71
1H3O	A B	B	91	F	2.3	85	106
1H3O	A B	B	92	I	1.8	85	106
1H3O	A B	B	96	V	1.8	85	106
1H3O	A B	B	113	V	1.6	113	125
1H3O	A D	D	80	V	1.0	78	82
1H3O	C B	B	80	V	1.1	78	82
1H3O	C D	C	875	P	1.3	873	887
1H3O	C D	C	879	R	1.1	873	887
1H3O	C D	C	883	I	1.1	873	887
1H3O	C D	C	899	Y	1.9	894	917
1H3O	C D	C	900	V	1.2	894	917
1H3O	C D	C	908	L	2.3	894	917
1H3O	C D	C	912	V	1.5	894	917
1H3O	C D	D	62	K	1.0	60	69
1H3O	C D	D	66	L	2.7	60	69
1H3O	C D	D	91	F	2.9	85	106
1H3O	C D	D	92	I	1.7	85	106
1H3O	C D	D	96	V	1.6	85	106
1H3O	C D	D	113	V	1.8	113	125
1H4J	A B	A	225	L	1.0	225	229
1H4J	A B	B	37	L	1.6	34	38
1H4J	A B	B	47	M	1.4	39	62
1H4J	A B	B	50	R	3.2	39	62
1H4J	A B	B	51	N	2.0	39	62
1H4J	A B	B	54	R	3.0	39	62
1H4J	A B	B	55	V	1.1	39	62
1H4J	A B	B	58	F	1.2	39	62
1H4J	C D	C	225	L	1.0	225	229
1H4J	C D	D	37	L	2.1	34	38
1H4J	C D	D	39	K	1.0	39	62
1H4J	C D	D	44	I	1.0	39	62
1H4J	C D	D	47	M	1.4	39	62
1H4J	C D	D	50	R	3.2	39	62
1H4J	C D	D	51	N	2.0	39	62
1H4J	C D	D	54	R	3.0	39	62
1H4J	C D	D	55	V	1.1	39	62
1H4J	C D	D	58	F	1.2	39	62
1H4J	E F	E	225	L	1.0	225	229
1H4J	E F	F	36	E	1.0	34	38
1H4J	E F	F	37	L	1.5	34	38
1H4J	E F	F	44	I	1.0	39	62
1H4J	E F	F	47	M	1.4	39	62
1H4J	E F	F	50	R	3.2	39	62
1H4J	E F	F	51	N	2.0	39	62
1H4J	E F	F	54	R	3.0	39	62

1H4J	E F	F	55	V	1.1	39	62
1H4J	E F	F	58	F	1.2	39	62
1H4J	G H	G	225	L	1.0	225	229
1H4J	G H	H	37	L	1.6	34	38
1H4J	G H	H	44	I	1.0	39	62
1H4J	G H	H	47	M	2.2	39	62
1H4J	G H	H	50	R	4.1	39	62
1H4J	G H	H	51	N	2.0	39	62
1H4J	G H	H	54	R	2.9	39	62
1H4J	G H	H	55	V	1.1	39	62
1H4J	G H	H	58	F	1.2	39	62
1H4L	A D	A	43	G	92.8	43	57
1H4L	A D	A	50	R	1.6	43	57
1H4L	A D	D	236	Y	1.6	219	237
1H4L	A D	D	258	W	3.2	254	268
1H4L	A D	D	262	L	2.4	254	268
1H4L	A D	D	273	L	1.7	269	278
1H4L	A D	D	282	F	1.2	279	291
1H4L	B E	B	49	L	1.6	44	57
1H4L	B E	B	50	R	1.4	44	57
1H4L	B E	E	236	Y	1.6	219	238
1H4L	B E	E	258	W	3.6	254	268
1H4L	B E	E	262	L	1.8	254	268
1H4L	B E	E	265	I	1.5	254	268
1H4L	B E	E	273	L	1.7	269	277
1H4L	B E	E	282	F	1.4	279	291
1H59	A B	A	16	F	3.4	8	19
1H59	A B	A	54	L	1.1	54	60
1H59	A B	A	58	E	1.4	54	60
1H59	A B	B	70	L	3.1	69	75
1H59	A B	B	74	L	1.3	69	75
1H5R	A B	A	67	L	1.2	58	69
1H5R	A B	A	230	H	1.5	230	248
1H5R	A B	A	281	Y	1.2	280	288
1H5R	A B	B	230	H	1.5	230	248
1H5R	A B	B	234	I	1.1	230	248
1H5R	A B	B	281	Y	2.0	280	291
1H5R	C B	C	239	F	2.1	230	248
1H5R	C B	C	246	R	3.9	230	248
1H5R	C B	C	247	Q	1.2	230	248
1H5R	C B	C	256	E	1.5	254	261
1H5R	C B	C	284	Y	1.5	280	289
1H5R	C B	B	239	F	1.8	230	248
1H5R	C B	B	246	R	4.1	230	248
1H5R	C B	B	247	Q	1.2	230	248
1H6K	A X	A	370	V	1.5	369	383
1H6K	A X	A	419	H	1.5	407	423
1H6K	A X	A	559	F	4.9	559	569
1H6K	A X	A	606	D	2.9	598	611
1H6K	A X	A	610	R	3.2	598	611
1H6K	A X	X	55	Q	2.2	53	63
1H6K	A X	X	58	E	1.4	53	63
1H6K	A X	X	99	R	1.7	91	102
1H6K	A X	X	100	Y	2.6	91	102
1H6K	B Y	B	370	V	1.6	369	383
1H6K	B Y	B	559	F	3.1	559	569
1H6K	B Y	Y	54	E	1.9	53	63
1H6K	B Y	Y	55	Q	1.7	53	63
1H6K	B Y	Y	99	R	1.3	91	102
1H6K	B Y	Y	100	Y	1.7	91	102

1H6K	B Z	B	768	L	1.8	762	770
1H6K	C X	C	768	L	1.8	762	770
1H6K	C Z	C	370	V	1.5	369	383
1H6K	C Z	C	559	F	1.6	559	569
1H6K	C Z	Z	55	Q	2.5	53	63
1H6K	C Z	Z	99	R	1.4	91	102
1H8B	A B	A	14	F	1.1	7	18
1H8B	A B	A	16	I	1.5	7	18
1H8B	A B	A	17	L	6.0	7	18
1H8B	A B	A	40	Y	1.2	35	45
1H8B	A B	A	67	L	1.3	60	68
1H8B	A B	B	16	V	1.8	8	26
1HBH	A B	A	31	R	1.4	21	36
1HBH	A B	A	35	V	1.3	21	36
1HBH	A B	B	34	V	1.3	20	35
1HBH	A B	B	127	Q	2.2	124	142
1HBH	A D	A	96	P	1.3	96	114
1HBH	A D	D	100	P	1.2	100	118
1HBH	C B	C	96	P	1.2	96	114
1HBH	C B	C	98	N	1.1	96	114
1HBH	C D	C	31	R	2.1	21	36
1HBH	C D	C	35	V	1.1	21	36
1HBH	C D	C	104	H	2.3	96	114
1HBH	C D	C	123	H	3.3	120	140
1HBH	C D	D	30	R	2.6	20	35
1HBH	C D	D	34	V	1.1	20	35
1HBH	C D	D	112	I	1.8	100	118
1HBH	C D	D	127	Q	1.1	124	142
1HBH	C D	D	131	Q	2.4	124	142
1HBM	A B	B	354	G	24.5	351	362
1HBM	A B	B	357	V	1.3	351	362
1HBM	A B	B	358	G	172.9	351	362
1HBM	A B	B	361	F	1.5	351	362
1HBM	A C	A	367	M	1.1	367	388
1HBM	A C	A	371	L	1.7	367	388
1HBM	A C	A	375	T	1.0	367	388
1HBM	A C	A	379	F	1.3	367	388
1HBM	A C	A	386	E	2.4	367	388
1HBM	A C	A	392	L	1.2	389	395
1HBM	A C	A	393	E	3.9	389	395
1HBM	A C	A	432	Y	1.2	420	438
1HBM	A C	C	15	R	2.2	10	20
1HBM	A C	C	234	M	1.4	228	247
1HBM	A C	C	238	H	4.0	228	247
1HBM	A C	C	239	V	1.2	228	247
1HBM	A C	C	241	R	1.1	228	247
1HBM	A C	C	245	G	141.0	228	247
1HBM	A E	A	199	E	1.9	190	201
1HBM	A E	A	232	G	4.2	220	239
1HBM	A E	A	253	Y	2.4	246	258
1HBM	A E	A	256	K	1.4	246	258
1HBM	A E	A	285	Y	1.1	283	290
1HBM	A E	E	139	V	1.8	128	146
1HBM	A E	E	150	M	1.1	150	161
1HBM	A E	E	151	Y	3.6	150	161
1HBM	A E	E	157	K	2.8	150	161
1HBM	B C	B	253	F	1.4	251	259
1HBM	B C	B	256	V	1.2	251	259
1HBM	B C	B	266	G	50.3	265	279
1HBM	B C	B	315	M	3.6	299	322

1HBM	B C	B	316	V	4.0	299	322
1HBM	B C	B	317	N	2.1	299	322
1HBM	B C	B	319	G	13.2	299	322
1HBM	B C	B	329	S	1.5	327	343
1HBM	B C	B	333	Y	1.5	327	343
1HBM	B C	B	336	D	2.8	327	343
1HBM	B C	B	337	L	1.4	327	343
1HBM	B C	B	339	E	1.4	327	343
1HBM	B C	B	340	F	1.7	327	343
1HBM	B C	B	341	E	2.2	327	343
1HBM	B C	C	66	I	3.2	65	70
1HBM	B C	C	67	R	2.3	65	70
1HBM	B C	C	69	M	2.4	65	70
1HBM	B C	C	103	R	2.9	98	106
1HBM	B C	C	233	I	1.5	228	247
1HBM	B C	C	236	R	3.0	228	247
1HBM	B C	C	237	I	1.3	228	247
1HBM	B C	C	241	R	1.8	228	247
1HBM	B C	C	244	G	262.7	228	247
1HBM	D B	D	199	E	1.5	190	201
1HBM	D B	D	232	G	2.5	220	239
1HBM	D B	D	253	Y	2.6	246	259
1HBM	D B	D	256	K	1.0	246	259
1HBM	D B	D	285	Y	1.2	283	290
1HBM	D B	D	421	Q	4.8	420	438
1HBM	D B	B	139	V	1.1	128	146
1HBM	D B	B	150	M	1.2	150	161
1HBM	D B	B	151	Y	3.4	150	161
1HBM	D B	B	152	D	1.1	150	161
1HBM	D B	B	157	K	2.9	150	161
1HBM	D E	E	354	G	32.7	351	362
1HBM	D E	E	357	V	1.2	351	362
1HBM	D E	E	358	G	186.2	351	362
1HBM	D E	E	361	F	1.5	351	362
1HBM	E C	E	150	M	1.0	150	161
1HBM	E C	C	246	F	2.8	228	247
1HBR	A D	A	95	P	1.0	95	114
1HBR	A D	D	37	W	3.4	36	42
1HBR	C D	C	31	R	3.2	21	36
1HBR	C D	C	107	V	1.1	95	114
1HBR	C D	C	119	P	1.1	119	137
1HBR	C D	C	122	H	2.8	119	137
1HBR	C D	D	30	R	3.1	20	35
1HBR	C D	D	34	V	1.3	20	35
1HBR	C D	D	112	I	1.2	100	118
1HBX	A G	A	155	L	1.4	154	180
1HBX	B G	B	170	K	1.2	154	179
1HBX	B G	B	173	Y	1.5	154	179
1HBX	E H	E	173	Y	1.3	154	179
1HBX	E H	E	219	L	1.7	209	221
1HC9	A C	A	36	R	1.5	33	37
1HC9	B D	B	36	R	1.1	33	37
1HDM	A B	A	59	F	2.1	57	62
1HDM	A B	A	73	D	3.9	70	84
1HDM	A B	A	79	W	1.5	70	84
1HDM	A B	A	80	M	1.4	70	84
1HDM	A B	A	81	I	1.4	70	84
1HDM	A B	B	49	L	1.1	47	59
1HDM	A B	B	56	H	1.2	47	59
1HDM	A B	B	63	L	2.1	61	67

1HDM	A B	B	66	R	2.6	61	67
1HDM	A B	B	76	H	1.6	69	86
1HDM	A B	B	80	F	1.7	69	86
1HDM	A B	B	81	W	1.3	69	86
1HDM	A B	B	84	L	1.9	69	86
1HDS	A B	A	119	P	1.6	119	136
1HDS	A D	D	36	W	1.9	35	41
1HDS	A D	D	39	R	3.8	35	41
1HDS	A D	D	100	Q	17.4	99	110
1HDS	C D	C	31	R	113.9	22	36
1HDS	C D	C	34	L	83.8	22	36
1HDS	C D	C	35	S	5.1	22	36
1HDS	C D	C	103	H	120.5	103	110
1HDS	C D	C	107	V	70.1	103	110
1HDS	C D	D	103	R	121.6	99	110
1HDS	C D	D	107	N	123.0	99	110
1HE1	A C	A	101	F	1.2	96	120
1HE1	A C	A	105	V	2.3	96	120
1HE1	A C	A	112	M	1.8	96	120
1HE1	A C	A	119	K	1.4	96	120
1HE1	A C	A	146	R	2.3	144	159
1HE1	A C	A	149	S	1.2	144	159
1HE1	A C	A	182	Q	2.0	181	185
1HE1	A C	A	183	Q	2.7	181	185
1HE1	A C	C	67	L	2.3	65	73
1HE1	A D	D	70	L	1.3	65	73
1HE1	B C	C	70	L	1.3	65	73
1HE1	B D	B	105	V	1.5	97	120
1HE1	B D	B	112	M	1.7	97	120
1HE1	B D	B	146	R	2.2	144	158
1HE1	B D	B	149	S	1.3	144	158
1HE1	B D	B	154	G	1.2	144	158
1HE1	B D	B	182	Q	1.9	181	185
1HE1	B D	B	183	Q	2.2	181	185
1HE1	B D	D	67	L	2.2	65	73
1HEZ	A E	E	853	Y	1.6	843	859
1HEZ	C E	E	843	F	1.3	843	859
1HEZ	C E	E	851	Y	1.1	843	859
1HEZ	C E	E	855	D	1.0	843	859
1HH4	A D	A	66	R	2.4	65	70
1HH4	A D	A	103	H	3.1	93	105
1HH4	A D	A	104	H	2.0	93	105
1HH4	A D	D	351	Y	2.3	346	357
1HH4	A D	D	355	L	1.4	346	357
1HH4	B E	B	66	R	2.4	65	69
1HH4	B E	B	67	L	1.9	65	69
1HH4	B E	E	351	Y	2.5	346	357
1HH4	B E	E	355	L	1.8	346	357
1HH9	A B	A	124	Q	1.7	122	126
1HIA	A B	B	237	W	2.8	235	245
1HIA	A B	B	242	I	3.0	235	245
1HIA	X Y	Y	237	W	3.3	235	245
1HIA	X Y	Y	241	T	1.0	235	245
1HIA	X Y	Y	242	I	1.5	235	245
1HL6	A B	A	19	G	2.0	17	28
1HL6	A B	A	26	L	2.4	17	28
1HL6	A B	B	57	V	1.1	55	69
1HL6	A B	B	60	E	1.1	55	69
1HL6	A B	B	63	R	1.4	55	69
1HL6	A B	B	125	Y	2.7	117	143

1HL6	A B	B	136	S	1.7	117	143
1HL6	A B	B	140	L	2.6	117	143
1HL6	A B	B	141	H	4.9	117	143
1HL6	C D	C	19	G	7.8	17	29
1HL6	C D	C	20	D	1.7	17	29
1HL6	C D	C	23	I	2.1	17	29
1HL6	C D	C	26	L	1.4	17	29
1HL6	C D	C	27	K	1.1	17	29
1HL6	C D	D	133	L	1.2	117	143
1HL6	C D	D	136	S	1.8	117	143
1HL6	C D	D	141	H	5.0	117	143
1HLE	A B	A	30	N	1.0	24	45
1HLE	A B	A	38	F	3.2	24	45
1HLE	A B	A	42	N	1.2	24	45
1HLE	A B	A	54	P	1.7	54	67
1HLE	A B	A	264	E	1.9	261	266
1HLU	A P	A	288	D	1.4	287	295
1HLU	A P	A	372	R	2.0	370	374
1HLU	A P	A	373	K	1.0	370	374
1HLU	A P	P	120	G	1.1	120	137
1HLU	A P	P	121	G	208.2	120	137
1HLU	A P	P	122	M	1.2	120	137
1HLU	A P	P	125	K	1.5	120	137
1HLU	A P	P	128	Y	1.3	120	137
1HLU	A P	P	129	E	1.8	120	137
1HMV	A B	A	380	I	1.5	364	384
1HMV	A B	B	258	Q	1.3	254	271
1HMV	A B	B	262	G	1.4	254	271
1HMV	C D	C	380	I	1.5	364	384
1HMV	C D	D	258	Q	1.5	254	271
1HMV	C D	D	262	G	1.6	254	271
1HMV	E F	E	380	I	1.5	364	384
1HMV	E F	F	396	E	1.6	395	406
1HMV	G H	G	380	I	1.5	364	384
1HQ4	C D	C	124	Q	1.2	122	127
1HQM	A C	C	692	E	1.0	692	697
1HQM	C E	C	1072	K	1.4	1060	1073
1HQR	A B	A	48	F	2.4	46	52
1HQR	A B	A	76	R	1.9	56	77
1HQR	A B	B	257	D	1.2	255	263
1HQR	B D	B	281	H	1.9	278	287
1HQR	B D	B	284	G	6.1	278	287
1HR0	C N	C	9	G	114.1	7	14
1HR0	C N	C	33	L	1.6	30	47
1HR0	C N	N	45	R	1.2	41	51
1HR0	D E	D	205	E	3.0	200	207
1HR0	E H	E	148	V	1.0	145	152
1HR0	F R	R	65	I	1.9	60	76
1HR0	G K	K	59	Y	2.1	58	75
1HR0	J N	N	42	I	1.2	41	51
1HR0	J N	N	44	L	1.7	41	51
1HR0	J N	N	45	R	1.1	41	51
1HR0	L Q	L	11	V	1.5	7	14
1HR8	A B	A	373	Q	1.0	364	382
1HR8	A B	B	93	E	1.0	85	95
1HR8	A B	B	386	L	3.3	370	388
1HR8	A B	B	415	F	1.1	411	421
1HR8	C D	C	85	E	1.4	77	87
1HR8	C D	C	376	S	1.0	364	382
1HR8	C D	D	90	L	4.0	85	95

1HR8	C D	D	386	L	3.2	370	388
1HR8	C D	D	415	F	1.0	411	421
1HR8	E F	E	85	E	1.5	77	87
1HR8	E F	E	369	R	1.0	364	382
1HR8	E F	E	380	M	1.5	364	382
1HR8	E F	F	94	N	1.5	85	95
1HR8	E F	F	386	L	3.3	370	388
1HR8	E F	F	415	F	1.2	411	421
1HR8	G H	G	85	E	1.0	77	87
1HR8	G H	G	86	L	1.0	77	87
1HR8	G H	G	369	R	1.2	364	382
1HR8	G H	G	380	M	1.0	364	382
1HR8	G H	H	386	L	3.2	370	388
1HR8	G H	H	415	F	1.2	411	421
1HRT	L H	L	14	L	1.0	14	14
1HT1	B F	B	58	E	1.1	55	66
1HT1	B F	B	62	R	1.8	55	66
1HT1	B F	B	65	E	1.1	55	66
1HT1	Z G	Z	65	E	1.1	50	66
1HTL	A C	C	211	L	2.7	197	226
1HTL	A C	C	214	Y	3.5	197	226
1HTL	A C	C	223	F	1.1	197	226
1HTL	A C	C	225	D	2.4	197	226
1HTL	D C	C	223	F	1.2	197	226
1HTL	D C	C	235	R	1.2	232	236
1HTL	F C	C	220	R	1.7	197	226
1HTL	G C	G	73	R	1.1	59	79
1HTL	H C	H	73	R	1.0	59	78
1HTL	H C	H	74	I	1.3	59	78
1HV2	A B	A	60	Y	2.6	51	71
1HV2	A B	B	158	L	3.2	158	171
1HV2	A B	B	161	R	1.1	158	171
1HV4	A B	A	31	R	1.7	21	36
1HV4	A B	A	103	H	1.1	95	113
1HV4	A B	A	107	V	1.2	95	113
1HV4	A B	A	122	H	2.6	119	136
1HV4	A B	B	30	R	1.7	20	35
1HV4	A B	B	34	V	1.4	20	35
1HV4	A B	B	112	I	2.2	100	118
1HV4	A D	A	95	P	2.0	95	113
1HV4	A D	D	37	W	2.7	36	41
1HV4	A F	A	12	G	6.2	4	18
1HV4	A F	F	15	W	1.1	5	18
1HV4	C B	C	95	P	1.5	95	113
1HV4	C B	B	37	W	1.3	36	41
1HV4	C D	C	31	R	1.6	21	36
1HV4	C D	C	103	H	1.7	95	113
1HV4	C D	C	107	V	1.1	95	113
1HV4	C D	C	122	H	2.6	119	136
1HV4	C D	D	30	R	2.0	20	35
1HV4	C D	D	34	V	1.4	20	35
1HV4	C D	D	111	I	1.0	100	118
1HV4	C D	D	112	I	2.2	100	118
1HV4	E F	E	31	R	2.3	21	36
1HV4	E F	E	103	H	1.3	95	113
1HV4	E F	E	107	V	1.2	95	113
1HV4	E F	E	122	H	2.4	119	136
1HV4	E F	F	30	R	1.6	20	35
1HV4	E F	F	34	V	1.4	20	35
1HV4	E F	F	112	I	2.2	100	118

1HV4	E H	E	95	P	2.1	95	113
1HV4	E H	H	36	P	1.2	36	41
1HV4	E H	H	37	W	2.1	36	41
1HV4	G F	G	95	P	1.9	95	113
1HV4	G F	F	37	W	3.2	36	41
1HV4	G H	G	31	R	1.7	21	36
1HV4	G H	G	103	H	1.1	95	113
1HV4	G H	G	107	V	1.0	95	113
1HV4	G H	G	122	H	2.3	119	136
1HV4	G H	H	30	R	1.7	20	35
1HV4	G H	H	34	V	1.4	20	35
1HV4	G H	H	112	I	2.2	100	118
1HVU	A B	A	500	Q	1.0	500	508
1HVU	A B	B	262	G	2.0	254	271
1HVU	A B	B	424	K	1.2	422	426
1HVU	A E	A	126	K	1.5	124	128
1HVU	D B	D	126	K	1.5	124	128
1HVU	D E	E	262	G	3.0	254	271
1HVU	D E	E	277	R	1.0	277	284
1HVU	D E	E	401	W	2.2	395	406
1HVU	G H	H	262	G	3.1	254	271
1HVU	G H	H	277	R	1.0	277	284
1HVU	G H	H	365	V	7.9	364	384
1HVU	G H	H	395	K	76.2	395	406
1HVU	J K	K	262	G	2.0	254	271
1HVU	J K	K	365	V	8.0	364	384
1HWM	A B	A	169	Y	2.1	168	180
1HWM	A B	A	172	Q	1.8	168	180
1HWM	A B	A	176	R	1.2	168	180
1HWM	A B	A	235	E	2.8	233	241
1HWM	A B	A	239	I	1.3	233	241
1HX1	A B	A	258	R	2.5	257	274
1HX1	A B	A	261	R	2.8	257	274
1HX1	A B	A	262	R	4.1	257	274
1HX1	A B	B	212	E	1.9	204	222
1HX1	A B	B	215	M	1.4	204	222
1HX1	A B	B	237	R	2.8	231	257
1HX1	A B	B	252	D	2.1	231	257
1HXY	A B	A	70	L	2.0	56	77
1HXY	A B	A	76	R	2.0	56	77
1HXY	A B	B	53	L	1.1	52	63
1HXY	A C	A	58	G	5.9	56	77
1HXY	B C	B	82	N	1.0	65	86
1HXY	B C	B	85	V	1.2	65	86
1HXY	B D	B	81	H	2.0	65	86
1HYM	A B	A	17	G	1.4	17	28
1HYR	A C	C	75	M	1.5	60	79
1HYR	B C	C	155	T	1.0	154	174
1HYR	B C	C	156	H	1.1	154	174
1I1A	A C	A	134	P	1.3	134	145
1I1A	A C	C	311	R	1.8	310	315
1I1Q	A B	A	360	S	1.0	356	376
1I1Q	A B	A	367	D	1.2	356	376
1I1Q	A B	A	370	R	1.5	356	376
1I1Q	A B	B	18	D	1.1	13	23
1I1R	A B	B	11	L	1.1	9	35
1I1R	A B	B	15	R	2.4	9	35
1I1R	A B	B	18	W	3.5	9	35
1I1R	A B	B	111	W	1.3	102	121
1I2M	A B	A	72	F	2.8	69	73

1I2M	A B	A	103	N	1.1	101	113
1I2M	A B	A	106	R	2.9	101	113
1I2M	A B	A	107	D	1.3	101	113
1I2M	A B	A	110	R	2.4	101	113
1I2M	C D	C	72	F	1.3	69	73
1I2M	C D	C	103	N	1.0	101	113
1I2M	C D	C	106	R	3.2	101	113
1I2M	C D	C	107	D	2.0	101	113
1I2M	C D	C	110	R	2.0	101	113
1I3O	A B	A	185	D	1.9	182	196
1I3O	A B	A	189	L	1.4	182	196
1I3O	A B	B	350	I	2.1	348	360
1I3O	A E	E	141	L	1.0	136	143
1I3O	B E	B	348	W	1.0	348	360
1I3O	B E	E	231	L	1.3	228	232
1I3O	C D	C	185	D	1.9	182	196
1I3O	C D	C	189	L	1.3	182	196
1I3O	C D	D	350	I	2.0	348	360
1I3O	D F	D	348	W	1.0	348	360
1I3O	D F	F	141	L	1.5	136	143
1I3O	D F	F	231	L	1.1	228	232
1I3Q	A B	A	26	E	1.0	24	31
1I3Q	A B	A	501	L	1.0	495	505
1I3Q	A B	A	654	N	1.4	639	659
1I3Q	A B	A	810	P	2.1	810	845
1I3Q	A B	A	813	F	1.6	810	845
1I3Q	A B	A	814	F	3.7	810	845
1I3Q	A B	A	820	G	137.7	810	845
1I3Q	A B	A	824	L	1.3	810	845
1I3Q	A B	A	1413	G	9.9	1406	1415
1I3Q	A B	A	1424	V	1.3	1424	1430
1I3Q	A B	A	1428	V	1.3	1424	1430
1I3Q	A B	B	699	E	1.2	695	700
1I3Q	A B	B	1023	V	1.0	1023	1038
1I3Q	A B	B	1026	L	1.2	1023	1038
1I3Q	A B	B	1132	E	2.0	1132	1142
1I3Q	A B	B	1134	E	2.6	1132	1142
1I3Q	A B	B	1138	M	1.1	1132	1142
1I3Q	A B	B	1139	I	1.3	1132	1142
1I3Q	A B	B	1141	H	1.0	1132	1142
1I3Q	A B	B	1147	L	1.4	1144	1152
1I3Q	A B	B	1148	K	2.1	1144	1152
1I3Q	A B	B	1151	L	1.1	1144	1152
1I3Q	A B	B	1200	A	1.5	1198	1210
1I3Q	A B	B	1204	F	1.8	1198	1210
1I3Q	A E	A	946	V	1.1	923	947
1I3Q	A E	A	1017	L	2.2	1005	1026
1I3Q	A E	A	1342	E	2.1	1341	1359
1I3Q	A E	E	183	P	1.0	183	188
1I3Q	A F	A	504	L	2.3	495	505
1I3Q	A F	F	87	K	1.0	87	103
1I3Q	A F	F	95	G	2.8	87	103
1I3Q	A K	A	543	L	2.0	543	553
1I3Q	A K	A	551	Y	3.9	543	553
1I3Q	A K	A	552	W	2.6	543	553
1I3Q	B C	C	35	R	1.4	27	39
1I3Q	B C	C	61	E	1.6	60	70
1I3Q	B C	C	62	F	2.1	60	70
1I3Q	B I	B	308	W	2.6	308	321
1I3Q	B J	B	190	Y	2.7	186	192

1I3Q	B J	J	33	G	38.6	32	39
1I3Q	B J	J	44	Y	2.1	44	53
1I3Q	B J	J	48	R	1.3	44	53
1I3Q	B J	J	51	L	1.3	44	53
1I3Q	B K	K	40	H	1.7	40	51
1I3Q	B L	B	119	L	1.0	114	120
1I3Q	C J	J	57	I	2.0	56	62
1I3Q	C J	J	61	L	2.4	56	62
1I3Q	C K	C	248	I	2.1	240	266
1I3Q	C K	C	254	K	2.1	240	266
1I3Q	C K	C	259	L	1.3	240	266
1I3Q	C K	C	262	L	2.2	240	266
1I3Q	C K	C	265	M	1.0	240	266
1I3Q	C K	K	42	L	1.0	40	51
1I3Q	C K	K	84	K	1.2	83	111
1I3Q	C K	K	87	L	1.2	83	111
1I3Q	C K	K	88	K	1.5	83	111
1I3Q	C K	K	95	I	1.3	83	111
1I3Q	C K	K	97	K	1.2	83	111
1I3Q	C K	K	98	L	2.4	83	111
1I3Q	C K	K	101	L	2.6	83	111
1I3Q	C K	K	102	K	1.1	83	111
1I3Q	C K	K	105	F	3.6	83	111
1I3Q	C L	C	68	G	73.9	60	70
1I3R	A B	A	48	F	1.8	46	50
1I3R	A B	A	62	N	1.4	56	77
1I3R	A B	A	66	N	10.0	56	77
1I3R	A B	A	69	N	11.1	56	77
1I3R	A B	A	70	L	1.5	56	77
1I3R	A B	A	74	K	2.2	56	77
1I3R	A B	A	76	R	1.5	56	77
1I3R	A B	B	82	P	13.0	81	89
1I3R	A B	B	112	F	2.4	91	113
1I3R	A B	B	115	F	3.2	114	118
1I3R	A B	B	116	L	3.2	114	118
1I3R	C D	C	48	F	2.9	46	50
1I3R	C D	C	69	N	1.3	56	77
1I3R	C D	C	70	L	2.0	56	77
1I3R	C D	C	74	K	1.9	56	77
1I3R	C D	C	76	R	3.2	56	77
1I3R	C D	D	83	D	1.8	81	89
1I3R	C D	D	112	F	2.7	91	113
1I3R	C D	D	115	F	3.3	114	118
1I3R	C D	D	116	L	2.8	114	118
1I3R	C F	C	57	Q	1.1	56	77
1I3R	E D	E	57	Q	1.6	56	77
1I3R	E D	D	93	F	1.0	91	113
1I3R	E F	E	48	F	1.7	46	50
1I3R	E F	E	69	N	1.8	56	77
1I3R	E F	E	70	L	2.0	56	77
1I3R	E F	E	74	K	2.6	56	77
1I3R	E F	E	76	R	4.5	56	77
1I3R	E F	F	80	G	8.0	78	89
1I3R	E F	F	83	D	2.1	78	89
1I3R	E F	F	112	F	1.4	100	113
1I3R	E F	F	115	F	3.1	114	119
1I3R	E F	F	116	L	4.8	114	119
1I3R	G H	G	48	F	2.7	46	51
1I3R	G H	G	62	N	1.4	56	77
1I3R	G H	G	69	N	1.9	56	77

1I3R	G H	G	70	L	1.8	56	77
1I3R	G H	G	74	K	1.8	56	77
1I3R	G H	G	76	R	4.1	56	77
1I3R	G H	H	83	D	2.9	81	89
1I3R	G H	H	109	Y	1.4	91	118
1I3R	G H	H	112	F	2.0	91	118
1I3R	G H	H	115	F	3.5	91	118
1I3R	G H	H	116	L	4.0	91	118
1I4D	A D	A	59	Y	1.1	29	78
1I4D	A D	A	66	H	2.1	29	78
1I4D	B D	B	57	H	1.2	29	78
1I4O	A C	A	240	W	1.2	240	252
1I4O	A C	C	141	L	2.2	136	143
1I4O	B D	D	141	L	2.9	136	143
1I51	A B	A	93	D	1.1	90	105
1I51	A B	A	97	L	1.3	90	105
1I51	A B	A	104	L	2.1	90	105
1I51	A B	B	242	V	1.2	240	252
1I51	A B	B	245	L	1.4	240	252
1I51	A B	B	249	L	1.1	240	252
1I51	B E	E	141	L	4.4	136	143
1I51	C D	C	97	L	1.5	90	105
1I51	C D	D	242	V	1.9	240	252
1I51	C D	D	245	L	1.2	240	252
1I51	C F	F	141	L	1.1	136	143
1I51	D F	F	141	L	1.6	136	143
1I5K	A C	C	310	L	2.5	306	327
1I5K	A C	C	313	L	1.5	306	327
1I5K	A C	C	317	R	4.0	306	327
1I5K	A D	D	409	E	1.1	406	427
1I5K	A D	D	419	E	1.3	406	427
1I5K	B C	C	316	E	1.5	306	327
1I5K	B C	C	319	E	2.0	306	327
1I5K	B C	C	320	E	1.7	306	327
1I5K	B D	D	414	K	1.9	406	427
1I7M	B A	B	40	W	2.1	37	47
1I7M	B A	A	94	L	1.2	91	102
1I7M	B A	A	101	Y	2.5	91	102
1I7M	D C	D	1040	W	2.6	1037	1047
1I7M	D C	D	1043	L	1.9	1037	1047
1I7M	D C	C	1094	L	1.2	1091	1102
1I7M	D C	C	1097	L	2.3	1091	1102
1I7M	D C	C	1101	Y	2.1	1091	1102
1I7Q	A B	A	115	D	1.0	114	119
1I7Q	A B	A	117	R	2.4	114	119
1I7Q	A B	A	364	M	1.0	356	376
1I7Q	A B	A	367	D	2.9	356	376
1I7Q	A B	A	370	R	3.0	356	376
1I7Q	A B	B	15	Y	2.8	14	24
1I7Q	A B	B	19	D	1.6	14	24
1I7Q	A B	B	22	R	1.4	14	24
1I7Q	A D	A	347	R	3.0	342	354
1I7Q	A D	D	181	G	3.0	181	194
1I7Q	C B	C	347	R	2.2	342	354
1I7Q	C B	C	350	L	1.6	342	354
1I7Q	C D	C	115	D	1.0	114	120
1I7Q	C D	C	364	M	1.2	356	376
1I7Q	C D	C	367	D	3.0	356	376
1I7Q	C D	C	368	L	1.5	356	376
1I7Q	C D	C	370	R	2.6	356	376

1I7Q	C D	C	372	D	4.8	356	376
1I7Q	C D	D	15	Y	1.2	14	24
1I7Q	C D	D	16	N	1.5	14	24
1I7Q	C D	D	19	D	1.2	14	24
1I7Q	C D	D	22	R	1.7	14	24
1I7W	A B	A	159	L	1.6	150	161
1I7W	A B	A	170	K	1.4	165	181
1I7W	A B	A	253	F	1.2	249	266
1I7W	A B	A	383	W	1.7	375	391
1I7W	A B	A	387	N	1.6	375	391
1I7W	A B	A	422	G	2.2	414	429
1I7W	A B	A	426	N	2.1	414	429
1I7W	A B	A	650	G	2.1	649	662
1I7W	A B	A	654	Y	1.9	649	662
1I7W	A B	B	665	D	1.3	662	667
1I7W	C D	C	148	L	1.5	144	151
1I7W	C D	C	155	E	1.1	152	161
1I7W	C D	C	156	L	1.2	152	161
1I7W	C D	C	159	L	1.2	152	161
1I7W	C D	C	174	M	3.0	165	179
1I7W	C D	C	253	F	1.6	249	266
1I7W	C D	C	508	K	1.3	504	518
1I7W	C D	C	512	G	3.6	504	518
1I7W	C D	C	653	T	1.0	649	662
1I7W	C D	D	657	I	1.2	657	666
1I7W	C D	D	665	D	1.2	657	666
1I7W	C D	D	717	K	1.1	716	722
1I7W	C D	D	718	L	3.0	716	722
1I7Y	A B	A	5	I	1.2	4	15
1I7Y	A B	A	6	T	1.1	4	15
1I7Y	A B	A	13	D	1.2	4	15
1I7Y	A B	A	24	L	1.6	21	47
1I7Y	A B	A	27	V	1.1	21	47
1I7Y	A B	A	31	F	1.8	21	47
1I7Y	A B	A	42	R	1.4	21	47
1I7Y	A B	A	93	R	2.9	78	102
1I7Y	A B	A	97	Y	4.7	78	102
1I7Y	A B	B	9	V	2.0	4	16
1I7Y	A B	B	24	F	2.7	21	33
1I7Y	A B	B	31	V	1.1	21	33
1I7Y	A B	B	34	G	5.7	34	47
1I7Y	A B	B	38	L	1.7	34	47
1I7Y	A B	B	93	R	2.1	78	102
1I7Y	A B	B	97	Y	3.9	78	102
1I7Z	A B	A	124	Q	1.4	122	127
1I7Z	C D	C	124	Q	1.9	122	128
1I84	S T	S	799	F	2.6	798	813
1I84	S T	S	802	Q	1.1	798	813
1I84	S T	S	805	G	1.9	798	813
1I84	S T	S	807	L	1.6	798	813
1I84	S T	S	808	A	2.7	798	813
1I84	S T	S	812	F	1.9	798	813
1I84	S T	T	33	D	1.2	28	38
1I84	S T	T	88	Y	1.7	85	93
1I84	V T	T	140	Y	120.7	140	150
1I84	V T	T	142	E	97.0	140	150
1I84	V W	V	796	I	1.4	793	813
1I84	V W	V	799	F	2.6	793	813
1I84	V W	V	802	Q	1.1	793	813
1I84	V W	V	812	F	1.9	793	813

1I84	V W	W	33	D	2.5	28	38
1I84	V W	W	44	N	1.9	44	50
1I84	V W	W	91	G	14.5	85	93
1I84	V W	W	127	L	1.0	121	129
1I94	C N	C	9	G	24.7	7	11
1I94	D E	D	205	E	2.2	202	207
1I94	D E	E	107	R	2.6	104	113
1I94	E H	E	140	R	1.2	128	141
1I94	E H	E	146	A	1.0	146	151
1I94	E H	E	149	E	1.3	146	151
1I94	E H	E	150	R	2.5	146	151
1I94	G K	K	58	P	23.6	58	65
1I94	J N	N	45	R	1.6	44	51
1I9R	H L	L	127	E	1.3	126	130
1I9R	H L	L	128	Q	2.4	126	130
1I9R	K M	M	127	E	1.5	126	130
1I9R	K M	M	128	Q	3.5	126	130
1I9R	X Y	Y	127	E	1.8	126	130
1I9R	X Y	Y	128	Q	1.0	126	130
1IA0	A K	A	420	E	1.1	418	436
1IAI	L H	L	124	Q	1.5	122	128
1IAK	A B	A	70	L	2.0	56	77
1IAK	A B	A	73	L	2.2	56	77
1IAK	A B	A	74	T	1.1	56	77
1IAK	A B	B	53	L	1.2	52	67
1IAK	A B	B	83	Y	1.0	68	88
1IAK	A B	B	86	E	1.2	68	88
1IAK	A P	A	65	T	1.4	56	77
1IAK	A P	A	68	H	1.3	56	77
1IAK	A P	A	69	N	2.6	56	77
1IAK	A P	A	71	E	1.1	56	77
1IAK	A P	A	72	I	3.0	56	77
1IAK	B P	B	61	W	2.1	52	67
1IAK	B P	B	78	V	1.2	68	88
1IAK	B P	B	81	H	1.1	68	88
1IAK	B P	B	82	N	1.8	68	88
1IAO	A B	A	62	N	3.1	56	77
1IAO	A B	A	68	H	1.8	56	77
1IAO	A B	A	69	N	2.0	56	77
1IAO	A B	A	70	L	1.5	56	77
1IAO	A B	A	72	I	1.1	56	77
1IAO	A B	A	73	L	2.1	56	77
1IAO	A B	A	74	T	1.1	56	77
1IAO	A B	A	76	R	1.2	56	77
1IAO	A B	B	53	L	1.2	52	64
1IAO	A B	B	57	D	1.0	52	64
1IB1	A E	A	127	R	1.0	112	132
1IB1	A E	A	169	G	12.2	165	183
1IB1	A E	A	172	L	1.5	165	183
1IB1	A E	A	180	E	1.8	165	183
1IB1	A E	A	217	I	1.0	215	228
1IB1	A E	A	224	N	2.8	215	228
1IB1	A E	E	47	G	80.3	45	61
1IB1	B F	B	169	G	7.9	165	183
1IB1	B F	B	172	L	1.5	165	183
1IB1	B F	B	180	E	1.5	165	183
1IB1	B F	B	217	I	1.1	215	228
1IB1	B F	B	224	N	2.4	215	228
1IB1	B F	F	47	G	40.3	45	61
1IB1	C G	C	46	V	1.7	38	68

1IB1	C G	C	60	R	1.0	38	68
1IB1	C G	C	169	G	2.4	165	183
1IB1	C G	C	172	L	1.4	165	183
1IB1	C G	C	180	E	1.5	165	183
1IB1	C G	C	217	I	1.1	215	228
1IB1	C G	C	224	N	2.5	215	228
1IB1	C G	G	47	G	74.9	45	60
1IB1	D H	D	45	S	1.8	38	69
1IB1	D H	D	46	V	2.1	38	69
1IB1	D H	D	49	K	1.1	38	69
1IB1	D H	D	56	R	1.7	38	69
1IB1	D H	D	117	F	1.2	112	132
1IB1	D H	D	120	K	1.3	112	132
1IB1	D H	D	169	G	3.3	165	183
1IB1	D H	D	172	L	1.8	165	183
1IB1	D H	D	180	E	1.2	165	183
1IB1	D H	D	217	I	1.1	215	228
1IB1	D H	D	219	Q	1.0	215	228
1IB1	D H	D	224	N	2.4	215	228
1IB1	D H	H	47	G	36.1	45	61
1IB1	D H	H	53	R	1.5	45	61
1IBC	A B	A	144	I	2.0	138	148
1IBC	A B	A	185	D	2.2	182	197
1IBC	A B	A	188	G	45.9	182	197
1IBC	A B	A	196	L	1.5	182	197
1IBC	A B	B	349	F	1.3	348	360
1IBC	A B	B	350	I	1.9	348	360
1IBC	A B	B	353	L	1.0	348	360
1IBC	A B	B	354	I	1.1	348	360
1IBG	L H	L	123	E	1.1	122	127
1IBG	L H	L	124	Q	1.6	122	127
1IBL	C E	C	131	R	1.4	130	144
1IBL	C N	C	9	G	184.5	7	11
1IBL	C N	N	49	H	1.5	41	51
1IBL	D E	E	107	R	1.1	104	112
1IBL	G K	K	59	Y	1.2	58	75
1IBL	J N	N	44	L	4.5	41	51
1IBL	L Q	L	11	V	1.2	7	14
1IBR	A B	A	104	W	1.0	101	110
1IBR	A B	A	107	D	1.3	101	110
1IBR	A B	A	140	R	3.1	138	142
1IBR	A B	A	166	R	1.2	157	170
1IBR	A B	B	15	R	1.2	15	32
1IBR	A B	B	18	L	1.6	15	32
1IBR	A B	B	59	L	1.6	51	63
1IBR	A B	B	156	Y	1.3	144	161
1IBR	A B	B	160	D	1.8	144	161
1IBR	A B	B	242	V	3.7	231	248
1IBR	A B	B	281	E	2.7	273	298
1IBR	A B	B	288	D	1.4	273	298
1IBR	C D	C	103	N	1.3	101	110
1IBR	C D	C	104	W	1.6	101	110
1IBR	C D	C	106	R	1.6	101	110
1IBR	C D	C	107	D	1.2	101	110
1IBR	C D	C	140	R	2.1	138	142
1IBR	C D	C	159	K	1.9	157	170
1IBR	C D	C	166	R	1.2	157	170
1IBR	C D	D	18	L	1.5	15	32
1IBR	C D	D	59	L	1.8	51	63
1IBR	C D	D	156	Y	1.2	144	161

1IBR	C D	D	239	Q	1.0	231	248
1IBR	C D	D	242	V	3.7	231	248
1IBR	C D	D	281	E	1.5	273	299
1IBR	C D	D	288	D	1.1	273	299
1IBT	A B	A	4	D	1.6	2	9
1IBT	A B	A	7	L	1.5	2	9
1IBT	A B	B	278	P	1.8	278	286
1IBT	A F	A	56	L	1.5	56	67
1IBT	A F	A	60	V	1.0	56	67
1IBT	A F	A	64	R	1.0	56	67
1IBT	A F	F	217	R	1.4	216	232
1IBT	C B	C	56	L	1.7	55	67
1IBT	C D	C	4	D	1.6	2	9
1IBT	C D	C	7	L	1.4	2	9
1IBT	C D	C	61	S	1.2	55	67
1IBT	C D	D	282	M	1.9	278	286
1IBT	E D	D	220	A	32.6	216	232
1IBT	E D	D	221	M	32.8	216	232
1IBT	E D	D	223	K	31.8	216	232
1IBT	E D	D	224	S	31.9	216	232
1IBT	E F	E	4	D	1.4	2	9
1IBT	E F	E	7	L	1.5	2	9
1IBT	E F	F	130	L	1.4	124	135
1IBT	E F	F	133	Y	1.0	124	135
1IBT	E F	F	282	M	1.9	278	286
1IBX	A B	B	74	D	6.0	74	79
1ICE	A B	A	144	I	2.1	138	148
1ICE	A B	A	185	D	1.8	182	196
1ICE	A B	A	188	G	2.7	182	196
1ICE	A B	A	192	L	1.9	182	196
1ICE	A B	A	262	F	2.0	260	265
1ICE	A B	B	349	F	1.0	348	360
1ICE	A B	B	350	I	1.7	348	360
1ICE	A B	B	354	I	1.4	348	360
1ICE	A B	B	357	M	1.5	348	360
1ICF	A B	A	37	Q	1.4	25	43
1ICF	A B	A	71	D	1.2	70	81
1ICF	A B	A	74	F	2.7	70	81
1ICF	A B	A	119	E	6.9	119	130
1ICF	A B	A	122	L	2.1	119	130
1ICF	A B	A	129	V	2.1	119	130
1ICF	A B	A	143	F	2.5	141	145
1ICF	C D	C	71	D	1.2	70	81
1ICF	C D	C	119	E	4.6	119	130
1ICF	C D	C	122	L	2.2	119	130
1ICF	C D	C	129	V	1.2	119	130
1ICF	C D	C	143	F	2.7	141	145
1ID3	A B	A	50	E	2.7	45	57
1ID3	A B	A	51	I	1.7	45	57
1ID3	A B	A	54	F	1.6	45	57
1ID3	A B	A	70	L	1.7	64	79
1ID3	A B	A	74	I	2.5	64	79
1ID3	A B	A	78	F	2.5	64	79
1ID3	A B	A	92	L	1.6	86	114
1ID3	A B	A	99	Y	2.3	86	114
1ID3	A B	A	100	L	2.2	86	114
1ID3	A B	A	101	V	1.6	86	114
1ID3	A B	A	104	F	2.1	86	114
1ID3	A B	A	121	K	1.0	121	130
1ID3	A B	A	124	I	2.1	121	130

1ID3	A B	B	28	G	1.9	25	29
1ID3	A B	B	36	R	1.7	31	42
1ID3	A B	B	37	L	1.7	31	42
1ID3	A B	B	39	R	2.9	31	42
1ID3	A B	B	40	R	2.5	31	42
1ID3	A B	B	41	G	14.0	31	42
1ID3	A B	B	53	E	1.0	48	76
1ID3	A B	B	58	L	1.4	48	76
1ID3	A B	B	59	K	10.3	48	76
1ID3	A B	B	61	F	10.8	48	76
1ID3	A B	B	62	L	3.7	48	76
1ID3	A B	B	66	I	2.8	48	76
1ID3	A B	B	70	V	1.3	48	76
1ID3	A B	B	86	V	1.0	85	93
1ID3	B D	B	72	Y	1.5	48	76
1ID3	B D	B	75	H	2.8	48	76
1ID3	B D	D	79	E	1.2	59	87
1ID3	B D	D	86	Y	1.1	59	87
1ID3	B D	D	103	L	1.6	94	104
1ID3	C D	C	50	V	1.7	46	74
1ID3	C D	C	55	V	1.5	46	74
1ID3	C D	C	56	L	1.2	46	74
1ID3	C D	C	81	P	1.0	81	90
1ID3	C D	D	69	V	1.0	59	87
1ID3	C D	D	73	F	1.3	59	87
1ID3	C D	D	76	I	1.1	59	87
1ID3	C D	D	109	L	1.8	107	127
1ID3	C D	D	117	G	33.4	107	127
1ID3	C D	D	124	Y	1.5	107	127
1ID3	E C	E	48	L	1.4	45	57
1ID3	E C	C	82	R	1.7	81	90
1ID3	E F	E	50	E	2.0	45	57
1ID3	E F	E	51	I	3.3	45	57
1ID3	E F	E	54	F	1.7	45	57
1ID3	E F	E	67	F	1.2	64	77
1ID3	E F	E	70	L	1.7	64	77
1ID3	E F	E	74	I	2.2	64	77
1ID3	E F	E	99	Y	2.2	86	114
1ID3	E F	E	100	L	2.5	86	114
1ID3	E F	E	101	V	1.7	86	114
1ID3	E F	E	124	I	2.0	121	132
1ID3	E F	F	35	R	1.0	31	41
1ID3	E F	F	36	R	2.3	31	41
1ID3	E F	F	40	R	3.2	31	41
1ID3	E F	F	50	I	1.8	50	60
1ID3	E F	F	57	V	1.0	50	60
1ID3	E F	F	58	L	2.4	50	60
1ID3	E F	F	61	F	1.6	61	76
1ID3	E F	F	66	I	1.9	61	76
1ID3	F D	F	91	K	1.3	85	93
1ID3	F H	F	75	H	2.3	61	76
1ID3	G H	G	50	V	1.9	46	74
1ID3	G H	G	51	Y	1.3	46	74
1ID3	G H	G	52	L	1.2	46	74
1ID3	G H	G	55	V	1.2	46	74
1ID3	G H	G	56	L	1.9	46	74
1ID3	G H	G	58	Y	4.0	46	74
1ID3	G H	G	59	L	2.2	46	74
1ID3	G H	G	63	I	2.0	46	74
1ID3	G H	G	64	L	2.0	46	74

1ID3	G H	G	81	P	1.3	81	91
1ID3	G H	G	84	L	2.3	81	91
1ID3	G H	G	97	L	1.0	92	98
1ID3	G H	H	64	I	1.2	59	87
1ID3	G H	H	68	F	2.5	59	87
1ID3	G H	H	72	I	1.3	59	87
1ID3	G H	H	73	F	2.6	59	87
1ID3	G H	H	97	I	1.7	94	105
1ID3	G H	H	109	L	1.8	108	123
1ID3	G H	H	117	G	120.9	108	123
1ID5	L H	L	14	E	2.4	14	14
1ID5	L H	L	14	E	2.6	14	14
1ID5	L H	L	14	L	3.0	14	14
1ID5	L H	L	14	F	1.7	14	14
1ID5	L H	L	14	Y	3.8	14	14
1IGC	H A	A	38	Y	1.0	28	42
1IGF	L H	L	124	Q	1.1	122	126
1IGT	A B	A	123	E	1.7	122	128
1IGT	C D	C	124	Q	1.3	122	128
1IHF	A B	A	8	M	1.0	5	16
1IHF	A B	A	11	Y	3.8	5	16
1IHF	A B	A	12	L	2.0	5	16
1IHF	A B	A	22	D	1.4	20	40
1IHF	A B	A	25	E	1.4	20	40
1IHF	A B	A	26	L	1.4	20	40
1IHF	A B	A	30	F	2.9	20	40
1IHF	A B	A	31	F	4.0	20	40
1IHF	A B	A	33	E	1.0	20	40
1IHF	A B	A	35	R	2.7	20	40
1IHF	A B	A	38	L	1.8	20	40
1IHF	A B	A	39	E	1.7	20	40
1IHF	A B	A	87	L	1.5	85	93
1IHF	A B	A	91	V	2.3	85	93
1IHF	A B	B	6	L	2.0	3	14
1IHF	A B	B	9	R	1.0	3	14
1IHF	A B	B	28	E	4.2	19	39
1IHF	A B	B	29	M	1.9	19	39
1IHF	A B	B	30	L	2.3	19	39
1IHF	A B	B	32	H	2.3	19	39
1IHF	A B	B	33	M	1.2	19	39
1IHF	A B	B	86	L	2.7	84	91
1IHF	A B	B	89	R	1.5	84	91
1II8	A B	A	36	K	1.2	36	48
1II8	A B	A	160	V	6.5	150	161
1II8	A B	A	170	Y	1.1	164	195
1II8	A B	A	177	K	2.1	164	195
1II8	A B	A	180	I	1.8	164	195
1II8	A B	A	184	I	1.1	164	195
1II8	A B	A	187	Y	1.8	164	195
1II8	A B	A	191	L	1.3	164	195
1II8	A B	B	712	V	1.4	710	720
1II8	A B	B	716	I	1.4	710	720
1II8	A B	B	723	K	1.1	723	760
1II8	A B	B	801	G	160.0	794	814
1II8	A B	B	812	L	1.2	794	814
1IJD	A B	B	12	L	1.1	6	35
1IJD	A B	B	13	H	1.8	6	35
1IJD	C D	D	12	L	1.1	6	35
1IJD	C D	D	13	H	1.8	6	35
1IJD	E F	F	12	L	1.1	6	35

1IJD	E F	F	13	H	1.8	6	35
1IK9	A C	A	177	Y	1.9	119	211
1IK9	A C	A	181	I	1.8	119	211
1IK9	A C	A	191	I	1.4	119	211
1IK9	A C	A	192	R	1.3	119	211
1IK9	A C	C	771	L	1.5	771	781
1IK9	A C	C	774	L	1.5	771	781
1IK9	A C	C	778	F	1.0	771	781
1IK9	B C	B	179	R	4.0	172	201
1IK9	B C	B	183	V	1.2	172	201
1IK9	B C	C	778	F	3.8	771	781
1IL1	A B	B	129	Q	1.1	127	131
1IM9	A D	A	79	R	2.6	57	85
1IM9	A D	A	146	K	1.7	138	150
1IND	L H	L	127	E	1.3	125	130
1IO4	C D	D	17	F	1.0	16	23
1IQ5	A B	A	11	E	1.2	6	20
1IQ5	A B	A	19	F	1.2	6	20
1IQ5	A B	A	51	M	1.2	45	56
1IQ5	A B	A	71	M	1.3	65	78
1IQ5	A B	A	91	V	1.1	83	93
1IQ5	A B	A	92	F	2.7	83	93
1IQ5	A B	A	124	M	3.7	118	129
1IQ5	A B	A	145	M	1.5	138	146
1IQ5	A B	B	337	L	2.0	337	349
1IQ5	A B	B	340	L	1.7	337	349
1IQ5	A B	B	342	L	1.1	337	349
1IQ5	A B	B	343	V	2.6	337	349
1IQ5	A B	B	344	K	2.2	337	349
1IQ5	A B	B	347	G	5.2	337	349
1IQ5	A B	B	348	H	1.3	337	349
1IQD	A B	A	125	Q	1.4	123	128
1IR2	A I	A	190	Y	1.5	182	195
1IR2	A I	A	194	R	1.1	182	195
1IR2	A I	A	421	R	2.0	413	433
1IR2	A I	A	432	N	1.4	413	433
1IR2	A I	A	454	E	1.2	453	462
1IR2	A I	I	25	Q	1.2	23	36
1IR2	A I	I	29	Q	4.4	23	36
1IR2	A I	I	32	Y	3.2	23	36
1IR2	A L	A	184	N	1.2	182	195
1IR2	A L	A	186	G	13.9	182	195
1IR2	A L	A	187	R	1.0	182	195
1IR2	A L	A	190	Y	1.6	182	195
1IR2	A L	A	223	E	3.3	214	233
1IR2	A L	A	226	Y	2.2	214	233
1IR2	A N	A	70	W	2.8	70	75
1IR2	A N	A	73	G	2.3	70	75
1IR2	A N	A	74	L	1.6	70	75
1IR2	B I	B	184	N	1.4	182	195
1IR2	B I	B	186	G	12.7	182	195
1IR2	B I	B	187	R	1.3	182	195
1IR2	B I	B	190	Y	1.7	182	195
1IR2	B I	B	220	F	1.1	214	233
1IR2	B I	B	223	E	2.8	214	233
1IR2	B I	B	226	Y	3.1	214	233
1IR2	B J	B	194	R	1.3	182	195
1IR2	B J	B	421	R	2.9	413	433
1IR2	B J	B	454	E	1.3	453	462
1IR2	B O	B	70	W	2.7	70	75

1IR2	B O	B	73	G	1.0	70	75
1IR2	B O	B	74	L	1.4	70	75
1IR2	C J	C	184	N	1.6	182	196
1IR2	C J	C	186	G	9.5	182	196
1IR2	C J	C	190	Y	1.5	182	196
1IR2	C J	C	191	E	1.0	182	196
1IR2	C J	C	223	E	3.2	214	233
1IR2	C J	C	226	Y	3.3	214	233
1IR2	C K	C	194	R	2.5	182	196
1IR2	C K	C	421	R	1.7	413	433
1IR2	C K	C	454	E	1.4	453	462
1IR2	C K	K	29	Q	1.7	23	36
1IR2	C K	K	32	Y	2.1	23	36
1IR2	C P	C	70	W	2.7	70	75
1IR2	C P	C	73	G	50.1	70	75
1IR2	C P	C	74	L	1.5	70	75
1IR2	D K	D	183	K	2.0	182	195
1IR2	D K	D	184	N	2.5	182	195
1IR2	D K	D	186	G	15.8	182	195
1IR2	D K	D	190	Y	1.1	182	195
1IR2	D K	D	191	E	1.1	182	195
1IR2	D K	D	220	F	2.1	214	233
1IR2	D K	D	223	E	5.5	214	233
1IR2	D K	D	226	Y	3.1	214	233
1IR2	D L	D	194	R	2.4	182	195
1IR2	D L	D	421	R	1.1	413	433
1IR2	D L	D	431	R	6.1	413	433
1IR2	D L	D	454	E	1.3	453	462
1IR2	D L	L	29	Q	5.8	23	36
1IR2	D L	L	32	Y	1.2	23	36
1IR2	D M	D	70	W	2.8	70	75
1IR2	D M	D	73	G	1.5	70	75
1IR2	D M	D	74	L	1.3	70	75
1IR2	E L	E	70	W	2.8	70	75
1IR2	E L	E	73	G	3.2	70	75
1IR2	E L	E	74	L	1.3	70	75
1IR2	E M	E	194	R	2.2	182	195
1IR2	E M	E	421	R	2.9	413	433
1IR2	E M	E	454	E	1.3	453	462
1IR2	E M	M	29	Q	1.5	23	36
1IR2	E M	M	32	Y	3.7	23	36
1IR2	E N	E	184	N	1.3	182	195
1IR2	E N	E	186	G	13.7	182	195
1IR2	E N	E	187	R	1.4	182	195
1IR2	E N	E	223	E	2.2	214	233
1IR2	E N	E	226	Y	2.2	214	233
1IR2	F I	F	70	W	2.5	70	75
1IR2	F I	F	73	G	74.4	70	75
1IR2	F I	F	74	L	1.3	70	75
1IR2	F N	F	194	R	1.1	182	195
1IR2	F N	F	421	R	2.9	413	433
1IR2	F N	F	432	N	1.2	413	433
1IR2	F N	F	454	E	1.4	453	462
1IR2	F N	N	25	Q	1.4	23	36
1IR2	F N	N	28	A	1.2	23	36
1IR2	F N	N	29	Q	2.0	23	36
1IR2	F N	N	32	Y	2.0	23	36
1IR2	F O	F	184	N	1.3	182	195
1IR2	F O	F	186	G	12.5	182	195
1IR2	F O	F	187	R	2.9	182	195

1IR2	F O	F	190	Y	1.2	182	195
1IR2	F O	F	191	E	1.2	182	195
1IR2	F O	F	219	L	2.4	214	233
1IR2	F O	F	220	F	2.5	214	233
1IR2	F O	F	223	E	4.8	214	233
1IR2	F O	F	226	Y	3.0	214	233
1IR2	F O	F	227	K	1.6	214	233
1IR2	G J	G	70	W	2.7	70	75
1IR2	G J	G	73	G	4.1	70	75
1IR2	G O	G	190	Y	1.3	182	195
1IR2	G O	G	421	R	1.3	413	433
1IR2	G O	G	454	E	1.3	453	462
1IR2	G O	O	29	Q	1.0	23	36
1IR2	G O	O	32	Y	2.6	23	36
1IR2	G P	G	184	N	1.2	182	195
1IR2	G P	G	186	G	12.6	182	195
1IR2	G P	G	187	R	1.6	182	195
1IR2	G P	G	190	Y	1.0	182	195
1IR2	G P	G	223	E	4.4	214	233
1IR2	G P	G	226	Y	5.1	214	233
1IR2	H K	H	70	W	2.7	70	75
1IR2	H K	H	73	G	2.0	70	75
1IR2	H K	H	74	L	1.1	70	75
1IR2	H M	H	183	K	2.0	182	196
1IR2	H M	H	184	N	1.5	182	196
1IR2	H M	H	186	G	11.8	182	196
1IR2	H M	H	187	R	1.7	182	196
1IR2	H M	H	190	Y	1.3	182	196
1IR2	H M	H	191	E	1.1	182	196
1IR2	H M	H	220	F	2.3	214	233
1IR2	H M	H	223	E	3.4	214	233
1IR2	H M	H	226	Y	2.1	214	233
1IR2	H P	H	194	R	2.7	182	196
1IR2	H P	H	195	G	1.0	182	196
1IR2	H P	H	421	R	2.1	413	433
1IR2	H P	H	454	E	1.4	453	462
1IR2	H P	P	32	Y	1.5	23	36
1IRE	A B	A	14	Q	1.1	10	32
1IRE	A B	A	17	I	2.2	10	32
1IRE	A B	A	21	V	2.2	10	32
1IRE	A B	A	22	K	2.7	10	32
1IRE	A B	A	24	L	2.8	10	32
1IRE	A B	A	27	M	2.4	10	32
1IRE	A B	A	28	L	1.8	10	32
1IRE	A B	A	29	I	1.6	10	32
1IRE	A B	A	38	M	2.8	36	46
1IRE	A B	A	39	I	1.6	36	46
1IRE	A B	A	41	R	2.8	36	46
1IRE	A B	A	42	M	2.1	36	46
1IRE	A B	A	45	I	1.2	36	46
1IRE	A B	A	125	W	2.5	124	128
1IRE	A B	A	129	P	1.2	129	138
1IRE	A B	A	130	Q	1.8	129	138
1IRE	A B	A	136	V	1.3	129	138
1IRE	A B	A	137	R	1.8	129	138
1IRE	A B	A	140	R	2.9	139	147
1IRE	A B	A	146	E	1.4	139	147
1IRE	A B	B	29	W	2.9	28	43
1IRE	A B	B	31	K	1.3	28	43
1IRE	A B	B	32	V	1.1	28	43

1IRE	A B	B	34	F	3.8	28	43
1IRE	A B	B	36	M	2.3	28	43
1IRE	A B	B	52	R	1.0	48	57
1IRE	A B	B	63	Y	1.5	60	65
1IRE	A B	B	73	I	1.1	68	83
1IRE	A B	B	91	L	1.5	88	101
1IRE	A B	B	94	R	1.5	88	101
1IRE	A B	B	98	Y	3.9	88	101
1IRE	A B	B	115	L	1.3	113	126
1IRE	A B	B	116	I	1.5	113	126
1IRE	A B	B	119	V	1.6	113	126
1IRE	A B	B	120	N	1.0	113	126
1IRE	A B	B	123	V	1.3	113	126
1IRU	A B	B	23	Y	3.4	19	30
1IRU	A B	B	79	G	1.7	79	101
1IRU	A B	B	80	P	1.3	79	101
1IRU	A G	A	24	Q	1.9	23	36
1IRU	A G	A	27	Y	2.0	23	36
1IRU	A G	A	84	T	1.4	84	106
1IRU	A G	A	86	D	1.8	84	106
1IRU	A G	G	117	M	1.1	108	122
1IRU	A G	G	120	H	2.8	108	122
1IRU	A H	A	95	R	1.3	84	106
1IRU	A H	A	103	Y	2.6	84	106
1IRU	A H	H	61	Y	2.8	49	71
1IRU	A H	H	65	F	1.6	49	71
1IRU	A H	H	68	I	1.2	49	71
1IRU	A I	A	105	Y	1.4	84	106
1IRU	A I	I	66	H	1.5	49	71
1IRU	A I	I	78	T	1.2	76	90
1IRU	B C	C	23	Y	3.0	19	29
1IRU	B C	C	82	D	1.6	80	102
1IRU	B J	B	100	Y	1.0	79	101
1IRU	B J	J	89	S	1.5	84	97
1IRU	C D	C	115	C	2.7	107	121
1IRU	C D	C	116	D	1.2	107	121
1IRU	C D	D	18	Q	1.1	17	28
1IRU	C D	D	21	Y	2.3	17	28
1IRU	C D	D	81	R	2.6	77	85
1IRU	C D	D	82	I	1.3	77	85
1IRU	C J	C	91	R	1.1	80	102
1IRU	C J	C	99	L	1.6	80	102
1IRU	C J	J	73	L	1.2	57	78
1IRU	C J	J	76	L	1.0	57	78
1IRU	C K	C	101	Y	2.7	80	102
1IRU	C K	K	67	Y	1.3	50	71
1IRU	C K	K	86	R	1.4	77	93
1IRU	D E	D	116	Q	2.0	104	118
1IRU	D E	E	23	Q	1.7	22	33
1IRU	D E	E	26	Y	3.4	22	33
1IRU	D E	E	84	D	1.1	82	103
1IRU	D K	D	96	L	3.1	86	98
1IRU	D K	K	62	K	1.0	50	71
1IRU	D K	K	66	L	1.5	50	71
1IRU	E F	F	24	Y	3.1	20	32
1IRU	E F	F	31	Q	1.1	20	32
1IRU	E L	E	100	W	1.6	82	103
1IRU	E L	E	101	F	3.3	82	103
1IRU	E L	L	57	R	1.1	49	70
1IRU	E L	L	61	R	1.4	49	70

1IRU	E L	L	64	R	1.4	49	70
1IRU	E L	L	65	I	1.1	49	70
1IRU	E L	L	68	L	1.5	49	70
1IRU	E M	M	71	R	1.0	58	79
1IRU	E M	M	75	Y	2.8	58	79
1IRU	E M	M	94	T	1.0	85	99
1IRU	F G	F	117	Q	14.6	117	121
1IRU	F M	F	97	F	1.2	78	99
1IRU	F N	N	86	R	1.2	85	102
1IRU	G H	G	102	F	3.3	81	103
1IRU	G H	H	66	H	2.3	49	71
1IRU	G N	N	76	L	1.8	57	78
1IRU	H I	I	88	F	1.8	76	90
1IRU	H N	H	136	Y	1.0	136	143
1IRU	H N	N	57	Y	1.1	57	78
1IRU	H N	N	61	Q	2.0	57	78
1IRU	I J	I	51	D	4.6	49	71
1IRU	I J	J	96	Y	3.0	84	97
1IRU	J K	J	59	D	2.9	57	78
1IRU	J Z	Z	165	Y	1.6	149	167
1IRU	K L	K	51	G	80.2	50	71
1IRU	K L	K	58	E	1.0	50	71
1IRU	K L	L	88	Y	2.1	76	90
1IRU	K Z	K	142	I	1.2	139	146
1IRU	K Z	K	144	D	1.5	139	146
1IRU	K Z	Z	134	Y	1.1	132	141
1IRU	K Z	Z	137	G	9.2	132	141
1IRU	K Z	Z	138	V	1.5	132	141
1IRU	K Z	Z	162	Q	1.5	149	167
1IRU	K Z	Z	166	R	1.5	149	167
1IRU	L M	L	51	D	3.5	49	70
1IRU	L M	L	54	F	2.1	49	70
1IRU	L M	M	97	Y	2.6	85	99
1IRU	M N	M	59	G	13.9	58	79
1IRU	M N	M	60	D	1.6	58	79
1IRU	O P	P	23	Y	3.4	19	30
1IRU	O P	P	79	G	1.8	79	101
1IRU	O P	P	80	P	1.3	79	101
1IRU	O U	O	24	Q	2.1	23	36
1IRU	O U	O	27	Y	1.7	23	36
1IRU	O U	O	84	T	1.2	84	106
1IRU	O U	U	117	M	1.0	108	122
1IRU	O U	U	120	H	1.1	108	122
1IRU	O V	O	95	R	1.4	84	106
1IRU	O V	O	103	Y	2.5	84	106
1IRU	O V	V	61	Y	2.8	49	71
1IRU	O V	V	65	F	1.6	49	71
1IRU	O V	V	68	I	1.2	49	71
1IRU	O W	O	105	Y	3.1	84	106
1IRU	O W	W	66	H	2.9	49	71
1IRU	O W	W	78	T	1.1	76	90
1IRU	P Q	P	118	Q	1.0	106	120
1IRU	P Q	Q	23	Y	2.8	19	29
1IRU	P W	P	98	L	1.1	79	101
1IRU	P X	P	100	Y	1.5	79	101
1IRU	P X	X	74	Y	1.0	57	78
1IRU	Q R	Q	116	D	1.2	107	121
1IRU	Q R	Q	119	Q	2.8	107	121
1IRU	Q R	R	18	Q	1.1	17	28
1IRU	Q R	R	21	Y	2.6	17	28

1IRU	Q R	R	81	R	2.5	77	85
1IRU	Q R	R	82	I	1.1	77	85
1IRU	Q X	Q	91	R	1.1	80	102
1IRU	Q X	Q	99	L	1.3	80	102
1IRU	Q X	X	73	L	1.2	57	78
1IRU	Q X	X	76	L	1.1	57	78
1IRU	Q Y	Q	101	Y	2.7	80	102
1IRU	Q Y	Y	67	Y	1.4	50	71
1IRU	Q Y	Y	86	R	1.5	77	93
1IRU	R S	R	116	Q	2.2	104	118
1IRU	R S	S	23	Q	1.5	22	33
1IRU	R S	S	26	Y	3.4	22	33
1IRU	R Y	R	96	L	3.1	86	98
1IRU	R Y	Y	66	L	1.5	50	71
1IRU	S T	T	24	Y	3.2	20	32
1IRU	S Z	S	100	W	1.6	82	103
1IRU	S Z	S	101	F	3.2	82	103
1IRU	S Z	Z	57	R	1.1	49	70
1IRU	S Z	Z	61	R	1.3	49	70
1IRU	S Z	Z	64	R	1.1	49	70
1IRU	S Z	Z	65	I	1.0	49	70
1IRU	S Z	Z	68	L	1.5	49	70
1IRU	T U	T	176	M	1.0	176	181
1IRU	T U	U	22	Q	1.7	21	32
1IRU	T U	U	25	Y	3.2	21	32
1IRU	T U	U	86	S	1.1	81	103
1IRU	U V	U	102	F	3.3	81	103
1IRU	U V	V	66	H	2.3	49	71
1IRU	V N	N	145	L	1.1	141	155
1IRU	V W	V	53	Q	1.3	49	71
1IRU	V W	W	88	F	1.8	76	90
1IRU	W M	W	164	F	1.3	148	165
1IRU	W M	M	177	D	1.0	168	186
1IRU	W M	M	180	I	1.1	168	186
1IRU	W M	M	184	E	1.7	168	186
1IRU	W N	W	132	L	1.0	131	141
1IRU	W N	N	149	L	1.5	141	155
1IRU	W N	N	175	V	1.0	162	180
1IRU	W X	W	51	D	4.1	49	71
1IRU	W X	X	96	Y	3.0	84	97
1IRU	X L	L	165	Y	1.6	149	167
1IRU	X M	X	148	G	23.3	143	151
1IRU	X M	X	149	M	1.1	143	151
1IRU	X Y	X	59	D	2.8	57	78
1IRU	Y L	Y	142	I	1.2	134	146
1IRU	Y L	Y	144	D	1.2	134	146
1IRU	Y L	L	134	Y	1.1	132	141
1IRU	Y L	L	137	G	4.7	132	141
1IRU	Y L	L	138	V	2.5	132	141
1IRU	Y L	L	162	Q	1.1	149	167
1IRU	Y L	L	166	R	1.4	149	167
1IRU	Y Z	Y	51	G	72.4	50	71
1IRU	Y Z	Y	58	E	1.0	50	71
1IRU	Y Z	Z	88	Y	2.1	76	90
1IW7	A C	A	41	R	1.0	32	48
1IW7	A C	A	42	R	1.3	32	48
1IW7	A C	A	77	E	2.0	75	85
1IW7	A C	A	83	K	1.7	75	85
1IW7	A C	A	154	E	1.5	153	157
1IW7	A C	C	929	R	1.3	911	933

1IW7	A C	C	932	E	1.1	911	933
1IW7	A C	C	938	K	1.5	938	951
1IW7	B C	B	41	R	1.4	32	48
1IW7	B C	C	692	E	1.1	692	697
1IW7	B D	D	813	L	1.5	810	816
1IW7	B D	D	851	L	1.1	846	855
1IW7	C D	C	1035	M	1.5	1034	1043
1IW7	C D	C	1039	A	1.0	1034	1043
1IW7	C D	C	1056	K	16.7	1046	1059
1IW7	C D	C	1067	Y	1.5	1060	1072
1IW7	C D	C	1071	I	1.3	1060	1072
1IW7	C D	D	648	M	1.7	646	653
1IW7	C D	D	652	L	4.2	646	653
1IW7	C D	D	939	F	1.4	924	946
1IW7	C D	D	1070	Y	4.2	1067	1090
1IW7	C D	D	1071	F	3.2	1067	1090
1IW7	C D	D	1078	R	1.9	1067	1090
1IW7	C D	D	1081	G	20.9	1067	1090
1IW7	C D	D	1092	G	73.5	1091	1095
1IW7	C D	D	1099	V	1.1	1096	1101
1IW7	C D	D	1223	I	1.3	1221	1236
1IW7	C F	C	773	L	1.1	769	779
1IW7	C F	C	774	L	1.0	769	779
1IW7	C F	C	775	R	1.9	769	779
1IW7	C F	C	1060	I	1.0	1060	1072
1IW7	C F	C	1067	Y	1.4	1060	1072
1IW7	D E	D	757	A	3.7	753	760
1IW7	D E	E	18	R	3.0	16	33
1IW7	D E	E	20	T	3.2	16	33
1IW7	D E	E	21	V	1.6	16	33
1IW7	D F	D	159	R	1.0	155	160
1IW7	D F	D	568	R	1.1	564	583
1IW7	D F	D	671	K	1.2	670	677
1IW7	D F	F	86	H	1.0	76	91
1IW7	D F	F	87	E	1.2	76	91
1IW7	D F	F	96	L	74.9	95	121
1IW7	D F	F	101	E	1.2	95	121
1IW7	D F	F	104	R	1.7	95	121
1IW7	D F	F	221	I	1.0	209	227
1IW7	D F	F	310	I	1.0	301	312
1IW7	K M	K	80	L	1.2	75	85
1IW7	K M	K	83	K	1.1	75	85
1IW7	K M	K	154	E	1.3	153	157
1IW7	K M	M	938	K	1.0	938	951
1IW7	L N	N	855	H	1.2	846	856
1IW7	M N	M	882	L	1.0	882	898
1IW7	M N	M	1038	W	1.1	1034	1043
1IW7	M N	M	1070	I	2.1	1060	1072
1IW7	M N	M	1085	F	1.7	1083	1095
1IW7	M N	M	1093	Q	1.1	1083	1095
1IW7	M N	N	21	W	3.6	15	22
1IW7	M N	N	85	V	1.1	83	88
1IW7	M N	N	656	F	1.6	654	664
1IW7	M N	N	754	F	1.9	753	760
1IW7	M N	N	1071	F	1.1	1067	1089
1IW7	M N	N	1081	G	3.4	1067	1089
1IW7	M N	N	1434	W	4.8	1434	1438
1IW7	M P	M	774	L	1.9	769	779
1IW7	M P	P	373	K	1.5	366	377
1IW7	M P	P	374	G	219.7	366	377

1IW7	N O	N	1495	I	1.0	1489	1503
1IW7	N O	O	21	V	1.7	16	33
1IW7	N O	O	61	E	1.3	60	70
1IW7	N O	O	88	E	1.5	82	93
1IW7	N P	N	159	R	1.1	155	160
1IW7	N P	N	546	R	1.3	539	561
1IW7	N P	N	550	R	1.2	539	561
1IW7	N P	N	553	R	4.4	539	561
1IW7	N P	N	557	L	3.5	539	561
1IW7	N P	N	565	I	3.9	564	583
1IW7	N P	N	566	I	1.9	564	583
1IW7	N P	N	572	R	1.1	564	583
1IW7	N P	N	576	E	1.0	564	583
1IW7	N P	N	616	Q	65.9	613	618
1IW7	N P	N	671	K	1.0	670	677
1IW7	N P	P	80	P	1.1	76	91
1IW7	N P	P	84	Y	2.9	76	91
1IW7	N P	P	96	L	41.6	95	121
1IW7	N P	P	97	E	21.2	95	121
1IW7	N P	P	140	R	2.0	139	145
1IW7	N P	P	188	I	3.3	168	191
1IW7	N P	P	192	L	3.8	192	202
1IW7	N P	P	211	D	3.5	209	227
1IW7	N P	P	214	Q	1.3	209	227
1IW7	N P	P	215	E	1.2	209	227
1IW7	N P	P	346	T	1.0	342	360
1IWA	A N	A	186	G	359.2	182	196
1IWA	A N	A	187	R	1.4	182	196
1IWA	A N	A	190	Y	1.1	182	196
1IWA	A P	A	431	R	1.4	413	433
1IWA	A P	P	28	K	2.1	23	36
1IWA	A P	P	32	Y	1.8	23	36
1IWA	C F	C	186	G	217.7	182	196
1IWA	C F	C	190	Y	1.1	182	196
1IWA	C H	C	156	I	1.2	155	163
1IWA	C H	C	219	L	1.0	214	231
1IWA	C J	C	70	W	1.7	70	74
1IWA	E D	E	156	I	1.1	155	163
1IWA	E D	E	219	L	1.1	214	231
1IWA	E D	D	28	K	1.5	23	35
1IWA	E H	E	186	G	259.4	182	196
1IWA	E H	E	190	Y	1.2	182	196
1IWA	E L	E	70	W	1.6	70	74
1IWA	G B	G	156	I	1.7	155	163
1IWA	G B	G	219	L	1.0	214	231
1IWA	G D	G	186	G	228.1	182	196
1IWA	G D	G	190	Y	1.9	182	196
1IWA	G D	G	194	K	1.0	182	196
1IWA	G D	G	227	K	1.4	214	231
1IWA	G P	P	86	E	1.0	80	94
1IWA	I B	I	186	G	178.2	182	196
1IWA	I F	I	156	I	1.8	155	163
1IWA	I N	N	86	E	1.0	80	94
1IWA	K L	K	156	I	1.2	155	163
1IWA	K L	K	429	L	2.0	413	433
1IWA	K L	K	431	R	4.8	413	433
1IWA	K L	L	25	Q	4.7	23	36
1IWA	K L	L	28	K	2.3	23	36
1IWA	K P	K	186	G	88.1	182	196
1IWA	M H	M	70	W	1.1	70	74

1IWA	M H	M	73	L	1.2	70	74
1IWA	M H	H	86	E	2.1	80	94
1IWA	M J	M	432	N	1.0	413	433
1IWA	M J	J	29	Q	1.3	23	36
1IWA	M L	M	186	G	219.8	182	196
1IWA	O F	F	86	E	1.1	80	94
1IWA	O J	O	186	G	213.0	182	196
1IWA	O J	O	190	Y	2.6	182	196
1IWA	O J	O	194	K	1.3	182	196
1IWA	O J	O	414	Q	1.3	413	433
1IWA	O N	O	156	I	1.1	155	163
1IWA	O N	O	219	L	1.0	214	231
1IWA	O N	O	429	L	1.5	413	433
1IWA	O N	O	432	N	1.6	413	433
1IWA	O N	N	28	K	1.4	23	36
1IWP	A B	A	178	R	2.3	177	195
1IWP	A B	A	305	G	102.1	304	310
1IWP	A B	A	458	L	2.4	454	467
1IWP	A B	B	82	F	1.0	80	91
1IWP	A B	B	142	Y	2.3	129	144
1IWP	A B	B	160	R	3.8	159	177
1IWP	A B	B	161	P	1.1	159	177
1IWP	A B	B	164	M	3.2	159	177
1IWP	A B	B	171	H	1.1	159	177
1IWP	A B	B	172	I	1.2	159	177
1IWP	A E	E	169	L	1.4	159	177
1IWP	A G	A	65	R	2.1	62	71
1IWP	A G	A	214	M	1.6	206	215
1IWP	A G	A	230	E	1.4	230	236
1IWP	A G	A	234	T	1.2	230	236
1IWP	A G	A	241	W	3.9	240	253
1IWP	A G	A	245	F	5.0	240	253
1IWP	A G	A	246	L	1.2	240	253
1IWP	A G	A	472	L	2.1	471	481
1IWP	A G	A	491	L	1.7	484	500
1IWP	A G	A	498	V	1.6	484	500
1IWP	A G	G	37	V	1.5	34	40
1IWP	A G	G	54	L	1.0	51	63
1IWP	A G	G	79	L	1.6	67	82
1IWP	A G	G	84	D	2.0	84	95
1IWP	A G	G	88	L	2.3	84	95
1IWP	A G	G	91	Y	3.4	84	95
1IWP	A G	G	123	F	1.5	118	134
1IWP	A G	G	129	E	1.7	118	134
1IWP	A G	G	131	Y	1.2	118	134
1IWP	L E	L	305	G	44.7	304	310
1IWP	L E	E	82	F	1.1	80	89
1IWP	L E	E	160	R	3.1	159	177
1IWP	L E	E	161	P	1.1	159	177
1IWP	L E	E	164	M	2.9	159	177
1IWP	L E	E	171	H	1.1	159	177
1IWP	L M	L	214	M	1.0	206	215
1IWP	L M	L	234	T	1.1	230	236
1IWP	L M	L	241	W	3.0	240	253
1IWP	L M	L	245	F	4.5	240	253
1IWP	L M	L	246	L	1.1	240	253
1IWP	L M	L	472	L	1.6	471	480
1IWP	L M	L	491	L	1.5	484	500
1IWP	L M	M	34	L	1.5	34	40
1IWP	L M	M	37	V	1.5	34	40

1IWP	L M	M	54	L	1.2	51	63
1IWP	L M	M	57	Q	1.3	51	63
1IWP	L M	M	61	A	1.0	51	63
1IWP	L M	M	69	V	1.9	67	82
1IWP	L M	M	73	F	1.6	67	82
1IWP	L M	M	79	L	5.0	67	82
1IWP	L M	M	80	I	6.1	67	82
1IWP	L M	M	88	L	1.8	84	95
1IWP	L M	M	91	Y	3.1	84	95
1IWP	L M	M	94	L	1.0	84	95
1IWP	L M	M	123	F	2.0	118	134
1IWQ	A B	A	11	E	1.3	6	20
1IWQ	A B	A	12	F	1.5	6	20
1IWQ	A B	A	14	E	1.5	6	20
1IWQ	A B	A	72	M	1.4	65	76
1IWQ	A B	A	92	F	1.1	82	93
1IWQ	A B	A	105	L	1.2	102	112
1IWQ	A B	A	109	M	3.7	102	112
1IWQ	A B	A	120	E	2.3	118	129
1IWQ	A B	A	123	E	2.1	118	129
1IWQ	A B	A	124	M	1.5	118	129
1IWQ	A B	A	127	E	1.4	118	129
1IWQ	A B	A	144	M	4.5	138	146
1IWQ	A B	B	200	F	5.4	200	207
1IWQ	A B	B	201	K	1.7	200	207
1IWQ	A B	B	202	L	3.3	200	207
1IXR	B C	B	184	K	1.5	179	189
1IXR	B C	B	187	L	1.2	179	189
1IXS	A B	A	184	K	1.0	179	188
1IXS	A B	A	187	L	1.4	179	188
1IXS	A B	B	78	G	134.2	77	88
1IXX	E F	F	23	W	1.0	23	34
1IYJ	A B	A	60	L	1.4	58	62
1IYJ	A B	A	61	E	1.4	58	62
1IYJ	A B	B	2566	F	1.2	2547	2568
1IYJ	A B	B	2589	R	1.3	2579	2596
1IYJ	C D	C	60	L	1.0	58	62
1IYJ	C D	C	61	E	2.2	58	62
1IYJ	C D	D	2440	L	1.0	2439	2446
1IYJ	C D	D	2453	L	1.3	2453	2458
1IYJ	C D	D	2560	K	1.0	2547	2568
1IYJ	C D	D	2564	M	1.0	2547	2568
1IYJ	C D	D	2585	Q	1.2	2579	2596
1IYJ	C D	D	2588	Y	1.0	2579	2596
1IYJ	C D	D	2589	R	1.3	2579	2596
1IZL	A D	A	150	P	226.7	144	152
1IZL	A D	A	209	A	2.2	199	216
1IZL	A D	A	213	A	2.2	199	216
1IZL	A D	A	215	H	2.2	199	216
1IZL	A D	A	276	A	2.2	271	279
1IZL	A D	D	141	Y	22.2	140	146
1IZL	A D	D	185	F	10.1	185	191
1IZL	A D	D	189	H	8.2	185	191
1IZL	A D	D	207	G	1.8	206	216
1IZL	A D	D	208	A	2.2	206	216
1IZL	A D	D	212	A	2.2	206	216
1IZL	A D	D	213	I	2.7	206	216
1IZL	A D	D	215	G	4.6	206	216
1IZL	A D	D	274	V	2.3	270	276
1IZL	A D	D	275	P	3.3	270	276

1IZL	A D	D	278	G	3.9	277	294
1IZL	A D	D	316	T	60.0	316	320
1IZL	E F	E	30	F	1.4	28	32
1IZL	E F	F	34	G	3.6	29	39
1IZL	J N	J	150	P	228.9	144	152
1IZL	J N	J	214	M	1.4	199	216
1IZL	J N	J	273	F	1.0	271	279
1IZL	J N	N	144	I	2.2	140	146
1IZL	J N	N	213	I	2.7	206	216
1IZL	J N	N	215	G	4.5	206	216
1IZL	J N	N	275	P	3.3	270	276
1IZL	J N	N	278	G	4.6	277	294
1IZL	P Q	Q	32	F	1.8	32	39
1IZL	P Q	Q	34	G	193.1	32	39
1IZN	A B	A	16	I	1.4	10	22
1IZN	A B	A	20	F	3.5	10	22
1IZN	A B	A	39	L	3.1	29	41
1IZN	A B	A	239	Y	1.0	221	252
1IZN	A B	A	243	I	1.5	221	252
1IZN	A B	A	244	S	1.2	221	252
1IZN	A B	A	247	Y	4.4	221	252
1IZN	A B	A	250	M	2.4	221	252
1IZN	A B	A	255	F	3.5	253	259
1IZN	A B	A	258	L	2.5	253	259
1IZN	A B	A	271	W	5.2	271	275
1IZN	A B	A	274	I	1.3	271	275
1IZN	A B	B	12	L	2.1	3	14
1IZN	A B	B	31	L	2.6	21	32
1IZN	A B	B	111	Y	3.1	91	113
1IZN	A B	B	112	F	1.0	91	113
1IZN	A B	B	214	G	87.6	209	244
1IZN	A B	B	218	E	3.0	209	244
1IZN	A B	B	221	E	1.8	209	244
1IZN	A B	B	222	N	1.2	209	244
1IZN	A B	B	225	R	4.9	209	244
1IZN	A B	B	231	I	1.3	209	244
1IZN	A B	B	232	Y	2.1	209	244
1IZN	A B	B	233	F	3.3	209	244
1IZN	A B	B	236	T	1.4	209	244
1IZN	A B	B	237	K	2.4	209	244
1IZN	A B	B	239	I	2.0	209	244
1IZN	A B	B	243	L	2.6	209	244
1IZN	C D	C	16	I	1.4	10	23
1IZN	C D	C	20	F	3.6	10	23
1IZN	C D	C	39	L	2.6	29	41
1IZN	C D	C	135	H	1.2	127	136
1IZN	C D	C	233	E	1.5	221	257
1IZN	C D	C	239	Y	2.4	221	257
1IZN	C D	C	247	Y	2.7	221	257
1IZN	C D	C	250	M	2.2	221	257
1IZN	C D	C	255	F	3.5	221	257
1IZN	C D	C	271	W	4.8	271	276
1IZN	C D	C	274	I	1.3	271	276
1IZN	C D	C	275	L	1.7	271	276
1IZN	C D	D	5	Q	1.4	3	14
1IZN	C D	D	12	L	2.1	3	14
1IZN	C D	D	31	L	2.3	21	32
1IZN	C D	D	111	Y	3.0	91	113
1IZN	C D	D	214	G	40.3	209	233
1IZN	C D	D	218	E	2.8	209	233

1IZN	C D	D	221	E	1.5	209	233
1IZN	C D	D	222	N	1.2	209	233
1IZN	C D	D	225	R	4.4	209	233
1IZN	C D	D	231	I	1.2	209	233
1IZN	C D	D	232	Y	1.2	209	233
1IZN	C D	D	236	T	1.5	234	244
1IZN	C D	D	237	K	1.3	234	244
1IZN	C D	D	239	I	1.6	234	244
1IZN	C D	D	243	L	2.7	234	244
1J19	A B	A	281	L	1.2	274	294
1J19	A B	A	288	H	1.1	274	294
1J19	A B	B	412	V	2.1	412	416
1J1D	A B	A	99	D	1.6	94	105
1J1D	A B	A	101	F	1.4	94	105
1J1D	A B	A	102	R	1.6	94	105
1J1D	A B	B	259	Y	2.0	226	270
1J1D	A B	B	263	V	1.1	226	270
1J1D	A C	A	60	M	1.5	54	64
1J1D	A C	A	103	M	1.4	94	105
1J1D	A C	A	136	L	1.7	130	141
1J1D	A C	A	138	K	1.4	130	141
1J1D	A C	A	156	F	1.0	150	157
1J1D	A C	C	45	R	1.8	43	62
1J1D	A C	C	49	L	1.2	43	62
1J1D	A C	C	53	L	1.5	43	62
1J1D	A C	C	54	L	1.1	43	62
1J1D	A C	C	61	L	1.3	43	62
1J1D	B C	B	217	K	1.5	204	224
1J1D	B C	B	221	I	2.1	204	224
1J1D	B C	B	230	R	1.9	226	270
1J1D	B C	B	236	L	2.1	226	270
1J1D	B C	B	237	W	2.2	226	270
1J1D	B C	B	240	I	2.4	226	270
1J1D	B C	B	243	L	1.3	226	270
1J1D	B C	B	247	K	1.1	226	270
1J1D	B C	B	248	F	2.3	226	270
1J1D	B C	B	249	D	1.8	226	270
1J1D	B C	B	250	L	2.1	226	270
1J1D	B C	B	253	K	1.5	226	270
1J1D	B C	B	264	L	1.6	226	270
1J1D	B C	B	267	R	1.3	226	270
1J1D	B C	C	72	K	2.9	63	80
1J1D	B C	C	76	L	1.1	63	80
1J1D	B C	C	90	F	1.6	90	136
1J1D	B C	C	98	R	1.5	90	136
1J1D	B C	C	100	L	1.2	90	136
1J1D	B C	C	101	H	1.6	90	136
1J1D	B C	C	104	V	1.5	90	136
1J1D	B C	C	107	V	1.5	90	136
1J1D	B C	C	110	E	1.3	90	136
1J1D	B C	C	111	R	2.9	90	136
1J1D	D E	D	99	D	1.2	94	105
1J1D	D E	D	102	R	1.3	94	105
1J1D	D E	E	256	Q	1.3	226	271
1J1D	D E	E	259	Y	2.6	226	271
1J1D	D F	D	6	K	1.4	4	11
1J1D	D F	D	20	F	1.6	14	28
1J1D	D F	D	48	L	1.3	38	49
1J1D	D F	D	81	M	1.1	74	82
1J1D	D F	D	103	M	1.2	94	105

1J1D	D F	D	104	F	1.8	94	105
1J1D	D F	D	121	L	1.1	114	123
1J1D	D F	D	136	L	1.7	131	141
1J1D	D F	D	138	K	1.1	131	141
1J1D	D F	F	45	R	1.4	44	80
1J1D	D F	F	47	L	1.3	44	80
1J1D	D F	F	53	L	2.8	44	80
1J1D	D F	F	54	L	3.0	44	80
1J1D	D F	F	56	I	1.2	44	80
1J1D	D F	F	61	L	1.1	44	80
1J1D	D F	F	154	M	1.2	151	156
1J1D	D F	F	155	M	1.3	151	156
1J1D	E F	E	216	R	1.3	202	223
1J1D	E F	E	236	L	1.6	226	271
1J1D	E F	E	237	W	3.0	226	271
1J1D	E F	E	240	I	3.4	226	271
1J1D	E F	E	241	Y	1.2	226	271
1J1D	E F	E	243	L	3.0	226	271
1J1D	E F	E	244	E	1.5	226	271
1J1D	E F	E	249	D	1.2	226	271
1J1D	E F	E	250	L	1.8	226	271
1J1D	E F	E	261	I	1.4	226	271
1J1D	E F	E	264	L	1.2	226	271
1J1D	E F	E	265	R	1.0	226	271
1J1D	E F	F	72	K	2.7	44	80
1J1D	E F	F	76	L	1.4	44	80
1J1D	E F	F	98	R	1.1	90	137
1J1D	E F	F	100	L	2.3	90	137
1J1D	E F	F	101	H	2.0	90	137
1J1D	E F	F	102	A	1.3	90	137
1J1D	E F	F	103	R	1.7	90	137
1J1D	E F	F	104	V	2.8	90	137
1J1D	E F	F	105	D	1.4	90	137
1J1D	E F	F	107	V	1.2	90	137
1J1D	E F	F	108	D	1.5	90	137
1J1D	E F	F	110	E	2.6	90	137
1J1D	E F	F	111	R	3.2	90	137
1J1D	E F	F	114	I	1.2	90	137
1J1D	E F	F	118	V	1.2	90	137
1J1D	E F	F	125	I	1.4	90	137
1J1D	E F	F	128	L	1.6	90	137
1J1D	E F	F	135	L	1.0	90	137
1J1E	A B	A	150	Y	1.3	150	157
1J1E	A B	B	270	D	1.0	226	271
1J1E	A C	A	45	M	1.0	38	48
1J1E	A C	A	100	L	3.5	94	105
1J1E	A C	A	102	R	1.1	94	105
1J1E	A C	A	103	M	1.6	94	105
1J1E	A C	A	104	F	1.2	94	105
1J1E	A C	A	132	D	1.2	130	141
1J1E	A C	A	136	L	1.9	130	141
1J1E	A C	C	45	R	8.0	43	80
1J1E	A C	C	49	L	2.1	43	80
1J1E	A C	C	53	L	1.0	43	80
1J1E	A C	C	54	L	1.3	43	80
1J1E	A C	C	64	E	1.0	43	80
1J1E	A C	C	155	M	1.0	151	160
1J1E	A C	C	158	L	1.1	151	160
1J1E	A C	C	159	L	1.6	151	160
1J1E	B C	B	217	K	1.0	204	224

1J1E	B C	B	221	I	1.3	204	224
1J1E	B C	B	229	L	1.5	226	271
1J1E	B C	B	236	L	1.8	226	271
1J1E	B C	B	237	W	2.4	226	271
1J1E	B C	B	241	Y	1.0	226	271
1J1E	B C	B	243	L	1.7	226	271
1J1E	B C	B	244	E	1.1	226	271
1J1E	B C	B	248	F	2.2	226	271
1J1E	B C	B	250	L	1.6	226	271
1J1E	B C	B	268	I	1.5	226	271
1J1E	B C	C	72	K	1.0	43	80
1J1E	B C	C	76	L	2.1	43	80
1J1E	B C	C	90	F	1.4	90	136
1J1E	B C	C	93	L	1.1	90	136
1J1E	B C	C	98	R	1.3	90	136
1J1E	B C	C	100	L	1.9	90	136
1J1E	B C	C	103	R	1.0	90	136
1J1E	B C	C	110	E	1.2	90	136
1J1E	B C	C	111	R	2.4	90	136
1J1E	B C	C	128	L	1.3	90	136
1J1E	B C	C	132	I	1.7	90	136
1J1E	D E	D	102	R	1.4	94	105
1J1E	D E	E	259	Y	1.7	226	271
1J1E	D E	E	263	V	1.1	226	271
1J1E	D F	D	48	L	1.0	38	51
1J1E	D F	D	100	L	1.3	94	105
1J1E	D F	D	102	R	1.0	94	105
1J1E	D F	D	131	D	1.0	131	141
1J1E	D F	D	136	L	2.0	131	141
1J1E	D F	D	139	D	1.7	131	141
1J1E	D F	D	153	F	13.6	150	157
1J1E	D F	F	44	S	1.9	43	81
1J1E	D F	F	46	K	2.1	43	81
1J1E	D F	F	47	L	1.3	43	81
1J1E	D F	F	50	K	3.3	43	81
1J1E	D F	F	158	L	2.0	153	159
1J1E	E F	E	229	L	1.8	226	271
1J1E	E F	E	230	R	1.7	226	271
1J1E	E F	E	236	L	1.6	226	271
1J1E	E F	E	237	W	4.7	226	271
1J1E	E F	E	240	I	1.9	226	271
1J1E	E F	E	247	K	2.3	226	271
1J1E	E F	E	250	L	1.1	226	271
1J1E	E F	E	254	F	1.2	226	271
1J1E	E F	E	258	K	3.0	226	271
1J1E	E F	E	260	E	3.1	226	271
1J1E	E F	E	261	I	1.5	226	271
1J1E	E F	E	268	I	2.4	226	271
1J1E	E F	F	72	K	2.2	43	81
1J1E	E F	F	76	L	2.0	43	81
1J1E	E F	F	79	R	1.2	43	81
1J1E	E F	F	90	F	1.2	90	136
1J1E	E F	F	93	L	1.6	90	136
1J1E	E F	F	100	L	1.8	90	136
1J1E	E F	F	110	E	1.4	90	136
1J1E	E F	F	111	R	2.0	90	136
1J1E	E F	F	114	I	1.2	90	136
1J1E	E F	F	118	V	1.2	90	136
1J1E	E F	F	121	N	2.9	90	136
1J1E	E F	F	124	E	3.5	90	136

1J1E	E F	F	128	L	4.5	90	136
1J1E	E F	F	131	K	2.5	90	136
1J1E	E F	F	132	I	1.3	90	136
1J1E	E F	F	135	L	1.3	90	136
1J2J	A B	A	77	L	2.7	75	81
1J2J	A B	A	80	H	2.0	75	81
1J2J	A B	B	182	L	1.7	172	183
1J2J	A B	B	197	I	1.7	187	206
1J34	A B	A	23	W	1.9	23	32
1J34	A B	A	27	E	1.0	23	32
1J34	A B	B	227	E	1.0	223	232
1J34	A C	C	442	W	2.1	442	446
1J3I	A D	A	57	Y	1.9	52	64
1J3I	A D	A	69	K	2.2	67	81
1J3I	A D	D	292	Y	3.0	287	293
1J3I	B C	B	57	Y	1.7	52	63
1J3I	B C	C	285	E	2.5	284	294
1J3I	B C	C	288	D	1.0	284	294
1J3I	B C	C	292	Y	2.9	284	294
1J3I	B C	C	293	F	1.8	284	294
1J7D	A B	A	13	F	4.6	11	25
1J7D	A B	A	17	E	1.0	11	25
1J7D	A B	A	20	E	1.0	11	25
1J7V	L R	L	20	P	3.0	18	32
1J7V	L R	L	24	R	1.8	18	32
1J7V	L R	L	34	K	1.5	34	41
1J8H	A B	A	69	N	1.4	56	77
1J8H	A B	A	70	L	1.9	56	77
1J8H	A B	A	73	M	1.5	56	77
1J8H	A B	A	76	R	2.5	56	77
1J8H	A B	B	56	P	1.2	55	63
1J8H	A B	B	57	D	2.6	55	63
1J8H	A C	A	58	G	6.1	56	77
1J8H	A C	A	65	V	1.0	56	77
1J8H	A C	A	69	N	1.0	56	77
1J8H	A C	A	72	I	1.6	56	77
1J8H	A E	A	60	L	1.0	56	77
1J8H	B C	B	60	Y	1.1	55	63
1J8H	B C	B	61	W	3.6	55	63
1J8H	B C	B	70	Q	3.6	65	73
1J8H	B C	B	71	K	3.0	65	73
1J8H	B C	B	82	N	1.2	78	86
1J8H	D E	E	137	E	1.2	135	142
1J9C	L H	H	128	F	1.2	126	129
1J9C	T L	T	62	E	1.5	60	66
1JB0	A B	A	125	I	1.0	123	127
1JB0	A B	A	463	D	1.0	455	468
1JB0	A B	A	464	T	2.5	455	468
1JB0	A B	A	597	L	1.9	591	620
1JB0	A B	A	655	W	2.5	646	657
1JB0	A B	A	662	I	1.0	659	663
1JB0	A B	A	674	L	2.4	670	692
1JB0	A B	A	677	L	1.3	670	692
1JB0	A B	A	691	F	5.6	670	692
1JB0	A B	A	695	G	95.4	694	711
1JB0	A B	A	698	Q	1.5	694	711
1JB0	A B	A	699	E	1.4	694	711
1JB0	A B	A	700	L	1.1	694	711
1JB0	A B	A	706	W	1.7	694	711
1JB0	A B	A	724	I	1.0	724	754

1JB0	A B	B	444	D	1.3	418	449
1JB0	A B	B	584	L	1.5	578	609
1JB0	A B	B	587	F	1.2	578	609
1JB0	A B	B	623	M	2.7	622	628
1JB0	A B	B	631	W	3.0	629	633
1JB0	A B	B	654	W	1.5	650	672
1JB0	A B	B	667	F	2.7	650	672
1JB0	A B	B	670	L	1.0	650	672
1JB0	A B	B	671	I	2.9	650	672
1JB0	A B	B	674	R	1.3	674	690
1JB0	A B	B	675	G	401.2	674	690
1JB0	A B	B	678	Q	1.1	674	690
1JB0	A B	B	686	W	1.6	674	690
1JB0	A B	B	708	I	1.0	708	738
1JB0	A C	C	52	R	4.1	52	57
1JB0	A D	A	431	D	1.2	429	435
1JB0	A D	D	62	E	1.2	61	75
1JB0	A F	A	706	W	1.5	694	711
1JB0	A F	F	89	R	1.3	62	90
1JB0	A J	J	3	H	1.4	2	8
1JB0	A J	J	7	Y	2.4	2	8
1JB0	A K	K	68	L	1.0	62	75
1JB0	B C	B	18	R	1.1	17	26
1JB0	B D	B	686	W	1.0	674	690
1JB0	B F	F	34	R	2.6	30	40
1JB0	B F	F	38	Y	1.2	30	40
1JB0	B I	B	19	R	2.2	17	26
1JB0	B I	B	69	W	3.4	38	70
1JB0	B L	B	686	W	1.7	674	690
1JB0	B L	L	96	Y	2.1	74	100
1JB0	B L	L	117	W	1.0	114	141
1JB0	B M	B	65	F	1.5	38	70
1JB0	B M	B	69	W	1.8	38	70
1JB0	B M	B	135	Y	3.1	131	155
1JB0	B M	B	139	I	1.3	131	155
1JB0	B M	B	149	L	1.8	131	155
1JB0	B M	B	152	G	2.3	131	155
1JB0	B M	B	153	W	1.2	131	155
1JB0	B M	M	8	V	1.6	5	30
1JB0	B M	M	14	I	1.0	5	30
1JB0	B M	M	21	L	1.2	5	30
1JB0	B M	M	25	L	2.0	5	30
1JB0	B M	M	29	L	1.6	5	30
1JB0	B X	B	465	F	2.9	461	470
1JB0	B X	X	11	F	1.1	11	31
1JB0	B X	X	30	Y	1.0	11	31
1JB0	C D	D	61	K	1.0	61	75
1JB0	C D	D	63	Q	1.1	61	75
1JB0	F J	F	38	Y	2.9	30	40
1JB0	I L	I	31	F	1.6	9	34
1JB0	I L	I	32	L	1.4	9	34
1JB0	I L	L	99	V	1.4	74	100
1JB7	A B	B	143	E	3.1	142	164
1JB7	A B	B	150	H	1.6	142	164
1JB7	A B	B	153	H	2.0	142	164
1JB7	A B	B	156	L	2.0	142	164
1JB7	A B	B	160	I	1.3	142	164
1JB7	A B	B	161	N	1.4	142	164
1JBU	H L	H	128	F	1.3	126	129
1JBU	H X	H	240	K	1.0	235	244

1JCH	A B	A	460	Y	2.3	457	463
1JCH	A B	A	461	G	48.0	457	463
1JCH	A B	B	53	E	1.1	53	60
1JCH	A B	B	54	W	1.1	53	60
1JCH	A B	B	57	L	2.6	53	60
1JCH	C D	C	460	Y	2.3	457	463
1JCH	C D	C	461	G	48.0	457	463
1JCH	C D	D	53	E	1.1	53	60
1JCH	C D	D	54	W	1.1	53	60
1JCH	C D	D	57	L	2.6	53	60
1JD2	A B	B	26	Y	2.6	22	33
1JD2	A B	B	86	E	1.0	82	103
1JD2	A G	A	26	Y	2.9	22	34
1JD2	A G	A	86	R	1.0	82	99
1JD2	A H	H	64	E	1.4	49	70
1JD2	A H	H	65	L	1.3	49	70
1JD2	A H	H	68	L	1.4	49	70
1JD2	B C	C	26	Y	1.9	22	34
1JD2	B C	C	33	R	1.1	22	34
1JD2	B I	B	93	R	1.8	82	103
1JD2	B I	B	97	Q	1.4	82	103
1JD2	B I	I	61	Y	1.7	49	70
1JD2	B I	I	64	N	1.3	49	70
1JD2	B I	I	65	L	1.2	49	70
1JD2	B J	J	66	Y	1.2	49	70
1JD2	B J	J	82	F	1.0	76	90
1JD2	C D	D	23	Q	1.9	22	34
1JD2	C D	D	26	Y	1.6	22	34
1JD2	C D	D	84	D	1.2	82	103
1JD2	C J	C	93	R	1.4	82	102
1JD2	C J	C	101	L	1.1	82	102
1JD2	C J	J	65	L	1.3	49	70
1JD2	C J	J	68	I	1.5	49	70
1JD2	C J	J	69	R	1.0	49	70
1JD2	D E	E	26	Y	2.4	22	33
1JD2	D E	E	83	P	1.1	82	103
1JD2	D K	D	101	L	1.2	82	103
1JD2	D K	K	65	L	1.1	56	70
1JD2	D K	K	68	L	1.4	56	70
1JD2	D L	D	99	H	1.0	82	103
1JD2	D L	L	66	Y	1.1	49	69
1JD2	D L	L	78	S	1.1	76	90
1JD2	D L	L	81	R	1.2	76	90
1JD2	D L	L	85	H	1.6	76	90
1JD2	E F	E	114	H	1.5	109	123
1JD2	E F	F	26	Y	2.3	22	33
1JD2	E F	F	84	D	1.5	82	103
1JD2	E L	E	93	R	3.1	82	103
1JD2	E L	E	97	N	3.0	82	103
1JD2	E L	L	65	W	5.1	49	69
1JD2	E L	L	68	F	2.7	49	69
1JD2	E M	M	82	Y	1.3	76	92
1JD2	F G	F	121	Q	2.3	109	123
1JD2	F G	G	26	Y	2.1	22	32
1JD2	F G	G	83	P	2.8	82	104
1JD2	F G	G	87	N	1.0	82	104
1JD2	F N	F	99	F	1.6	82	103
1JD2	F N	N	66	Y	2.2	49	70
1JD2	F N	N	78	T	2.0	76	90
1JD2	G H	G	110	D	1.3	109	126

1JD2	G N	G	93	K	1.1	82	104
1JD2	G N	G	100	R	1.1	82	104
1JD2	G N	G	101	Y	2.0	82	104
1JD2	G N	N	61	Y	1.5	49	70
1JD2	G N	N	64	E	1.4	49	70
1JD2	G N	N	65	L	1.2	49	70
1JD2	H I	H	51	D	1.9	49	70
1JD2	H I	I	88	Y	3.1	76	90
1JD2	H I	I	139	E	1.1	131	142
1JD2	H I	I	153	E	1.0	148	165
1JD2	H N	H	85	Q	1.0	76	90
1JD2	H N	H	88	F	3.1	76	90
1JD2	H N	N	50	A	1.0	49	70
1JD2	H S	S	153	K	1.4	148	166
1JD2	H T	T	132	H	1.1	129	141
1JD2	H T	T	133	M	1.2	129	141
1JD2	H T	T	137	L	1.3	129	141
1JD2	H T	T	161	V	1.2	148	166
1JD2	I R	R	164	H	1.7	148	166
1JD2	I R	R	197	W	1.9	192	204
1JD2	I S	I	136	G	53.4	131	142
1JD2	I S	I	164	D	1.1	148	165
1JD2	I S	S	161	S	1.0	148	166
1JD2	J K	J	50	G	41.2	49	70
1JD2	J K	J	57	E	1.1	49	70
1JD2	J K	K	88	Y	2.0	76	90
1JD2	J R	J	139	D	1.5	129	141
1JD2	J R	J	164	K	1.5	148	165
1JD2	J R	R	133	F	1.6	131	142
1JD2	J R	R	139	D	1.0	131	142
1JD2	K L	K	51	D	3.0	49	55
1JD2	K L	K	53	Q	1.8	49	55
1JD2	K L	K	54	F	3.0	49	55
1JD2	K L	L	88	Y	4.9	76	90
1JD2	L M	L	51	D	1.2	49	69
1JD2	L M	M	139	R	1.0	129	141
1JD2	M N	M	53	Q	2.2	49	68
1JD2	M N	N	88	Y	1.8	76	90
1JD2	M U	M	129	F	1.8	129	141
1JD2	M U	M	165	R	1.6	148	166
1JD2	M U	U	165	W	2.1	148	166
1JD2	M U	U	187	P	1.2	187	187
1JD2	O L	O	164	W	1.2	148	165
1JD2	O L	L	164	E	1.2	148	165
1JD2	O M	O	137	V	1.1	131	141
1JD2	O M	O	139	E	1.7	131	141
1JD2	O P	P	139	E	1.0	131	142
1JD2	O P	P	152	F	1.2	148	165
1JD2	O P	P	153	E	2.1	148	165
1JD2	O U	O	88	F	2.0	76	90
1JD2	O U	O	132	L	1.1	131	141
1JD2	P K	K	133	F	1.5	131	141
1JD2	P K	K	164	H	1.2	148	166
1JD2	P K	K	165	R	1.6	148	166
1JD2	P K	K	193	G	1.8	192	204
1JD2	P K	K	196	F	1.9	192	204
1JD2	P K	K	197	W	1.0	192	204
1JD2	P L	P	136	G	43.9	131	142
1JD2	P L	P	164	D	5.4	148	165
1JD2	Q K	Q	133	Y	1.1	129	141

1JD2	Q K	K	136	G	1.7	131	141
1JD2	Q R	Q	50	G	79.3	49	70
1JD2	Q R	Q	57	E	1.2	49	70
1JD2	Q R	R	88	Y	1.2	76	90
1JD2	R S	R	51	D	3.0	49	70
1JD2	R S	R	53	Q	1.8	49	70
1JD2	R S	R	54	F	1.0	49	70
1JD2	R S	S	88	Y	4.4	76	90
1JD2	S T	S	51	D	1.2	49	69
1JD2	S T	T	131	A	1.9	129	141
1JD2	T N	T	129	F	1.5	129	141
1JD2	T N	T	165	R	1.0	148	166
1JD2	T N	N	165	W	1.9	148	166
1JD2	T N	N	187	P	1.0	187	187
1JD2	T U	U	88	Y	1.6	76	90
1JD2	V O	O	64	E	1.3	49	70
1JD2	V O	O	65	L	1.6	49	70
1JD2	V W	V	121	Q	1.1	109	123
1JD2	V W	W	26	Y	2.3	22	33
1JD2	W P	W	93	R	1.7	82	103
1JD2	W P	P	61	Y	1.4	49	70
1JD2	W P	P	65	L	1.0	49	70
1JD2	W P	P	68	L	1.4	49	70
1JD2	W Q	Q	66	Y	1.9	49	70
1JD2	W Q	Q	82	F	1.1	76	90
1JD2	W X	X	26	Y	1.5	22	34
1JD2	X Q	X	93	R	1.0	82	102
1JD2	X Q	X	101	L	1.4	82	102
1JD2	X Q	Q	65	L	1.4	49	70
1JD2	X Q	Q	68	I	1.5	49	70
1JD2	X R	R	81	K	1.2	76	90
1JD2	X Y	Y	23	Q	1.7	22	34
1JD2	X Y	Y	26	Y	1.8	22	34
1JD2	Y R	Y	93	R	1.1	82	103
1JD2	Y R	Y	101	L	1.1	82	103
1JD2	Y R	R	64	R	1.0	49	70
1JD2	Y R	R	65	L	1.6	49	70
1JD2	Y R	R	68	L	1.8	49	70
1JD2	Y S	Y	102	Y	1.2	82	103
1JD2	Y S	S	66	Y	1.7	49	69
1JD2	Y Z	Z	26	Y	2.3	22	33
1JD2	Y Z	Z	83	P	2.4	82	103
1JD2	Z S	Z	93	R	2.2	82	103
1JD2	Z S	S	65	W	1.2	49	69
1JD2	Z S	S	68	F	1.9	49	69
1JD2	Z T	T	66	N	1.1	49	68
1JDP	B H	B	173	E	1.0	167	183
1JEB	A B	A	31	R	2.0	21	36
1JEB	A B	A	103	H	1.6	95	113
1JEB	A B	A	107	V	1.0	95	113
1JEB	A B	A	122	H	2.0	119	137
1JEB	A B	B	30	R	1.8	20	35
1JEB	A B	B	112	I	2.1	100	119
1JEB	A B	B	115	G	1.3	100	119
1JEB	A B	B	116	H	2.0	100	119
1JEB	A D	D	37	W	3.0	36	41
1JEB	A D	D	102	N	1.4	100	119
1JEB	C B	C	95	P	1.4	95	113
1JEB	C B	C	96	V	1.4	95	113
1JEB	C B	B	37	W	4.0	36	41

1JEB	C B	B	102	N	1.4	100	119
1JEB	C D	C	31	R	2.4	21	36
1JEB	C D	C	107	V	1.4	95	113
1JEB	C D	C	122	H	2.8	119	137
1JEB	C D	D	30	R	2.4	20	35
1JEB	C D	D	112	I	1.6	100	119
1JEB	C D	D	115	G	3.3	100	119
1JEB	C D	D	116	H	1.6	100	119
1JEK	A B	A	558	V	1.1	547	585
1JEK	A B	A	565	M	1.7	547	585
1JEK	A B	A	568	H	2.6	547	585
1JEK	A B	A	572	G	1.3	547	585
1JEK	A B	B	631	W	1.7	629	661
1JEK	A B	B	635	I	1.3	629	661
1JEK	A B	B	638	H	3.1	629	661
1JEK	A B	B	642	L	2.5	629	661
1JEY	A B	A	333	E	1.0	331	337
1JEY	A B	A	381	L	2.0	378	392
1JEY	A B	A	385	L	1.0	378	392
1JEY	A B	A	387	I	1.0	378	392
1JEY	A B	A	388	K	2.6	378	392
1JEY	A B	A	391	E	1.7	378	392
1JEY	A B	A	459	V	1.3	456	469
1JEY	A B	A	462	M	1.2	456	469
1JEY	A B	A	463	K	1.6	456	469
1JEY	A B	A	466	V	2.5	456	469
1JEY	A B	A	486	H	1.4	481	495
1JEY	A B	A	490	L	2.3	481	495
1JEY	A B	A	493	L	1.0	481	495
1JEY	A B	A	522	V	1.1	521	530
1JEY	A B	A	525	F	1.8	521	530
1JEY	A B	A	529	V	1.3	521	530
1JEY	A B	B	47	F	1.5	30	48
1JEY	A B	B	88	F	1.6	88	98
1JEY	A B	B	451	L	1.7	448	461
1JEY	A B	B	454	V	1.2	448	461
1JEY	A B	B	455	D	1.2	448	461
1JEY	A B	B	458	I	3.1	448	461
1JEY	A B	B	459	D	1.0	448	461
1JEY	A B	B	485	P	1.1	485	500
1JEY	A B	B	513	W	1.5	510	516
1JFI	A B	A	16	R	1.8	14	22
1JFI	A B	A	20	I	3.1	14	22
1JFI	A B	A	34	V	1.5	32	58
1JFI	A B	A	38	I	1.4	32	58
1JFI	A B	A	40	R	1.3	32	58
1JFI	A B	A	42	L	1.7	32	58
1JFI	A B	A	44	L	1.4	32	58
1JFI	A B	A	45	F	3.4	32	58
1JFI	A B	A	50	L	2.0	32	58
1JFI	A B	A	70	L	1.0	67	72
1JFI	A B	B	121	M	1.8	115	126
1JFI	A B	B	125	T	1.2	115	126
1JFI	A B	B	138	L	2.0	133	161
1JFI	A B	B	146	F	3.4	133	161
1JFI	A B	B	147	I	2.6	133	161
1JFI	A B	B	148	H	1.0	133	161
1JFI	A B	B	168	P	1.0	168	179
1JFI	A B	B	171	V	1.1	168	179
1JFI	A B	B	183	Y	2.5	183	211

1JFI	B C	B	219	L	1.1	215	242
1JFI	B C	B	222	Q	1.2	215	242
1JFI	B C	B	225	L	5.8	215	242
1JGL	L H	L	123	E	1.1	122	127
1JGL	L H	L	124	Q	1.3	122	127
1JGN	A B	A	45	G	1.9	40	47
1JGN	A B	A	68	K	1.0	62	82
1JGV	L H	L	124	Q	1.6	122	127
1JH4	A B	A	44	T	2.1	40	48
1JH4	A B	A	45	G	90.4	40	48
1JH4	A B	A	52	N	5.4	52	60
1JH4	A B	A	55	L	2.3	52	60
1JH4	A B	A	71	E	1.6	62	80
1JHL	H A	A	112	R	1.6	109	116
1JHL	H A	A	113	K	1.7	109	116
1JIW	P I	P	169	Y	3.2	169	183
1JIW	P I	P	176	H	1.1	169	183
1JIW	P I	P	177	E	1.3	169	183
1JJ2	A Y	Y	76	G	14.3	74	82
1JJ2	A Y	Y	79	V	1.6	74	82
1JJ2	F L	F	34	N	1.0	33	42
1JJ2	F L	F	41	E	1.0	33	42
1JJ2	F L	F	57	E	1.8	57	69
1JJ2	F L	F	62	H	2.0	57	69
1JJ2	F L	L	7	Y	3.5	4	12
1JJ2	F L	L	8	I	2.5	4	12
1JJ2	F L	L	23	L	1.1	19	33
1JJ2	F L	L	27	R	1.4	19	33
1JJ2	M P	M	24	L	1.1	20	30
1JJ2	R U	U	28	L	1.0	13	36
1JJ2	R U	U	31	R	1.0	13	36
1JJO	A C	A	57	I	1.8	54	65
1JJO	A C	A	62	G	15.0	54	65
1JJO	B C	B	55	L	1.0	54	65
1JJO	B C	C	132	Q	1.1	130	138
1JJO	B C	C	136	M	1.2	130	138
1JJO	B D	B	57	I	1.8	54	65
1JJO	B D	B	62	G	15.0	54	65
1JJO	C E	C	272	I	3.9	271	276
1JJO	C F	C	135	K	1.4	130	138
1JJO	D E	D	135	K	1.6	130	138
1JJO	D F	D	272	I	4.0	271	276
1JJU	A B	A	121	H	1.8	116	130
1JJU	A B	A	128	G	74.8	116	130
1JJU	B C	C	36	G	88.0	34	40
1JJU	B C	C	39	D	3.6	34	40
1JK0	A B	A	171	F	1.1	163	188
1JK0	A B	A	201	F	2.2	194	205
1JK0	A B	B	50	K	1.1	43	55
1JK0	A B	B	53	E	1.0	43	55
1JK9	C D	C	58	V	1.2	57	61
1JL4	A B	A	70	L	1.6	56	77
1JL4	A B	A	73	L	2.0	56	77
1JL4	A B	A	74	T	1.1	56	77
1JL4	A C	A	68	H	1.0	56	77
1JM7	A B	A	81	Q	1.1	80	98
1JM7	A B	A	85	E	2.2	80	98
1JM7	A B	A	86	L	7.7	80	98
1JM7	A B	A	96	D	1.0	80	98
1JM7	A B	B	43	R	1.8	35	49

1JMO	H A	A	63	L	1.2	63	69
1JMO	H A	A	66	I	1.2	63	69
1JMO	H A	A	67	F	2.3	63	69
1JMO	L H	L	14	E	1.8	14	14
1JMO	L H	L	14	E	1.0	14	14
1JMO	L H	L	14	L	1.8	14	14
1JMT	A B	A	88	E	1.2	64	94
1JMT	A B	B	104	P	1.6	104	111
1JMT	A B	B	107	Y	1.3	104	111
1JMT	A B	B	108	K	1.4	104	111
1JMU	A B	A	41	L	1.3	38	42
1JMU	A B	B	111	F	1.0	105	121
1JMU	A B	B	213	Q	1.1	212	223
1JMU	A B	B	267	A	1.8	264	270
1JMU	B G	B	526	S	1.7	524	530
1JMU	B G	G	9	H	2.9	8	19
1JMU	B G	G	10	Q	2.6	8	19
1JMU	B G	G	313	Y	3.8	308	316
1JMU	B G	G	333	I	1.0	331	335
1JMU	B G	G	334	V	2.3	331	335
1JMU	B H	H	161	T	1.2	159	177
1JMU	C D	C	41	L	1.4	38	42
1JMU	C D	D	111	F	1.1	105	121
1JMU	C D	D	213	Q	1.3	212	223
1JMU	D H	D	526	S	1.8	524	530
1JMU	D H	H	9	H	2.9	8	19
1JMU	D H	H	10	Q	2.8	8	19
1JMU	D H	H	313	Y	2.3	308	316
1JMU	D H	H	333	I	1.1	331	335
1JMU	E F	E	41	L	1.4	38	42
1JMU	E F	F	111	F	1.2	105	121
1JMU	E F	F	212	M	1.0	212	223
1JMU	E F	F	213	Q	1.2	212	223
1JMU	F G	G	161	T	1.0	159	177
1JMU	F I	F	518	L	1.0	515	519
1JMU	F I	F	526	S	1.7	524	530
1JMU	F I	I	9	H	2.2	8	19
1JMU	F I	I	10	Q	2.5	8	19
1JMU	F I	I	313	Y	2.1	308	316
1JMU	F I	I	333	I	1.0	331	335
1JMX	A B	A	121	H	1.0	116	130
1JMX	A B	A	128	G	4.4	116	130
1JMX	A G	A	47	M	15.5	34	48
1JMX	A G	A	57	R	2.3	54	68
1JMX	A G	A	129	Q	1.2	116	130
1JMX	A G	G	53	T	1.3	50	54
1JMX	B G	G	36	G	54.0	34	40
1JMX	B G	G	39	D	1.6	34	40
1JN5	A B	A	6	F	2.5	6	30
1JN5	A B	A	10	V	1.1	6	30
1JN5	A B	A	18	E	1.0	6	30
1JN5	A B	B	452	F	2.2	448	455
1JNH	A B	A	126	E	1.9	124	129
1JNH	C D	C	126	E	2.3	124	129
1JNH	E F	E	126	E	1.3	124	129
1JNH	G H	G	126	E	2.0	124	129
1JNL	L H	L	124	Q	1.3	122	128
1JNR	A B	A	39	Y	3.2	32	48
1JNR	A B	A	40	E	1.0	32	48
1JNR	A B	A	43	Y	4.9	32	48

1JNR	A B	A	44	W	3.7	32	48
1JNR	A B	A	47	L	3.0	32	48
1JNR	A B	A	90	E	1.8	89	100
1JNR	A B	A	118	G	1.2	106	126
1JNR	A B	A	122	L	1.5	106	126
1JNR	A B	A	156	I	1.1	153	166
1JNR	A B	A	159	E	3.8	153	166
1JNR	A B	A	359	F	2.2	348	364
1JNR	A B	A	363	L	2.8	348	364
1JNR	A B	A	367	V	1.4	367	376
1JNR	A B	A	368	S	1.1	367	376
1JNR	A B	A	371	L	1.7	367	376
1JNR	A B	A	375	C	1.1	367	376
1JNR	A B	A	461	K	1.3	449	471
1JNR	A B	A	566	H	3.0	565	591
1JNR	A B	A	570	R	3.6	565	591
1JNR	A B	B	126	L	3.4	123	127
1JNR	A D	A	556	D	3.0	540	558
1JNR	C B	C	520	R	1.0	514	529
1JNR	C B	C	556	D	3.6	540	559
1JNR	C D	C	39	Y	2.7	32	48
1JNR	C D	C	40	E	1.4	32	48
1JNR	C D	C	43	Y	5.0	32	48
1JNR	C D	C	44	W	3.7	32	48
1JNR	C D	C	47	L	2.4	32	48
1JNR	C D	C	90	E	2.1	89	100
1JNR	C D	C	118	G	6.7	106	126
1JNR	C D	C	122	L	1.5	106	126
1JNR	C D	C	156	I	2.0	153	166
1JNR	C D	C	159	E	4.8	153	166
1JNR	C D	C	359	F	2.0	348	364
1JNR	C D	C	363	L	2.9	348	364
1JNR	C D	C	367	V	1.4	367	376
1JNR	C D	C	371	L	1.6	367	376
1JNR	C D	C	375	C	1.0	367	376
1JNR	C D	C	566	H	2.3	565	591
1JNR	C D	C	570	R	2.4	565	591
1JNR	C D	D	23	Y	1.1	20	25
1JNR	C D	D	24	I	1.6	20	25
1JNR	C D	D	55	K	1.0	52	56
1JNR	C D	D	126	L	2.9	123	127
1JOU	A B	A	1	F	1.8	1	1
1JOU	A B	A	14	E	1.1	14	14
1JOU	A B	A	14	E	2.2	14	14
1JOU	A B	A	14	L	1.9	14	14
1JOU	A B	A	14	L	1.4	14	14
1JOU	A B	B	129	L	1.0	126	130
1JOU	C B	B	57	H	1.8	56	60
1JOU	C D	C	14	E	1.4	14	14
1JOU	C D	C	14	E	1.1	14	14
1JOU	C D	C	14	L	1.4	14	14
1JOU	C D	C	14	L	1.5	14	14
1JOU	E F	E	14	E	1.5	14	14
1JOU	E F	E	14	E	2.6	14	14
1JOU	E F	E	14	L	1.7	14	14
1JOU	E F	E	14	L	1.2	14	14
1JOW	A B	A	26	N	2.7	23	32
1JOW	A B	A	108	I	1.2	91	109
1JOW	A B	A	154	D	1.3	152	163
1JOW	A B	A	171	P	1.1	167	187

1JOW	A B	A	174	Y	2.7	167	187
1JOW	A B	B	59	I	1.6	59	68
1JPS	L H	L	124	Q	1.3	122	127
1JPW	A D	A	253	F	1.5	249	266
1JPW	A D	A	260	H	1.6	249	266
1JPW	A D	A	296	I	1.8	291	306
1JPW	A D	A	386	R	1.2	375	390
1JPW	A D	A	422	G	1.7	414	428
1JPW	A D	A	426	N	1.1	414	428
1JPW	A D	D	44	V	1.1	42	47
1JPW	A D	D	45	K	1.6	42	47
1JPW	B E	B	253	F	1.3	249	266
1JPW	B E	B	256	I	1.0	249	266
1JPW	B E	B	260	H	1.7	249	266
1JPW	B E	B	292	K	1.2	291	306
1JPW	B E	B	296	I	2.1	291	306
1JPW	B E	B	349	V	1.1	334	350
1JPW	B E	B	387	N	1.0	375	391
1JPW	B E	B	426	N	1.6	414	428
1JPW	B E	E	44	V	2.0	42	47
1JPW	B E	E	45	K	2.1	42	47
1JPW	C F	C	253	F	1.0	249	266
1JPW	C F	C	256	I	1.2	249	266
1JPW	C F	C	260	H	3.5	249	266
1JPW	C F	C	292	K	4.6	291	306
1JPW	C F	C	296	I	2.1	291	306
1JPW	C F	C	349	V	1.4	334	350
1JPW	C F	C	426	N	1.2	414	428
1JPW	C F	C	435	K	2.1	432	441
1JPW	C F	C	470	H	2.3	459	472
1JPW	C F	F	41	L	4.5	41	47
1JPW	C F	F	44	V	1.3	41	47
1JPW	C F	F	45	K	3.0	41	47
1JQJ	A C	C	65	F	1.0	61	69
1JR3	B E	B	220	L	1.2	214	223
1JR3	B E	B	334	I	1.1	322	338
1JR3	B E	B	345	R	1.0	345	359
1JR3	B E	B	347	M	1.9	345	359
1JR3	B E	E	253	M	2.3	241	260
1JR3	B E	E	283	P	1.2	283	303
1JR3	B E	E	295	H	1.0	283	303
1JR3	C D	C	30	N	1.0	22	34
1JR3	C D	D	179	L	1.0	178	192
1JR3	C D	D	190	L	1.3	178	192
1JR3	C D	D	191	L	1.9	178	192
1JR3	D E	D	262	R	1.0	249	263
1JR3	D E	D	299	R	2.0	295	313
1JR3	D E	D	302	V	1.0	295	313
1JR3	D E	D	310	L	1.0	295	313
1JR3	D E	E	310	L	2.8	308	324
1JR3	D E	E	313	T	1.0	308	324
1JR3	D E	E	317	L	1.1	308	324
1JRO	A B	A	28	R	2.2	23	30
1JRO	A B	A	92	Q	1.2	90	98
1JRO	A B	A	96	I	1.9	90	98
1JRO	A B	A	434	Y	2.0	432	451
1JRO	A B	A	448	R	1.2	432	451
1JRO	A B	B	107	R	1.1	106	113
1JRO	A B	B	666	G	129.9	657	675
1JRO	A B	B	673	G	1.6	657	675

1JRO	C D	C	25	E	1.6	23	30
1JRO	C D	C	28	R	3.1	23	30
1JRO	C D	C	96	I	2.3	90	98
1JRO	C D	C	213	T	1.6	206	216
1JRO	C D	C	434	Y	3.8	432	451
1JRO	C D	C	444	L	2.3	432	451
1JRO	C D	C	448	R	3.0	432	451
1JRO	C D	D	15	H	1.5	12	17
1JRO	C D	D	16	V	1.6	12	17
1JRO	C D	D	107	R	2.4	106	115
1JRO	C D	D	666	G	147.7	657	675
1JRO	C D	D	673	G	1.9	657	675
1JRO	C D	D	763	P	1.9	763	775
1JRO	C D	D	764	E	2.6	763	775
1JRO	E F	E	25	E	1.2	23	30
1JRO	E F	E	28	R	2.0	23	30
1JRO	E F	E	96	I	2.5	90	98
1JRO	E F	E	434	Y	2.1	432	451
1JRO	E F	F	15	H	1.1	12	17
1JRO	E F	F	16	V	1.3	12	17
1JRO	E F	F	106	H	1.0	106	114
1JRO	E F	F	107	R	1.8	106	114
1JRO	E F	F	659	L	1.0	657	675
1JRO	E F	F	666	G	138.6	657	675
1JRO	E F	F	764	E	1.6	763	775
1JRO	G H	G	92	Q	2.6	90	98
1JRO	G H	G	96	I	2.1	90	98
1JRO	G H	G	126	D	1.2	125	129
1JRO	G H	G	434	Y	3.0	432	451
1JRO	G H	H	15	H	1.1	12	17
1JRO	G H	H	16	V	1.4	12	17
1JRO	G H	H	107	R	1.4	106	114
1JRO	G H	H	666	G	156.7	657	675
1JRO	G H	H	763	P	3.6	763	775
1JRO	G H	H	764	E	2.0	763	775
1JSD	A B	A	102	R	2.1	98	108
1JSD	A B	B	100	V	1.5	75	127
1JSD	A B	B	104	N	2.6	75	127
1JSD	A B	B	108	L	2.2	75	127
1JSD	A B	B	111	H	2.4	75	127
1JSM	A B	B	93	T	1.6	75	126
1JSM	A B	B	100	V	1.7	75	126
1JSM	A B	B	104	N	2.5	75	126
1JSM	A B	B	108	L	2.0	75	126
1JSM	A B	B	111	H	2.6	75	126
1JSU	A B	A	278	K	2.4	277	282
1JSU	A B	B	181	D	2.5	179	193
1JSU	A B	B	182	I	1.7	179	193
1JSU	A B	B	185	Y	1.2	179	193
1JSU	A B	B	186	L	1.3	179	193
1JSU	A B	B	267	F	1.5	253	269
1JSU	A B	B	295	E	1.1	288	302
1JSU	B C	B	213	I	1.1	208	225
1JSU	B C	B	217	W	1.9	208	225
1JSU	B C	B	254	Q	1.6	253	269
1JSU	B C	B	255	L	2.0	253	269
1JSU	B C	B	281	I	1.4	275	282
1JSU	B C	B	294	M	1.5	288	302
1JSU	B C	B	297	L	2.2	288	302
1JSU	B C	B	300	K	1.0	288	302

1JSU	B C	C	38	H	1.3	38	50
1JSU	B C	C	48	H	1.8	38	50
1JTD	A B	A	111	K	1.9	107	112
1JTG	A B	A	111	K	1.1	107	112
1JTG	C D	C	111	K	1.4	107	112
1JTG	C D	C	270	M	1.1	270	287
1JTH	A B	A	33	L	1.8	12	72
1JTH	A B	A	36	V	1.2	12	72
1JTH	A B	A	43	G	2.3	12	72
1JTH	A B	A	47	L	1.9	12	72
1JTH	A B	A	50	L	1.2	12	72
1JTH	A B	A	57	L	1.2	12	72
1JTH	A B	A	64	M	1.1	12	72
1JTH	A B	A	71	M	1.0	12	72
1JTH	A B	B	198	R	1.1	192	257
1JTH	A B	B	201	E	1.1	192	257
1JTH	A B	B	205	L	2.8	192	257
1JTH	A B	B	212	L	1.1	192	257
1JTH	A B	B	215	M	1.4	192	257
1JTH	A B	B	233	I	1.1	192	257
1JTH	A D	A	21	L	1.1	12	72
1JTH	A D	A	31	R	1.8	12	72
1JTH	A D	A	32	M	1.4	12	72
1JTH	A D	A	35	L	1.4	12	72
1JTH	A D	A	49	M	1.4	12	72
1JTH	A D	A	56	Q	1.1	12	72
1JTH	A D	A	57	L	1.2	12	72
1JTH	A D	A	59	R	1.6	12	72
1JTH	A D	A	60	I	2.4	12	72
1JTH	A D	A	63	G	14.2	12	72
1JTH	A D	A	67	I	1.3	12	72
1JTH	A D	D	199	H	1.6	196	239
1JTH	A D	D	206	E	2.9	196	239
1JTH	A D	D	213	H	2.1	196	239
1JTH	A D	D	216	F	1.2	196	239
1JTH	A D	D	230	I	1.4	196	239
1JTH	A D	D	234	E	2.5	196	239
1JTH	A D	D	237	V	1.3	196	239
1JTH	C B	C	32	M	1.7	11	78
1JTH	C B	C	35	L	1.4	11	78
1JTH	C B	C	49	M	1.4	11	78
1JTH	C B	C	59	R	1.9	11	78
1JTH	C B	C	60	I	1.6	11	78
1JTH	C B	C	63	G	55.1	11	78
1JTH	C B	C	67	I	1.8	11	78
1JTH	C B	B	202	I	1.3	192	257
1JTH	C B	B	206	E	1.2	192	257
1JTH	C B	B	209	I	1.4	192	257
1JTH	C B	B	213	H	3.1	192	257
1JTH	C B	B	223	V	1.1	192	257
1JTH	C B	B	230	I	1.2	192	257
1JTH	C B	B	234	E	2.5	192	257
1JTH	C B	B	251	T	1.0	192	257
1JTH	C D	C	33	L	1.5	11	78
1JTH	C D	C	36	V	1.3	11	78
1JTH	C D	C	40	K	1.0	11	78
1JTH	C D	C	47	L	1.1	11	78
1JTH	C D	C	57	L	1.6	11	78
1JTH	C D	C	71	M	1.2	11	78
1JTH	C D	D	198	R	1.2	196	239

1JTH	C D	D	201	E	1.0	196	239
1JTH	C D	D	205	L	2.1	196	239
1JTH	C D	D	211	E	1.0	196	239
1JTH	C D	D	212	L	1.2	196	239
1JTH	C D	D	215	M	1.5	196	239
1JTH	C D	D	233	I	2.2	196	239
1JTO	A L	L	109	V	1.0	109	114
1JW9	B D	B	176	L	2.3	173	178
1JXP	B D	B	20	S	1.4	13	23
1JY2	N O	N	51	G	42.8	51	77
1JY2	N O	N	53	R	1.6	51	77
1JY2	N O	N	55	K	1.8	51	77
1JY2	N O	N	56	G	94.3	51	77
1JY2	N O	N	57	L	1.7	51	77
1JY2	N O	N	59	D	1.2	51	77
1JY2	N O	N	69	I	1.4	51	77
1JY2	N O	N	76	L	2.0	51	77
1JY2	N O	O	89	L	1.8	86	113
1JY2	N O	O	100	I	1.1	86	113
1JY2	N O	O	107	L	1.5	86	113
1JY2	N P	N	54	M	1.6	51	77
1JY2	N P	N	65	F	3.7	51	77
1JY2	N P	N	68	R	3.8	51	77
1JY2	N P	N	72	L	2.2	51	77
1JY2	N P	P	29	L	2.2	22	48
1JY2	N P	P	37	D	1.8	22	48
1JY2	N P	P	40	L	1.2	22	48
1JY2	N P	P	44	E	1.5	22	48
1JY2	O P	O	86	G	143.6	86	113
1JY2	O P	O	93	L	1.3	86	113
1JY2	O P	O	104	I	1.5	86	113
1JY2	O P	O	111	V	1.2	86	113
1JY2	O P	P	25	I	2.5	22	48
1JY2	O P	P	43	L	1.7	22	48
1JY2	O S	O	90	Q	1.3	86	113
1JY2	Q R	Q	51	G	47.2	51	77
1JY2	Q R	Q	53	R	1.7	51	77
1JY2	Q R	Q	54	M	1.1	51	77
1JY2	Q R	Q	55	K	2.2	51	77
1JY2	Q R	Q	56	G	105.7	51	77
1JY2	Q R	Q	58	I	1.8	51	77
1JY2	Q R	Q	59	D	1.0	51	77
1JY2	Q R	Q	69	I	1.6	51	77
1JY2	Q R	R	89	L	2.2	86	112
1JY2	Q R	R	93	L	1.2	86	112
1JY2	Q R	R	100	I	1.0	86	112
1JY2	Q S	Q	65	F	3.8	51	77
1JY2	Q S	Q	68	R	3.5	51	77
1JY2	Q S	Q	72	L	1.8	51	77
1JY2	Q S	S	27	D	1.0	22	48
1JY2	Q S	S	29	L	2.3	22	48
1JY2	Q S	S	36	V	2.9	22	48
1JY2	Q S	S	37	D	1.8	22	48
1JY2	Q S	S	40	L	1.9	22	48
1JY2	Q S	S	44	E	1.4	22	48
1JY2	R S	R	86	G	123.7	86	112
1JY2	R S	R	93	L	1.1	86	112
1JY2	R S	R	111	V	1.3	86	112
1JY2	R S	S	25	I	2.3	22	48
1JY2	R S	S	32	Y	1.3	22	48

1JY2	R S	S	43	L	1.9	22	48
1JY7	A B	A	31	R	2.6	19	36
1JY7	A B	A	107	V	1.2	95	110
1JY7	A B	A	122	H	1.3	119	137
1JY7	A B	B	34	V	1.0	22	35
1JY7	A B	B	116	H	1.7	100	118
1JY7	A B	B	124	P	1.6	124	146
1JY7	A D	A	95	P	1.7	95	110
1JY7	C B	C	95	P	1.6	95	110
1JY7	C B	B	102	N	1.1	100	118
1JY7	C D	C	31	R	1.8	19	36
1JY7	C D	C	122	H	2.1	119	137
1JY7	C D	D	34	V	1.1	22	35
1JY7	C D	D	116	H	1.6	100	118
1JY7	C D	D	124	P	1.4	124	146
1JY7	P Q	P	31	R	2.2	19	36
1JY7	P Q	P	103	H	1.0	95	110
1JY7	P Q	P	107	V	1.2	95	110
1JY7	P Q	P	122	H	1.5	119	137
1JY7	P Q	Q	34	V	1.2	22	35
1JY7	P Q	Q	116	H	1.6	100	118
1JY7	P S	P	95	P	1.4	95	110
1JY7	R Q	R	95	P	1.5	95	110
1JY7	R Q	Q	102	N	1.0	100	118
1JY7	R S	R	31	R	1.0	19	36
1JY7	R S	R	122	H	2.0	119	137
1JY7	R S	S	34	V	1.2	22	35
1JY7	R S	S	116	H	1.4	100	118
1JY7	R S	S	124	P	1.7	124	146
1JY7	U V	U	122	H	1.3	119	137
1JY7	U V	V	34	V	1.1	22	35
1JY7	U V	V	116	H	1.4	100	118
1JY7	U V	V	125	P	2.6	124	146
1JY7	U X	U	95	P	1.2	95	110
1JY7	W X	W	31	R	1.4	19	36
1JY7	W X	W	107	V	1.5	95	110
1JY7	W X	W	122	H	1.2	119	137
1JY7	W X	X	116	H	1.3	100	118
1JYO	A E	E	130	F	3.6	130	137
1JYO	A E	E	133	L	2.0	130	137
1JYO	A F	A	111	E	2.2	103	124
1JYO	A F	A	118	E	2.8	103	124
1JYO	A F	F	105	I	1.1	93	106
1JYO	A F	F	120	T	1.0	120	128
1JYO	B E	B	111	E	1.9	103	124
1JYO	B E	B	118	E	2.0	103	124
1JYO	B F	F	133	L	2.0	130	137
1JYO	C F	F	83	F	4.5	77	91
1JYO	C F	F	85	H	1.1	77	91
1JYO	C F	F	89	E	1.3	77	91
1JYO	C F	F	90	K	2.4	77	91
1JYO	D E	D	15	L	1.0	2	16
1JYO	D E	E	83	F	4.5	77	91
1JYO	D E	E	85	H	1.2	77	91
1JZD	A C	A	99	G	128.0	99	107
1JZD	A C	A	100	Y	3.5	99	107
1JZD	B C	B	99	G	26.7	99	107
1JZD	B C	B	100	Y	2.4	99	107
1JZD	B C	B	102	H	1.5	99	107
1K3B	A B	B	280	Y	1.7	279	291

1K3B	A B	B	281	L	2.3	279	291
1K3B	A B	B	290	F	1.4	279	291
1K3B	A C	A	8	Y	2.0	8	12
1K3B	B C	B	241	G	14.0	234	251
1K3B	B C	B	242	M	1.5	234	251
1K3B	B C	B	243	L	1.3	234	251
1K3B	B C	B	246	R	3.7	234	251
1K3B	B C	B	247	I	1.2	234	251
1K3B	B C	B	336	M	4.9	333	344
1K3B	B C	B	340	L	2.0	333	344
1K3B	B C	B	356	F	2.7	354	358
1K3M	A B	A	13	L	1.2	13	18
1K3Z	A D	A	298	I	2.2	294	305
1K3Z	A D	A	301	K	1.2	294	305
1K3Z	A D	A	302	R	1.1	294	305
1K3Z	A D	A	309	F	4.0	306	315
1K3Z	A D	A	312	I	1.3	306	315
1K3Z	A D	D	67	I	1.5	61	69
1K3Z	A D	D	68	H	2.5	61	69
1K3Z	A D	D	76	F	1.2	71	78
1K3Z	A D	D	103	I	1.0	97	105
1K3Z	A D	D	250	E	1.6	244	251
1K4C	A B	B	124	Q	1.2	122	127
1K4C	A C	C	49	L	2.1	24	52
1K4C	A C	C	62	Y	2.0	62	74
1K5D	A B	A	29	R	2.2	23	31
1K5D	A B	A	30	H	1.6	23	31
1K5D	A B	A	167	K	1.4	159	170
1K5D	A B	A	201	L	1.5	197	203
1K5D	A C	A	96	V	2.9	95	105
1K5D	A C	A	97	T	1.2	95	105
1K5D	D E	D	167	K	1.9	159	170
1K5D	D F	D	95	R	1.8	95	105
1K5D	D F	D	96	V	3.9	95	105
1K5D	D F	D	97	T	4.2	95	105
1K5D	G H	G	167	K	1.5	159	170
1K5D	G I	G	95	R	2.0	95	105
1K5D	G I	G	96	V	4.1	95	105
1K5D	G I	G	97	T	3.6	95	105
1K5D	J C	C	327	E	1.2	320	333
1K5D	J K	J	167	K	1.9	159	170
1K5D	J K	J	201	L	2.2	197	203
1K5D	J L	J	97	T	4.8	95	105
1K6L	L H	L	7	R	1.5	6	10
1K6L	L H	H	242	M	1.3	227	248
1K6L	L M	L	6	E	2.3	6	10
1K6L	L M	L	9	Y	2.0	6	10
1K6L	L M	L	107	I	1.8	84	112
1K6L	L M	L	111	L	2.4	84	112
1K6L	L M	L	116	H	3.4	116	132
1K6L	L M	L	117	I	2.3	116	132
1K6L	L M	L	180	F	1.0	171	199
1K6L	L M	L	187	L	3.3	171	199
1K6L	L M	L	190	H	1.3	171	199
1K6L	L M	L	191	G	2.7	171	199
1K6L	L M	L	195	L	2.6	171	199
1K6L	L M	L	214	T	1.6	209	220
1K6L	L M	L	215	F	2.1	209	220
1K6L	L M	L	219	L	1.7	209	220
1K6L	L M	L	231	R	2.3	226	251

1K6L	L M	L	233	G	260.7	226	251
1K6L	L M	L	263	W	1.8	259	268
1K6L	L M	M	87	R	2.2	82	88
1K6L	L M	M	132	R	1.1	113	139
1K6L	L M	M	145	H	1.5	145	161
1K6L	L M	M	180	F	2.6	179	193
1K6L	L M	M	183	L	1.0	179	193
1K6L	L M	M	209	L	1.9	200	226
1K6L	L M	M	216	F	2.6	200	226
1K6L	L M	M	220	G	2.3	200	226
1K6L	L M	M	224	L	1.0	200	226
1K6L	L M	M	234	E	1.1	234	240
1K6L	L M	M	235	L	2.4	234	240
1K6L	L M	M	243	T	1.4	243	256
1K6L	L M	M	247	R	2.6	243	256
1K6L	L M	M	250	L	1.6	243	256
1K6L	L M	M	251	F	3.1	243	256
1K6L	L M	M	252	W	1.1	243	256
1K6L	L M	M	254	W	6.2	243	256
1K6L	M H	M	37	T	1.6	37	43
1K6L	M H	M	41	W	2.4	37	43
1K6L	M H	M	201	F	1.7	200	226
1K6L	M H	M	271	W	2.3	262	287
1K6L	M H	M	297	W	1.2	294	301
1K6L	M H	H	17	I	1.1	12	35
1K6L	M H	H	20	F	1.5	12	35
1K6L	M H	H	31	L	1.9	12	35
1K6L	M H	H	34	E	1.1	12	35
1K6L	M H	H	230	E	1.0	227	248
1K6L	M H	H	231	D	2.3	227	248
1K74	A D	A	393	R	1.5	386	408
1K74	A D	A	397	Y	3.2	386	408
1K74	A D	A	426	R	1.2	421	437
1K74	A D	A	430	L	1.2	421	437
1K74	A D	D	434	K	1.2	431	459
1K74	A D	D	436	L	1.5	431	459
1K74	A D	D	437	Q	1.6	431	459
1K74	A D	D	443	R	1.0	431	459
1K74	D E	D	315	V	1.1	311	333
1K74	D E	D	468	L	1.1	467	474
1K74	D E	D	471	E	1.1	467	474
1K74	D E	E	690	L	1.9	688	697
1K74	D E	E	693	L	1.2	688	697
1K74	D E	E	694	L	1.4	688	697
1K7L	A B	A	462	E	2.4	458	465
1K7L	A B	B	690	L	1.8	688	697
1K7L	C D	C	310	K	1.4	302	324
1K7L	C D	C	462	E	1.5	458	465
1K7L	C D	D	690	L	1.2	688	697
1K7L	C D	D	693	L	1.1	688	697
1K7L	C D	D	694	L	1.3	688	697
1K7L	C F	F	689	I	1.0	688	697
1K7L	C F	F	692	R	1.7	688	697
1K7L	E F	E	306	V	3.0	302	324
1K7L	E F	F	694	L	1.6	688	697
1K7L	G H	G	288	T	1.0	268	293
1K7L	G H	H	690	L	1.8	688	697
1K7L	G H	H	694	L	1.4	688	697
1K8I	A B	A	59	W	1.6	58	62
1K8I	A B	A	71	F	2.0	66	87

1K8I	A B	A	72	D	1.1	66	87
1K8I	A B	A	75	F	2.2	66	87
1K8I	A B	A	79	L	1.0	66	87
1K8I	A B	A	83	V	1.0	66	87
1K8I	A B	B	61	L	2.1	51	63
1K8I	A B	B	70	R	1.3	65	74
1K8I	A B	B	81	H	1.0	75	85
1K8I	A B	B	86	W	1.5	86	91
1K8I	A B	B	89	L	1.6	86	91
1KA9	H F	H	187	L	1.1	184	197
1KAT	W X	W	17	F	2.4	17	25
1KAT	W X	W	18	M	2.6	17	25
1KAT	W X	W	21	Y	2.5	17	25
1KAT	W X	W	22	Q	2.6	17	25
1KAT	W X	X	13	W	2.6	13	18
1KAT	W X	X	16	F	1.7	13	18
1KBH	A B	A	13	L	2.3	4	17
1KBH	A B	A	14	H	1.2	4	17
1KBH	A B	A	24	G	74.5	23	32
1KBH	A B	A	34	I	3.0	34	41
1KBH	A B	A	38	V	1.3	34	41
1KBH	A B	B	86	L	2.4	84	100
1KBH	A B	B	91	I	1.2	84	100
1KBH	A B	B	94	R	3.5	84	100
1KBH	A B	B	97	K	1.0	84	100
1KBH	A B	B	98	Y	1.4	84	100
1KC5	L H	L	123	E	1.3	122	127
1KCG	A C	C	73	M	1.1	65	87
1KCG	A C	C	76	E	1.0	65	87
1KCG	A C	C	164	M	1.9	156	186
1KCG	B C	C	82	R	1.2	65	87
1KCG	B C	C	83	L	2.5	65	87
1KCS	L H	L	124	Q	1.4	122	127
1KD8	A B	A	5	L	1.6	2	35
1KD8	A B	A	9	V	1.2	2	35
1KD8	A B	A	13	E	1.2	2	35
1KD8	A B	B	5	L	1.2	2	35
1KD8	A B	B	8	K	1.3	2	35
1KD8	A B	B	19	L	1.2	2	35
1KD8	A B	B	27	K	2.0	2	35
1KD8	A B	B	29	K	1.8	2	35
1KD8	A B	B	33	C	1.4	2	35
1KD8	C D	C	2	V	1.0	2	35
1KD8	C D	C	5	L	1.6	2	35
1KD8	C D	C	9	V	1.2	2	35
1KD8	C D	C	12	I	1.1	2	35
1KD8	C D	C	13	E	1.0	2	35
1KD8	C D	C	19	L	1.6	2	35
1KD8	C D	C	22	E	1.5	2	35
1KD8	C D	C	23	V	1.1	2	35
1KD8	C D	C	26	L	1.4	2	35
1KD8	C D	C	27	E	1.0	2	35
1KD8	C D	D	5	L	1.6	2	35
1KD8	C D	D	8	K	1.5	2	35
1KD8	C D	D	12	L	1.1	2	35
1KD8	C D	D	19	L	1.5	2	35
1KD8	C D	D	22	K	1.7	2	35
1KD8	C D	D	23	V	1.1	2	35
1KD8	C D	D	26	L	2.0	2	35
1KD8	F E	F	5	L	2.3	2	35

1KD8	F E	F	12	I	1.2	2	35
1KD8	F E	F	13	E	1.1	2	35
1KD8	F E	F	19	L	1.6	2	35
1KD8	F E	F	20	E	1.3	2	35
1KD8	F E	F	23	V	1.0	2	35
1KD8	F E	F	27	E	1.3	2	35
1KD8	F E	E	5	L	2.4	2	34
1KD8	F E	E	8	K	1.1	2	34
1KD8	F E	E	12	L	1.1	2	34
1KD8	F E	E	15	K	1.1	2	34
1KD8	F E	E	19	L	2.0	2	34
1KD8	F E	E	22	K	1.2	2	34
1KDD	B A	B	5	L	1.0	2	34
1KDD	B A	B	12	L	1.6	2	34
1KDD	B A	B	15	K	1.3	2	34
1KDD	B A	B	19	L	1.5	2	34
1KDD	B A	B	22	K	1.5	2	34
1KDD	B A	B	26	L	1.3	2	34
1KDD	B A	A	12	L	1.7	2	35
1KDD	B A	A	16	I	2.2	2	35
1KDD	B A	A	20	E	1.4	2	35
1KDD	B A	A	23	V	1.2	2	35
1KDD	B A	A	26	L	1.7	2	35
1KDD	B A	A	27	E	1.0	2	35
1KDD	B A	A	29	E	1.4	2	35
1KDD	D C	D	5	L	1.6	2	33
1KDD	D C	D	8	K	1.7	2	33
1KDD	D C	D	12	L	1.6	2	33
1KDD	D C	D	15	K	1.2	2	33
1KDD	D C	D	23	V	1.4	2	33
1KDD	D C	D	26	L	1.3	2	33
1KDD	D C	C	2	V	1.1	2	33
1KDD	D C	C	5	L	2.0	2	33
1KDD	D C	C	9	V	1.2	2	33
1KDD	D C	C	12	L	2.4	2	33
1KDD	D C	C	13	E	1.0	2	33
1KDD	D C	C	16	I	1.4	2	33
1KDD	D C	C	19	L	1.5	2	33
1KDD	D C	C	23	V	1.1	2	33
1KDD	D C	C	26	L	1.5	2	33
1KDD	E F	E	5	L	1.8	2	34
1KDD	E F	E	6	K	1.1	2	34
1KDD	E F	E	8	K	1.2	2	34
1KDD	E F	E	12	L	1.0	2	34
1KDD	E F	E	15	K	1.4	2	34
1KDD	E F	E	19	L	1.4	2	34
1KDD	E F	E	22	K	1.6	2	34
1KDD	E F	E	26	L	2.6	2	34
1KDD	E F	E	33	C	1.0	2	34
1KDD	E F	F	5	L	1.6	2	34
1KDD	E F	F	12	L	2.8	2	34
1KDD	E F	F	16	I	1.6	2	34
1KDD	E F	F	19	L	1.3	2	34
1KDD	E F	F	20	E	1.5	2	34
1KDD	E F	F	27	E	1.2	2	34
1KDX	A B	A	599	L	1.7	597	612
1KDX	A B	A	606	K	1.8	597	612
1KDX	A B	A	655	E	1.2	646	666
1KDX	A B	A	657	I	1.1	646	666
1KDX	A B	A	658	Y	2.7	646	666

1KDX	A B	B	124	R	1.0	120	130
1KDX	A B	B	128	L	1.6	120	130
1KDX	A B	B	137	I	2.1	135	145
1KDX	A B	B	141	L	1.0	135	145
1KDX	A B	B	144	D	1.0	135	145
1KEG	L H	L	124	Q	1.5	122	127
1KEL	L H	L	129	Q	1.1	127	132
1KEN	A B	B	89	I	1.2	77	97
1KEN	A B	B	92	W	2.0	77	97
1KEN	A B	B	101	A	1.0	98	109
1KEN	A B	B	105	Q	5.3	98	109
1KEN	A B	B	108	I	1.2	98	109
1KEN	A D	D	50	G	1.8	50	56
1KEN	A D	D	54	R	1.2	50	56
1KEN	C D	D	89	I	2.1	77	97
1KEN	C D	D	92	W	2.5	77	97
1KEN	C D	D	105	Q	1.8	103	109
1KEN	C D	D	108	I	1.3	103	109
1KEN	C F	F	50	G	30.4	50	56
1KEN	C T	C	190	E	1.6	188	195
1KEN	E B	B	50	G	17.4	50	56
1KEN	E D	D	79	D	1.2	77	97
1KEN	E F	F	89	I	3.0	77	97
1KEN	E F	F	92	W	1.7	77	97
1KEN	E F	F	105	Q	3.0	98	109
1KF6	A B	A	46	V	1.3	44	48
1KF6	A B	A	97	E	1.6	89	99
1KF6	A B	A	98	L	1.5	89	99
1KF6	A B	A	133	F	1.0	131	145
1KF6	A B	A	141	Q	1.0	131	145
1KF6	A B	A	144	L	1.1	131	145
1KF6	A B	A	338	Y	2.5	329	339
1KF6	A B	A	452	R	1.8	448	463
1KF6	A B	B	45	D	1.9	36	48
1KF6	A B	B	110	I	1.6	107	116
1KF6	A B	B	114	E	1.2	107	116
1KF6	A B	B	136	P	1.0	136	145
1KF6	B C	B	209	Y	2.9	209	214
1KF6	B C	B	225	Q	1.1	220	240
1KF6	B C	B	226	Q	1.5	220	240
1KF6	B C	C	21	F	2.4	20	51
1KF6	B C	C	22	Y	2.3	20	51
1KF6	B C	C	25	Y	1.0	20	51
1KF6	B D	B	160	Q	1.0	159	164
1KF6	B D	B	196	N	2.5	188	197
1KF6	B D	B	231	S	1.0	220	240
1KF6	B D	B	235	F	2.2	220	240
1KF6	B D	D	11	P	1.4	10	24
1KF6	B D	D	14	W	2.7	10	24
1KF6	C D	C	38	F	3.0	20	51
1KF6	C D	C	42	L	1.3	20	51
1KF6	C D	C	43	I	1.2	20	51
1KF6	C D	C	46	L	1.9	20	51
1KF6	C D	C	49	L	2.0	20	51
1KF6	C D	C	56	W	2.4	53	65
1KF6	C D	C	63	L	1.2	53	65
1KF6	C D	C	76	L	1.7	67	94
1KF6	C D	C	86	W	3.5	67	94
1KF6	C D	C	87	F	1.2	67	94
1KF6	C D	C	124	L	1.2	105	127

1KF6	C D	D	17	F	1.7	10	24
1KF6	C D	D	21	G	2.9	10	24
1KF6	C D	D	22	M	1.2	10	24
1KF6	C D	D	26	I	1.2	25	41
1KF6	C D	D	32	I	2.5	25	41
1KF6	C D	D	34	L	1.7	25	41
1KF6	C D	D	36	G	6.2	25	41
1KF6	C D	D	39	L	1.7	25	41
1KF6	C D	D	51	Y	2.7	51	59
1KF6	C D	D	54	V	1.0	51	59
1KF6	C D	D	71	I	2.0	61	89
1KF6	C D	D	78	G	1.0	61	89
1KF6	C D	D	81	R	1.0	61	89
1KF6	C D	D	114	G	14.6	96	115
1KF6	M N	M	46	V	1.1	44	48
1KF6	M N	M	98	L	1.2	89	99
1KF6	M N	M	137	H	2.7	135	143
1KF6	M N	M	330	F	1.1	329	339
1KF6	M N	M	333	E	1.2	329	339
1KF6	M N	M	338	Y	2.0	329	339
1KF6	M N	M	452	R	1.3	448	463
1KF6	M N	M	504	Y	2.1	500	525
1KF6	M N	N	45	D	1.4	36	48
1KF6	M N	N	136	P	1.5	136	142
1KF6	N D	D	98	W	1.5	96	115
1KF6	N O	N	141	K	1.2	136	142
1KF6	N O	N	159	P	1.1	159	164
1KF6	N O	N	209	Y	2.2	209	214
1KF6	N O	N	225	Q	1.6	220	240
1KF6	N O	O	21	F	3.5	20	51
1KF6	N O	O	25	Y	1.6	20	51
1KF6	N O	O	89	L	3.7	66	92
1KF6	N P	N	235	F	1.6	220	240
1KF6	N P	P	14	W	1.7	10	36
1KF6	O P	O	42	L	1.4	20	51
1KF6	O P	O	46	L	1.6	20	51
1KF6	O P	O	49	L	2.3	20	51
1KF6	O P	O	56	W	1.7	53	64
1KF6	O P	O	63	L	1.5	53	64
1KF6	O P	O	76	L	3.0	66	92
1KF6	O P	O	82	H	1.2	66	92
1KF6	O P	O	86	W	4.0	66	92
1KF6	O P	O	87	F	1.0	66	92
1KF6	O P	O	123	I	1.5	105	130
1KF6	O P	P	17	F	1.3	10	36
1KF6	O P	P	21	G	1.3	10	36
1KF6	O P	P	26	I	1.1	10	36
1KF6	O P	P	30	V	1.2	10	36
1KF6	O P	P	34	L	1.8	10	36
1KF6	O P	P	35	V	1.0	10	36
1KF6	O P	P	71	I	2.2	61	89
1KF6	O P	P	78	G	13.9	61	89
1KF9	A B	A	25	F	1.4	6	33
1KF9	A B	A	64	K	2.1	64	70
1KF9	A B	A	171	S	1.2	109	182
1KF9	A B	A	172	K	1.4	109	182
1KF9	A B	A	175	T	1.2	109	182
1KF9	A C	A	8	R	1.1	6	33
1KF9	A C	A	19	R	1.5	6	33
1KF9	A C	A	116	D	25.5	109	182

1KF9	A C	A	120	G	67.4	109	182
1KF9	D C	D	1091	Q	1.0	1087	1093
1KF9	D C	D	1094	R	1.3	1094	1099
1KF9	D E	D	1025	F	1.4	1006	1033
1KF9	D E	D	1064	K	2.2	1064	1070
1KF9	D E	D	1171	S	1.2	1109	1182
1KF9	D E	D	1172	K	1.4	1109	1182
1KF9	D E	D	1175	T	1.0	1109	1182
1KF9	D F	D	1008	R	1.2	1006	1033
1KF9	D F	D	1019	R	1.5	1006	1033
1KF9	D F	D	1116	D	1.0	1109	1182
1KF9	D F	D	1120	G	46.1	1109	1182
1KFA	M I	M	129	Q	1.3	127	132
1KFU	L S	L	13	E	1.3	4	17
1KFU	L S	L	16	E	1.2	4	17
1KFU	L S	L	641	Q	1.0	640	648
1KFU	L S	L	642	L	1.9	640	648
1KFU	L S	L	661	N	1.1	659	680
1KFU	L S	L	664	R	1.3	659	680
1KFU	L S	L	668	R	1.5	659	680
1KFU	L S	L	676	F	2.5	659	680
1KFU	L S	L	691	L	1.6	691	699
1KFU	L S	L	694	W	3.5	691	699
1KFU	L S	S	842	D	1.5	841	851
1KFU	L S	S	943	F	3.1	940	946
1KFU	L S	S	961	W	3.9	958	967
1KFU	L S	S	962	L	1.0	958	967
1KFU	L S	S	963	Q	1.2	958	967
1KFU	L S	S	964	L	1.9	958	967
1KFU	L S	S	966	M	2.4	958	967
1KFY	A B	A	97	E	1.7	89	99
1KFY	A B	A	98	L	1.4	89	99
1KFY	A B	A	133	F	1.5	131	143
1KFY	A B	A	330	F	1.7	329	339
1KFY	A B	A	334	L	1.0	329	339
1KFY	A B	A	338	Y	2.1	329	339
1KFY	A B	A	452	R	1.8	448	463
1KFY	A B	A	504	Y	1.6	500	525
1KFY	A B	B	45	D	1.9	36	48
1KFY	A B	B	110	I	1.1	107	116
1KFY	A B	B	136	P	1.1	136	145
1KFY	A B	B	179	Y	1.5	170	181
1KFY	B C	B	209	Y	2.0	209	214
1KFY	B C	C	21	F	3.5	20	51
1KFY	B C	C	22	Y	2.5	20	51
1KFY	B D	B	235	F	1.3	220	240
1KFY	B D	D	14	W	1.5	12	36
1KFY	B P	P	98	W	1.0	96	118
1KFY	C D	C	42	L	1.2	20	51
1KFY	C D	C	46	L	1.4	20	51
1KFY	C D	C	49	L	4.5	20	51
1KFY	C D	C	50	K	2.4	20	51
1KFY	C D	C	56	W	1.9	53	64
1KFY	C D	C	63	L	1.2	53	64
1KFY	C D	C	76	L	1.8	67	92
1KFY	C D	C	86	W	2.7	67	92
1KFY	C D	C	124	L	1.4	105	130
1KFY	C D	C	128	L	2.2	105	130
1KFY	C D	D	21	G	3.5	12	36
1KFY	C D	D	26	I	1.2	12	36

1KFY	C D	D	30	V	1.4	12	36
1KFY	C D	D	34	L	1.8	12	36
1KFY	C D	D	51	Y	3.5	51	60
1KFY	C D	D	71	I	2.1	61	89
1KFY	C D	D	78	G	3.9	61	89
1KFY	C D	D	114	G	1.5	96	116
1KFY	M N	M	134	H	1.0	131	143
1KFY	M N	M	330	F	1.0	329	339
1KFY	M N	M	338	Y	1.2	329	339
1KFY	M N	M	448	W	1.0	448	463
1KFY	M N	M	452	R	1.3	448	463
1KFY	M N	M	504	Y	2.7	500	525
1KFY	M N	N	45	D	1.0	36	48
1KFY	M N	N	114	E	1.1	107	116
1KFY	M N	N	136	P	1.2	136	145
1KFY	M N	N	139	M	1.3	136	145
1KFY	N D	N	239	T	1.0	220	240
1KFY	N D	D	98	W	1.2	96	116
1KFY	N O	N	209	Y	1.7	209	214
1KFY	N O	N	225	Q	1.6	220	240
1KFY	N O	O	21	F	3.3	20	51
1KFY	N O	O	22	Y	2.0	20	51
1KFY	N O	O	25	Y	1.6	20	51
1KFY	N O	O	89	L	3.5	67	92
1KFY	N P	N	235	F	1.7	220	240
1KFY	N P	P	11	P	1.1	10	36
1KFY	N P	P	14	W	2.4	10	36
1KFY	O P	O	26	M	1.1	20	51
1KFY	O P	O	42	L	1.3	20	51
1KFY	O P	O	46	L	1.2	20	51
1KFY	O P	O	49	L	2.0	20	51
1KFY	O P	O	63	L	1.4	53	65
1KFY	O P	O	76	L	1.6	67	92
1KFY	O P	O	82	H	1.6	67	92
1KFY	O P	O	86	W	2.8	67	92
1KFY	O P	P	26	I	1.2	10	36
1KFY	O P	P	30	V	1.5	10	36
1KFY	O P	P	71	I	2.1	61	90
1KFY	O P	P	78	G	4.2	61	90
1KFY	O P	P	89	L	1.2	61	90
1KG0	A B	A	47	E	1.0	46	50
1KG0	A B	A	48	F	2.5	46	50
1KG0	A B	A	70	L	1.9	56	77
1KG0	A D	A	58	G	127.9	56	77
1KG0	A D	A	65	V	1.3	56	77
1KG0	B C	B	65	K	1.4	65	73
1KG0	B C	B	72	R	2.5	65	73
1KG0	B D	B	61	W	2.5	52	62
1KG0	B D	B	70	Q	7.4	65	73
1KG0	B D	B	71	R	5.6	65	73
1KG0	B D	B	85	V	1.6	74	86
1KI1	A B	A	67	L	3.0	67	73
1KI1	A B	A	70	L	2.3	67	73
1KI1	A B	B	1379	M	1.6	1371	1383
1KI1	C B	B	1265	K	1.0	1233	1269
1KI1	C D	C	67	L	2.1	67	73
1KI1	C D	C	70	L	2.4	67	73
1KI1	C D	D	1244	E	3.2	1233	1269
1KI1	C D	D	1379	M	1.6	1371	1383
1KI1	C D	D	1384	R	2.6	1384	1395

1KI1	C D	D	1424	V	1.0	1403	1438
1KI6	A B	A	87	Y	1.8	85	93
1KI6	A B	A	91	L	1.5	85	93
1KI6	A B	A	126	I	1.7	114	143
1KI6	A B	A	130	M	1.7	114	143
1KI6	A B	A	185	Q	1.8	184	193
1KI6	A B	A	190	F	1.3	184	193
1KI6	A B	A	307	V	1.7	306	321
1KI6	A B	A	308	F	1.3	306	321
1KI6	A B	A	310	W	3.2	306	321
1KI6	A B	A	371	E	2.6	357	373
1KI6	A B	B	87	Y	1.8	85	93
1KI6	A B	B	91	L	1.6	85	93
1KI6	A B	B	130	M	2.0	130	143
1KI6	A B	B	185	Q	1.6	184	193
1KI6	A B	B	308	F	1.3	306	321
1KI6	A B	B	368	F	1.3	357	373
1KI6	A B	B	371	E	2.1	357	373
1KI6	A B	B	372	M	1.2	357	373
1KIL	A B	A	39	V	1.6	39	88
1KIL	A B	A	43	V	1.5	39	88
1KIL	A B	A	46	M	1.7	39	88
1KIL	A B	A	47	R	2.1	39	88
1KIL	A B	A	60	L	1.2	39	88
1KIL	A B	A	71	Q	1.1	39	88
1KIL	A B	A	78	E	1.4	39	88
1KIL	A B	B	205	L	1.4	193	231
1KIL	A B	B	212	L	1.8	193	231
1KIL	A B	B	215	M	1.5	193	231
1KIL	A B	B	216	F	3.3	193	231
1KIL	A B	B	229	M	1.2	193	231
1KIL	A B	B	233	I	1.0	232	248
1KIL	A B	B	243	Y	1.8	232	248
1KIL	A D	A	41	E	1.3	39	88
1KIL	A D	A	45	I	1.1	39	88
1KIL	A D	A	56	R	1.3	39	88
1KIL	A D	A	59	K	1.3	39	88
1KIL	A D	A	63	L	2.2	39	88
1KIL	A D	A	66	R	1.8	39	88
1KIL	A D	A	70	L	1.2	39	88
1KIL	A D	A	77	F	1.6	39	88
1KIL	A D	A	84	L	1.6	39	88
1KIL	A D	D	150	L	1.2	141	202
1KIL	A D	D	157	I	1.2	141	202
1KIL	A D	D	161	R	2.3	141	202
1KIL	A D	D	168	G	6.8	141	202
1KIL	A D	D	174	Q	1.2	141	202
1KIL	A D	D	178	I	1.5	141	202
1KIL	A D	D	181	I	1.0	141	202
1KIL	A D	D	182	M	1.6	141	202
1KIL	A D	D	189	K	1.2	141	202
1KIL	A D	D	192	I	1.5	141	202
1KIL	A D	D	193	D	1.1	141	202
1KIL	A E	A	54	L	2.0	39	88
1KIL	A E	A	57	D	1.0	39	88
1KIL	A E	E	63	R	1.9	34	70
1KIL	B C	B	195	I	1.0	193	231
1KIL	B C	B	199	H	1.9	193	231
1KIL	B C	B	206	E	1.3	193	231
1KIL	B C	B	209	I	1.3	193	231

1KIL	B C	B	213	H	1.4	193	231
1KIL	B C	B	223	V	1.4	193	231
1KIL	B C	B	234	E	1.8	232	248
1KIL	B C	B	244	V	1.0	232	248
1KIL	B C	C	21	L	1.1	11	80
1KIL	B C	C	35	L	2.2	11	80
1KIL	B C	C	49	M	1.5	11	80
1KIL	B C	C	59	R	1.8	11	80
1KIL	B C	C	63	G	5.6	11	80
1KIL	B C	C	67	I	2.0	11	80
1KIL	B D	B	216	F	1.8	193	231
1KIL	B D	D	160	L	1.8	141	202
1KIL	B E	B	215	M	1.0	193	231
1KIL	C D	C	26	L	1.2	11	80
1KIL	C D	C	29	T	1.5	11	80
1KIL	C D	C	33	L	1.0	11	80
1KIL	C D	C	47	L	1.7	11	80
1KIL	C D	C	64	M	1.0	11	80
1KIL	C D	D	146	M	1.0	141	202
1KIL	C D	D	149	N	1.0	141	202
1KIL	C D	D	153	V	1.5	141	202
1KIL	C D	D	160	L	1.6	141	202
1KIL	C D	D	181	I	2.1	141	202
1KIL	C D	D	184	K	1.1	141	202
1KIL	C D	D	191	R	1.1	141	202
1KIL	C D	D	198	R	1.3	141	202
1KJ2	I D	I	62	R	2.0	57	85
1KJ2	I E	I	76	V	1.1	57	85
1KJ2	I E	I	155	R	1.1	152	162
1KJY	A B	A	108	F	2.2	98	112
1KJY	C D	C	1086	R	2.2	1070	1091
1KJY	C D	C	1108	F	2.0	1098	1113
1KJY	C D	C	1248	K	1.4	1242	1255
1KJY	C D	C	1249	L	1.2	1242	1255
1KJY	C D	D	1497	I	1.3	1497	1508
1KJY	C D	D	1500	L	1.3	1497	1508
1KJY	C D	D	1501	V	1.3	1497	1508
1KJY	C D	D	1503	L	1.1	1497	1508
1KJY	C D	D	1504	L	1.0	1497	1508
1KJY	C D	D	1507	V	1.7	1497	1508
1KKL	A I	A	297	F	1.1	293	309
1KKL	A I	A	301	L	1.3	293	309
1KKL	A I	A	305	I	2.1	293	309
1KKL	B J	B	301	L	1.4	293	306
1KKL	B J	B	305	I	1.8	293	306
1KKL	C H	C	301	L	1.4	293	309
1KKL	C H	C	305	I	1.4	293	309
1KKL	C H	C	308	N	1.3	293	309
1KKQ	A E	A	288	T	3.1	281	292
1KKQ	A E	E	686	E	1.5	686	692
1KKQ	B F	F	689	I	1.2	687	694
1KKQ	C G	G	693	L	2.3	686	694
1KKQ	D H	D	281	V	1.3	277	294
1KKQ	D H	D	310	K	2.3	302	312
1KKQ	D H	H	686	E	1.5	686	691
1KKQ	D H	H	689	I	1.5	686	691
1KLI	L H	H	128	F	1.5	126	129
1KMC	A C	C	141	L	2.4	136	143
1KMI	Y Z	Y	20	I	2.6	15	28
1KMI	Y Z	Z	137	M	2.1	104	152

1KMI	Y Z	Z	144	L	1.6	104	152
1KMI	Y Z	Z	146	G	10.5	104	152
1KN1	A B	A	5	V	1.5	4	15
1KN1	A B	A	9	I	2.5	4	15
1KN1	A B	A	27	I	1.1	21	32
1KN1	A B	A	28	K	1.1	21	32
1KN1	A B	A	30	F	1.4	21	32
1KN1	A B	A	34	G	62.5	33	47
1KN1	A B	A	97	Y	1.8	78	102
1KN1	A B	B	9	I	2.2	4	14
1KN1	A B	B	31	F	2.7	21	33
1KN1	A B	B	34	G	49.5	34	47
1KN1	A B	B	38	V	1.6	34	47
1KN1	A B	B	93	R	2.9	78	102
1KN1	A B	B	97	Y	2.1	78	102
1KN1	A B	B	100	L	1.3	78	102
1KN2	L H	L	124	Q	1.1	122	127
1KPE	A B	A	71	E	1.3	71	87
1KPE	A B	A	75	G	247.2	71	87
1KPE	A B	A	79	I	1.8	71	87
1KPE	A B	B	71	E	1.2	71	88
1KPE	A B	B	75	G	258.6	71	88
1KPE	A B	B	79	I	2.1	71	88
1KPE	A B	B	82	K	1.1	71	88
1KPS	A B	A	134	Y	1.9	131	140
1KPS	A B	B	564	F	2.2	557	566
1KPS	A D	D	580	H	1.1	577	589
1KPS	C B	B	577	F	2.4	577	589
1KQF	A B	A	93	P	1.2	93	97
1KQF	A B	A	100	D	3.0	98	103
1KQF	A B	A	241	F	1.8	238	250
1KQF	A B	A	264	R	2.9	264	268
1KQF	A B	A	913	I	2.6	909	915
1KQF	A B	B	47	V	1.6	44	53
1KQF	A B	B	52	W	4.6	44	53
1KQF	A B	B	165	D	1.7	164	169
1KQF	A B	B	166	R	3.0	164	169
1KQF	A B	B	177	K	1.8	174	179
1KQF	B C	B	253	W	2.8	248	255
1KQF	B C	B	257	L	1.6	256	280
1KQF	B C	B	272	L	2.5	256	280
1KQF	B C	B	275	H	1.9	256	280
1KQF	B C	B	276	Y	1.2	256	280
1KQF	B C	B	279	I	1.2	256	280
1KQF	B C	C	54	R	1.6	50	78
1KQF	B C	C	149	R	1.3	145	176
1KQF	B C	C	152	L	1.8	145	176
1KQF	B C	C	153	L	1.5	145	176
1KQF	B C	C	171	Y	3.7	145	176
1KQF	B C	C	175	W	2.9	145	176
1KQF	B C	C	195	K	1.4	190	197
1KQF	B C	C	196	H	1.1	190	197
1KQS	A Y	Y	30	E	1.0	20	34
1KQS	A Y	Y	76	G	6.3	74	82
1KQS	A Y	Y	79	V	1.3	74	82
1KQS	F L	F	37	T	1.2	33	42
1KQS	F L	F	38	K	1.2	33	42
1KQS	F L	F	62	H	2.1	57	69
1KQS	F L	L	7	Y	2.8	4	12
1KQS	F L	L	8	I	3.2	4	12

1KQS	F L	L	23	L	1.0	19	33
1KTD	A B	A	48	F	2.7	46	52
1KTD	A B	A	51	F	2.1	46	52
1KTD	A B	A	58	G	101.5	56	77
1KTD	A B	A	62	N	3.5	56	77
1KTD	A B	A	69	N	2.3	56	77
1KTD	A B	A	70	L	1.4	56	77
1KTD	A B	A	72	V	1.1	56	77
1KTD	A B	A	73	M	3.0	56	77
1KTD	A B	A	74	K	1.7	56	77
1KTD	A B	A	76	R	3.3	56	77
1KTD	A B	B	84	D	5.5	82	91
1KTD	A B	B	113	F	1.8	92	119
1KTD	A B	B	116	F	3.3	92	119
1KTD	A B	B	117	L	2.0	92	119
1KTD	C D	C	48	F	1.2	46	50
1KTD	C D	C	58	G	81.5	56	77
1KTD	C D	C	62	N	1.8	56	77
1KTD	C D	C	69	N	2.3	56	77
1KTD	C D	C	72	V	1.1	56	77
1KTD	C D	C	74	K	1.3	56	77
1KTD	C D	C	76	R	4.3	56	77
1KTD	C D	D	80	L	1.0	79	90
1KTD	C D	D	81	G	1.6	79	90
1KTD	C D	D	84	D	2.9	79	90
1KTD	C D	D	113	F	1.7	105	114
1KTK	A E	A	15	Y	1.5	9	18
1KTK	B F	B	15	Y	1.4	12	17
1KTK	B F	B	182	S	2.5	181	185
1KUP	A B	A	3	K	3.1	2	6
1KUP	A B	A	4	V	1.8	2	6
1KUP	A B	A	7	F	2.5	7	11
1KUP	A B	A	8	K	1.1	7	11
1KUP	A B	B	17	I	3.2	14	20
1KV6	A C	A	298	M	1.1	294	317
1KV6	A C	A	449	L	1.0	448	455
1KV6	A C	C	693	L	1.0	688	696
1KVD	A B	A	51	V	1.2	50	71
1KVD	A B	A	54	I	2.1	50	71
1KVD	A B	A	57	G	14.4	50	71
1KVD	A B	A	58	I	2.7	50	71
1KVD	A B	A	61	I	2.2	50	71
1KVD	A B	A	65	F	4.0	50	71
1KVD	A B	A	69	W	2.7	50	71
1KVD	A B	A	70	H	1.3	50	71
1KVD	A B	B	176	D	1.4	167	183
1KVD	A B	B	177	L	1.5	167	183
1KVD	A B	B	181	G	4.2	167	183
1KVD	A B	B	182	F	1.4	167	183
1KVD	C D	C	51	V	1.1	50	65
1KVD	C D	C	54	I	1.8	50	65
1KVD	C D	C	57	G	14.8	50	65
1KVD	C D	C	58	I	2.0	50	65
1KVD	C D	C	61	I	2.2	50	65
1KVD	C D	C	62	L	1.8	50	65
1KVD	C D	C	69	W	3.0	66	72
1KVD	C D	D	171	Q	1.2	167	183
1KVD	C D	D	173	M	1.0	167	183
1KVD	C D	D	176	D	1.5	167	183
1KVD	C D	D	181	G	3.5	167	183

1KVD	C D	D	182	F	1.3	167	183
1KX4	A B	A	50	E	1.4	45	57
1KX4	A B	A	51	I	2.0	45	57
1KX4	A B	A	54	Y	1.5	45	57
1KX4	A B	A	67	F	3.1	64	79
1KX4	A B	A	70	L	2.0	64	79
1KX4	A B	A	73	E	3.3	64	79
1KX4	A B	A	74	I	2.0	64	79
1KX4	A B	A	78	F	1.9	64	79
1KX4	A B	A	92	L	2.1	86	114
1KX4	A B	A	97	E	1.1	86	114
1KX4	A B	A	99	Y	2.7	86	114
1KX4	A B	A	100	L	2.3	86	114
1KX4	A B	A	101	V	1.6	86	114
1KX4	A B	A	104	F	3.3	86	114
1KX4	A B	A	121	P	1.1	121	132
1KX4	A B	A	124	I	1.4	121	132
1KX4	A B	B	28	G	21.7	25	29
1KX4	A B	B	36	R	3.0	31	41
1KX4	A B	B	37	L	2.1	31	41
1KX4	A B	B	39	R	2.4	31	41
1KX4	A B	B	40	R	4.0	31	41
1KX4	A B	B	58	L	1.5	50	76
1KX4	A B	B	61	F	2.9	50	76
1KX4	A B	B	62	L	2.3	50	76
1KX4	A B	B	66	I	2.9	50	76
1KX4	A B	B	70	V	1.7	50	76
1KX4	A B	B	86	V	1.8	83	93
1KX4	A G	A	48	L	1.1	45	57
1KX4	B D	B	72	Y	1.9	50	76
1KX4	B D	B	75	H	2.3	50	76
1KX4	B D	B	88	Y	1.6	83	93
1KX4	B D	D	80	Y	2.1	53	81
1KX4	B D	D	97	L	1.5	88	99
1KX4	C D	C	49	V	1.7	45	73
1KX4	C D	C	51	L	1.5	45	73
1KX4	C D	C	54	V	1.6	45	73
1KX4	C D	C	55	L	2.2	45	73
1KX4	C D	C	57	Y	2.4	45	73
1KX4	C D	C	58	L	1.8	45	73
1KX4	C D	C	63	L	2.2	45	73
1KX4	C D	C	67	G	48.3	45	73
1KX4	C D	C	83	L	1.7	80	89
1KX4	C D	C	96	L	1.3	91	97
1KX4	C D	D	58	I	1.8	53	81
1KX4	C D	D	67	F	2.9	53	81
1KX4	C D	D	91	I	2.5	88	99
1KX4	C D	D	95	V	1.0	88	99
1KX4	C D	D	103	L	1.3	102	121
1KX4	C D	D	111	G	267.2	102	121
1KX4	C D	D	115	V	1.2	102	121
1KX4	C D	D	117	K	1.2	102	121
1KX4	C D	D	118	Y	2.3	102	121
1KX4	E C	E	48	L	1.5	45	55
1KX4	E C	E	94	E	1.3	86	114
1KX4	E C	E	112	I	1.5	86	114
1KX4	E F	E	50	E	2.0	45	55
1KX4	E F	E	51	I	1.8	45	55
1KX4	E F	E	67	F	1.3	64	77
1KX4	E F	E	70	L	1.8	64	77

1KX4	E F	E	74	I	1.4	64	77
1KX4	E F	E	92	L	1.9	86	114
1KX4	E F	E	99	Y	2.7	86	114
1KX4	E F	E	100	L	1.8	86	114
1KX4	E F	E	101	V	1.3	86	114
1KX4	E F	E	104	F	2.8	86	114
1KX4	E F	E	121	P	1.8	121	132
1KX4	E F	E	124	I	1.3	121	132
1KX4	E F	F	37	L	2.2	31	41
1KX4	E F	F	39	R	3.2	31	41
1KX4	E F	F	40	R	2.0	31	41
1KX4	E F	F	50	I	2.4	50	76
1KX4	E F	F	53	E	1.2	50	76
1KX4	E F	F	57	V	1.4	50	76
1KX4	E F	F	58	L	1.2	50	76
1KX4	E F	F	61	F	3.3	50	76
1KX4	E F	F	62	L	1.8	50	76
1KX4	E F	F	66	I	2.9	50	76
1KX4	E F	F	70	V	1.2	50	76
1KX4	E F	F	86	V	1.5	83	93
1KX4	F H	F	72	Y	3.0	50	76
1KX4	F H	F	75	H	2.3	50	76
1KX4	F H	H	73	E	1.9	53	81
1KX4	F H	H	77	L	1.5	53	81
1KX4	F H	H	97	L	1.8	88	99
1KX4	G H	G	49	V	1.8	45	73
1KX4	G H	G	50	Y	3.4	45	73
1KX4	G H	G	51	L	3.0	45	73
1KX4	G H	G	54	V	1.5	45	73
1KX4	G H	G	55	L	2.0	45	73
1KX4	G H	G	63	L	1.8	45	73
1KX4	G H	G	67	G	99.9	45	73
1KX4	G H	G	80	P	1.2	80	89
1KX4	G H	G	83	L	1.2	80	89
1KX4	G H	G	96	L	1.6	91	97
1KX4	G H	H	41	V	1.0	35	46
1KX4	G H	H	58	I	1.8	53	81
1KX4	G H	H	62	F	2.2	53	81
1KX4	G H	H	67	F	2.5	53	81
1KX4	G H	H	75	S	1.0	53	81
1KX4	G H	H	91	I	2.0	88	99
1KX4	G H	H	106	H	1.5	103	120
1KX4	G H	H	111	G	68.6	103	120
1KX4	G H	H	115	V	1.3	103	120
1KX4	G H	H	118	Y	3.0	103	120
1KXP	A D	A	143	Y	1.3	137	145
1KXP	A D	A	283	M	1.3	274	284
1KXP	A D	D	141	N	2.4	141	151
1KXP	A D	D	143	E	1.5	141	151
1KXP	A D	D	200	L	2.4	195	227
1KXP	A D	D	201	K	1.4	195	227
1KXP	A D	D	203	R	1.9	195	227
1KXP	A D	D	204	L	1.1	195	227
1KXP	A D	D	310	V	1.0	305	315
1KXP	A D	D	314	F	2.4	305	315
1KXP	A D	D	415	F	1.4	415	430
1KXV	A C	A	155	Y	2.8	154	160
1KXV	A C	A	205	G	241.7	204	214
1KXV	B D	B	155	Y	3.0	154	160
1KXV	B D	B	205	G	12.4	204	213

1KYO	A B	A	368	L	1.2	359	378
1KYO	A B	A	371	L	1.9	359	378
1KYO	A B	A	374	G	58.1	359	378
1KYO	A B	B	68	V	1.0	64	75
1KYO	A B	B	129	Y	2.3	116	136
1KYO	A C	A	344	H	1.6	339	356
1KYO	A C	A	345	F	1.5	339	356
1KYO	A C	A	446	R	1.4	444	450
1KYO	A C	C	4	R	1.5	3	7
1KYO	A E	A	162	H	2.0	155	168
1KYO	A R	A	300	K	1.1	300	308
1KYO	B R	B	65	L	1.1	64	75
1KYO	B R	B	69	R	1.0	64	75
1KYO	B R	B	117	H	1.2	116	136
1KYO	B R	B	121	E	1.0	116	136
1KYO	B R	R	62	R	1.9	54	63
1KYO	B R	R	120	L	2.6	102	121
1KYO	C D	C	70	R	1.5	58	72
1KYO	C D	C	224	Y	2.3	224	247
1KYO	C D	C	225	F	1.0	224	247
1KYO	C D	C	227	F	1.1	224	247
1KYO	C D	C	231	V	1.2	224	247
1KYO	C D	C	235	L	1.7	224	247
1KYO	C D	C	238	L	2.0	224	247
1KYO	C D	C	245	F	2.4	224	247
1KYO	C D	C	246	Y	1.3	224	247
1KYO	C D	D	270	G	33.0	261	292
1KYO	C D	D	277	L	1.8	261	292
1KYO	C D	D	281	Y	2.4	261	292
1KYO	C D	D	288	K	1.5	261	292
1KYO	C D	D	295	I	1.1	293	298
1KYO	C E	C	49	F	2.8	31	52
1KYO	C E	E	78	F	2.4	51	80
1KYO	C G	C	376	V	1.3	346	381
1KYO	C G	C	377	L	1.6	346	381
1KYO	C G	C	378	F	2.4	346	381
1KYO	C G	C	379	Y	3.7	346	381
1KYO	C G	C	380	I	1.6	346	381
1KYO	C G	G	5	F	1.0	5	18
1KYO	C G	G	12	G	172.6	5	18
1KYO	C G	G	16	L	2.0	5	18
1KYO	C G	G	32	F	5.4	19	37
1KYO	C G	G	45	F	4.4	45	49
1KYO	C G	G	76	I	1.1	65	84
1KYO	C G	G	79	H	2.1	65	84
1KYO	C H	C	323	K	1.1	320	342
1KYO	C H	C	324	F	1.5	320	342
1KYO	C H	C	327	F	2.0	320	342
1KYO	C H	C	331	F	2.4	320	342
1KYO	C H	C	338	Q	4.2	320	342
1KYO	C H	C	346	V	1.0	346	381
1KYO	C H	C	351	M	1.4	346	381
1KYO	C H	C	355	A	4.3	346	381
1KYO	C H	H	62	P	2.2	53	81
1KYO	C H	H	66	Y	2.9	53	81
1KYO	C H	H	69	W	2.7	53	81
1KYO	C H	H	73	G	2.5	53	81
1KYO	C H	H	80	L	1.0	53	81
1KYO	C P	C	142	W	1.3	138	152
1KYO	C P	C	164	W	1.7	155	167

1KYO	C P	C	288	K	1.0	288	301
1KYO	D E	D	280	L	1.4	261	292
1KYO	D E	D	283	L	2.8	261	292
1KYO	D E	D	287	V	1.3	261	292
1KYO	D E	E	66	L	1.4	51	80
1KYO	D F	F	98	Y	1.1	89	111
1KYO	D F	F	124	V	1.9	124	145
1KYO	D F	F	127	F	2.4	124	145
1KYO	D F	F	128	F	4.0	124	145
1KYO	D F	F	143	F	4.4	124	145
1KYO	D G	G	73	Y	2.4	65	84
1KYO	D H	D	290	F	2.0	261	292
1KYO	D I	D	87	H	1.5	87	105
1KYO	D I	D	268	R	1.8	261	292
1KYO	D I	D	272	K	1.6	261	292
1KYO	D I	I	32	F	3.2	18	44
1KYO	D I	I	33	D	1.1	18	44
1KYO	D I	I	36	I	1.8	18	44
1KYO	D I	I	40	Y	3.2	18	44
1KYO	D I	I	43	H	1.4	18	44
1KYO	D I	I	49	W	3.6	49	55
1KYO	E H	E	52	G	4.3	51	80
1KYO	E H	E	53	R	1.0	51	80
1KYO	E H	E	55	Y	1.3	51	80
1KYO	E H	E	57	Y	1.2	51	80
1KYO	E I	E	57	Y	2.3	51	80
1KYO	E I	E	61	G	3.1	51	80
1KYO	E I	I	7	Y	1.7	5	11
1KYO	G H	G	69	Y	1.9	65	84
1KYO	G H	G	76	I	1.0	65	84
1KYO	L M	L	368	L	1.1	359	378
1KYO	L M	L	371	L	1.8	359	378
1KYO	L M	L	374	G	84.8	359	378
1KYO	L M	L	406	F	1.0	402	412
1KYO	L M	M	68	V	1.2	64	75
1KYO	L M	M	73	L	1.0	64	75
1KYO	L M	M	129	Y	1.8	116	136
1KYO	L N	L	341	D	1.1	339	356
1KYO	L P	L	151	E	1.0	135	154
1KYO	L P	L	162	H	2.4	155	168
1KYO	L P	L	182	E	1.0	181	185
1KYO	L T	T	19	G	2.3	18	44
1KYO	M G	M	65	L	1.2	64	75
1KYO	M G	M	69	R	1.4	64	75
1KYO	M G	M	73	L	1.5	64	75
1KYO	M G	M	117	H	1.2	116	136
1KYO	M G	G	62	R	1.8	54	63
1KYO	M G	G	109	E	1.0	102	122
1KYO	M G	G	120	L	2.2	102	122
1KYO	N E	N	142	W	1.3	138	152
1KYO	N E	N	164	W	2.5	158	167
1KYO	N E	N	178	R	2.0	173	205
1KYO	N E	N	279	Y	1.1	275	284
1KYO	N E	E	79	I	1.5	51	80
1KYO	N O	N	70	R	1.1	58	72
1KYO	N O	N	76	Y	2.6	75	103
1KYO	N O	N	80	Y	1.7	75	103
1KYO	N O	N	227	F	1.0	225	247
1KYO	N O	N	231	V	1.7	225	247
1KYO	N O	N	234	F	2.3	225	247

1KYO	N O	N	238	L	2.0	225	247
1KYO	N O	N	245	F	2.4	225	247
1KYO	N O	N	246	Y	1.5	225	247
1KYO	N O	O	266	R	2.0	264	297
1KYO	N O	O	270	G	44.8	264	297
1KYO	N O	O	277	L	2.3	264	297
1KYO	N O	O	281	Y	2.2	264	297
1KYO	N O	O	288	K	1.5	264	297
1KYO	N O	O	292	W	2.7	264	297
1KYO	N P	N	49	F	3.4	31	54
1KYO	N P	P	78	F	2.5	51	81
1KYO	N R	N	375	N	1.6	347	381
1KYO	N R	N	376	V	1.2	347	381
1KYO	N R	N	378	F	2.4	347	381
1KYO	N R	N	379	Y	3.5	347	381
1KYO	N R	N	380	I	2.0	347	381
1KYO	N R	R	5	F	1.2	5	18
1KYO	N R	R	12	G	207.0	5	18
1KYO	N R	R	16	L	1.9	5	18
1KYO	N R	R	32	F	6.1	19	37
1KYO	N R	R	45	F	4.7	45	49
1KYO	N R	R	76	I	1.0	65	85
1KYO	N R	R	79	H	2.6	65	85
1KYO	N S	N	324	F	1.0	320	342
1KYO	N S	N	327	F	1.6	320	342
1KYO	N S	N	331	F	2.4	320	342
1KYO	N S	N	335	L	1.0	320	342
1KYO	N S	N	339	I	1.0	320	342
1KYO	N S	N	347	P	1.1	347	381
1KYO	N S	N	351	M	1.5	347	381
1KYO	N S	S	58	Y	1.8	53	81
1KYO	N S	S	66	Y	3.1	53	81
1KYO	N S	S	69	W	3.3	53	81
1KYO	O P	O	280	L	1.0	264	297
1KYO	O P	O	283	L	1.2	264	297
1KYO	O P	O	287	V	1.2	264	297
1KYO	O P	P	66	L	1.4	51	81
1KYO	O Q	O	246	Q	2.3	244	260
1KYO	O Q	Q	98	Y	1.6	89	111
1KYO	O Q	Q	124	V	2.7	124	140
1KYO	O Q	Q	127	F	1.3	124	140
1KYO	O Q	Q	128	F	5.6	124	140
1KYO	O Q	Q	143	F	6.2	141	146
1KYO	O R	R	73	Y	1.3	65	85
1KYO	O S	O	290	F	2.7	264	297
1KYO	O T	O	87	H	1.1	87	102
1KYO	O T	O	268	R	1.8	264	297
1KYO	O T	O	272	K	2.5	264	297
1KYO	O T	O	276	I	1.2	264	297
1KYO	O T	T	32	F	3.9	18	44
1KYO	O T	T	36	I	1.8	18	44
1KYO	O T	T	39	W	1.1	18	44
1KYO	O T	T	40	Y	3.0	18	44
1KYO	O T	T	43	H	1.1	18	44
1KYO	O T	T	49	W	3.3	49	55
1KYO	P T	P	53	R	1.0	51	81
1KYO	P T	P	57	Y	2.6	51	81
1KYO	P T	P	61	G	1.3	51	81
1KYO	P T	P	65	L	1.3	51	81
1KYO	P T	T	28	F	1.1	18	44

1KYO	P U	P	127	Q	1.2	123	130
1KYO	R S	R	69	Y	1.5	65	85
1KZ7	A B	A	639	E	1.9	639	661
1KZ7	A B	A	733	P	1.9	721	742
1KZ7	A B	A	766	L	1.1	761	773
1KZ7	A B	A	769	V	1.2	761	773
1KZ7	A B	B	67	L	1.6	66	73
1KZ7	A B	B	70	L	1.7	66	73
1KZ7	A B	B	103	H	1.4	87	105
1KZ7	C D	C	1639	E	3.1	1639	1661
1KZ7	C D	C	1766	L	1.0	1761	1773
1KZ7	C D	C	1769	V	1.0	1761	1773
1KZ7	C D	C	1810	N	1.5	1792	1812
1KZ7	C D	D	1065	D	1.7	1065	1071
1KZ7	C D	D	1067	L	1.6	1065	1071
1KZ7	C D	D	1070	L	1.8	1065	1071
1KZ7	C D	D	1103	H	1.0	1087	1105
1L0O	A C	A	34	M	1.0	34	56
1L0O	A C	C	151	L	1.1	146	158
1L0O	B C	B	21	V	1.0	16	30
1L0O	B C	B	35	D	1.2	34	56
1L0X	A B	B	23	F	1.6	21	27
1L0X	C D	D	23	F	1.7	21	27
1L0X	C D	D	194	Q	1.2	194	198
1L1O	A B	B	153	N	1.6	153	170
1L1O	A B	B	155	F	1.2	153	170
1L1O	A B	B	160	L	1.0	153	170
1L1O	A B	B	163	I	2.3	153	170
1L1O	A B	B	167	M	1.3	153	170
1L1O	A C	A	98	L	1.6	96	109
1L1O	A C	A	105	I	1.7	96	109
1L1O	B C	B	160	L	1.1	153	170
1L1O	B C	B	169	L	1.3	153	170
1L1O	B C	C	599	Y	1.0	599	616
1L1O	B C	C	606	L	2.1	599	616
1L1O	B C	C	610	I	2.2	599	616
1L1O	D E	D	99	Y	2.1	96	109
1L1O	D E	E	156	T	1.1	153	171
1L1O	D E	E	160	L	1.6	153	171
1L1O	D F	D	98	L	1.8	96	109
1L1O	D F	D	105	I	1.7	96	109
1L1O	D F	F	603	G	1.3	599	615
1L1O	D F	F	610	I	1.2	599	615
1L1O	E F	E	160	L	1.5	153	171
1L1O	E F	E	169	L	1.4	153	171
1L1O	E F	F	599	Y	1.5	599	615
1L1O	E F	F	606	L	1.4	599	615
1L1O	E F	F	610	I	1.8	599	615
1L2I	A C	A	358	I	1.7	339	363
1L2I	A C	A	376	V	1.3	372	382
1L2I	A C	A	539	L	1.2	538	547
1L2I	A C	A	542	E	1.0	538	547
1L2I	A C	C	690	L	1.1	688	696
1L2I	A C	C	694	L	2.3	688	696
1L2W	A I	I	39	Y	1.9	38	45
1L2W	A I	I	43	L	2.2	38	45
1L2W	B I	B	108	E	2.0	102	117
1L2W	B I	B	115	E	1.5	102	117
1L2W	B I	I	73	F	2.0	68	77
1L2W	B I	I	74	I	1.3	68	77

1L2W	C J	C	108	E	2.3	102	117
1L2W	C J	C	115	E	1.4	102	117
1L2W	C J	J	73	F	2.0	68	77
1L2W	C J	J	74	I	1.2	68	77
1L2W	D J	D	104	Y	1.2	104	119
1L2W	D J	J	39	Y	1.7	38	45
1L2W	D J	J	43	L	2.1	38	45
1L2W	E K	E	108	E	2.6	102	117
1L2W	E K	E	115	E	1.0	102	117
1L2W	E K	K	73	F	1.4	68	77
1L2W	E K	K	74	I	1.1	68	77
1L2W	F K	K	39	Y	1.0	38	45
1L2W	F K	K	43	L	1.4	38	45
1L2W	G L	L	39	Y	2.2	38	45
1L2W	G L	L	43	L	2.0	38	45
1L2W	H L	H	108	E	1.6	102	117
1L2W	H L	H	115	E	2.1	102	117
1L2W	H L	L	73	F	1.8	68	77
1L2W	H L	L	74	I	1.1	68	77
1L3E	A B	B	112	K	1.0	110	131
1L3E	A B	B	179	S	1.8	169	184
1L4A	A B	A	41	L	2.2	40	69
1L4A	A B	A	48	V	1.2	40	69
1L4A	A B	A	55	M	2.2	40	69
1L4A	A B	A	62	V	1.4	40	69
1L4A	A B	A	94	K	1.9	90	96
1L4A	A B	B	208	L	1.0	188	229
1L4A	A B	B	215	L	2.7	188	229
1L4A	A B	B	219	F	1.3	188	229
1L4A	A D	A	54	I	1.4	40	69
1L4A	A D	A	64	E	1.2	40	69
1L4A	A D	A	68	K	1.8	40	69
1L4A	A D	A	82	G	378.5	79	84
1L4A	A E	A	63	L	2.3	40	69
1L4A	A E	E	66	R	1.7	53	74
1L4A	B C	B	195	L	1.8	188	229
1L4A	B C	B	202	H	1.2	188	229
1L4A	B C	B	205	I	1.0	188	229
1L4A	B C	B	209	E	1.2	188	229
1L4A	B C	B	212	I	1.1	188	229
1L4A	B C	B	216	H	1.9	188	229
1L4A	B C	C	17	I	1.1	13	57
1L4A	B C	C	35	M	1.2	13	57
1L4A	B C	C	38	M	1.0	13	57
1L4A	B C	C	52	M	1.3	13	57
1L4A	B C	C	63	I	1.1	61	67
1L4A	B C	C	70	I	2.2	68	73
1L4A	B D	B	201	R	2.5	188	229
1L4A	B D	B	219	F	2.3	188	229
1L4A	B D	D	150	E	1.3	148	162
1L4A	B D	D	153	M	1.0	148	162
1L4A	B D	D	157	M	1.1	148	162
1L4A	B D	D	167	L	1.3	164	192
1L4A	C D	C	36	L	1.9	13	57
1L4A	C D	C	40	E	1.1	13	57
1L4A	C D	C	43	K	1.1	13	57
1L4A	C D	D	167	L	1.5	164	192
1L4A	C D	D	188	I	1.8	164	192
1L4A	C D	D	191	K	1.3	164	192
1L5G	A B	B	293	G	7.2	292	302

1L5G	A B	B	297	E	1.1	292	302
1L5G	A B	B	324	L	1.5	315	325
1L7T	L H	L	129	Q	1.3	127	132
1L8C	A B	A	6	R	2.1	3	29
1L8C	A B	A	8	L	1.4	3	29
1L8C	A B	A	9	I	1.0	3	29
1L8C	A B	A	15	L	1.2	3	29
1L8C	A B	A	20	H	2.0	3	29
1L8C	A B	A	43	M	1.2	40	53
1L8C	A B	A	71	I	2.5	62	77
1L8C	A B	A	73	H	1.1	62	77
1L8C	A B	A	75	K	1.1	62	77
1L8C	A B	B	124	E	1.1	120	127
1L8C	A B	B	141	L	2.4	139	149
1L8C	A B	B	145	L	2.2	139	149
1L9B	L C	L	261	D	1.6	259	263
1L9B	L H	L	8	K	1.5	6	10
1L9B	L H	L	9	Y	1.6	6	10
1L9B	L H	H	242	M	1.1	227	244
1L9B	L M	L	6	E	1.6	6	10
1L9B	L M	L	103	R	1.0	84	112
1L9B	L M	L	107	I	1.7	84	112
1L9B	L M	L	111	L	3.0	84	112
1L9B	L M	L	116	H	1.0	116	139
1L9B	L M	L	117	I	2.3	116	139
1L9B	L M	L	151	W	1.3	150	162
1L9B	L M	L	187	L	2.4	171	199
1L9B	L M	L	189	L	1.2	171	199
1L9B	L M	L	190	H	1.4	171	199
1L9B	L M	L	191	G	1.9	171	199
1L9B	L M	L	194	V	1.8	171	199
1L9B	L M	L	195	L	2.1	171	199
1L9B	L M	L	215	F	2.6	209	221
1L9B	L M	L	217	R	1.6	209	221
1L9B	L M	L	218	D	1.3	209	221
1L9B	L M	L	233	G	240.7	226	251
1L9B	L M	L	234	L	1.1	226	251
1L9B	L M	M	87	R	2.5	82	88
1L9B	L M	M	132	R	2.6	113	140
1L9B	L M	M	136	R	1.6	113	140
1L9B	L M	M	145	H	1.8	145	169
1L9B	L M	M	146	T	1.3	145	169
1L9B	L M	M	180	F	2.5	179	193
1L9B	L M	M	209	L	1.7	200	226
1L9B	L M	M	216	F	4.0	200	226
1L9B	L M	M	220	G	14.0	200	226
1L9B	L M	M	224	L	1.3	200	226
1L9B	L M	M	235	L	2.5	234	240
1L9B	L M	M	250	L	1.2	243	256
1L9B	L M	M	251	F	3.0	243	256
1L9B	L M	M	252	W	1.1	243	256
1L9B	L M	M	253	R	1.1	243	256
1L9B	L M	M	254	W	5.5	243	256
1L9B	M H	M	201	F	2.5	200	226
1L9B	M H	M	263	E	1.4	262	266
1L9B	M H	M	264	G	271.6	262	266
1L9B	M H	M	271	W	2.6	267	287
1L9B	M H	M	286	L	1.2	267	287
1L9B	M H	M	297	W	2.2	294	301
1L9B	M H	H	17	I	1.8	12	35

1L9B	M H	H	27	L	2.4	12	35
1L9B	M H	H	31	L	1.7	12	35
1L9B	M H	H	231	D	1.0	227	244
1L9J	L M	L	103	R	1.3	84	111
1L9J	L M	L	107	I	1.4	84	111
1L9J	L M	L	116	H	1.9	116	132
1L9J	L M	L	151	W	1.7	150	162
1L9J	L M	L	187	L	1.5	171	199
1L9J	L M	L	190	H	1.7	171	199
1L9J	L M	L	194	V	1.0	171	199
1L9J	L M	L	215	F	3.1	209	218
1L9J	L M	L	233	G	323.6	226	243
1L9J	L M	L	234	L	1.2	226	243
1L9J	L M	L	263	W	1.8	259	268
1L9J	L M	L	266	W	1.0	259	268
1L9J	L M	M	133	T	1.1	113	140
1L9J	L M	M	136	R	1.6	113	140
1L9J	L M	M	180	F	2.2	179	193
1L9J	L M	M	209	L	1.4	200	226
1L9J	L M	M	216	F	2.6	200	226
1L9J	L M	M	220	G	12.9	200	226
1L9J	L M	M	224	L	1.5	200	226
1L9J	L M	M	235	L	2.5	234	240
1L9J	L M	M	250	L	1.8	246	256
1L9J	L M	M	251	F	1.0	246	256
1L9J	L M	M	254	W	5.6	246	256
1L9J	L M	M	266	H	1.2	262	275
1L9J	M H	M	200	P	6.8	200	226
1L9J	M H	M	201	F	1.5	200	226
1L9J	M H	M	236	E	1.3	234	240
1L9J	M H	M	264	G	362.8	262	275
1L9J	M H	M	271	W	2.4	262	275
1L9J	M H	M	286	L	1.0	276	287
1L9J	M H	H	27	L	2.6	12	35
1L9J	M H	H	31	L	1.3	12	35
1L9J	M H	H	230	E	1.1	227	244
1L9J	R S	R	107	I	1.9	84	111
1L9J	R S	R	151	W	1.3	150	162
1L9J	R S	R	190	H	1.8	171	199
1L9J	R S	R	191	G	1.9	171	199
1L9J	R S	R	194	V	1.1	171	199
1L9J	R S	R	195	L	2.2	171	199
1L9J	R S	R	215	F	2.1	209	218
1L9J	R S	R	217	R	2.1	209	218
1L9J	R S	R	233	G	400.2	226	251
1L9J	R S	R	234	L	1.9	226	251
1L9J	R S	R	236	L	2.0	226	251
1L9J	R S	R	272	W	7.0	270	274
1L9J	R S	S	132	R	1.9	113	141
1L9J	R S	S	133	T	2.3	113	141
1L9J	R S	S	136	R	4.1	113	141
1L9J	R S	S	140	L	3.5	113	141
1L9J	R S	S	145	H	1.2	145	161
1L9J	R S	S	180	F	2.6	179	193
1L9J	R S	S	183	L	1.1	179	193
1L9J	R S	S	216	F	2.2	200	226
1L9J	R S	S	220	G	17.1	200	226
1L9J	R S	S	224	L	1.7	200	226
1L9J	R S	S	235	L	2.2	234	240
1L9J	R S	S	247	R	1.4	243	254

1L9J	R S	S	266	H	1.5	262	287
1L9J	S T	S	201	F	2.9	200	226
1L9J	S T	S	208	F	1.0	200	226
1L9J	S T	S	238	I	1.2	234	240
1L9J	S T	S	263	E	1.3	262	287
1L9J	S T	S	264	G	230.6	262	287
1L9J	S T	S	265	I	1.3	262	287
1L9J	S T	S	271	W	2.4	262	287
1L9J	S T	S	275	L	1.1	262	287
1L9J	S T	T	27	L	2.6	15	35
1L9J	S T	T	32	Q	1.4	15	35
1L9J	S T	T	34	E	1.8	15	35
1LB1	A B	A	639	E	2.7	625	657
1LB1	A B	A	740	R	1.0	719	742
1LB1	A B	A	766	L	3.0	761	773
1LB1	A B	A	778	L	1.0	774	785
1LB1	A B	A	814	H	2.0	792	816
1LB1	A B	B	69	L	1.1	69	75
1LB1	A B	B	72	L	1.4	69	75
1LB1	A B	B	105	H	1.5	89	107
1LB1	A B	B	106	F	1.8	89	107
1LB1	C D	C	639	E	2.7	625	663
1LB1	C D	C	766	L	2.5	761	773
1LB1	C D	C	813	M	1.0	792	816
1LB1	C D	C	814	H	3.5	792	816
1LB1	C D	D	69	L	1.9	69	75
1LB1	C D	D	72	L	2.2	69	75
1LB1	C D	D	105	H	1.8	89	107
1LB1	C D	D	106	F	1.8	89	107
1LB1	E F	E	639	E	1.5	625	663
1LB1	E F	E	770	Q	2.6	761	773
1LB1	E F	E	813	M	1.2	792	816
1LB1	E F	F	69	L	1.7	69	75
1LB1	E F	F	72	L	2.0	69	75
1LB1	E F	F	105	H	2.0	89	107
1LB1	E F	F	106	F	1.9	89	107
1LB1	G H	G	639	E	1.9	625	663
1LB1	G H	G	766	L	2.0	761	773
1LB1	G H	G	814	H	1.1	792	816
1LB1	G H	H	69	L	1.6	69	75
1LB1	G H	H	72	L	1.1	69	75
1LB1	G H	H	105	H	1.1	89	107
1LDK	A B	A	363	P	6.5	363	385
1LDK	A B	A	367	V	1.0	363	385
1LDK	A B	B	418	S	1.0	417	431
1LDK	A B	B	425	Y	1.3	417	431
1LDK	A D	A	43	M	1.3	40	53
1LDK	A D	A	46	Y	1.0	40	53
1LDK	A D	A	50	Y	4.6	40	53
1LDK	A D	A	139	Y	1.1	138	142
1LDK	A D	D	2109	Y	2.4	2097	2110
1LDK	D E	D	2105	L	1.7	2097	2110
1LDK	D E	D	2123	V	1.0	2113	2126
1LEN	A B	B	12	L	1.9	12	16
1LGH	A B	A	7	Y	1.9	6	10
1LGH	A B	A	15	P	1.1	15	40
1LGH	A B	A	45	W	1.2	45	56
1LGH	A B	B	16	V	1.0	10	42
1LGH	A B	B	17	H	2.9	10	42
1LGH	D B	D	49	G	94.7	45	56

1LGH	D E	D	7	Y	1.9	6	10
1LGH	D E	D	15	P	1.1	15	40
1LGH	D E	D	45	W	1.2	45	56
1LGH	D E	E	16	V	1.0	10	42
1LGH	D E	E	17	H	2.9	10	42
1LGH	G H	G	7	Y	1.9	6	10
1LGH	G H	G	15	P	1.1	15	40
1LGH	G H	G	45	W	1.2	45	56
1LGH	G H	H	16	V	1.0	10	42
1LGH	G H	H	17	H	2.9	10	42
1LGH	J H	J	49	G	62.5	45	56
1LGH	J K	J	7	Y	1.9	6	10
1LGH	J K	J	15	P	1.1	15	40
1LGH	J K	J	45	W	1.2	45	56
1LGH	J K	K	16	V	1.0	10	42
1LGH	J K	K	17	H	2.9	10	42
1LIA	A B	A	9	I	3.3	4	15
1LIA	A B	A	24	L	2.0	21	47
1LIA	A B	A	48	H	1.0	48	63
1LIA	A B	A	89	D	1.2	78	102
1LIA	A B	A	93	R	3.1	78	102
1LIA	A B	A	96	N	1.3	78	102
1LIA	A B	A	97	Y	4.1	78	102
1LIA	A B	A	100	V	1.3	78	102
1LIA	A B	A	101	V	1.0	78	102
1LIA	A B	A	110	W	1.5	105	113
1LIA	A B	B	9	V	1.8	4	15
1LIA	A B	B	13	D	1.2	4	15
1LIA	A B	B	34	G	3.8	34	47
1LIA	A B	B	45	V	1.3	34	47
1LIA	A B	B	93	R	1.7	78	102
1LIA	A B	B	97	Y	2.7	78	102
1LIA	A B	B	100	L	1.7	78	102
1LIA	A L	A	167	D	1.7	165	174
1LIA	K L	K	9	I	3.3	4	15
1LIA	K L	K	13	D	2.1	4	15
1LIA	K L	K	24	L	1.0	21	33
1LIA	K L	K	30	N	1.2	21	33
1LIA	K L	K	31	I	1.2	21	33
1LIA	K L	K	48	H	4.8	48	63
1LIA	K L	K	93	R	1.2	78	102
1LIA	K L	K	96	N	5.4	78	102
1LIA	K L	K	97	Y	1.2	78	102
1LIA	K L	L	34	G	1.2	34	47
1LIA	K L	L	45	V	1.4	34	47
1LIA	K L	L	93	R	1.6	78	102
1LIA	K L	L	97	Y	3.5	78	102
1LIA	K L	L	100	L	2.0	78	102
1LJ2	A D	A	298	M	1.0	274	306
1LJ2	A D	A	301	G	160.5	274	306
1LJ2	A D	A	302	L	1.0	274	306
1LJ2	A D	D	156	I	1.1	153	158
1LJ2	A D	D	157	M	1.5	153	158
1LJ2	B C	B	298	M	1.0	274	306
1LJ2	B C	B	301	G	235.5	274	306
1LJ2	B C	C	156	I	1.0	153	157
1LJ2	B D	B	299	F	1.0	274	306
1LK3	A L	A	134	K	1.2	133	142
1LK3	B L	L	121	T	1.2	121	125
1LK3	B M	B	133	E	1.7	133	142

1LK3	B M	B	137	Y	1.1	133	142
1LK3	L H	L	122	E	1.1	121	125
1LK3	L H	L	123	Q	1.4	121	125
1LK3	M I	M	123	Q	1.4	121	126
1LKY	A B	A	64	L	2.3	59	65
1LKY	A B	A	73	R	1.6	67	74
1LKY	A B	B	67	K	1.2	67	74
1LKY	A B	B	80	V	1.0	75	91
1LKY	C D	C	64	L	2.9	59	65
1LKY	C D	D	80	V	1.3	78	91
1LKY	E F	F	67	K	1.4	67	74
1LKY	E F	F	79	D	1.3	78	91
1LNU	A B	A	49	F	4.2	47	53
1LNU	A B	A	63	N	1.3	57	77
1LNU	A B	A	70	N	2.3	57	77
1LNU	A B	A	71	L	1.6	57	77
1LNU	A B	A	74	L	1.6	57	77
1LNU	A B	A	75	T	1.7	57	77
1LNU	A B	B	83	D	1.4	80	88
1LNU	C D	C	49	F	4.5	47	53
1LNU	C D	C	59	G	1.5	57	77
1LNU	C D	C	63	N	1.1	57	77
1LNU	C D	C	70	N	1.1	57	77
1LNU	C D	C	71	L	1.5	57	77
1LNU	E F	E	49	F	4.3	47	53
1LNU	E F	E	59	G	2.0	57	77
1LNU	E F	E	63	N	1.6	57	77
1LNU	E F	E	71	L	1.4	57	77
1LNU	E F	F	109	Y	1.2	105	115
1LNU	G H	G	49	F	2.7	47	53
1LNU	G H	G	59	G	1.2	57	78
1LNU	G H	G	63	N	1.3	57	78
1LNU	G H	G	71	L	2.1	57	78
1LNU	G H	G	74	L	1.6	57	78
1LNU	G H	G	77	R	1.5	57	78
1LO0	L H	L	129	Q	2.0	127	132
1LO0	X Y	X	129	Q	1.7	127	132
1LO4	L H	L	128	E	1.4	127	132
1LO5	A B	A	47	E	2.2	46	50
1LO5	A B	A	48	F	1.0	46	50
1LO5	A B	A	73	M	1.4	56	77
1LO5	A B	A	74	T	1.6	56	77
1LO5	A B	B	53	L	1.0	52	60
1LO5	A C	A	58	G	134.5	56	77
1LO5	A C	A	65	V	1.3	56	77
1LO5	A C	A	72	I	1.0	56	77
1LO5	B C	B	81	H	1.0	75	84
1LOC	A B	B	12	L	1.9	12	16
1LOC	C D	D	12	L	2.4	12	16
1LOC	G H	H	12	L	2.1	12	16
1LOF	A B	B	12	L	1.3	12	16
1LOF	A B	B	15	F	1.2	12	16
1LOT	A B	A	125	N	1.6	125	135
1LOT	A B	A	127	E	1.1	125	135
1LOT	A B	A	184	L	2.2	179	211
1LOT	A B	A	187	R	1.7	179	211
1LOT	A B	A	188	L	1.2	179	211
1LOT	A B	A	298	F	1.4	289	299
1LOT	A B	A	399	F	1.7	399	414
1LOT	A B	B	143	Y	1.3	137	145

1LP1	A B	A	13	G	35.0	6	18
1LP1	A B	A	17	V	1.0	6	18
1LP1	A B	A	28	K	1.6	24	37
1LP1	A B	A	31	I	1.7	24	37
1LP1	A B	A	32	F	2.3	24	37
1LP1	A B	A	35	W	1.1	24	37
1LP1	A B	B	13	F	4.1	6	18
1LP1	A B	B	14	Y	1.9	6	18
1LP1	A B	B	17	L	1.2	6	18
1LP9	A E	A	65	R	1.0	57	85
1LP9	A E	A	66	K	1.7	57	85
1LP9	A E	A	162	G	34.8	152	175
1LP9	E F	F	136	E	1.3	134	140
1LP9	H L	H	65	R	1.2	57	85
1LP9	H L	H	66	K	1.5	57	85
1LP9	H L	H	162	G	33.9	152	175
1LQ8	A B	A	31	F	1.2	29	41
1LQ8	A B	A	34	Y	1.1	29	41
1LQ8	A B	A	50	P	1.4	50	63
1LQ8	A B	A	260	E	1.6	256	262
1LQ8	A B	A	268	L	1.2	265	275
1LQ8	C D	C	50	P	1.7	50	63
1LQ8	C D	C	268	L	1.1	265	273
1LQ8	C D	C	271	W	3.3	265	273
1LQ8	E F	E	50	P	1.5	50	63
1LQ8	E F	E	256	M	1.2	256	261
1LQ8	E F	E	260	E	1.7	256	261
1LQ8	E H	E	127	V	1.2	124	134
1LQ8	G H	G	31	F	1.2	29	41
1LQ8	G H	G	34	Y	1.1	29	41
1LQ8	G H	G	50	P	1.8	50	63
1LQ8	G H	G	268	L	1.2	265	275
1LQB	A B	A	34	I	1.9	24	35
1LQB	A B	B	68	H	3.0	67	83
1LQB	A B	B	75	M	1.1	67	83
1LQB	A B	B	79	Y	1.4	67	83
1LQB	A B	B	82	R	3.5	67	83
1LQB	B C	B	76	Y	5.3	67	83
1LQB	B C	B	101	L	1.4	100	110
1LQB	B C	B	104	L	3.1	100	110
1LQB	B C	C	158	L	3.5	158	168
1LQB	B C	C	159	K	1.2	158	168
1LQB	B C	C	161	R	2.9	158	168
1LQM	A B	A	88	S	1.1	87	100
1LQM	A B	A	191	L	1.6	190	195
1LQM	A B	B	31	E	1.1	26	34
1LQM	C D	C	191	L	2.5	190	195
1LQM	C D	D	28	E	1.3	26	34
1LQM	E F	E	87	P	1.0	87	98
1LQM	E F	E	88	S	1.0	87	98
1LQM	E F	F	28	E	1.7	26	34
1LQS	R L	L	24	Q	1.4	20	33
1LQS	R L	L	34	K	1.9	34	38
1LQS	R M	M	151	E	1.9	143	157
1LQS	R M	M	155	H	1.1	143	157
1LQS	S M	M	34	K	1.5	34	38
1LQV	A C	A	78	G	1.1	59	87
1LRW	A B	B	36	E	1.2	34	62
1LRW	A B	B	37	L	1.4	34	62
1LRW	A B	B	40	Q	1.8	34	62

1LRW	A B	B	47	M	1.6	34	62
1LRW	A B	B	51	N	3.7	34	62
1LRW	A B	B	54	R	2.4	34	62
1LRW	C D	D	37	L	1.3	34	38
1LRW	C D	D	40	Q	1.1	39	62
1LRW	C D	D	47	M	1.4	39	62
1LRW	C D	D	48	D	1.0	39	62
1LRW	C D	D	51	N	2.3	39	62
1LRW	C D	D	54	R	2.6	39	62
1LRW	C D	D	55	V	1.1	39	62
1LT4	D A	A	223	F	1.5	197	226
1LT4	F A	A	233	Y	1.6	232	236
1LT4	H A	H	74	I	1.3	59	78
1LTX	A B	A	64	T	1.6	63	74
1LTX	A B	A	111	H	11.7	107	117
1LTX	A B	A	178	Y	2.9	178	190
1LTX	A B	A	182	H	1.1	178	190
1LTX	A B	A	230	F	2.1	226	236
1LTX	A B	A	421	Y	3.7	419	442
1LTX	A B	A	424	D	3.2	419	442
1LTX	A B	B	217	W	3.1	212	223
1LTX	A B	B	218	W	1.1	212	223
1LTX	A B	B	221	E	1.2	212	223
1LTX	A R	A	216	Q	2.4	205	222
1LTX	A R	A	220	F	2.3	205	222
1LTX	A R	A	377	L	1.9	359	378
1LTX	A R	R	275	R	3.5	275	281
1LTX	A R	R	279	F	2.8	275	281
1LTX	A R	R	286	M	2.3	286	301
1LTX	A R	R	294	K	1.1	286	301
1LUJ	A B	A	312	K	1.2	309	318
1LUJ	A B	A	435	K	1.1	432	441
1LUJ	A B	A	619	C	1.9	608	622
1LUJ	A B	A	653	T	1.3	649	662
1LUJ	A B	A	654	Y	1.8	649	662
1LUJ	A B	A	660	F	2.7	649	662
1LUJ	A B	A	661	R	2.1	649	662
1LUJ	A B	B	22	V	1.9	11	29
1LUJ	A B	B	37	E	2.8	35	44
1LVC	A D	A	527	K	1.0	522	539
1LVC	A D	A	533	L	1.0	522	539
1LVC	A D	A	538	I	1.1	522	539
1LVC	A D	A	649	I	2.4	648	655
1LVC	A D	A	664	I	1.5	660	665
1LVC	A D	A	745	Y	1.5	743	779
1LVC	A D	A	766	H	1.1	743	779
1LVC	A D	D	11	E	1.3	11	17
1LVC	A D	D	14	E	2.2	11	17
1LVC	A D	D	83	E	1.5	83	93
1LVC	A D	D	84	E	2.2	83	93
1LVC	A D	D	91	V	1.2	83	93
1LVC	A D	D	112	L	1.3	102	113
1LVC	B E	B	533	L	1.2	528	536
1LVC	B E	B	714	Q	1.2	714	718
1LVC	B E	E	83	E	1.1	83	93
1LVC	B E	E	84	E	1.1	83	93
1LVC	B E	E	140	E	6.9	138	145
1LVC	C F	C	501	L	1.0	501	508
1LVC	C F	C	513	W	1.1	511	516
1LVC	C F	C	523	L	1.1	522	536

1LVC	C F	C	525	K	3.0	522	536
1LVC	C F	C	527	K	1.2	522	536
1LVC	C F	C	529	V	1.1	522	536
1LVC	C F	C	531	N	4.5	522	536
1LVC	C F	C	533	L	1.2	522	536
1LVC	C F	C	534	I	1.0	522	536
1LVC	C F	C	704	Y	1.1	694	705
1LVC	C F	C	718	R	1.0	714	731
1LVC	C F	C	763	L	1.1	743	766
1LVC	C F	F	14	E	1.4	11	17
1LVC	C F	F	87	E	1.5	83	93
1LVC	C F	F	89	F	1.0	83	93
1LVC	C F	F	91	V	1.3	83	93
1LVC	C F	F	92	F	1.3	83	93
1LVC	C F	F	124	M	2.6	119	129
1LVC	C F	F	127	E	1.7	119	129
1LVC	C F	F	128	A	1.0	119	129
1LVC	C F	F	139	E	1.7	138	147
1LVC	C F	F	140	E	2.3	138	147
1LVC	C F	F	141	F	1.3	138	147
1LWU	A B	A	112	I	1.3	111	123
1LWU	A B	A	126	L	1.4	124	135
1LWU	A B	A	133	I	1.5	124	135
1LWU	A B	A	140	I	1.5	136	156
1LWU	A B	A	144	E	1.8	136	156
1LWU	A B	A	149	V	1.0	136	156
1LWU	A B	A	151	L	1.5	136	156
1LWU	A B	A	171	N	1.2	170	181
1LWU	A B	B	181	T	1.0	174	188
1LWU	A B	B	192	V	1.4	191	213
1LWU	A B	B	196	L	1.7	191	213
1LWU	A B	B	199	K	2.3	191	213
1LWU	A B	B	207	I	1.2	191	213
1LWU	A C	A	115	L	1.8	111	123
1LWU	A C	A	118	R	1.7	111	123
1LWU	A C	A	147	I	1.0	136	156
1LWU	A C	C	99	G	1.4	89	134
1LWU	A C	C	106	I	1.8	89	134
1LWU	B C	B	178	I	1.4	174	188
1LWU	B C	B	182	V	1.8	174	188
1LWU	B C	B	186	L	1.5	174	188
1LWU	B C	B	193	L	1.7	191	213
1LWU	B C	C	95	L	2.0	89	134
1LWU	B C	C	109	L	1.8	89	134
1LWU	B C	C	112	M	1.5	89	134
1LWU	B C	C	113	W	1.1	89	134
1LWU	B C	C	123	L	1.2	89	134
1LWU	D E	D	112	I	1.6	111	123
1LWU	D E	D	126	L	1.4	124	135
1LWU	D E	D	133	I	1.5	124	135
1LWU	D E	D	140	I	1.6	136	156
1LWU	D E	D	144	E	1.8	136	156
1LWU	D E	D	149	V	1.0	136	156
1LWU	D E	D	151	L	1.5	136	156
1LWU	D E	D	152	R	1.0	136	156
1LWU	D E	D	171	N	1.1	170	181
1LWU	D E	E	167	I	1.4	164	173
1LWU	D E	E	177	R	1.7	174	188
1LWU	D E	E	181	T	1.3	174	188
1LWU	D E	E	192	V	1.4	191	213

1LWU	D E	E	196	L	3.6	191	213
1LWU	D E	E	199	K	2.3	191	213
1LWU	D E	E	207	I	1.2	191	213
1LWU	D F	D	115	L	1.9	111	123
1LWU	D F	D	118	R	1.5	111	123
1LWU	D F	F	99	G	1.4	89	134
1LWU	E F	E	182	V	1.3	174	188
1LWU	E F	E	186	L	1.4	174	188
1LWU	E F	E	193	L	2.8	191	213
1LWU	E F	F	95	L	1.6	89	134
1LWU	E F	F	109	L	1.0	89	134
1LWU	E F	F	112	M	1.5	89	134
1LWU	E F	F	113	W	1.1	89	134
1LWU	E F	F	115	V	1.0	89	134
1LWU	E F	F	119	F	1.4	89	134
1LWU	E F	F	123	L	1.6	89	134
1LWU	G F	F	89	L	1.4	89	134
1LWU	G H	G	145	V	1.4	120	156
1LWU	G H	G	146	D	1.4	120	156
1LWU	G H	G	147	I	1.8	120	156
1LWU	G H	G	151	L	1.6	120	156
1LWU	G H	G	155	K	3.5	120	156
1LWU	G H	H	170	R	1.4	168	173
1LWU	G H	H	177	R	2.7	174	182
1LWU	G H	H	196	L	1.0	187	202
1LWU	G H	H	206	A	1.5	203	214
1LWU	G H	H	209	T	1.7	203	214
1LWU	G H	H	210	Q	1.3	203	214
1LWU	G H	H	213	L	1.1	203	214
1LWU	G I	G	126	L	1.0	120	156
1LWU	G I	G	129	L	1.1	120	156
1LWU	G I	I	92	V	1.0	89	96
1LWU	G I	I	109	L	1.2	104	134
1LWU	H I	H	190	K	1.3	187	202
1LWU	H I	H	193	L	1.3	187	202
1LWU	J C	C	89	L	1.3	89	134
1LWU	J K	J	123	L	8.7	120	156
1LWU	J K	J	142	R	1.6	120	156
1LWU	J K	J	149	V	1.1	120	156
1LWU	J K	J	151	L	1.6	120	156
1LWU	J K	K	177	R	1.0	176	182
1LWU	J L	J	126	L	1.0	120	156
1LWU	J L	L	92	V	1.0	89	96
1LWU	J L	L	106	I	1.1	104	134
1LWU	J L	L	109	L	1.2	104	134
1LWU	K L	K	190	K	1.2	187	202
1LWU	K L	K	193	L	2.3	187	202
1LWU	K L	L	119	F	1.1	104	134
1LWU	K L	L	130	I	1.4	104	134
1LYW	A D	A	54	W	1.8	51	56
1LYW	A D	A	55	I	1.6	51	56
1LYW	C B	C	54	W	1.7	51	56
1LYW	C D	D	323	D	1.4	323	329
1LYW	G F	F	242	D	1.2	241	251
1LZW	A B	A	64	E	2.2	63	80
1LZW	A B	A	65	V	1.4	63	80
1LZW	A B	A	67	E	1.7	63	80
1LZW	A B	A	69	K	1.3	63	80
1LZW	A B	B	177	R	1.7	173	190
1LZW	A B	B	213	Y	1.8	210	218

1M1E	A B	A	312	K	1.6	309	318
1M1E	A B	A	426	N	1.4	414	428
1M1E	A B	A	470	H	1.2	458	472
1M1E	A B	A	653	T	1.1	649	663
1M1E	A B	A	660	F	3.7	649	663
1M1E	A B	B	19	K	1.1	11	29
1M1E	A B	B	22	V	1.5	11	29
1M1J	A B	A	49	G	60.0	49	53
1M1J	A B	A	54	G	275.0	54	80
1M1J	A B	A	56	I	1.5	54	80
1M1J	A B	A	74	L	1.8	54	80
1M1J	A B	A	127	V	1.2	88	161
1M1J	A B	A	134	I	2.3	88	161
1M1J	A B	A	138	Q	1.7	88	161
1M1J	A B	A	141	I	1.6	88	161
1M1J	A B	A	148	M	1.4	88	161
1M1J	A B	A	149	K	1.3	88	161
1M1J	A B	A	154	D	1.9	88	161
1M1J	A B	A	155	I	1.9	88	161
1M1J	A B	A	157	I	1.6	88	161
1M1J	A B	A	159	I	1.4	88	161
1M1J	A B	A	160	R	1.6	88	161
1M1J	A B	A	179	Y	1.6	178	192
1M1J	A B	A	182	I	1.3	178	192
1M1J	A B	B	87	L	1.2	84	96
1M1J	A B	B	105	L	1.9	99	198
1M1J	A B	B	112	F	3.7	99	198
1M1J	A B	B	122	Y	1.4	99	198
1M1J	A B	B	126	I	3.2	99	198
1M1J	A B	B	129	K	1.5	99	198
1M1J	A B	B	143	I	1.3	99	198
1M1J	A B	B	158	I	1.8	99	198
1M1J	A B	B	160	D	1.1	99	198
1M1J	A B	B	161	N	1.3	99	198
1M1J	A B	B	166	I	1.7	99	198
1M1J	A B	B	173	L	1.2	99	198
1M1J	A B	B	176	V	2.5	99	198
1M1J	A B	B	180	L	2.5	99	198
1M1J	A B	B	183	K	1.0	99	198
1M1J	A B	B	191	I	1.1	99	198
1M1J	A B	B	197	Y	2.7	99	198
1M1J	A C	A	63	Y	1.4	54	80
1M1J	A C	A	70	I	1.2	54	80
1M1J	A C	A	109	Y	1.6	88	161
1M1J	A C	A	112	V	1.8	88	161
1M1J	A C	A	116	L	1.8	88	161
1M1J	A C	A	119	R	1.6	88	161
1M1J	A C	A	123	L	1.5	88	161
1M1J	A C	A	137	L	1.0	88	161
1M1J	A C	A	141	I	1.4	88	161
1M1J	A C	A	151	L	1.9	88	161
1M1J	A C	A	155	I	2.9	88	161
1M1J	A C	C	29	F	2.8	23	53
1M1J	A C	C	40	L	1.3	23	53
1M1J	A C	C	47	L	1.7	23	53
1M1J	A C	C	90	I	1.4	79	134
1M1J	A C	C	93	I	2.0	79	134
1M1J	A C	C	104	E	1.0	79	134
1M1J	A C	C	107	I	1.5	79	134
1M1J	A C	C	114	H	2.0	79	134

1M1J	A C	C	125	K	1.2	79	134
1M1J	A C	C	128	I	1.9	79	134
1M1J	B C	B	84	G	188.8	84	96
1M1J	B C	B	91	L	1.8	84	96
1M1J	B C	B	102	L	1.0	99	198
1M1J	B C	B	106	K	1.3	99	198
1M1J	B C	B	109	V	1.7	99	198
1M1J	B C	B	123	V	1.5	99	198
1M1J	B C	B	162	L	1.1	99	198
1M1J	B C	B	170	L	2.0	99	198
1M1J	B C	B	174	R	1.7	99	198
1M1J	B C	B	177	I	2.0	99	198
1M1J	B C	B	191	I	1.3	99	198
1M1J	B C	C	25	I	1.3	23	53
1M1J	B C	C	32	Y	1.6	23	53
1M1J	B C	C	43	I	2.9	23	53
1M1J	B C	C	57	I	1.7	54	65
1M1J	B C	C	110	L	2.3	79	134
1M1J	B C	C	120	K	1.1	79	134
1M1J	B C	C	124	L	1.2	79	134
1M1J	B C	C	131	L	1.9	79	134
1M1J	B C	C	210	Q	1.0	208	214
1M1J	D E	D	49	G	60.5	49	53
1M1J	D E	D	99	L	3.4	88	102
1M1J	D E	D	120	I	1.1	103	161
1M1J	D E	D	141	I	2.2	103	161
1M1J	D E	D	149	K	1.3	103	161
1M1J	D E	D	152	E	2.5	103	161
1M1J	D E	D	154	D	1.6	103	161
1M1J	D E	D	155	I	1.5	103	161
1M1J	D E	D	157	I	1.4	103	161
1M1J	D E	D	159	I	1.2	103	161
1M1J	D E	D	160	R	1.5	103	161
1M1J	D E	D	178	G	1.5	177	192
1M1J	D E	D	179	Y	1.3	177	192
1M1J	D E	D	182	I	2.1	177	192
1M1J	D E	E	165	N	1.2	165	198
1M1J	D E	E	173	L	2.5	165	198
1M1J	D E	E	176	V	1.2	165	198
1M1J	D E	E	180	L	2.2	165	198
1M1J	D E	E	183	K	2.7	165	198
1M1J	D E	E	187	L	2.5	165	198
1M1J	D E	E	194	Q	1.1	165	198
1M1J	D E	E	197	Y	2.6	165	198
1M1J	D F	D	109	Y	1.0	103	161
1M1J	D F	D	119	R	1.3	103	161
1M1J	D F	D	137	L	1.1	103	161
1M1J	D F	D	151	L	1.8	103	161
1M1J	D F	D	155	I	1.0	103	161
1M1J	D F	D	158	K	2.1	103	161
1M1J	D F	D	159	I	5.6	103	161
1M1J	D F	F	40	L	1.5	40	51
1M1J	D F	F	47	L	1.0	40	51
1M1J	D F	F	90	I	1.8	79	97
1M1J	D F	F	107	I	1.2	98	134
1M1J	D F	F	121	I	2.6	98	134
1M1J	D F	F	131	L	5.2	98	134
1M1J	E F	E	84	G	195.4	84	88
1M1J	E F	E	120	Y	1.2	112	123
1M1J	E F	E	162	L	2.0	159	164

1M1J	E F	E	170	L	2.3	165	198
1M1J	E F	E	177	I	2.1	165	198
1M1J	E F	F	25	I	1.4	23	29
1M1J	E F	F	32	Y	1.0	32	36
1M1J	E F	F	89	I	2.1	79	97
1M1J	E F	F	96	Y	1.3	79	97
1M1J	E F	F	110	L	2.3	98	134
1M1J	E F	F	120	K	1.0	98	134
1M1J	E F	F	131	L	2.2	98	134
1M1J	E F	F	210	Q	1.2	208	214
1M1Y	A B	A	23	K	1.1	22	31
1M1Y	A B	A	86	V	1.1	86	93
1M1Y	A B	A	87	G	5.8	86	93
1M1Y	A B	A	91	Y	3.1	86	93
1M1Y	A B	A	123	I	1.7	120	125
1M1Y	A B	A	134	L	1.9	128	142
1M1Y	A B	A	158	L	1.5	154	159
1M1Y	A B	A	240	I	1.7	234	245
1M1Y	A B	A	334	E	1.6	318	345
1M1Y	A B	A	429	F	1.9	429	434
1M1Y	A B	B	20	Y	2.7	18	31
1M1Y	A B	B	52	Y	1.4	50	57
1M1Y	A B	B	94	G	218.5	93	108
1M1Y	A B	B	98	Y	1.6	93	108
1M1Y	A B	B	102	Y	1.7	93	108
1M1Y	A B	B	133	D	1.1	128	142
1M1Y	A B	B	137	N	1.3	128	142
1M1Y	A B	B	157	V	1.7	153	158
1M1Y	A B	B	428	W	1.7	427	437
1M1Y	I J	I	86	V	1.1	86	93
1M1Y	I J	I	87	G	7.5	86	93
1M1Y	I J	I	91	Y	2.5	86	93
1M1Y	I J	I	123	I	1.3	120	125
1M1Y	I J	I	133	K	1.6	128	142
1M1Y	I J	I	134	L	1.4	128	142
1M1Y	I J	I	141	L	1.7	128	142
1M1Y	I J	I	158	L	1.3	154	159
1M1Y	I J	I	240	I	1.8	234	245
1M1Y	I J	I	334	E	1.9	318	345
1M1Y	I J	I	429	F	2.5	429	434
1M1Y	I J	I	430	I	1.0	429	434
1M1Y	I J	J	20	Y	2.7	18	31
1M1Y	I J	J	52	Y	1.6	50	58
1M1Y	I J	J	94	G	299.1	93	108
1M1Y	I J	J	98	Y	1.3	93	108
1M1Y	I J	J	102	Y	1.2	93	108
1M1Y	I J	J	157	V	1.6	153	158
1M1Y	I J	J	428	W	1.1	427	437
1M1Y	I J	J	454	D	1.0	446	459
1M1Y	I L	L	348	R	2.7	342	358
1M1Y	J N	J	400	K	1.3	400	412
1M1Y	K J	J	348	R	1.9	342	358
1M1Y	K L	K	86	V	1.2	86	93
1M1Y	K L	K	87	G	3.6	86	93
1M1Y	K L	K	91	Y	2.6	86	93
1M1Y	K L	K	123	I	1.5	120	125
1M1Y	K L	K	133	K	1.6	128	142
1M1Y	K L	K	134	L	1.3	128	142
1M1Y	K L	K	141	L	1.9	128	142
1M1Y	K L	K	236	W	2.6	234	245

1M1Y	K L	K	240	I	1.6	234	245
1M1Y	K L	K	334	E	1.9	318	345
1M1Y	K L	K	429	F	2.6	429	434
1M1Y	K L	K	461	R	1.0	453	468
1M1Y	K L	L	20	Y	2.4	18	31
1M1Y	K L	L	23	M	1.3	18	31
1M1Y	K L	L	24	L	1.2	18	31
1M1Y	K L	L	52	Y	1.6	50	57
1M1Y	K L	L	94	G	253.8	93	108
1M1Y	K L	L	98	Y	1.2	93	108
1M1Y	K L	L	102	Y	3.3	93	108
1M1Y	K L	L	157	V	1.6	153	158
1M1Y	K L	L	428	W	1.5	427	437
1M2O	A B	A	723	F	1.7	722	726
1M2O	A B	B	41	H	1.0	36	43
1M2O	A B	B	82	R	1.2	82	87
1M2O	A B	B	83	L	1.1	82	87
1M2O	C D	D	41	H	1.2	36	45
1M2O	C D	D	42	M	1.2	36	45
1M2O	C D	D	82	R	1.4	82	87
1M2O	C D	D	83	L	1.4	82	87
1M2Z	A B	A	572	I	1.9	556	581
1M2Z	A B	A	590	D	1.7	589	598
1M2Z	A B	A	593	M	1.2	589	598
1M2Z	A B	A	752	M	1.1	751	763
1M2Z	A B	B	744	L	1.0	743	749
1M2Z	A B	B	745	L	2.0	743	749
1M2Z	A B	B	746	R	1.4	743	749
1M2Z	D E	D	579	K	1.2	556	581
1M2Z	D E	D	760	Q	1.6	751	761
1M2Z	D E	E	745	L	1.4	743	751
1M45	A B	A	13	L	1.2	10	15
1M45	A B	A	29	D	1.0	27	34
1M45	A B	A	32	R	1.7	27	34
1M45	A B	A	125	L	1.4	119	126
1M45	A B	A	146	V	1.8	139	147
1M45	A B	B	812	K	1.1	807	830
1M45	A B	B	814	L	2.3	807	830
1M45	A B	B	815	Q	1.8	807	830
1M45	A B	B	818	I	2.0	807	830
1M45	A B	B	820	G	98.1	807	830
1M45	A B	B	821	F	2.2	807	830
1M45	A B	B	822	I	1.4	807	830
1M45	A B	B	823	I	1.2	807	830
1M45	A B	B	824	R	2.9	807	830
1M46	A B	A	86	F	1.9	83	93
1M46	A B	A	110	L	1.0	103	113
1M46	A B	A	125	L	1.0	119	128
1M46	A B	A	146	V	1.0	139	148
1M46	A B	B	859	I	1.5	855	878
1M46	A B	B	862	L	1.8	855	878
1M46	A B	B	863	Q	2.6	855	878
1M46	A B	B	866	I	1.3	855	878
1M46	A B	B	870	L	1.0	855	878
1M4U	L A	L	86	I	2.2	83	95
1M56	A B	A	92	G	47.7	92	109
1M56	A B	A	342	L	1.8	342	371
1M56	A B	A	353	M	1.2	342	371
1M56	A B	A	357	V	1.0	342	371
1M56	A B	A	364	F	2.6	342	371

1M56	A B	A	367	I	2.0	342	371
1M56	A B	A	368	A	3.9	342	371
1M56	A B	A	409	Y	2.0	404	411
1M56	A B	A	493	W	1.2	491	519
1M56	A B	B	61	I	1.9	49	65
1M56	A B	B	104	W	3.7	98	118
1M56	A B	B	112	L	1.8	98	118
1M56	A B	B	119	S	1.3	119	127
1M56	A B	B	123	L	1.7	119	127
1M56	A C	A	137	R	1.0	136	158
1M56	A C	A	144	W	2.4	136	158
1M56	A C	A	152	L	2.0	136	158
1M56	A C	A	192	F	1.1	188	215
1M56	A C	A	206	I	1.7	188	215
1M56	A C	A	248	G	14.1	227	259
1M56	A C	A	274	L	1.6	272	280
1M56	A C	A	278	I	1.5	272	280
1M56	A C	C	16	I	1.6	16	36
1M56	A C	C	19	F	2.0	16	36
1M56	A C	C	26	F	2.0	16	36
1M56	A C	C	82	G	11.4	73	107
1M56	A C	C	86	F	7.3	73	107
1M56	A C	C	92	M	1.2	73	107
1M56	A C	C	97	W	3.8	73	107
1M56	A C	C	99	W	4.6	73	107
1M56	A C	C	103	K	1.6	73	107
1M56	A C	C	104	H	1.0	73	107
1M56	G H	G	92	G	32.4	92	109
1M56	G H	G	342	L	1.0	342	371
1M56	G H	G	353	M	1.0	342	371
1M56	G H	G	357	V	1.0	342	371
1M56	G H	G	364	F	1.9	342	371
1M56	G H	G	367	I	1.6	342	371
1M56	G H	H	61	I	2.5	49	83
1M56	G H	H	76	I	1.6	49	83
1M56	G H	H	112	L	1.7	105	118
1M56	G I	G	17	F	2.8	16	22
1M56	G I	G	137	R	4.2	136	157
1M56	G I	G	138	M	1.4	136	157
1M56	G I	G	141	L	3.2	136	157
1M56	G I	G	144	W	2.3	136	157
1M56	G I	G	152	L	2.1	136	157
1M56	G I	G	188	D	1.0	186	192
1M56	G I	G	214	N	3.8	209	215
1M56	G I	G	248	G	19.0	227	259
1M56	G I	G	278	I	1.6	272	280
1M56	G I	I	18	P	1.1	16	36
1M56	G I	I	19	F	2.1	16	36
1M56	G I	I	26	F	2.2	16	36
1M56	G I	I	29	L	2.0	16	36
1M56	G I	I	33	V	2.5	16	36
1M56	G I	I	58	W	2.1	41	68
1M56	G I	I	65	E	1.8	41	68
1M56	G I	I	82	G	30.7	73	107
1M56	G I	I	85	L	1.6	73	107
1M56	G I	I	92	M	1.1	73	107
1M56	G I	I	97	W	1.5	73	107
1M56	G I	I	99	W	4.3	73	107
1M56	G I	I	104	H	1.4	73	107
1M56	G I	I	204	M	16.4	197	229

1M56	I J	J	28	F	1.2	19	51
1M63	A B	A	350	F	4.8	349	363
1M63	A B	A	352	W	1.5	349	363
1M63	A B	A	354	L	1.1	349	363
1M63	A B	A	360	K	1.1	349	363
1M63	A B	A	361	V	1.4	349	363
1M63	A B	B	93	F	1.3	87	96
1M63	A B	B	108	N	1.0	108	120
1M63	A B	B	109	G	133.0	108	120
1M63	A B	B	112	F	2.1	108	120
1M63	A B	B	118	M	1.2	108	120
1M63	A B	B	130	Q	1.0	125	140
1M63	A B	B	131	I	2.2	125	140
1M63	A B	B	134	K	1.5	125	140
1M63	A B	B	135	T	1.1	125	140
1M63	A B	B	136	I	1.1	125	140
1M63	A B	B	137	I	1.6	125	140
1M63	A B	B	152	F	1.5	149	156
1M63	A C	A	356	F	1.2	349	363
1M63	E F	E	350	F	4.3	349	360
1M63	E F	E	353	S	1.0	349	360
1M63	E F	E	354	L	1.6	349	360
1M63	E F	E	357	V	1.1	349	360
1M63	E F	E	358	G	6.3	349	360
1M63	E F	F	29	L	1.0	18	30
1M63	E F	F	111	L	1.5	110	120
1M63	E F	F	112	F	1.6	110	120
1M63	E F	F	130	Q	1.2	125	138
1M63	E F	F	131	I	2.4	125	138
1M63	E F	F	137	I	1.2	125	138
1M63	E F	F	152	F	1.5	150	154
1M8Q	A B	A	818	Y	10.0	784	826
1M8Q	A B	A	819	N	52.6	784	826
1M8Q	A B	B	50	T	45.3	44	54
1M8Q	A B	B	84	F	1.1	77	88
1M8Q	A B	B	87	K	1.0	77	88
1M8Q	A C	A	788	T	1.2	784	826
1M8Q	A C	A	793	R	1.0	784	826
1M8Q	A C	A	795	R	1.0	784	826
1M8Q	A C	A	796	G	1.0	784	826
1M8Q	A C	A	799	M	1.0	784	826
1M8Q	A C	A	800	R	1.2	784	826
1M8Q	A C	A	806	M	1.3	784	826
1M8Q	A C	C	17	F	1.4	9	18
1M8Q	A C	C	87	F	1.4	85	93
1M8Q	D F	D	800	R	3.3	784	826
1M8Q	G I	G	800	R	5.7	784	826
1M8Q	G I	G	803	Y	1.4	784	826
1M8Q	G I	I	146	I	1.4	140	147
1M8Q	G V	V	141	S	1.1	137	145
1M8Q	G V	V	142	L	1.2	137	145
1M8Q	G V	V	338	S	1.7	338	349
1M8Q	G X	G	556	D	80.3	555	559
1M8Q	G X	G	557	E	26.9	555	559
1M8Q	P Q	P	818	Y	36.1	807	826
1M8Q	P R	P	800	R	19.9	788	806
1M8Q	P R	R	87	F	1.0	85	93
1M8Q	P R	R	122	E	8.4	120	126
1M8Q	P R	R	146	I	1.3	140	147
1M93	A B	A	5	R	1.2	2	11

1M93	A B	A	6	E	1.2	2	11
1M93	A B	A	23	I	2.3	20	33
1M93	A B	A	26	V	2.7	20	33
1M93	A B	A	27	L	1.3	20	33
1M93	A B	A	29	I	1.9	20	33
1M93	A B	A	30	L	1.6	20	33
1M93	A B	A	32	Y	1.2	20	33
1M93	A B	A	38	T	2.7	37	45
1M93	A B	A	41	Q	2.0	37	45
1M93	A B	A	42	L	1.4	37	45
1M93	A B	B	77	F	1.2	75	82
1M93	A B	B	246	L	1.2	246	253
1M93	A B	B	250	L	1.3	246	253
1M93	A C	A	4	F	3.6	2	11
1M93	A C	A	20	P	1.3	20	33
1M93	B C	B	207	L	1.9	207	212
1M93	B C	B	211	E	1.0	207	212
1M93	B C	B	219	F	1.3	216	225
1MCP	L H	L	130	Q	2.5	128	132
1MDU	A B	A	75	G	6.4	71	88
1MDU	A B	A	79	I	2.3	71	88
1MDU	A B	A	80	F	3.2	71	88
1MDU	A B	A	82	V	1.0	71	88
1MDU	A B	B	145	Y	1.3	139	147
1MDU	A B	B	347	I	2.5	340	351
1MDU	A B	B	353	T	13.6	352	356
1MDU	D E	D	75	G	8.0	71	88
1MDU	D E	D	79	I	1.6	71	88
1MDU	D E	D	80	F	1.8	71	88
1MDU	D E	D	82	V	1.0	71	88
1MDU	D E	E	145	Y	1.2	139	147
1MDU	D E	E	347	I	2.5	340	351
1MDY	A B	A	129	F	1.7	109	134
1MDY	A B	A	132	L	2.0	109	134
1MDY	A B	A	150	L	3.1	146	163
1MDY	A B	A	157	I	1.6	146	163
1MDY	A B	B	132	L	1.6	108	135
1MDY	A B	B	147	V	2.7	146	163
1MDY	A B	B	150	L	2.8	146	163
1MDY	A B	B	154	I	2.2	146	163
1MEE	A I	A	104	Y	2.5	104	117
1MEX	L H	L	124	Q	1.1	122	127
1MF8	A B	A	350	F	4.8	349	358
1MF8	A B	A	352	W	1.4	349	358
1MF8	A B	A	354	L	2.4	349	358
1MF8	A B	A	361	V	1.6	359	370
1MF8	A B	A	364	M	3.7	359	370
1MF8	A B	A	365	L	1.8	359	370
1MF8	A B	A	368	V	1.8	359	370
1MF8	A B	A	369	L	1.5	359	370
1MF8	A B	B	25	R	4.3	16	30
1MF8	A B	B	29	L	1.9	16	30
1MF8	A B	B	48	L	4.8	46	50
1MF8	A B	B	98	Y	2.4	87	99
1MF8	A B	B	152	F	1.6	149	156
1MF8	A B	B	161	I	2.9	161	165
1MF8	A C	A	159	Y	1.0	154	160
1MFB	L H	L	127	E	3.1	125	130
1MG2	A F	A	15	G	13.4	9	28
1MG2	A F	A	26	L	1.8	9	28

1MG2	E B	E	15	G	35.0	10	28
1MG2	E B	E	26	L	1.7	10	28
1MG2	I N	I	14	Q	1.1	9	29
1MG2	I N	I	15	G	14.3	9	29
1MG2	I N	I	26	L	1.4	9	29
1MG2	M J	M	15	G	13.7	9	28
1MG2	M J	M	26	L	1.7	9	28
1MHM	B A	B	48	I	2.2	42	52
1MHM	B A	B	49	L	1.1	42	52
1MHM	B A	A	99	I	1.4	96	106
1MHM	B A	A	102	L	1.1	96	106
1MHP	H L	L	122	E	1.0	121	125
1MHY	B D	B	19	R	1.4	17	27
1MHY	B D	B	23	I	2.5	17	27
1MHY	B D	B	55	L	1.7	51	57
1MHY	B D	B	109	H	2.7	109	134
1MHY	B D	B	110	H	1.4	109	134
1MHY	B D	B	113	V	1.1	109	134
1MHY	B D	B	116	K	1.4	109	134
1MHY	B D	B	156	L	1.5	141	166
1MHY	B D	B	157	Y	2.3	141	166
1MHY	B D	B	160	Y	3.2	141	166
1MHY	B D	B	161	G	88.0	141	166
1MHY	B D	B	163	F	1.8	141	166
1MHY	B D	B	170	G	14.6	167	173
1MHY	B D	B	171	R	2.9	167	173
1MHY	B D	B	179	R	1.7	176	207
1MHY	B D	B	183	V	1.3	176	207
1MHY	B D	B	187	L	2.3	176	207
1MHY	B D	B	191	D	1.2	176	207
1MHY	B D	B	194	Q	1.8	176	207
1MHY	B D	B	195	M	2.5	176	207
1MHY	B D	B	197	Q	1.2	176	207
1MHY	B D	B	198	M	1.0	176	207
1MHY	B D	B	201	L	1.6	176	207
1MHY	B D	B	202	F	1.1	176	207
1MHY	B D	B	205	K	1.4	176	207
1MHY	B D	B	235	Q	1.5	228	239
1MHY	B D	B	238	W	3.4	228	239
1MHY	B D	D	28	V	1.7	25	31
1MHY	B D	D	65	K	2.5	64	89
1MHY	B D	D	67	Y	1.5	64	89
1MHY	B D	D	69	R	1.0	64	89
1MHY	B D	D	79	F	1.4	64	89
1MHY	B D	D	97	P	1.3	97	128
1MHY	B D	D	115	Y	4.3	97	128
1MHY	B D	D	125	W	5.2	97	128
1MHY	B D	D	138	L	1.3	131	162
1MHY	B D	D	142	L	1.9	131	162
1MHY	B D	D	145	I	1.8	131	162
1MHY	B D	D	149	H	3.9	131	162
1MHY	B D	D	172	R	1.2	171	178
1MHY	B D	D	173	R	1.2	171	178
1MHY	B D	D	181	W	1.7	179	188
1MHY	B D	D	182	K	1.1	179	188
1MHY	B D	D	185	K	1.5	179	188
1MHY	B D	D	186	R	1.7	179	188
1MHY	B D	D	190	D	3.8	189	193
1MHY	B G	B	246	E	1.2	244	273
1MHY	B G	B	315	H	2.3	313	339

1MHY	B G	B	319	F	2.5	313	339
1MHY	B G	G	59	R	1.7	53	73
1MHY	B G	G	62	E	2.5	53	73
1MHY	B G	G	63	E	2.0	53	73
1MHY	B G	G	66	S	1.0	53	73
1MHY	B G	G	116	R	4.5	105	119
1MHY	B G	G	126	V	1.6	126	145
1MHY	B G	G	127	N	3.4	126	145
1MHY	B G	G	130	L	1.2	126	145
1MHY	B G	G	133	D	2.4	126	145
1MHY	D G	D	266	F	1.9	261	293
1MHY	D G	D	454	E	3.4	451	460
1MHY	D G	D	455	R	3.4	451	460
1MHY	D G	D	458	L	2.4	451	460
1MHY	D G	D	459	I	7.0	451	460
1MHY	D G	D	484	E	1.3	478	485
1MHY	D G	G	113	I	1.6	105	119
1MHY	D G	G	141	M	1.3	126	145
1MHY	D G	G	144	R	2.5	126	145
1MHY	D G	G	153	L	1.5	153	161
1MHY	D G	G	156	L	1.0	153	161
1MHY	D G	G	157	R	3.5	153	161
1MHY	D G	G	160	R	3.4	153	161
1MI5	A E	A	76	E	1.5	57	85
1MI5	D E	E	137	E	1.0	135	141
1MI5	D E	E	140	H	2.7	135	141
1MIM	L H	L	121	Q	1.0	119	124
1MIO	A B	A	77	I	1.6	77	82
1MIO	A B	A	78	G	78.4	77	82
1MIO	A B	A	81	F	1.1	77	82
1MIO	A B	A	115	I	1.4	112	117
1MIO	A B	A	149	L	2.2	145	151
1MIO	A B	A	446	H	1.1	446	457
1MIO	A B	A	469	F	2.5	465	472
1MIO	A B	A	470	V	1.5	465	472
1MIO	A B	B	47	G	59.2	46	61
1MIO	A B	B	51	Y	1.9	46	61
1MIO	A B	B	83	N	1.2	81	96
1MIO	A B	B	94	L	2.1	81	96
1MIO	A B	B	95	Y	2.7	81	96
1MIO	A B	B	107	L	2.1	106	112
1MIO	A B	B	394	Y	3.2	393	402
1MIO	A B	B	397	F	1.0	393	402
1MIO	A D	A	506	G	1.3	493	508
1MIO	A D	D	274	D	1.7	270	285
1MIO	A D	D	278	M	1.0	270	285
1MIO	A D	D	296	R	1.3	290	306
1MIO	A D	D	300	I	1.0	290	306
1MIO	A D	D	304	I	2.1	290	306
1MIO	C B	C	223	W	1.3	221	233
1MIO	C B	B	281	S	4.6	270	284
1MIO	C B	B	296	R	2.4	290	306
1MIO	C B	B	300	I	1.4	290	306
1MIO	C B	B	304	I	1.8	290	306
1MIO	C D	C	77	I	1.2	77	82
1MIO	C D	C	78	G	4.4	77	82
1MIO	C D	C	81	F	1.6	77	82
1MIO	C D	C	149	L	1.4	145	150
1MIO	C D	C	446	H	2.6	446	457
1MIO	C D	C	470	V	1.2	470	474

1MIO	C D	C	473	K	1.1	470	474
1MIO	C D	D	47	G	218.1	47	60
1MIO	C D	D	51	Y	2.3	47	60
1MIO	C D	D	94	L	1.1	81	95
1MIO	C D	D	107	L	1.4	106	111
1MIO	C D	D	375	F	1.1	374	384
1MIU	B A	A	2551	K	1.6	2538	2555
1MJE	B A	B	51	D	1.6	50	54
1MJE	B A	B	52	F	2.2	50	54
1MJE	B A	B	56	L	1.6	56	62
1MJE	B A	A	2435	K	1.6	2430	2437
1MJE	B A	A	2550	W	2.3	2542	2555
1MJE	B A	A	2579	Y	2.3	2570	2588
1MJG	A M	A	95	W	1.2	94	129
1MJG	A M	A	232	F	1.6	227	256
1MJG	A M	A	615	L	1.3	614	629
1MJG	A M	A	622	Q	1.4	614	629
1MJG	A M	A	623	I	1.7	614	629
1MJG	A M	A	627	V	1.1	614	629
1MJG	A M	A	654	W	2.5	638	666
1MJG	A M	A	658	V	2.0	638	666
1MJG	A M	A	659	H	1.9	638	666
1MJG	A M	A	665	R	1.6	638	666
1MJG	A M	M	30	I	1.0	19	48
1MJG	A M	M	35	Y	2.6	19	48
1MJG	A M	M	188	E	1.4	188	196
1MJG	A M	M	191	E	3.1	188	196
1MJG	A M	M	260	M	2.1	260	272
1MJG	A N	N	45	R	2.1	19	48
1MJG	A N	N	87	R	1.0	76	89
1MJG	B M	M	45	R	1.2	19	48
1MJG	B M	M	87	R	1.1	76	89
1MJG	B N	B	95	W	1.2	94	129
1MJG	B N	B	228	V	1.3	227	256
1MJG	B N	B	232	F	1.6	227	256
1MJG	B N	B	615	L	1.4	614	629
1MJG	B N	B	622	Q	1.2	614	629
1MJG	B N	B	623	I	1.8	614	629
1MJG	B N	B	627	V	1.1	614	629
1MJG	B N	B	651	Y	2.1	638	666
1MJG	B N	B	654	W	2.7	638	666
1MJG	B N	B	658	V	2.3	638	666
1MJG	B N	B	659	H	1.1	638	666
1MJG	B N	N	27	H	1.2	19	48
1MJG	B N	N	30	I	1.0	19	48
1MJG	B N	N	35	Y	2.7	19	48
1MJG	B N	N	38	I	1.7	19	48
1MJG	B N	N	188	E	1.6	188	196
1MJG	B N	N	191	E	1.1	188	196
1MJG	B N	N	192	Q	2.0	188	196
1MJG	B N	N	260	M	2.1	260	272
1MJG	C O	C	95	W	1.3	94	129
1MJG	C O	C	228	V	1.3	227	256
1MJG	C O	C	232	F	1.6	227	256
1MJG	C O	C	615	L	1.4	614	629
1MJG	C O	C	622	Q	1.1	614	629
1MJG	C O	C	623	I	1.2	614	629
1MJG	C O	C	627	V	1.1	614	629
1MJG	C O	C	654	W	1.6	638	666
1MJG	C O	C	658	V	1.2	638	666

1MJG	C O	C	659	H	2.0	638	666
1MJG	C O	C	662	V	1.8	638	666
1MJG	C O	O	27	H	1.0	19	48
1MJG	C O	O	30	I	1.0	19	48
1MJG	C O	O	35	Y	2.7	19	48
1MJG	C O	O	188	E	1.0	188	196
1MJG	C O	O	191	E	2.2	188	196
1MJG	C O	O	194	L	1.2	188	196
1MJG	C O	O	260	M	2.0	260	272
1MJG	C P	P	37	E	1.7	19	48
1MJG	D O	O	37	E	1.8	19	48
1MJG	D O	O	45	R	1.1	19	48
1MJG	D P	D	95	W	1.3	94	129
1MJG	D P	D	232	F	1.5	227	256
1MJG	D P	D	615	L	1.4	614	629
1MJG	D P	D	623	I	1.7	614	629
1MJG	D P	D	627	V	1.1	614	629
1MJG	D P	D	654	W	1.2	638	666
1MJG	D P	D	659	H	2.4	638	666
1MJG	D P	D	662	V	1.2	638	666
1MJG	D P	P	35	Y	2.8	19	48
1MJG	D P	P	38	I	1.1	19	48
1MJG	D P	P	188	E	1.2	188	196
1MJG	D P	P	191	E	2.4	188	196
1MJG	D P	P	260	M	2.0	260	272
1MK2	A B	A	405	W	1.6	400	414
1MK2	A B	B	689	Q	1.1	686	692
1MK9	E F	F	296	V	1.2	291	305
1MKW	L H	L	14	E	1.7	14	14
1MKW	L H	L	14	E	1.0	14	14
1MKW	L H	L	14	Y	2.9	14	14
1MMO	B D	B	16	M	1.6	14	23
1MMO	B D	B	20	I	2.5	14	23
1MMO	B D	B	110	V	1.2	107	131
1MMO	B D	B	113	K	1.9	107	131
1MMO	B D	B	117	W	5.0	107	131
1MMO	B D	B	153	L	1.1	138	163
1MMO	B D	B	154	F	2.6	138	163
1MMO	B D	B	157	Y	2.8	138	163
1MMO	B D	B	158	G	57.6	138	163
1MMO	B D	B	160	F	1.5	138	163
1MMO	B D	B	176	R	1.7	173	204
1MMO	B D	B	184	F	4.8	173	204
1MMO	B D	B	188	D	1.1	173	204
1MMO	B D	B	191	Q	1.6	173	204
1MMO	B D	B	194	Q	1.2	173	204
1MMO	B D	B	215	K	2.0	212	220
1MMO	B D	B	218	W	1.3	212	220
1MMO	B D	B	232	E	1.6	227	236
1MMO	B D	B	235	W	2.9	227	236
1MMO	B D	D	27	E	1.5	25	31
1MMO	B D	D	28	V	1.7	25	31
1MMO	B D	D	30	R	1.6	25	31
1MMO	B D	D	65	K	3.6	64	79
1MMO	B D	D	67	Y	1.9	64	79
1MMO	B D	D	69	R	1.1	64	79
1MMO	B D	D	97	P	1.2	97	128
1MMO	B D	D	115	Y	4.4	97	128
1MMO	B D	D	122	G	17.3	97	128
1MMO	B D	D	125	W	4.9	97	128

1MMO	B D	D	138	L	1.4	131	161
1MMO	B D	D	142	L	2.6	131	161
1MMO	B D	D	145	I	1.4	131	161
1MMO	B D	D	149	H	3.2	131	161
1MMO	B D	D	153	Y	1.0	131	161
1MMO	B D	D	156	Y	1.2	131	161
1MMO	B D	D	172	R	2.7	171	178
1MMO	B D	D	173	R	1.1	171	178
1MMO	B D	D	181	W	1.6	179	188
1MMO	B D	D	185	K	2.9	179	188
1MMO	B D	D	190	D	3.2	189	194
1MMO	B G	B	243	E	1.5	241	250
1MMO	B G	B	312	Y	2.7	310	324
1MMO	B G	B	318	R	1.0	310	324
1MMO	B G	G	12	R	2.1	10	20
1MMO	B G	G	54	L	1.9	53	72
1MMO	B G	G	61	E	2.0	53	72
1MMO	B G	G	77	F	3.1	74	79
1MMO	B G	G	115	R	3.7	114	118
1MMO	B G	G	126	N	2.7	125	144
1MMO	C E	C	16	M	1.6	14	24
1MMO	C E	C	20	I	2.2	14	24
1MMO	C E	C	52	L	2.3	48	54
1MMO	C E	C	53	T	1.3	48	54
1MMO	C E	C	106	H	2.9	106	131
1MMO	C E	C	110	V	1.0	106	131
1MMO	C E	C	113	K	4.7	106	131
1MMO	C E	C	118	R	1.1	106	131
1MMO	C E	C	120	T	5.6	106	131
1MMO	C E	C	153	L	1.5	138	163
1MMO	C E	C	154	F	1.2	138	163
1MMO	C E	C	157	Y	2.7	138	163
1MMO	C E	C	158	G	40.8	138	163
1MMO	C E	C	160	F	1.2	138	163
1MMO	C E	C	176	R	1.2	173	204
1MMO	C E	C	184	F	4.2	173	204
1MMO	C E	C	188	D	3.5	173	204
1MMO	C E	C	192	M	3.8	173	204
1MMO	C E	C	194	Q	1.2	173	204
1MMO	C E	C	195	L	1.1	173	204
1MMO	C E	C	215	K	1.4	212	220
1MMO	C E	C	218	W	1.4	212	220
1MMO	C E	C	232	E	1.3	225	236
1MMO	C E	C	235	W	1.1	225	236
1MMO	C E	E	27	E	1.2	25	31
1MMO	C E	E	28	V	1.8	25	31
1MMO	C E	E	30	R	1.3	25	31
1MMO	C E	E	66	E	1.9	64	79
1MMO	C E	E	67	Y	1.6	64	79
1MMO	C E	E	69	R	1.0	64	79
1MMO	C E	E	97	P	1.1	97	121
1MMO	C E	E	115	Y	6.1	97	121
1MMO	C E	E	122	G	13.7	122	128
1MMO	C E	E	125	W	4.3	122	128
1MMO	C E	E	138	L	1.6	131	161
1MMO	C E	E	142	L	2.1	131	161
1MMO	C E	E	145	I	1.2	131	161
1MMO	C E	E	146	R	1.2	131	161
1MMO	C E	E	149	H	3.8	131	161
1MMO	C E	E	156	Y	1.4	131	161

1MMO	C E	E	172	R	2.7	171	176
1MMO	C E	E	190	D	4.4	189	194
1MMO	C E	E	193	I	2.9	189	194
1MMO	C H	C	243	E	1.4	241	250
1MMO	C H	C	312	Y	2.6	310	324
1MMO	C H	H	12	R	1.6	10	21
1MMO	C H	H	54	L	1.3	50	72
1MMO	C H	H	61	E	1.9	50	72
1MMO	C H	H	74	E	1.5	74	79
1MMO	C H	H	111	H	1.1	104	112
1MMO	C H	H	115	R	2.7	114	118
1MMO	C H	H	126	N	1.0	125	144
1MMO	C H	H	133	R	1.2	125	144
1MMO	D G	D	266	Y	1.9	261	293
1MMO	D G	D	452	W	1.6	452	460
1MMO	D G	D	455	R	1.5	452	460
1MMO	D G	D	458	L	4.0	452	460
1MMO	D G	D	471	E	1.0	469	473
1MMO	D G	G	136	G	18.6	125	144
1MMO	D G	G	139	L	3.7	125	144
1MMO	D G	G	140	M	1.0	125	144
1MMO	D G	G	143	R	3.6	125	144
1MMO	D G	G	155	L	1.7	152	160
1MMO	D G	G	156	R	2.5	152	160
1MMO	D G	G	159	R	2.5	152	160
1MMO	E H	E	266	Y	2.7	261	293
1MMO	E H	E	454	E	2.5	451	460
1MMO	E H	E	455	R	3.5	451	460
1MMO	E H	E	458	L	1.9	451	460
1MMO	E H	H	136	G	8.5	125	144
1MMO	E H	H	139	L	1.7	125	144
1MMO	E H	H	143	R	2.7	125	144
1MMO	E H	H	152	L	1.3	152	160
1MMO	E H	H	155	L	1.6	152	160
1MMO	E H	H	156	R	3.7	152	160
1MMO	E H	H	159	R	2.9	152	160
1MNM	B C	B	48	F	1.1	29	54
1MNM	B C	B	87	R	1.6	84	94
1MO1	A B	A	74	L	1.8	70	82
1MO1	A B	A	81	V	1.3	70	82
1MO1	A B	B	74	L	1.9	70	82
1MO1	A B	B	80	Y	1.1	70	82
1MO1	A B	B	81	V	1.3	70	82
1MO1	A D	A	24	Q	1.3	16	28
1MO1	A D	A	27	N	1.4	16	28
1MO1	C D	C	74	L	1.8	70	82
1MO1	C D	C	80	Y	2.1	70	82
1MO1	C D	C	81	V	2.4	70	82
1MO1	C D	D	74	L	1.7	70	82
1MO1	C D	D	80	Y	1.1	70	82
1MO1	C D	D	81	V	1.3	70	82
1MPA	L H	L	128	E	1.0	127	133
1MPA	L H	L	129	Q	1.1	127	133
1MR1	A D	A	414	L	2.4	412	419
1MR1	A D	D	284	Y	2.0	281	285
1MT1	E D	E	35	D	2.5	30	42
1MT1	E F	E	34	F	2.4	30	42
1MT1	E F	E	38	L	1.5	30	42
1MT1	G H	G	34	F	2.8	30	42
1MT1	G J	G	35	D	2.5	30	42

1MT1	I J	I	34	F	2.5	30	42
1MT1	I L	I	35	D	2.2	30	42
1MT1	K H	K	35	D	2.4	30	42
1MT1	K L	K	34	F	2.3	30	42
1MTP	A B	A	20	H	2.8	10	27
1MTP	A B	A	36	P	1.9	36	49
1MTY	B G	B	243	E	1.6	241	250
1MTY	B G	B	312	Y	2.3	310	342
1MTY	B G	G	12	R	1.4	10	21
1MTY	B G	G	61	E	1.9	50	72
1MTY	B G	G	77	F	1.2	74	79
1MTY	B G	G	115	R	3.3	104	118
1MTY	B G	G	125	V	2.4	125	144
1MTY	B G	G	126	N	2.3	125	144
1MTY	B G	G	129	L	1.8	125	144
1MTY	B G	G	133	R	1.2	125	144
1MTY	C H	C	243	E	1.4	241	250
1MTY	C H	C	312	Y	2.3	310	342
1MTY	C H	H	12	R	1.3	10	22
1MTY	C H	H	61	E	2.4	53	72
1MTY	C H	H	111	H	1.1	104	118
1MTY	C H	H	125	V	1.4	125	144
1MTY	C H	H	126	N	1.2	125	144
1MTY	D B	D	27	E	1.5	25	31
1MTY	D B	D	28	V	1.7	25	31
1MTY	D B	D	30	R	1.3	25	31
1MTY	D B	D	65	K	3.6	64	84
1MTY	D B	D	66	E	1.5	64	84
1MTY	D B	D	67	Y	2.2	64	84
1MTY	D B	D	69	R	1.4	64	84
1MTY	D B	D	97	P	1.3	97	128
1MTY	D B	D	115	Y	2.4	97	128
1MTY	D B	D	122	G	55.4	97	128
1MTY	D B	D	125	W	5.0	97	128
1MTY	D B	D	138	L	1.1	131	161
1MTY	D B	D	142	L	2.5	131	161
1MTY	D B	D	145	I	1.5	131	161
1MTY	D B	D	149	H	3.6	131	161
1MTY	D B	D	172	R	8.2	171	178
1MTY	D B	D	173	R	1.2	171	178
1MTY	D B	D	181	W	1.3	179	188
1MTY	D B	D	185	K	1.5	179	188
1MTY	D B	D	186	R	1.2	179	188
1MTY	D B	D	190	D	3.2	189	193
1MTY	D B	B	16	M	1.8	14	24
1MTY	D B	B	20	I	2.2	14	24
1MTY	D B	B	52	L	2.1	48	54
1MTY	D B	B	53	T	1.1	48	54
1MTY	D B	B	106	H	1.2	106	130
1MTY	D B	B	110	V	1.0	106	130
1MTY	D B	B	113	K	1.6	106	130
1MTY	D B	B	117	W	4.8	106	130
1MTY	D B	B	153	L	1.4	138	163
1MTY	D B	B	154	F	1.2	138	163
1MTY	D B	B	157	Y	3.3	138	163
1MTY	D B	B	158	G	69.1	138	163
1MTY	D B	B	160	F	1.0	138	163
1MTY	D B	B	176	R	1.6	173	204
1MTY	D B	B	184	F	4.3	173	204
1MTY	D B	B	188	D	1.4	173	204

1MTY	D B	B	191	Q	1.4	173	204
1MTY	D B	B	195	L	1.1	173	204
1MTY	D B	B	215	K	1.4	212	221
1MTY	D B	B	232	E	1.5	225	237
1MTY	D B	B	235	W	2.3	225	237
1MTY	D G	D	266	Y	2.5	261	293
1MTY	D G	D	454	E	1.8	451	460
1MTY	D G	D	455	R	3.5	451	460
1MTY	D G	D	458	L	2.6	451	460
1MTY	D G	G	112	I	1.4	104	118
1MTY	D G	G	136	G	13.0	125	144
1MTY	D G	G	139	L	4.0	125	144
1MTY	D G	G	140	M	1.0	125	144
1MTY	D G	G	143	R	3.0	125	144
1MTY	D G	G	152	L	1.3	152	160
1MTY	D G	G	155	L	1.7	152	160
1MTY	D G	G	156	R	2.2	152	160
1MTY	D G	G	159	R	7.5	152	160
1MTY	E B	B	289	Q	1.0	276	305
1MTY	E C	E	28	V	1.7	25	31
1MTY	E C	E	30	R	1.6	25	31
1MTY	E C	E	65	K	2.8	64	84
1MTY	E C	E	66	E	2.3	64	84
1MTY	E C	E	67	Y	2.0	64	84
1MTY	E C	E	69	R	1.6	64	84
1MTY	E C	E	97	P	1.2	97	128
1MTY	E C	E	122	G	78.4	97	128
1MTY	E C	E	123	M	1.4	97	128
1MTY	E C	E	125	W	4.9	97	128
1MTY	E C	E	142	L	2.4	131	161
1MTY	E C	E	145	I	1.7	131	161
1MTY	E C	E	146	R	1.8	131	161
1MTY	E C	E	149	H	3.8	131	161
1MTY	E C	E	153	Y	1.8	131	161
1MTY	E C	E	172	R	2.3	171	178
1MTY	E C	E	181	W	1.5	179	188
1MTY	E C	E	185	K	1.6	179	188
1MTY	E C	E	186	R	1.2	179	188
1MTY	E C	E	190	D	3.4	189	194
1MTY	E C	E	193	I	13.8	189	194
1MTY	E C	C	20	I	2.3	14	24
1MTY	E C	C	52	L	2.2	48	54
1MTY	E C	C	53	T	1.1	48	54
1MTY	E C	C	106	H	1.1	106	130
1MTY	E C	C	110	V	1.0	106	130
1MTY	E C	C	111	K	1.3	106	130
1MTY	E C	C	113	K	1.7	106	130
1MTY	E C	C	117	W	5.8	106	130
1MTY	E C	C	153	L	1.0	138	170
1MTY	E C	C	154	F	1.2	138	170
1MTY	E C	C	157	Y	3.2	138	170
1MTY	E C	C	158	G	65.6	138	170
1MTY	E C	C	160	F	1.0	138	170
1MTY	E C	C	181	F	1.0	173	203
1MTY	E C	C	184	F	4.4	173	203
1MTY	E C	C	188	D	1.3	173	203
1MTY	E C	C	191	Q	1.5	173	203
1MTY	E C	C	194	Q	1.0	173	203
1MTY	E C	C	195	L	1.5	173	203
1MTY	E C	C	215	K	1.4	212	220

1MTY	E C	C	235	W	1.9	225	237
1MTY	E H	E	266	Y	2.7	261	292
1MTY	E H	E	454	E	2.4	451	460
1MTY	E H	E	455	R	2.2	451	460
1MTY	E H	E	458	L	2.4	451	460
1MTY	E H	E	484	E	2.1	478	485
1MTY	E H	H	136	G	14.3	125	144
1MTY	E H	H	139	L	2.5	125	144
1MTY	E H	H	140	M	1.0	125	144
1MTY	E H	H	141	E	1.6	125	144
1MTY	E H	H	152	L	1.5	152	160
1MTY	E H	H	155	L	1.6	152	160
1MTY	E H	H	156	R	3.2	152	160
1MTY	E H	H	159	R	3.8	152	160
1MU2	A B	A	162	H	2.1	154	175
1MU2	A B	A	165	R	1.0	154	175
1MU2	A B	A	169	E	3.0	154	175
1MU2	A B	A	172	R	1.6	154	175
1MU2	A B	A	379	L	1.6	363	382
1MU2	A B	B	363	G	29.3	363	382
1MU2	A B	B	364	I	1.2	363	382
1MU2	A B	B	395	E	1.3	394	404
1MU2	A B	B	400	W	4.3	394	404
1MU2	A B	B	421	L	1.0	420	426
1MU2	A B	B	423	R	1.6	420	426
1MUJ	A B	A	48	F	1.7	46	52
1MUJ	A B	A	76	R	1.6	56	77
1MUJ	A B	B	57	D	1.7	52	63
1MUJ	A B	B	89	T	1.0	85	91
1MUJ	A C	A	58	G	242.4	56	77
1MUJ	A C	A	65	V	1.0	56	77
1MUJ	A C	A	68	H	1.2	56	77
1MUJ	A C	A	69	N	1.0	56	77
1MUJ	A C	A	72	V	2.0	56	77
1MUJ	B C	B	60	Y	1.5	52	63
1MUJ	B C	B	61	W	2.1	52	63
1MUJ	B C	B	74	E	1.5	66	84
1MUJ	B C	B	81	H	1.3	66	84
1MVF	A E	E	23	Q	1.6	19	25
1MVF	B D	D	23	Q	1.0	19	25
1MVW	G H	H	47	L	87.8	44	54
1MVW	G H	H	80	F	1.1	77	88
1MVW	G I	G	734	E	1.0	730	739
1MVW	G I	G	796	G	182.4	784	826
1MVW	G I	I	35	R	4.2	27	36
1MVW	G I	I	106	E	1.1	104	113
1MVW	G I	I	109	H	1.6	104	113
1MVW	G V	V	141	S	1.1	137	145
1MVW	G V	V	142	L	1.2	137	145
1MVW	G V	V	338	S	2.2	338	349
1MVW	G X	G	556	D	80.2	555	559
1MVW	G X	G	557	E	26.9	555	559
1MVW	J K	J	819	N	3.6	784	826
1MVW	J K	J	823	F	2.0	784	826
1MVW	J K	J	824	M	3.8	784	826
1MVW	J K	K	51	F	1.2	44	54
1MVW	J K	K	157	I	4.3	152	159
1MVW	J L	J	795	R	41.9	784	826
1MVW	J L	J	796	G	72.1	784	826
1MVW	J W	J	631	E	20.3	619	633

1MVW	J W	J	632	G	621.8	619	633
1MVW	J W	J	655	E	19.9	650	658
1MVW	J W	W	141	S	1.1	137	145
1MVW	J W	W	142	L	1.2	137	145
1MVW	J W	W	143	Y	1.7	137	145
1MVW	J W	W	342	G	5.8	338	349
1MVW	J W	W	344	S	109.5	338	349
1MVW	J Y	J	556	D	26.4	555	559
1MVW	J Y	J	557	E	86.3	555	559
1MVW	M O	M	796	G	8.6	788	826
1MVW	M O	M	800	R	1.9	788	826
1MVW	M O	O	17	F	1.1	9	18
1MVW	M O	O	32	D	1.5	27	36
1MVW	P Q	P	823	F	2.4	788	826
1MVW	P Q	Q	47	L	19.6	44	54
1MVW	P Q	Q	51	F	33.9	44	54
1MVW	P Q	Q	67	M	38.8	61	69
1MVW	P Q	Q	80	F	1.0	77	88
1MVW	P Q	Q	132	E	1.6	132	140
1MVW	P R	R	17	F	1.3	9	18
1MVW	P R	R	43	N	1.6	43	53
1MWA	A B	B	134	K	1.2	134	140
1MWA	A B	B	136	E	1.6	134	140
1MWA	A H	H	155	R	1.3	152	161
1MWA	A H	H	162	G	2.0	162	175
1MWA	B H	H	76	V	1.9	57	85
1MWA	D I	I	76	V	1.0	58	85
1MWN	A X	A	55	K	6.1	50	61
1MWN	A X	X	11	L	2.2	7	12
1MWN	B Y	B	55	K	1.3	50	61
1MXE	A E	A	18	L	1.3	6	20
1MXE	A E	A	19	F	2.0	6	20
1MXE	A E	A	51	M	1.4	45	55
1MXE	A E	A	75	K	2.2	65	79
1MXE	A E	A	84	E	1.2	81	93
1MXE	A E	A	92	F	1.3	81	93
1MXE	A E	A	105	L	1.2	102	112
1MXE	A E	A	120	E	1.2	118	129
1MXE	A E	A	124	M	2.5	118	129
1MXE	A E	A	127	E	1.0	118	129
1MXE	A E	A	144	M	1.3	138	147
1MXE	A E	A	145	M	1.9	138	147
1MXE	A E	E	298	F	2.8	298	318
1MXE	A E	E	302	K	1.6	298	318
1MXE	A E	E	303	W	6.9	298	318
1MXE	A E	E	304	K	1.1	298	318
1MXE	A E	E	307	F	2.6	298	318
1MXE	A E	E	312	V	1.4	298	318
1MXE	A E	E	313	V	1.6	298	318
1MXE	A E	E	314	R	2.1	298	318
1MXE	A E	E	315	H	1.8	298	318
1MXE	A E	E	316	M	1.9	298	318
1MXE	B F	B	11	E	1.9	6	20
1MXE	B F	B	14	E	1.3	6	20
1MXE	B F	B	18	L	1.0	6	20
1MXE	B F	B	19	F	1.9	6	20
1MXE	B F	B	47	E	1.1	45	56
1MXE	B F	B	51	M	2.1	45	56
1MXE	B F	B	71	M	1.0	65	78
1MXE	B F	B	92	F	1.0	81	93

1MXE	B F	B	105	L	1.2	102	112
1MXE	B F	B	120	E	1.2	118	129
1MXE	B F	B	124	M	2.6	118	129
1MXE	B F	B	144	M	1.3	138	147
1MXE	B F	B	145	M	1.8	138	147
1MXE	B F	F	298	F	3.7	298	318
1MXE	B F	F	302	K	2.5	298	318
1MXE	B F	F	303	W	6.9	298	318
1MXE	B F	F	304	K	2.5	298	318
1MXE	B F	F	305	Q	1.9	298	318
1MXE	B F	F	307	F	2.8	298	318
1MXE	B F	F	312	V	1.5	298	318
1MXE	B F	F	313	V	1.6	298	318
1MXE	B F	F	314	R	1.0	298	318
1MXE	B F	F	315	H	1.7	298	318
1MXE	B F	F	316	M	2.1	298	318
1MXE	B F	F	317	R	1.0	298	318
1MZN	A B	A	277	F	1.4	264	285
1MZN	A B	A	280	V	1.5	264	285
1MZN	A B	A	294	L	1.9	294	304
1MZN	A B	A	298	V	1.5	294	304
1MZN	A B	A	450	F	2.0	449	456
1MZN	A B	A	453	E	2.8	449	456
1MZN	A B	B	474	I	2.2	473	481
1MZN	A B	B	475	L	2.6	473	481
1MZN	A B	B	476	H	1.3	473	481
1MZN	A B	B	478	L	1.3	473	481
1MZN	A B	B	479	L	2.8	473	481
1MZN	A B	B	480	Q	1.3	473	481
1MZN	C D	C	1280	V	1.4	1264	1285
1MZN	C D	C	1294	L	1.2	1294	1304
1MZN	C D	C	1450	F	1.4	1449	1455
1MZN	C D	C	1453	E	2.5	1449	1455
1MZN	C D	D	1475	L	2.2	1473	1481
1MZN	C D	D	1478	L	1.4	1473	1481
1MZN	C D	D	1479	L	2.6	1473	1481
1MZN	E F	E	2280	V	1.5	2264	2285
1MZN	E F	E	2298	V	1.2	2294	2304
1MZN	E F	E	2450	F	1.9	2449	2456
1MZN	E F	E	2453	E	2.1	2449	2456
1MZN	E F	F	2474	I	1.2	2473	2481
1MZN	E F	F	2475	L	2.6	2473	2481
1MZN	E F	F	2478	L	1.3	2473	2481
1MZN	E F	F	2479	L	2.6	2473	2481
1N0W	A B	A	199	H	1.7	197	209
1N0W	A B	A	205	Y	1.0	197	209
1N0X	L H	L	124	Q	1.3	122	126
1N0X	M K	M	124	Q	1.6	122	128
1N1J	A B	A	65	I	2.4	59	69
1N1J	A B	A	84	V	1.1	78	106
1N1J	A B	A	92	I	2.9	78	106
1N1J	A B	A	116	I	1.5	113	123
1N1J	A B	A	128	Y	2.4	126	140
1N1J	A B	A	132	L	1.5	126	140
1N1J	A B	A	135	Y	1.4	126	140
1N1J	A B	A	136	L	12.0	126	140
1N1J	A B	B	47	R	1.5	45	53
1N1J	A B	B	51	I	3.6	45	53
1N1J	A B	B	67	V	1.1	63	91
1N1J	A B	B	68	L	2.7	63	91

1N1J	A B	B	69	F	4.7	63	91
1N1J	A B	B	71	K	1.5	63	91
1N1J	A B	B	75	I	1.3	63	91
1N1J	A B	B	77	I	3.0	63	91
1N1J	A B	B	85	W	2.9	63	91
1N1J	A B	B	101	I	1.4	98	106
1N2D	A C	A	13	L	1.0	4	15
1N2D	A C	A	125	L	1.3	119	128
1N2D	A C	A	146	V	1.5	139	148
1N2D	A C	C	812	K	1.4	808	853
1N2D	A C	C	814	L	2.5	808	853
1N2D	A C	C	815	Q	2.8	808	853
1N2D	A C	C	818	I	1.7	808	853
1N2D	A C	C	820	G	69.0	808	853
1N2D	A C	C	821	F	2.4	808	853
1N2D	A C	C	822	I	1.4	808	853
1N2D	A C	C	823	I	1.1	808	853
1N2D	A C	C	824	R	2.4	808	853
1N2D	B C	B	32	R	2.2	27	34
1N2D	B C	B	86	F	1.5	83	93
1N2D	B C	B	90	F	1.9	83	93
1N2D	B C	B	92	V	1.9	83	93
1N2D	B C	B	109	M	1.6	103	113
1N2D	B C	C	832	K	2.6	808	853
1N2D	B C	C	839	L	1.4	808	853
1N2D	B C	C	840	Q	2.2	808	853
1N2D	B C	C	843	Y	2.1	808	853
1N2D	B C	C	844	R	2.2	808	853
1N2D	B C	C	845	G	115.8	808	853
1N2D	B C	C	848	I	1.3	808	853
1N2D	B C	C	849	R	2.0	808	853
1N34	C N	C	40	R	6.6	38	43
1N34	D E	D	205	E	1.8	200	207
1N34	D E	E	107	R	2.2	104	114
1N34	E H	E	151	L	1.2	145	153
1N34	G K	K	58	P	1.1	58	74
1N34	G K	K	59	Y	1.9	58	74
1N4M	A C	A	533	E	1.4	525	539
1N4M	B D	B	460	M	18.3	439	468
1N4M	B D	B	476	L	1.6	474	478
1N4M	B D	B	533	E	1.2	525	537
1N4M	B D	B	555	H	1.4	544	562
1N4M	B E	B	756	Y	2.0	752	764
1N4M	B E	B	757	N	1.1	752	764
1N4M	B E	B	769	L	1.0	765	772
1N4Q	A B	A	96	F	1.4	94	109
1N4Q	A B	A	104	R	1.8	94	109
1N4Q	A B	A	131	Y	1.9	131	144
1N4Q	A B	A	135	H	1.3	131	144
1N4Q	A B	A	170	H	1.5	166	180
1N4Q	A B	A	200	Y	4.4	200	213
1N4Q	A B	A	234	N	1.4	234	246
1N4Q	A B	A	241	H	1.2	234	246
1N4Q	A B	A	274	E	1.2	274	283
1N4Q	A B	A	275	S	1.3	274	283
1N4Q	A B	A	282	G	110.0	274	283
1N4Q	A B	A	317	D	1.5	309	325
1N4Q	A B	A	355	Y	3.1	353	365
1N4Q	A B	A	358	Y	1.8	353	365
1N4Q	A B	B	47	R	3.5	47	61

1N4Q	A B	B	75	W	3.0	69	79
1N4Q	A B	B	250	R	2.5	242	254
1N4Q	A B	B	253	I	1.8	242	254
1N4Q	C D	C	131	Y	2.0	131	144
1N4Q	C D	C	135	H	1.3	131	144
1N4Q	C D	C	170	H	1.5	166	180
1N4Q	C D	C	200	Y	4.2	200	213
1N4Q	C D	C	235	S	1.1	234	246
1N4Q	C D	C	241	H	1.2	234	246
1N4Q	C D	C	274	E	2.3	274	283
1N4Q	C D	C	275	S	1.3	274	283
1N4Q	C D	C	278	N	1.4	274	283
1N4Q	C D	C	282	G	124.8	274	283
1N4Q	C D	C	317	D	1.5	309	325
1N4Q	C D	C	355	Y	4.3	353	365
1N4Q	C D	C	358	Y	2.4	353	365
1N4Q	C D	D	47	R	3.5	47	61
1N4Q	C D	D	75	W	3.2	69	79
1N4Q	C D	D	250	R	2.1	242	256
1N4Q	C D	D	251	W	1.8	242	256
1N4Q	C D	D	253	I	2.1	242	256
1N4Q	C D	D	255	R	1.7	242	256
1N4Q	E F	E	104	R	1.8	94	109
1N4Q	E F	E	131	Y	2.2	131	144
1N4Q	E F	E	135	H	1.3	131	144
1N4Q	E F	E	170	H	1.5	166	180
1N4Q	E F	E	200	Y	3.5	200	213
1N4Q	E F	E	235	S	1.2	234	246
1N4Q	E F	E	241	H	1.2	234	246
1N4Q	E F	E	274	E	2.7	274	283
1N4Q	E F	E	275	S	1.7	274	283
1N4Q	E F	E	278	N	1.8	274	283
1N4Q	E F	E	282	G	115.9	274	283
1N4Q	E F	E	286	D	1.1	284	288
1N4Q	E F	E	317	D	1.3	309	325
1N4Q	E F	E	324	E	1.1	309	325
1N4Q	E F	E	355	Y	3.9	353	365
1N4Q	E F	E	358	Y	1.4	353	365
1N4Q	E F	F	47	R	3.1	47	61
1N4Q	E F	F	75	W	3.1	69	79
1N4Q	E F	F	243	K	1.7	242	254
1N4Q	E F	F	250	R	2.1	242	254
1N4Q	E F	F	251	W	2.2	242	254
1N4Q	E F	F	253	I	1.9	242	254
1N4Q	G H	G	96	F	1.7	94	109
1N4Q	G H	G	131	Y	2.3	131	144
1N4Q	G H	G	135	H	1.3	131	144
1N4Q	G H	G	170	H	1.4	166	180
1N4Q	G H	G	200	Y	4.2	200	213
1N4Q	G H	G	234	N	1.4	234	246
1N4Q	G H	G	241	H	1.2	234	246
1N4Q	G H	G	274	E	2.9	274	283
1N4Q	G H	G	275	S	1.2	274	283
1N4Q	G H	G	278	N	1.6	274	283
1N4Q	G H	G	282	G	110.4	274	283
1N4Q	G H	G	317	D	1.9	309	325
1N4Q	G H	G	355	Y	3.0	353	365
1N4Q	G H	G	358	Y	2.3	353	365
1N4Q	G H	H	47	R	3.2	47	61
1N4Q	G H	H	75	W	3.1	69	79

1N4Q	G H	H	243	K	1.0	242	254
1N4Q	G H	H	250	R	2.6	242	254
1N4Q	G H	H	251	W	2.4	242	254
1N4Q	G H	H	253	I	1.5	242	254
1N4Q	I J	I	131	Y	1.8	131	144
1N4Q	I J	I	135	H	1.1	131	144
1N4Q	I J	I	170	H	1.5	166	180
1N4Q	I J	I	200	Y	4.5	200	213
1N4Q	I J	I	234	N	1.0	234	246
1N4Q	I J	I	235	S	1.0	234	246
1N4Q	I J	I	241	H	1.2	234	246
1N4Q	I J	I	274	E	1.5	274	283
1N4Q	I J	I	275	S	1.5	274	283
1N4Q	I J	I	282	G	111.4	274	283
1N4Q	I J	I	317	D	1.3	309	325
1N4Q	I J	I	355	Y	2.8	353	365
1N4Q	I J	I	358	Y	1.4	353	365
1N4Q	I J	J	47	R	1.3	47	61
1N4Q	I J	J	75	W	3.5	69	79
1N4Q	I J	J	250	R	2.7	242	254
1N4Q	I J	J	253	I	1.2	242	254
1N4Q	K D	K	361	R	1.2	353	365
1N4Q	K L	K	104	R	1.9	94	109
1N4Q	K L	K	131	Y	1.7	131	144
1N4Q	K L	K	135	H	1.4	131	144
1N4Q	K L	K	170	H	1.5	166	180
1N4Q	K L	K	200	Y	4.1	200	213
1N4Q	K L	K	235	S	1.2	234	246
1N4Q	K L	K	241	H	1.2	234	246
1N4Q	K L	K	274	E	2.6	274	283
1N4Q	K L	K	275	S	1.5	274	283
1N4Q	K L	K	282	G	120.8	274	283
1N4Q	K L	K	355	Y	3.0	353	365
1N4Q	K L	K	358	Y	1.2	353	365
1N4Q	K L	L	47	R	1.6	47	61
1N4Q	K L	L	75	W	3.5	69	79
1N4Q	K L	L	250	R	3.1	242	254
1N4Q	K L	L	251	W	1.2	242	254
1N4Q	K L	L	253	I	1.3	242	254
1N52	A B	A	329	R	3.8	329	338
1N52	A B	A	374	T	1.3	369	383
1N52	A B	A	458	R	1.8	444	459
1N52	A B	A	559	F	2.8	559	569
1N52	A B	B	54	E	1.0	53	63
1N52	A B	B	55	Q	1.6	53	63
1N52	A B	B	58	E	2.6	53	63
1N52	A B	B	99	R	1.4	91	100
1N5W	A B	A	27	H	1.9	25	33
1N5W	A B	A	30	R	1.9	25	33
1N5W	A B	A	91	Q	1.9	89	97
1N5W	A B	A	95	R	1.0	89	97
1N5W	A B	A	129	R	1.9	125	132
1N5W	A B	B	33	F	1.2	28	34
1N5W	A B	B	127	Y	4.1	126	136
1N5W	A B	B	131	D	1.3	126	136
1N5W	A B	B	301	R	4.5	301	306
1N5W	A B	B	693	M	1.4	692	713
1N5W	A B	B	697	G	8.5	692	713
1N5W	A B	B	701	G	122.9	692	713
1N5W	A B	B	705	E	1.8	692	713

1N5W	A C	C	38	I	2.0	36	43
1N5W	A C	C	42	K	1.7	36	43
1N5W	A C	C	105	Q	3.4	104	110
1N5W	A C	C	108	Y	3.1	104	110
1N5W	B C	B	127	Y	1.5	126	136
1N5W	B C	B	131	D	1.4	126	136
1N5W	B C	B	796	W	1.6	795	805
1N5W	B C	B	799	W	2.3	795	805
1N5W	B C	C	266	Y	3.6	264	286
1N5W	D E	D	27	H	1.9	25	34
1N5W	D E	D	30	R	1.9	25	34
1N5W	D E	D	91	Q	2.0	89	97
1N5W	D E	D	104	Y	4.7	104	120
1N5W	D E	D	125	E	1.2	125	132
1N5W	D E	D	129	R	1.1	125	132
1N5W	D E	E	33	F	1.4	28	34
1N5W	D E	E	126	R	3.6	126	136
1N5W	D E	E	127	Y	6.0	126	136
1N5W	D E	E	131	D	2.4	126	136
1N5W	D E	E	301	R	2.9	301	306
1N5W	D E	E	693	M	1.2	692	713
1N5W	D E	E	697	G	29.2	692	713
1N5W	D E	E	701	G	124.5	692	713
1N5W	D E	E	705	E	2.0	692	713
1N5W	D F	F	38	I	2.1	36	43
1N5W	D F	F	42	K	1.5	36	43
1N5W	D F	F	105	Q	3.3	104	110
1N5W	D F	F	108	Y	2.7	104	110
1N5W	E F	E	127	Y	1.6	126	136
1N5W	E F	E	131	D	1.1	126	136
1N5W	E F	E	796	W	1.7	795	805
1N5W	E F	E	799	W	2.1	795	805
1N5W	E F	F	266	Y	3.4	264	286
1N73	B C	B	171	Y	1.2	164	177
1N73	B C	B	200	M	1.9	180	214
1N73	B C	C	119	F	3.6	88	134
1N73	B C	C	123	L	4.8	88	134
1N73	B C	C	130	I	1.1	88	134
1N73	D E	D	126	L	1.2	112	156
1N73	D E	D	133	I	1.2	112	156
1N73	D E	D	140	I	1.3	112	156
1N73	D E	D	144	E	1.1	112	156
1N73	D E	D	147	I	1.7	112	156
1N73	D E	D	151	L	1.1	112	156
1N73	D E	D	152	R	1.2	112	156
1N73	D E	E	189	M	1.0	173	214
1N73	D E	E	195	H	1.2	173	214
1N73	D E	E	196	L	1.5	173	214
1N73	D E	E	199	K	1.0	173	214
1N73	D E	E	202	R	1.3	173	214
1N73	D E	E	203	M	1.2	173	214
1N73	D E	E	207	I	1.0	173	214
1N73	D E	E	209	T	2.7	173	214
1N73	D F	D	115	L	1.3	112	156
1N73	D F	D	118	R	1.2	112	156
1N73	D F	D	129	L	1.4	112	156
1N73	D F	D	132	N	2.5	112	156
1N73	D F	D	136	Q	1.5	112	156
1N73	D F	D	143	V	1.1	112	156
1N73	D F	F	106	I	1.7	96	134

1N73	D F	F	120	V	1.0	96	134
1N73	D F	F	127	L	1.4	96	134
1N73	E F	E	178	I	1.0	173	214
1N73	E F	E	182	V	2.2	173	214
1N73	E F	E	186	L	2.0	173	214
1N73	E F	E	189	M	1.1	173	214
1N73	E F	E	193	L	1.3	173	214
1N73	E F	E	207	I	1.3	173	214
1N73	E F	F	106	I	1.5	96	134
1N73	E F	F	108	E	1.6	96	134
1N73	E F	F	109	L	2.6	96	134
1N73	E F	F	123	L	1.8	96	134
1N73	E F	F	130	I	1.0	96	134
1N73	E F	F	143	A	1.5	141	145
1N86	A B	A	148	K	1.4	146	163
1N86	A B	A	149	R	1.7	146	163
1N86	A B	A	156	I	1.1	146	163
1N86	A B	A	158	I	1.0	146	163
1N86	A B	B	178	K	1.8	162	193
1N86	A C	A	136	L	1.6	133	138
1N86	A C	A	161	C	2.2	146	163
1N86	A C	C	114	Y	2.6	102	121
1N86	B C	B	172	L	1.6	162	193
1N86	B C	B	176	R	1.4	162	193
1N86	B C	B	179	I	1.1	162	193
1N86	B C	B	186	V	1.5	162	193
1N86	B C	B	190	M	1.1	162	193
1N86	B C	C	103	H	1.1	102	121
1N86	B C	C	120	K	1.8	102	121
1N86	B C	C	124	L	1.5	122	135
1N86	B C	C	131	L	2.0	122	135
1N86	D E	D	140	V	3.2	135	143
1N86	D E	D	144	L	2.6	144	161
1N86	D E	D	147	M	2.0	144	161
1N86	D E	D	148	K	4.3	144	161
1N86	D E	D	149	R	1.2	144	161
1N86	D E	D	150	L	3.4	144	161
1N86	D E	D	156	I	1.6	144	161
1N86	D E	D	158	I	1.0	144	161
1N86	D E	E	168	L	4.8	165	170
1N86	D E	E	171	I	3.5	171	178
1N86	D E	E	174	N	4.0	171	178
1N86	D E	E	175	L	1.8	171	178
1N86	D E	E	192	Y	1.8	179	193
1N86	D F	D	136	L	1.2	135	143
1N86	D F	D	150	L	1.0	144	161
1N86	D F	F	114	Y	2.3	105	118
1N86	E F	E	165	L	1.3	165	170
1N86	E F	E	168	L	4.9	165	170
1N86	E F	E	169	R	4.6	165	170
1N86	E F	E	172	L	1.5	171	178
1N86	E F	E	175	L	4.5	171	178
1N86	E F	E	179	I	3.2	179	193
1N86	E F	E	183	E	1.1	179	193
1N86	E F	E	186	V	1.2	179	193
1N86	E F	F	109	Y	4.5	105	118
1N86	E F	F	110	L	5.4	105	118
1N86	E F	F	117	N	2.0	105	118
1N86	E F	F	120	K	5.6	119	134
1N86	E F	F	124	L	2.0	119	134

1N86	E F	F	131	L	2.0	119	134
1N8O	B C	C	235	V	1.4	235	245
1N8O	B C	C	237	W	3.2	235	245
1N8O	B C	C	238	V	1.3	235	245
1N8O	B C	C	241	T	1.2	235	245
1N8O	B C	C	242	L	2.3	235	245
1N8Z	A B	A	124	Q	1.2	122	126
1N95	A B	A	96	F	1.4	94	110
1N95	A B	A	131	Y	3.4	131	144
1N95	A B	A	132	T	1.9	131	144
1N95	A B	A	170	H	2.5	166	180
1N95	A B	A	203	W	1.3	200	213
1N95	A B	A	207	Q	3.5	200	213
1N95	A B	A	234	N	2.9	234	246
1N95	A B	A	241	H	1.0	234	246
1N95	A B	A	242	F	3.8	234	246
1N95	A B	A	274	E	1.2	274	286
1N95	A B	A	275	S	2.8	274	286
1N95	A B	A	282	G	8.3	274	286
1N95	A B	A	354	E	1.4	353	366
1N95	A B	A	355	Y	2.2	353	366
1N95	A B	A	358	Y	2.5	353	366
1N95	A B	B	100	R	2.3	100	108
1N95	A B	B	129	F	1.1	121	134
1N95	A B	B	271	K	1.6	270	280
1N9G	F E	F	311	Y	2.1	308	314
1N9G	F E	F	312	I	2.1	308	314
1N9G	F E	F	313	F	3.6	308	314
1N9G	F E	E	311	Y	1.2	308	314
1N9G	F E	E	312	I	2.4	308	314
1N9G	F E	E	313	F	3.5	308	314
1NAK	M I	M	124	Q	1.9	122	126
1NB3	B J	B	68	P	1.3	68	78
1NBF	A D	A	297	Q	2.3	296	312
1NBF	A D	A	367	Y	1.1	360	368
1NBF	B C	B	301	R	1.6	296	312
1NBF	B C	B	366	D	1.2	360	368
1NBU	A C	A	54	Y	1.9	54	66
1NBU	A C	C	74	E	1.1	73	87
1NBU	A D	A	74	E	1.6	73	87
1NBU	B C	B	74	E	1.5	73	87
1NBU	B C	C	54	Y	1.4	54	66
1NBW	A B	A	143	F	1.7	143	156
1NBW	A B	A	175	N	1.0	170	176
1NBW	A B	B	27	W	2.6	19	32
1NBW	A B	B	30	E	1.8	19	32
1NBW	A B	B	31	E	2.1	19	32
1NBW	C D	C	143	F	1.5	143	157
1NBW	C D	C	172	L	1.9	170	176
1NBW	C D	D	27	W	2.3	19	32
1NBW	C D	D	30	E	3.1	19	32
1NBW	C D	D	31	E	2.4	19	32
1NBW	C D	D	98	R	1.2	94	109
1NC2	C D	C	126	E	1.2	125	130
1NC2	C D	C	127	E	1.5	125	130
1NCA	L H	L	124	Q	1.8	122	127
1ND0	A B	A	124	Q	1.1	122	127
1ND0	E F	E	123	E	1.2	122	127
1ND0	E F	E	124	Q	1.7	122	127
1ND0	G H	G	123	E	1.1	122	127

1ND0	G H	G	124	Q	1.9	122	127
1NDO	A B	A	346	D	1.0	338	352
1NDO	A B	A	357	F	1.1	357	375
1NDO	A B	A	361	D	1.2	357	375
1NDO	A B	A	364	D	2.2	357	375
1NDO	A B	B	597	V	1.0	592	603
1NDO	A B	B	598	R	2.1	592	603
1NDO	A B	B	601	H	3.9	592	603
1NDO	C D	C	346	D	1.8	338	352
1NDO	C D	C	350	R	2.7	338	352
1NDO	C D	C	361	D	1.7	357	375
1NDO	C D	C	364	D	2.3	357	375
1NDO	C D	C	367	E	1.0	357	375
1NDO	C D	D	597	V	1.1	592	603
1NDO	C D	D	598	R	2.0	592	603
1NDO	C D	D	601	H	2.6	592	603
1NDO	E F	E	218	R	1.2	214	221
1NDO	E F	E	350	R	1.0	338	352
1NDO	E F	E	357	F	2.0	357	375
1NDO	E F	E	364	D	2.7	357	375
1NDO	E F	F	597	V	1.1	592	603
1NDO	E F	F	598	R	2.7	592	603
1NDO	E F	F	601	H	3.1	592	603
1NEK	A B	A	100	E	3.8	92	102
1NEK	A B	A	101	H	1.7	92	102
1NEK	A B	B	137	P	1.0	137	144
1NEK	A B	B	143	L	2.0	137	144
1NEK	A B	B	180	R	1.1	172	183
1NEK	B C	B	163	W	1.8	160	165
1NEK	B C	B	224	R	1.2	222	237
1NEK	B C	C	103	F	1.4	103	129
1NEK	B C	C	106	G	30.8	103	129
1NEK	B D	D	12	G	182.3	12	38
1NEK	B D	D	13	V	1.5	12	38
1NEK	C D	C	41	V	1.1	22	54
1NEK	C D	C	42	G	17.0	22	54
1NEK	C D	C	45	L	1.3	22	54
1NEK	C D	C	48	L	1.2	22	54
1NEK	C D	C	49	G	11.4	22	54
1NEK	C D	C	51	S	2.5	22	54
1NEK	C D	C	58	F	3.8	55	67
1NEK	C D	C	92	M	1.0	68	97
1NEK	C D	D	45	Y	2.6	45	53
1NEK	C D	D	52	F	2.1	45	53
1NEK	C D	D	79	V	1.1	55	84
1NEK	C D	D	104	Y	1.6	87	114
1NEX	A B	A	166	I	1.4	163	170
1NEX	A B	A	167	R	1.1	163	170
1NEX	A B	B	274	L	1.5	274	278
1NEX	A B	B	286	I	1.8	280	288
1NEX	A B	B	305	W	2.3	303	310
1NEX	C B	B	339	S	1.3	331	342
1NEX	C D	C	132	Y	1.0	132	141
1NEX	C D	C	135	I	1.0	132	141
1NEX	C D	C	147	L	1.4	144	156
1NEX	C D	C	152	K	1.0	144	156
1NEX	C D	C	166	I	1.3	163	170
1NEX	C D	C	167	R	1.3	163	170
1NEX	C D	D	274	L	3.9	274	278
1NEX	C D	D	282	I	1.4	280	288

1NEX	C D	D	294	D	1.0	292	300
1NEX	C D	D	305	W	2.2	303	310
1NF3	A C	A	23	Y	1.4	16	25
1NF3	B D	B	166	K	1.2	165	179
1NF3	B D	B	170	D	1.1	165	179
1NF5	A B	A	31	F	1.7	23	34
1NF5	A B	A	32	H	1.2	23	34
1NF5	A B	A	105	K	1.0	105	111
1NF5	A B	B	360	F	3.5	359	365
1NF5	C D	C	31	F	1.5	23	34
1NF5	C D	D	360	F	3.3	359	365
1NFD	A B	B	136	E	1.6	134	140
1NFD	C D	D	134	K	4.9	134	141
1NFD	C D	D	136	E	5.7	134	141
1NFD	E F	E	124	E	1.8	122	127
1NFU	A B	A	127	W	3.4	125	131
1NGM	A B	A	138	K	1.1	129	140
1NGM	A B	A	141	R	1.8	141	146
1NGM	A B	A	142	I	2.6	141	146
1NGM	A B	B	487	W	2.3	477	491
1NGM	A B	B	494	F	2.2	492	505
1NGM	E F	E	83	K	1.4	82	87
1NGM	E F	E	137	R	1.4	129	147
1NGM	E F	E	138	K	1.3	129	147
1NGM	E F	E	141	R	3.2	129	147
1NGM	E F	E	224	Y	3.5	220	237
1NGM	E F	F	452	L	1.6	448	453
1NGM	E F	F	469	E	1.4	468	472
1NGM	E F	F	470	L	1.1	468	472
1NGM	E F	F	480	S	1.5	477	491
1NGM	E F	F	487	W	3.7	477	491
1NGM	E F	F	494	F	1.4	492	502
1NGM	I F	I	131	D	1.7	131	147
1NGM	I J	I	133	K	2.0	131	147
1NGM	I J	I	141	R	2.6	131	147
1NGM	I J	I	145	K	1.0	131	147
1NGM	I J	J	470	L	2.3	468	472
1NGM	I J	J	494	F	1.6	492	502
1NGM	M N	M	141	R	1.8	129	147
1NGM	M N	M	142	I	1.0	129	147
1NGM	M N	N	483	K	1.2	477	491
1NGM	M N	N	487	W	3.5	477	491
1NGM	M N	N	494	F	2.1	492	497
1NGW	A B	A	122	D	1.0	122	127
1NGW	L H	L	123	E	1.0	122	127
1NH2	A C	A	142	I	1.3	129	147
1NH2	B D	B	9	V	1.0	4	21
1NH2	B D	B	10	Y	5.0	4	21
1NH2	B D	B	13	I	2.4	4	21
1NH2	B D	B	17	V	1.6	4	21
1NH2	B D	B	25	F	1.6	22	28
1NH2	B D	B	38	L	2.1	32	48
1NH2	B D	B	42	W	3.7	32	48
1NH2	B D	B	45	K	1.6	32	48
1NH2	B D	B	46	L	1.3	32	48
1NH2	B D	D	15	I	3.3	14	29
1NH2	B D	D	19	L	2.0	14	29
1NH2	B D	D	26	L	1.5	14	29
1NH2	B D	D	36	L	1.7	34	55
1NH2	B D	D	40	V	1.3	34	55

1NH2	B D	D	47	V	1.8	34	55
1NH2	C D	D	52	L	1.7	34	55
1NHG	A C	A	111	Y	2.3	111	122
1NHG	A C	A	114	G	90.6	111	122
1NHG	A C	A	115	I	1.1	111	122
1NHG	A C	A	268	H	1.4	268	272
1NHG	A C	C	368	F	2.9	368	380
1NHG	A C	C	369	I	2.1	368	380
1NHG	A C	C	373	I	1.2	368	380
1NHG	A C	C	391	I	1.9	388	400
1NHG	A C	C	392	G	45.0	388	400
1NHG	A C	C	399	L	3.5	388	400
1NHG	A D	A	300	G	8.2	281	303
1NHG	B C	B	297	Y	1.1	281	303
1NHG	B C	B	300	G	2.3	281	303
1NHG	B C	B	301	R	1.4	281	303
1NHG	B D	B	111	Y	1.9	111	122
1NHG	B D	B	114	G	57.3	111	122
1NHG	B D	B	115	I	1.0	111	122
1NHG	B D	B	293	R	1.4	281	303
1NHG	B D	D	368	F	2.2	368	380
1NHG	B D	D	391	I	2.4	388	400
1NHG	B D	D	392	G	43.6	388	400
1NHG	B D	D	399	L	3.0	388	400
1NI4	A B	A	147	G	168.4	140	155
1NI4	A B	A	154	Y	4.2	140	155
1NI4	A B	B	64	G	22.2	62	70
1NI4	A B	B	65	I	1.4	62	70
1NI4	A B	B	68	G	118.0	62	70
1NI4	A B	B	101	Y	3.5	90	102
1NI4	A B	B	278	R	1.3	271	279
1NI4	A D	D	307	I	1.0	306	311
1NI4	A D	D	308	L	2.7	306	311
1NI4	A D	D	325	K	1.2	316	328
1NI4	C B	B	308	L	2.6	306	311
1NI4	C B	B	321	F	1.2	316	327
1NI4	C B	B	322	A	1.2	316	327
1NI4	C B	B	325	K	1.0	316	327
1NI4	C D	C	147	G	173.8	140	156
1NI4	C D	C	150	L	1.0	140	156
1NI4	C D	C	154	Y	3.7	140	156
1NI4	C D	D	64	G	34.8	62	70
1NI4	C D	D	68	G	157.2	62	70
1NI4	C D	D	101	Y	4.0	90	102
1NIK	A B	A	501	L	1.3	495	505
1NIK	A B	A	658	L	1.9	639	659
1NIK	A B	A	761	M	1.2	755	763
1NIK	A B	A	810	P	1.1	810	830
1NIK	A B	A	813	F	2.1	810	830
1NIK	A B	A	814	F	3.5	810	830
1NIK	A B	A	820	G	182.0	810	830
1NIK	A B	A	824	L	1.9	810	830
1NIK	A B	A	1261	K	1.0	1261	1271
1NIK	A B	A	1413	G	34.7	1405	1415
1NIK	A B	B	699	E	1.6	695	700
1NIK	A B	B	1023	V	1.1	1023	1038
1NIK	A B	B	1026	L	1.4	1023	1038
1NIK	A B	B	1052	V	1.8	1052	1062
1NIK	A B	B	1134	E	1.0	1132	1141
1NIK	A B	B	1135	R	1.6	1132	1141

1NIK	A B	B	1139	I	1.8	1132	1141
1NIK	A B	B	1202	L	4.4	1198	1210
1NIK	A B	B	1207	L	1.0	1198	1210
1NIK	A E	A	942	F	1.3	923	947
1NIK	A E	A	946	V	1.2	923	947
1NIK	A E	A	1006	I	1.3	1005	1014
1NIK	A F	A	504	L	1.9	495	505
1NIK	A F	F	92	R	1.7	87	103
1NIK	A F	F	95	G	22.7	87	103
1NIK	A I	A	710	L	1.0	710	737
1NIK	A K	A	551	Y	2.8	544	553
1NIK	A K	A	552	W	6.4	544	553
1NIK	B C	C	35	R	1.2	27	40
1NIK	B C	C	38	I	1.3	27	40
1NIK	B C	C	61	E	1.5	60	70
1NIK	B C	C	62	F	2.8	60	70
1NIK	B C	C	65	H	1.9	60	70
1NIK	B I	B	298	L	1.8	296	302
1NIK	B I	B	308	W	3.6	308	316
1NIK	B I	B	311	L	1.4	308	316
1NIK	B J	B	190	Y	2.5	186	192
1NIK	B J	J	59	K	1.4	56	62
1NIK	B K	K	40	H	1.1	40	51
1NIK	C J	C	62	F	1.3	60	70
1NIK	C J	J	19	E	1.3	18	28
1NIK	C J	J	58	E	1.3	56	62
1NIK	C J	J	61	L	1.7	56	62
1NIK	C K	C	29	M	1.4	27	40
1NIK	C K	C	33	L	2.8	27	40
1NIK	C K	C	241	D	1.2	240	264
1NIK	C K	C	248	I	4.3	240	264
1NIK	C K	C	251	L	1.2	240	264
1NIK	C K	C	255	V	1.3	240	264
1NIK	C K	C	258	I	1.1	240	264
1NIK	C K	C	259	L	1.4	240	264
1NIK	C K	C	262	L	2.2	240	264
1NIK	C K	K	42	L	1.1	40	51
1NIK	C K	K	45	L	2.2	40	51
1NIK	C K	K	84	K	2.3	83	111
1NIK	C K	K	88	K	1.0	83	111
1NIK	C K	K	97	K	1.5	83	111
1NIK	C K	K	98	L	2.1	83	111
1NIK	C K	K	101	L	2.0	83	111
1NIK	C K	K	105	F	3.9	83	111
1NIK	C L	C	68	G	9.9	60	70
1NIW	A B	A	12	F	1.1	6	20
1NIW	A B	A	92	F	1.9	81	93
1NIW	A B	A	141	F	1.0	138	143
1NIW	A B	B	496	F	2.7	496	507
1NIW	A B	B	498	E	1.0	496	507
1NIW	A B	B	503	V	1.4	496	507
1NIW	A B	B	504	K	1.1	496	507
1NIW	A B	B	505	I	2.2	496	507
1NIW	C D	C	12	F	1.3	6	20
1NIW	C D	C	14	E	1.4	6	20
1NIW	C D	C	84	E	1.3	81	93
1NIW	C D	C	92	F	2.3	81	93
1NIW	C D	C	141	F	1.2	138	143
1NIW	C D	D	496	F	2.9	496	509
1NIW	C D	D	498	E	1.2	496	509

1NIW	C D	D	503	V	1.0	496	509
1NIW	C D	D	504	K	1.9	496	509
1NIW	C D	D	505	I	2.3	496	509
1NIW	E F	E	11	E	1.7	6	20
1NIW	E F	E	14	E	2.0	6	20
1NIW	E F	E	92	F	2.8	81	93
1NIW	E F	E	105	L	1.9	102	108
1NIW	E F	E	141	F	1.0	138	143
1NIW	E F	F	496	F	4.7	496	508
1NIW	E F	F	497	K	1.4	496	508
1NIW	E F	F	498	E	1.4	496	508
1NIW	E F	F	499	V	1.2	496	508
1NIW	E F	F	503	V	1.8	496	508
1NIW	E F	F	504	K	1.1	496	508
1NIW	E F	F	505	I	1.3	496	508
1NIW	G H	G	12	F	1.1	6	20
1NIW	G H	G	19	F	1.0	6	20
1NIW	G H	G	92	F	3.0	83	93
1NIW	G H	G	105	L	1.0	102	108
1NIW	G H	G	141	F	1.0	138	143
1NIW	G H	H	496	F	3.1	496	509
1NIW	G H	H	503	V	2.0	496	509
1NIW	G H	H	504	K	1.7	496	509
1NIW	G H	H	505	I	2.1	496	509
1NJ9	A B	A	125	E	1.6	123	127
1NJ9	L H	L	125	E	1.3	123	128
1NKP	A B	A	921	F	2.0	898	927
1NKP	A B	A	924	L	1.9	898	927
1NKP	A B	A	943	L	3.3	939	982
1NKP	A B	A	949	Y	1.6	939	982
1NKP	A B	A	950	I	1.9	939	982
1NKP	A B	A	960	L	1.0	939	982
1NKP	A B	A	968	R	1.0	939	982
1NKP	A B	A	971	R	1.1	939	982
1NKP	A B	A	975	K	1.3	939	982
1NKP	A B	A	978	L	1.6	939	982
1NKP	A B	A	981	L	1.3	939	982
1NKP	A B	B	222	F	2.1	203	229
1NKP	A B	B	225	L	1.7	203	229
1NKP	A B	B	243	L	3.0	239	280
1NKP	A B	B	249	Y	1.3	239	280
1NKP	A B	B	250	I	1.7	239	280
1NKP	A B	B	254	R	1.7	239	280
1NKP	A B	B	267	L	2.1	239	280
1NKP	A B	B	270	Q	1.4	239	280
1NKP	A B	B	274	L	2.7	239	280
1NKP	A B	B	278	V	1.0	239	280
1NKP	D E	D	521	F	2.0	500	527
1NKP	D E	D	524	L	1.6	500	527
1NKP	D E	D	543	L	3.4	539	581
1NKP	D E	D	550	I	2.1	539	581
1NKP	D E	D	560	L	1.4	539	581
1NKP	D E	D	564	E	1.2	539	581
1NKP	D E	D	567	L	1.1	539	581
1NKP	D E	D	568	R	1.1	539	581
1NKP	D E	D	571	R	1.1	539	581
1NKP	D E	D	574	L	1.8	539	581
1NKP	D E	D	578	L	1.9	539	581
1NKP	D E	E	722	F	2.0	705	727
1NKP	D E	E	725	L	2.2	705	727

1NKP	D E	E	743	L	3.0	739	780
1NKP	D E	E	749	Y	1.3	739	780
1NKP	D E	E	750	I	1.6	739	780
1NKP	D E	E	760	H	1.5	739	780
1NKP	D E	E	764	I	1.2	739	780
1NKP	D E	E	767	L	2.1	739	780
1NKP	D E	E	770	Q	1.5	739	780
1NKP	D E	E	774	L	2.1	739	780
1NL0	L H	L	125	E	1.3	123	128
1NLD	L H	L	124	Q	1.0	122	127
1NLW	A B	A	17	L	1.0	5	27
1NLW	A B	A	24	L	1.3	5	27
1NLW	A B	A	43	L	2.9	40	80
1NLW	A B	A	47	K	1.0	40	80
1NLW	A B	A	50	I	2.2	40	80
1NLW	A B	A	53	L	2.1	40	80
1NLW	A B	A	54	E	1.1	40	80
1NLW	A B	A	64	I	1.8	40	80
1NLW	A B	A	67	L	2.0	40	80
1NLW	A B	A	74	L	1.9	40	80
1NLW	A B	A	78	L	1.2	40	80
1NLW	A B	B	222	F	1.2	204	227
1NLW	A B	B	225	L	1.8	204	227
1NLW	A B	B	249	Y	1.4	239	278
1NLW	A B	B	250	I	2.3	239	278
1NLW	A B	B	253	M	1.4	239	278
1NLW	A B	B	260	H	1.3	239	278
1NLW	A B	B	264	I	1.8	239	278
1NLW	D E	D	524	L	1.4	503	527
1NLW	D E	D	543	L	3.0	539	578
1NLW	D E	D	550	I	1.6	539	578
1NLW	D E	D	553	L	1.4	539	578
1NLW	D E	D	564	I	1.2	539	578
1NLW	D E	D	567	L	1.8	539	578
1NLW	D E	D	574	L	1.7	539	578
1NLW	D E	E	722	F	1.4	706	727
1NLW	D E	E	725	L	2.0	706	727
1NLW	D E	E	743	L	1.4	739	778
1NLW	D E	E	750	I	1.8	739	778
1NLW	D E	E	760	H	1.2	739	778
1NLW	D E	E	764	I	1.8	739	778
1NLW	D E	E	767	L	1.0	739	778
1NLW	D E	E	774	L	1.9	739	778
1NMU	C B	C	92	F	2.1	91	97
1NMU	C B	B	35	R	2.3	27	36
1NMU	C B	B	58	Y	1.1	53	63
1NMU	C B	B	61	M	1.4	53	63
1NMU	C B	B	62	L	1.5	53	63
1NOV	A D	D	366	F	3.5	366	377
1NOV	A D	D	367	W	4.1	366	377
1NOV	A D	D	373	I	1.9	366	377
1NOV	B E	B	349	K	1.1	341	353
1NOV	B E	B	350	I	1.3	341	353
1NOV	B E	E	366	F	3.0	366	377
1NOV	B E	E	367	W	4.1	366	377
1NOV	B E	E	373	I	2.1	366	377
1NOV	B E	E	374	L	1.4	366	377
1NOV	C F	C	68	K	1.0	61	72
1NOV	C F	C	349	K	1.4	341	354
1NOV	C F	F	367	W	4.7	366	377

1NOV	C F	F	369	R	1.2	366	377
1NOV	C F	F	373	I	1.5	366	377
1NOV	C F	F	374	L	1.6	366	377
1NPQ	A B	B	123	R	1.1	119	126
1NPQ	A B	B	125	L	1.6	119	126
1NRJ	A B	A	34	I	1.7	27	40
1NRJ	A B	A	38	I	2.4	27	40
1NRL	A C	A	255	I	1.1	240	261
1NRL	A C	A	270	E	1.1	269	279
1NRL	A C	A	273	I	3.6	269	279
1NRL	A C	A	424	L	1.0	423	429
1NRL	A C	A	427	E	2.6	423	429
1NRL	A C	C	690	L	2.0	688	695
1NRL	A C	C	691	H	1.0	688	695
1NRL	A C	C	693	L	1.0	688	695
1NRL	A C	C	694	L	1.1	688	695
1NRL	B D	B	255	I	1.1	240	260
1NRL	B D	B	259	K	2.8	240	260
1NRL	B D	B	273	I	3.8	269	279
1NRL	B D	B	424	L	1.1	423	429
1NRL	B D	B	427	E	2.4	423	429
1NRL	B D	D	690	L	2.6	688	696
1NRL	B D	D	691	H	1.0	688	696
1NRL	B D	D	694	L	2.4	688	696
1NRO	L H	L	14	L	1.5	14	14
1NRO	L H	L	14	Y	1.5	14	14
1NSN	H S	S	124	H	1.5	124	135
1NSN	L H	L	124	Q	1.2	122	127
1NT2	A B	A	149	F	3.1	139	151
1NT2	A B	B	36	F	1.9	32	38
1NT2	A B	B	65	L	1.0	59	80
1NT2	A B	B	77	V	1.1	59	80
1NT2	A B	B	173	E	1.2	172	177
1NT2	A B	B	247	F	1.5	230	249
1NTK	A B	A	4	Y	2.1	4	11
1NTK	A B	A	76	E	1.9	75	82
1NTK	A B	A	80	E	2.1	75	82
1NTK	A B	A	366	V	1.7	351	369
1NTK	A B	A	372	T	1.9	372	386
1NTK	A B	B	370	M	1.4	354	372
1NTK	A B	B	375	S	1.4	375	389
1NTK	A C	A	332	D	1.1	331	348
1NTK	A C	A	336	F	1.6	331	348
1NTK	A C	A	436	R	1.1	434	440
1NTK	A E	A	141	N	1.4	124	143
1NTK	A E	A	142	D	1.7	124	143
1NTK	A E	A	147	D	2.0	145	158
1NTK	A G	A	434	Y	1.2	434	440
1NTK	A I	A	140	E	1.3	124	143
1NTK	A I	A	146	R	9.3	145	158
1NTK	B I	B	150	V	1.0	134	152
1NTK	B I	B	368	Y	8.7	354	372
1NTK	C D	C	72	D	1.3	59	73
1NTK	C D	C	77	W	1.9	76	104
1NTK	C D	C	81	Y	2.3	76	104
1NTK	C D	C	233	L	2.5	228	244
1NTK	C D	C	234	L	1.2	228	244
1NTK	C D	C	237	L	1.6	228	244
1NTK	C D	D	50	H	1.3	48	56
1NTK	C D	D	204	M	1.0	196	219

1NTK	C D	D	205	G	37.8	196	219
1NTK	C D	D	208	M	3.5	196	219
1NTK	C D	D	209	L	1.8	196	219
1NTK	C D	D	212	M	1.4	196	219
1NTK	C D	D	216	L	1.8	196	219
1NTK	C D	D	220	Y	1.1	220	232
1NTK	C D	D	227	W	3.8	220	232
1NTK	C D	D	230	L	1.5	220	232
1NTK	C E	E	58	F	2.0	29	61
1NTK	C F	C	319	P	1.4	319	340
1NTK	C F	C	376	L	1.3	345	378
1NTK	C F	F	20	Y	2.5	8	25
1NTK	C F	F	21	Y	1.2	8	25
1NTK	C F	F	62	I	1.0	52	71
1NTK	C G	C	326	W	1.5	319	340
1NTK	C G	C	333	L	1.1	319	340
1NTK	C G	C	337	W	3.5	319	340
1NTK	C G	C	347	Y	2.9	345	378
1NTK	C G	G	52	F	3.4	45	68
1NTK	C G	G	55	F	2.0	45	68
1NTK	C G	G	59	Y	1.1	45	68
1NTK	C G	G	62	G	24.6	45	68
1NTK	C G	G	66	F	2.5	45	68
1NTK	D E	D	211	M	1.0	196	219
1NTK	D E	D	215	L	1.2	196	219
1NTK	D E	D	218	L	1.3	196	219
1NTK	D E	E	39	V	1.0	29	61
1NTK	D F	F	60	F	2.6	52	71
1NTK	D F	F	70	M	1.0	52	71
1NTK	D G	D	225	H	1.3	220	232
1NTK	D G	D	229	V	1.5	220	232
1NTK	D H	H	17	L	1.4	16	25
1NTK	D H	H	59	L	1.0	55	77
1NTK	D J	D	203	R	1.4	196	219
1NTK	D J	D	206	L	1.2	196	219
1NTK	D J	D	207	K	1.3	196	219
1NTK	D J	J	35	F	2.3	17	46
1NTK	D J	J	40	D	1.1	17	46
1NTK	D J	J	43	Y	2.7	17	46
1NTK	E G	E	32	R	2.5	29	61
1NTK	E J	E	34	G	11.1	29	61
1NTK	E J	E	45	V	2.0	29	61
1NTK	E J	E	49	Y	2.8	29	61
1NTK	E J	J	10	Y	2.1	5	16
1NTK	E J	J	14	F	1.2	5	16
1NTK	E J	J	20	F	1.5	17	46
1NTK	E J	J	31	F	1.0	17	46
1NTK	E J	J	32	E	1.0	17	46
1NTK	E K	K	34	W	2.4	18	36
1NTK	F G	F	55	Y	1.0	52	71
1NTK	F G	F	60	F	1.1	52	71
1NU7	A B	A	14	E	1.4	14	14
1NU7	A B	A	14	E	1.7	14	14
1NU7	A B	A	14	L	1.3	14	14
1NU7	B D	D	42	L	1.0	24	47
1NU7	B D	D	46	E	1.3	24	47
1NU7	B D	D	67	L	3.0	56	95
1NU7	B D	D	71	Q	2.1	56	95
1NU7	B D	D	74	L	1.0	56	95
1NU7	B D	D	194	L	1.7	182	197

1NU7	B D	D	213	E	1.0	208	230
1NU7	E F	E	14	E	2.6	14	14
1NU7	E F	E	14	L	1.7	14	14
1NU7	F H	H	42	L	1.0	24	46
1NU7	F H	H	56	K	1.1	56	95
1NU7	F H	H	63	M	2.1	56	95
1NU7	F H	H	67	L	1.1	56	95
1NU7	F H	H	194	L	1.7	182	197
1NU9	D F	F	42	L	1.1	24	46
1NU9	D F	F	59	K	4.9	56	95
1NU9	D F	F	67	L	1.4	56	95
1NVM	A B	A	124	Q	1.0	123	133
1NVM	A B	A	125	H	1.7	123	133
1NVM	A B	A	331	D	3.7	326	341
1NVM	A B	A	335	D	1.4	326	341
1NVM	A B	B	169	R	3.8	166	170
1NVM	A B	B	173	D	2.2	172	188
1NVM	C D	C	125	H	1.1	123	133
1NVM	C D	C	331	D	4.4	326	339
1NVM	C D	C	335	D	1.6	326	339
1NVM	C D	D	169	R	2.5	166	170
1NVM	C D	D	173	D	2.5	172	188
1NVM	C F	C	74	E	1.7	69	80
1NVM	C F	F	85	V	1.4	84	95
1NVM	E F	E	125	H	1.4	123	133
1NVM	E F	E	331	D	3.2	326	339
1NVM	E F	E	335	D	1.5	326	339
1NVM	E F	F	169	R	3.2	166	171
1NVM	E F	F	172	I	1.5	172	188
1NVM	E F	F	173	D	2.0	172	188
1NVM	G H	G	328	M	1.6	326	340
1NVM	G H	G	331	D	3.6	326	340
1NVM	G H	G	335	D	1.1	326	340
1NVM	G H	H	169	R	3.1	166	171
1NVP	B D	B	13	L	1.6	10	25
1NVP	B D	B	14	Y	1.7	10	25
1NVP	B D	B	17	V	1.8	10	25
1NVP	B D	B	21	V	1.3	10	25
1NVP	B D	B	38	V	1.1	36	51
1NVP	B D	B	42	L	2.0	36	51
1NVP	B D	B	45	L	1.1	36	51
1NVP	B D	B	46	W	4.4	36	51
1NVP	B D	B	49	K	1.9	36	51
1NVP	B D	D	11	L	2.8	10	25
1NVP	B D	D	15	L	2.1	10	25
1NVP	B D	D	22	L	1.7	10	25
1NVP	B D	D	36	V	1.2	30	52
1NW9	A B	A	323	W	3.9	316	324
1NW9	A B	A	343	H	3.5	336	344
1NWD	A B	A	92	F	1.0	82	93
1NWD	A B	A	141	F	5.3	138	146
1NWD	A B	B	12	L	1.4	7	26
1NWD	A B	B	19	K	2.4	7	26
1NWD	A B	B	22	V	2.9	7	26
1NWD	A C	A	19	F	2.2	7	20
1NWD	A C	C	18	W	2.0	7	26
1NWD	A C	C	19	K	1.8	7	26
1NX0	A C	A	102	L	1.2	95	108
1NX0	A C	A	106	L	2.7	95	108
1NX0	A C	A	125	V	3.8	115	128

1NX0	A C	A	166	W	4.7	159	179
1NX0	A C	C	603	I	2.4	602	610
1NX0	A C	C	606	L	2.9	602	610
1NX0	A C	C	609	D	1.4	602	610
1NX0	B D	B	406	L	1.1	395	408
1NX0	B D	B	466	W	1.4	459	479
1NX0	B D	D	703	I	2.4	702	710
1NX0	B D	D	706	L	1.8	702	710
1NZY	A B	A	82	F	2.0	75	99
1NZY	A B	A	158	M	2.3	158	168
1NZY	A B	A	159	R	5.4	158	168
1NZY	A B	A	160	R	2.0	158	168
1NZY	A B	A	162	M	3.5	158	168
1NZY	A B	A	163	E	1.0	158	168
1NZY	A B	A	165	M	2.6	158	168
1NZY	A B	A	166	L	3.2	158	168
1NZY	A B	A	167	T	2.3	158	168
1NZY	A B	A	221	W	1.4	207	222
1NZY	A B	B	155	I	1.0	150	156
1NZY	A B	B	209	L	1.9	207	222
1NZY	A B	B	217	F	4.4	207	222
1NZY	A B	B	220	G	92.2	207	222
1NZY	A B	B	221	W	2.6	207	222
1NZY	A B	B	225	V	1.8	225	242
1NZY	A B	B	232	E	2.2	225	242
1NZY	A B	B	236	V	1.0	225	242
1NZY	A B	B	239	S	1.4	225	242
1NZY	A B	B	240	V	2.0	225	242
1NZY	A B	B	245	F	2.8	243	255
1NZY	A B	B	249	L	1.5	243	255
1NZY	C B	C	155	I	1.0	150	156
1NZY	C B	C	209	L	1.2	207	222
1NZY	C B	C	216	R	1.6	207	222
1NZY	C B	C	217	F	4.5	207	222
1NZY	C B	C	220	G	157.9	207	222
1NZY	C B	C	221	W	2.1	207	222
1NZY	C B	C	225	V	1.8	225	240
1NZY	C B	C	226	E	1.1	225	240
1NZY	C B	C	232	E	2.3	225	240
1NZY	C B	C	236	V	1.1	225	240
1NZY	C B	C	237	I	1.0	225	240
1NZY	C B	C	239	S	1.2	225	240
1NZY	C B	C	245	F	2.9	243	255
1NZY	C B	C	249	L	1.7	243	255
1NZY	C B	B	78	V	1.0	75	99
1NZY	C B	B	79	R	1.1	75	99
1NZY	C B	B	82	F	2.1	75	99
1NZY	C B	B	94	H	1.1	75	99
1NZY	C B	B	150	Y	3.8	150	156
1NZY	C B	B	158	M	1.7	158	168
1NZY	C B	B	159	R	5.1	158	168
1NZY	C B	B	160	R	3.2	158	168
1NZY	C B	B	162	M	4.2	158	168
1NZY	C B	B	166	L	5.3	158	168
1NZY	C B	B	221	W	1.3	207	222
1O0P	A B	A	397	E	1.4	392	407
1O18	D E	D	812	S	3.0	784	826
1O18	D E	D	815	C	1.2	784	826
1O18	D E	D	816	I	1.1	784	826
1O18	D E	D	818	Y	42.3	784	826

1O18	D E	E	100	A	3.1	94	105
1O18	D E	E	101	F	3.6	94	105
1O18	D E	E	132	E	7.9	132	140
1O18	D F	D	787	I	1.2	784	826
1O18	D F	D	796	G	42.0	784	826
1O18	D F	D	799	M	1.1	784	826
1O18	D F	D	800	R	1.1	784	826
1O18	D F	D	806	M	1.2	784	826
1O18	D F	F	17	F	1.3	9	18
1O18	D F	F	87	F	1.2	85	93
1O18	G H	G	824	M	1.8	784	826
1O18	G H	H	80	F	1.1	77	88
1O18	G H	H	135	N	1.8	132	140
1O18	G H	H	157	I	2.1	152	159
1O18	G I	G	730	S	4.4	730	739
1O18	G I	G	800	R	182.7	784	826
1O18	G V	V	141	S	1.1	137	145
1O18	G V	V	142	L	1.1	137	145
1O18	G X	G	556	D	80.3	555	559
1O18	G X	G	557	E	27.0	555	559
1O18	J K	J	816	I	1.2	784	826
1O18	J K	J	820	V	4.0	784	826
1O18	J K	J	823	F	2.8	784	826
1O18	J K	K	87	K	1.2	77	88
1O18	J L	J	795	R	38.4	784	826
1O18	J L	J	796	G	72.3	784	826
1O18	J L	J	801	V	1.5	784	826
1O18	J W	J	632	G	584.7	619	633
1O18	J W	W	141	S	1.1	137	145
1O18	J W	W	142	L	1.2	137	145
1O18	J W	W	344	S	109.5	338	349
1O18	J Y	J	556	D	26.4	555	559
1O18	J Y	J	557	E	86.6	555	559
1O18	M N	M	809	R	16.5	808	826
1O18	M N	M	816	I	1.6	808	826
1O18	M N	M	822	S	41.4	808	826
1O18	M N	M	823	F	1.7	808	826
1O18	M N	N	34	I	75.8	21	35
1O18	M N	N	80	F	7.9	77	88
1O18	M N	N	116	F	15.1	114	123
1O18	M N	N	132	E	14.9	132	140
1O18	M N	N	136	M	15.0	132	140
1O18	M O	M	730	S	1.6	730	739
1O18	M Z	M	536	L	578.1	532	537
1O18	M Z	M	631	E	149.7	619	633
1O18	M Z	M	632	G	749.5	619	633
1O18	M Z	M	655	E	146.5	650	658
1O18	M Z	Z	141	S	1.1	137	145
1O18	M Z	Z	142	L	1.2	137	145
1O18	M Z	Z	143	Y	1.7	137	145
1O18	M Z	Z	342	G	5.6	338	349
1O18	M Z	Z	344	S	683.2	338	349
1O18	M Z	Z	345	I	70.5	338	349
1O18	M Z	Z	346	L	574.7	338	349
1O18	M Z	Z	348	S	148.7	338	349
1O18	P Q	P	822	S	29.3	808	826
1O18	P Q	P	823	F	1.4	808	826
1O18	P Q	Q	34	I	64.6	21	35
1O18	P Q	Q	80	F	11.1	77	88
1O18	P R	P	796	G	195.4	784	805

1O18	P R	P	803	Y	1.9	784	805
1O18	P R	R	17	F	1.0	9	18
1O18	P R	R	111	L	13.2	104	113
1O2F	A B	A	41	F	2.0	39	43
1O2F	A B	B	378	D	1.0	377	389
1O4X	A B	B	265	R	1.0	251	272
1O5E	L H	H	235	R	1.1	235	245
1O5E	L H	H	236	E	1.1	235	245
1O94	B E	B	456	K	1.3	438	458
1O94	B E	E	194	L	2.8	194	203
1O94	C D	C	98	I	1.6	97	112
1O94	C D	C	132	I	1.1	129	139
1O94	C D	C	133	S	1.6	129	139
1O94	C D	D	73	D	1.9	72	86
1O94	C D	D	101	G	3.5	97	111
1O94	E F	E	98	I	1.8	97	112
1O94	E F	E	132	I	2.1	129	139
1O94	E F	E	133	S	1.7	129	139
1O94	E F	F	73	D	1.8	72	86
1O96	A B	A	132	I	3.6	129	139
1O96	A B	A	133	S	1.5	129	139
1O96	A B	A	254	I	2.1	247	262
1O96	A B	A	255	I	1.2	247	262
1O96	A B	A	257	I	2.0	247	262
1O96	A B	A	258	I	1.4	247	262
1O96	A B	B	108	S	1.0	102	110
1O96	A B	B	236	R	4.2	236	242
1O96	A B	B	240	D	1.1	236	242
1O96	A B	B	314	L	2.0	307	318
1O96	C D	C	37	E	1.0	37	53
1O96	C D	C	98	I	1.1	97	112
1O96	C D	C	254	I	1.3	248	261
1O96	C D	C	257	I	1.8	248	261
1O96	C D	C	258	I	1.3	248	261
1O96	C D	D	310	I	1.6	307	318
1O96	C D	D	314	L	1.8	307	318
1O96	E F	E	37	E	1.3	37	52
1O96	E F	E	98	I	1.3	97	112
1O96	E F	E	133	S	1.5	129	139
1O96	E F	E	247	I	2.1	247	261
1O96	E F	E	254	I	1.8	247	261
1O96	E F	E	257	I	1.4	247	261
1O96	E F	E	258	I	1.2	247	261
1O96	E F	F	97	V	1.6	97	110
1O96	E F	F	310	I	1.1	308	314
1O96	Q Z	Q	37	E	1.2	37	53
1O96	Q Z	Q	133	S	1.5	129	139
1O96	Q Z	Q	247	I	1.8	247	260
1O96	Q Z	Q	251	A	1.1	247	260
1O96	Q Z	Q	254	I	2.3	247	260
1O96	Q Z	Q	257	I	2.3	247	260
1O96	Q Z	Q	258	I	1.2	247	260
1O96	Q Z	Z	97	V	2.1	97	110
1O96	Q Z	Z	100	L	1.1	97	110
1O96	Q Z	Z	310	I	1.4	307	318
1O96	Q Z	Z	314	L	2.1	307	318
1O96	Q Z	Z	317	Q	1.3	307	318
1O9U	A B	A	228	I	3.5	225	229
1O9U	A B	A	263	V	1.2	262	274
1O9U	A B	A	267	V	1.1	262	274

1O9U	A B	A	270	I	1.2	262	274
1O9U	A B	B	388	F	2.5	384	400
1O9U	A B	B	392	L	1.6	384	400
1O9U	A B	B	393	I	1.3	384	400
1OAO	A C	C	45	R	2.4	19	48
1OAO	A C	C	84	N	2.6	76	89
1OAO	A C	C	87	R	1.5	76	89
1OAO	A D	A	95	W	1.2	94	129
1OAO	A D	A	228	V	1.5	227	257
1OAO	A D	A	232	F	1.5	227	257
1OAO	A D	A	615	L	1.5	614	629
1OAO	A D	A	622	Q	2.4	614	629
1OAO	A D	A	623	I	1.8	614	629
1OAO	A D	A	626	D	2.3	614	629
1OAO	A D	A	654	W	2.1	638	666
1OAO	A D	A	658	V	1.5	638	666
1OAO	A D	A	659	H	1.4	638	666
1OAO	A D	A	662	V	1.5	638	666
1OAO	A D	D	30	I	1.0	19	48
1OAO	A D	D	35	Y	2.6	19	48
1OAO	A D	D	38	I	1.8	19	48
1OAO	A D	D	39	L	1.1	19	48
1OAO	A D	D	188	E	2.2	188	196
1OAO	A D	D	191	E	2.1	188	196
1OAO	A D	D	260	M	2.1	260	272
1OAO	B C	B	95	W	1.1	94	129
1OAO	B C	B	232	F	1.6	227	256
1OAO	B C	B	615	L	1.6	614	629
1OAO	B C	B	622	Q	1.5	614	629
1OAO	B C	B	651	Y	1.6	638	666
1OAO	B C	B	654	W	3.2	638	666
1OAO	B C	B	655	K	1.2	638	666
1OAO	B C	B	658	V	1.4	638	666
1OAO	B C	B	659	H	2.5	638	666
1OAO	B C	B	662	V	1.0	638	666
1OAO	B C	C	35	Y	1.3	19	48
1OAO	B C	C	39	L	1.1	19	48
1OAO	B C	C	188	E	1.9	188	196
1OAO	B C	C	191	E	2.8	188	196
1OAO	B C	C	195	E	1.0	188	196
1OAO	B C	C	260	M	2.0	260	273
1OAO	B D	D	45	R	2.1	19	48
1OAO	B D	D	84	N	2.8	76	89
1OC0	A B	A	131	R	1.3	129	143
1OC0	A B	A	135	I	2.2	129	143
1OCC	A B	A	299	V	1.5	299	328
1OCC	A B	A	310	M	1.7	299	328
1OCC	A B	A	314	I	1.3	299	328
1OCC	A B	A	321	F	3.7	299	328
1OCC	A B	A	346	F	1.8	336	360
1OCC	A B	A	353	L	1.0	336	360
1OCC	A B	A	363	L	2.6	361	368
1OCC	A B	A	366	V	1.0	361	368
1OCC	A B	A	367	L	1.1	361	368
1OCC	A B	A	430	F	1.4	407	434
1OCC	A B	A	433	L	1.1	407	434
1OCC	A B	A	450	W	2.7	448	479
1OCC	A B	B	20	L	1.2	15	46
1OCC	A B	B	23	F	2.1	15	46
1OCC	A B	B	38	V	1.3	15	46

1OCC	A B	B	39	L	1.0	15	46
1OCC	A B	B	73	L	2.3	66	88
1OCC	A B	B	80	S	1.6	66	88
1OCC	A B	B	84	L	2.1	66	88
1OCC	A B	B	85	Y	2.0	66	88
1OCC	A C	A	95	P	3.4	95	116
1OCC	A C	A	103	W	1.0	95	116
1OCC	A C	A	107	P	1.9	95	116
1OCC	A C	A	111	L	1.0	95	116
1OCC	A C	A	148	F	2.5	141	171
1OCC	A C	A	152	L	1.4	141	171
1OCC	A C	A	162	I	1.4	141	171
1OCC	A C	A	165	I	1.8	141	171
1OCC	A C	A	196	L	1.7	183	213
1OCC	A C	A	210	L	1.3	183	213
1OCC	A C	A	212	D	2.0	183	213
1OCC	A C	A	230	L	1.8	228	261
1OCC	A C	C	15	P	1.2	15	37
1OCC	A C	C	17	P	1.2	15	37
1OCC	A C	C	18	L	1.8	15	37
1OCC	A C	C	25	L	1.6	15	37
1OCC	A C	C	35	F	1.5	15	37
1OCC	A C	C	36	H	1.3	15	37
1OCC	A C	C	81	Y	1.1	73	107
1OCC	A C	C	82	G	2.4	73	107
1OCC	A C	C	85	L	2.6	73	107
1OCC	A C	C	86	F	1.0	73	107
1OCC	A C	C	93	F	1.4	73	107
1OCC	A C	C	96	G	137.6	73	107
1OCC	A C	C	99	W	3.9	73	107
1OCC	A C	C	103	H	3.0	73	107
1OCC	A D	A	412	I	1.8	407	434
1OCC	A D	A	416	I	1.2	407	434
1OCC	A D	A	459	F	1.5	448	479
1OCC	A D	A	463	T	1.1	448	479
1OCC	A D	D	81	V	1.5	77	104
1OCC	A D	D	88	F	1.1	77	104
1OCC	A D	D	89	I	1.5	77	104
1OCC	A D	D	96	L	2.2	77	104
1OCC	A F	A	492	L	3.2	492	496
1OCC	A F	A	495	L	1.6	492	496
1OCC	A J	J	50	L	1.1	26	55
1OCC	A L	A	25	W	2.2	12	41
1OCC	A L	A	36	L	1.9	12	41
1OCC	A L	A	53	I	1.2	52	87
1OCC	A L	A	469	V	1.4	448	479
1OCC	A L	A	473	W	2.7	448	479
1OCC	A L	A	476	F	2.0	448	479
1OCC	A L	L	25	M	1.6	18	45
1OCC	A L	L	28	F	2.3	18	45
1OCC	A L	L	29	F	1.9	18	45
1OCC	A L	L	32	G	13.3	18	45
1OCC	A L	L	33	F	2.6	18	45
1OCC	A L	L	36	P	1.2	18	45
1OCC	A L	L	37	F	1.9	18	45
1OCC	A L	L	40	V	1.1	18	45
1OCC	A M	A	409	W	1.0	407	434
1OCC	A M	A	466	M	2.1	448	479
1OCC	A M	A	470	F	3.4	448	479
1OCC	A M	A	473	W	1.5	448	479

1OCC	A M	M	18	G	1.0	12	36
1OCC	A M	M	19	L	1.7	12	36
1OCC	A M	M	26	F	2.1	12	36
1OCC	A T	A	275	W	1.5	270	286
1OCC	A T	A	281	G	341.3	270	286
1OCC	A T	T	18	F	1.8	13	22
1OCC	B D	D	115	W	4.9	113	126
1OCC	B D	D	133	G	22.5	130	136
1OCC	B E	E	38	G	1.1	26	39
1OCC	B H	H	68	W	2.4	66	78
1OCC	B I	B	22	H	1.0	15	46
1OCC	B I	B	29	M	1.0	15	46
1OCC	B I	B	33	L	1.0	15	46
1OCC	B I	B	37	L	1.3	15	46
1OCC	B I	B	40	Y	2.5	15	46
1OCC	B I	B	44	L	1.2	15	46
1OCC	B I	B	218	Y	1.4	216	225
1OCC	B I	I	13	L	1.3	12	51
1OCC	B I	I	35	Y	2.3	12	51
1OCC	B I	I	47	Y	1.8	12	51
1OCC	B I	I	60	F	2.5	56	66
1OCC	C G	C	34	W	1.2	15	37
1OCC	C G	C	132	L	1.3	129	153
1OCC	C G	C	135	S	1.0	129	153
1OCC	C G	C	142	V	1.0	129	153
1OCC	C G	C	146	W	2.2	129	153
1OCC	C G	C	149	H	1.3	129	153
1OCC	C G	C	165	I	1.8	156	184
1OCC	C G	C	169	L	1.4	156	184
1OCC	C G	C	182	Y	1.4	156	184
1OCC	C G	G	16	W	1.0	13	22
1OCC	C G	G	20	T	1.6	13	22
1OCC	C G	G	21	F	1.7	13	22
1OCC	C G	G	25	L	1.0	23	38
1OCC	C G	G	28	V	1.6	23	38
1OCC	C H	H	30	W	1.6	26	45
1OCC	C J	C	15	P	2.1	15	37
1OCC	C J	C	16	W	1.4	15	37
1OCC	C J	C	33	M	1.8	15	37
1OCC	C J	C	42	L	1.7	40	69
1OCC	C J	C	53	T	3.7	40	69
1OCC	C J	C	59	R	1.7	40	69
1OCC	C J	C	63	R	3.7	40	69
1OCC	C J	C	64	E	2.1	40	69
1OCC	C J	C	67	F	3.6	40	69
1OCC	C J	C	68	Q	2.8	40	69
1OCC	C J	J	5	V	3.2	5	14
1OCC	C J	J	8	K	1.1	5	14
1OCC	C J	J	9	Q	2.0	5	14
1OCC	C J	J	12	F	2.7	5	14
1OCC	C J	J	28	D	1.6	26	55
1OCC	C J	J	32	Y	1.0	26	55
1OCC	C J	J	42	G	31.3	26	55
1OCC	C J	J	52	W	1.1	26	55
1OCC	D E	D	44	E	4.1	35	46
1OCC	D E	D	56	K	2.6	53	64
1OCC	D E	D	60	Y	2.3	53	64
1OCC	D E	D	68	F	2.0	68	72
1OCC	D E	E	30	R	1.0	26	39
1OCC	D E	E	34	N	1.4	26	39

1OCC	D E	E	56	R	1.2	45	58
1OCC	D E	E	61	F	2.6	61	76
1OCC	D I	D	131	I	3.3	130	136
1OCC	D I	I	47	Y	1.7	12	51
1OCC	D I	I	50	F	2.9	12	51
1OCC	D I	I	62	E	1.2	56	66
1OCC	D K	D	83	G	157.4	77	104
1OCC	D K	D	87	F	1.0	77	104
1OCC	D K	D	90	G	36.4	77	104
1OCC	D K	D	118	K	1.1	113	126
1OCC	D K	D	121	K	2.2	113	126
1OCC	D K	D	122	R	1.1	113	126
1OCC	D K	D	134	F	1.2	130	136
1OCC	D K	K	10	H	1.3	9	35
1OCC	D K	K	14	G	2.4	9	35
1OCC	D K	K	18	L	2.0	9	35
1OCC	D K	K	21	G	27.5	9	35
1OCC	D K	K	24	F	1.4	9	35
1OCC	D K	K	32	M	1.0	9	35
1OCC	D M	D	103	V	1.0	77	104
1OCC	E F	E	27	W	1.2	26	39
1OCC	E I	E	84	Y	4.0	79	89
1OCC	G H	H	75	R	1.0	66	78
1OCC	J L	L	42	H	1.0	18	45
1OCC	L M	L	33	F	1.1	18	45
1OCC	L M	L	37	F	2.1	18	45
1OCC	L M	L	38	F	1.4	18	45
1OCC	L M	M	26	F	1.4	12	36
1OCC	L M	M	33	V	2.0	12	36
1OCC	N G	N	186	W	3.0	183	213
1OCC	N G	N	189	M	2.8	183	213
1OCC	N G	N	275	W	1.5	270	286
1OCC	N G	N	281	G	339.9	270	286
1OCC	N G	G	18	F	2.4	13	22
1OCC	N O	N	299	V	1.5	299	328
1OCC	N O	N	310	M	1.7	299	328
1OCC	N O	N	314	I	1.3	299	328
1OCC	N O	N	321	F	3.7	299	328
1OCC	N O	N	342	L	1.3	336	360
1OCC	N O	N	346	F	1.8	336	360
1OCC	N O	N	353	L	1.0	336	360
1OCC	N O	N	363	L	1.6	361	368
1OCC	N O	N	430	F	1.5	407	434
1OCC	N O	N	433	L	1.0	407	434
1OCC	N O	N	450	W	2.7	448	479
1OCC	N O	O	20	L	1.0	15	46
1OCC	N O	O	38	V	1.3	15	46
1OCC	N O	O	39	L	1.0	15	46
1OCC	N O	O	73	L	2.3	66	88
1OCC	N O	O	80	S	1.0	66	88
1OCC	N O	O	84	L	2.2	66	88
1OCC	N O	O	85	Y	2.0	66	88
1OCC	N P	N	95	P	2.8	95	116
1OCC	N P	N	103	W	1.1	95	116
1OCC	N P	N	107	P	1.9	95	116
1OCC	N P	N	111	L	1.0	95	116
1OCC	N P	N	148	F	2.5	141	171
1OCC	N P	N	152	L	1.4	141	171
1OCC	N P	N	162	I	1.3	141	171
1OCC	N P	N	165	I	1.8	141	171

1OCC	N P	N	196	L	1.7	183	213
1OCC	N P	N	208	M	1.2	183	213
1OCC	N P	N	210	L	1.3	183	213
1OCC	N P	N	212	D	1.9	183	213
1OCC	N P	N	230	L	1.8	228	261
1OCC	N P	N	234	L	1.7	228	261
1OCC	N P	P	15	P	1.2	15	37
1OCC	N P	P	17	P	1.2	15	37
1OCC	N P	P	18	L	1.8	15	37
1OCC	N P	P	25	L	1.6	15	37
1OCC	N P	P	35	F	1.5	15	37
1OCC	N P	P	36	H	1.3	15	37
1OCC	N P	P	81	Y	1.0	73	107
1OCC	N P	P	82	G	1.4	73	107
1OCC	N P	P	85	L	1.7	73	107
1OCC	N P	P	93	F	1.4	73	107
1OCC	N P	P	96	G	137.5	73	107
1OCC	N P	P	97	F	2.4	73	107
1OCC	N P	P	99	W	3.9	73	107
1OCC	N P	P	103	H	3.0	73	107
1OCC	N P	P	199	V	3.4	192	224
1OCC	N Q	N	412	I	1.8	407	434
1OCC	N Q	N	459	F	1.2	448	479
1OCC	N Q	Q	81	V	1.5	77	104
1OCC	N Q	Q	89	I	1.2	77	104
1OCC	N Q	Q	96	L	2.2	77	104
1OCC	N S	N	492	L	3.2	492	496
1OCC	N S	N	495	L	1.6	492	496
1OCC	N W	W	50	L	1.1	26	55
1OCC	N Y	N	25	W	2.2	12	41
1OCC	N Y	N	36	L	1.9	12	41
1OCC	N Y	N	469	V	1.4	448	479
1OCC	N Y	N	473	W	2.7	448	479
1OCC	N Y	N	476	F	2.0	448	479
1OCC	N Y	Y	25	M	1.6	18	45
1OCC	N Y	Y	28	F	2.3	18	45
1OCC	N Y	Y	29	F	1.9	18	45
1OCC	N Y	Y	32	G	13.3	18	45
1OCC	N Y	Y	33	F	2.6	18	45
1OCC	N Y	Y	36	P	1.2	18	45
1OCC	N Y	Y	37	F	1.9	18	45
1OCC	N Y	Y	40	V	1.1	18	45
1OCC	N Z	N	409	W	1.0	407	434
1OCC	N Z	N	466	M	1.9	448	479
1OCC	N Z	N	470	F	4.4	448	479
1OCC	N Z	N	473	W	1.4	448	479
1OCC	N Z	Z	19	L	2.2	12	36
1OCC	N Z	Z	23	F	1.7	12	36
1OCC	N Z	Z	26	F	2.3	12	36
1OCC	N Z	Z	27	L	1.3	12	36
1OCC	O Q	Q	115	W	4.9	113	126
1OCC	O Q	Q	133	G	22.5	130	136
1OCC	O R	R	38	G	1.1	26	39
1OCC	O U	U	62	S	1.2	54	64
1OCC	O U	U	68	W	2.4	66	78
1OCC	O V	O	22	H	1.0	15	46
1OCC	O V	O	29	M	1.0	15	46
1OCC	O V	O	33	L	1.0	15	46
1OCC	O V	O	37	L	1.3	15	46
1OCC	O V	O	40	Y	2.5	15	46

1OCC	O V	O	44	L	1.2	15	46
1OCC	O V	O	218	Y	1.4	216	225
1OCC	O V	V	13	L	1.3	12	51
1OCC	O V	V	35	Y	2.3	12	51
1OCC	O V	V	47	Y	1.8	12	51
1OCC	O V	V	60	F	2.5	56	66
1OCC	P T	P	34	W	1.2	15	37
1OCC	P T	P	132	L	1.2	129	153
1OCC	P T	P	135	S	1.0	129	153
1OCC	P T	P	142	V	1.0	129	153
1OCC	P T	P	146	W	2.2	129	153
1OCC	P T	P	149	H	1.3	129	153
1OCC	P T	P	165	I	1.6	156	184
1OCC	P T	P	169	L	1.3	156	184
1OCC	P T	P	182	Y	1.4	156	184
1OCC	P T	T	16	W	1.0	13	22
1OCC	P T	T	20	T	1.3	13	22
1OCC	P T	T	21	F	1.7	13	22
1OCC	P T	T	25	L	1.0	23	38
1OCC	P T	T	28	V	1.5	23	38
1OCC	P U	U	30	W	2.1	26	45
1OCC	P W	P	15	P	2.2	15	37
1OCC	P W	P	16	W	1.1	15	37
1OCC	P W	P	42	L	1.7	40	69
1OCC	P W	P	63	R	1.8	40	69
1OCC	P W	P	67	F	2.0	40	69
1OCC	P W	W	5	V	1.4	5	14
1OCC	P W	W	12	F	1.4	5	14
1OCC	P W	W	28	D	1.6	26	55
1OCC	P W	W	32	Y	1.6	26	55
1OCC	P W	W	42	G	31.2	26	55
1OCC	P W	W	52	W	1.1	26	55
1OCC	Q R	Q	44	E	1.4	35	46
1OCC	Q R	Q	56	K	2.6	53	64
1OCC	Q R	Q	60	Y	6.3	53	64
1OCC	Q R	Q	68	F	2.0	68	72
1OCC	Q R	R	30	R	1.0	26	39
1OCC	Q R	R	34	N	1.4	26	39
1OCC	Q R	R	56	R	1.2	45	58
1OCC	Q R	R	61	F	2.2	61	76
1OCC	Q R	R	69	E	1.8	61	76
1OCC	Q R	R	104	L	1.7	101	105
1OCC	Q V	Q	131	I	3.3	130	136
1OCC	Q V	V	47	Y	1.7	12	51
1OCC	Q V	V	50	F	2.9	12	51
1OCC	Q V	V	62	E	1.2	56	66
1OCC	Q X	Q	83	G	157.0	77	104
1OCC	Q X	Q	90	G	36.3	77	104
1OCC	Q X	Q	118	K	1.1	113	126
1OCC	Q X	Q	121	K	2.0	113	126
1OCC	Q X	Q	122	R	1.1	113	126
1OCC	Q X	Q	134	F	1.4	130	136
1OCC	Q X	X	10	H	1.3	9	35
1OCC	Q X	X	14	G	2.4	9	35
1OCC	Q X	X	18	L	2.0	9	35
1OCC	Q X	X	21	G	27.3	9	35
1OCC	Q X	X	24	F	1.4	9	35
1OCC	Q X	X	32	M	1.0	9	35
1OCC	Q Z	Q	103	V	1.0	77	104
1OCC	R S	R	27	W	1.2	26	39

1OCC	R V	R	84	Y	4.0	79	89
1OCC	W Y	Y	42	H	1.0	18	45
1OCC	Y Z	Y	22	L	1.2	18	45
1OCC	Y Z	Y	33	F	1.1	18	45
1OCC	Y Z	Y	37	F	2.1	18	45
1OCC	Y Z	Y	38	F	1.4	18	45
1OCC	Y Z	Z	26	F	1.4	12	36
1OCC	Y Z	Z	33	V	2.0	12	36
1OE9	A B	A	774	I	3.1	755	793
1OE9	A B	A	781	W	1.8	755	793
1OE9	A B	A	782	L	1.5	755	793
1OE9	A B	B	93	F	1.7	86	96
1OE9	A B	B	95	V	1.4	86	96
1OE9	A B	B	113	L	1.4	106	114
1OE9	A B	B	128	V	1.1	122	130
1OED	A B	A	224	L	2.0	213	239
1OED	A B	A	231	L	1.7	213	239
1OED	A B	A	238	D	7.7	213	239
1OED	A B	A	252	S	8.7	243	271
1OED	A B	B	250	S	20.1	250	277
1OED	A B	B	253	I	2.2	250	277
1OED	A B	B	264	L	1.0	250	277
1OED	A B	B	299	V	1.0	283	308
1OED	A B	B	302	L	68.9	283	308
1OED	A E	A	255	V	1.1	243	271
1OED	A E	E	265	F	1.6	251	280
1OED	B C	B	219	F	1.3	219	245
1OED	B C	B	262	F	2.1	250	277
1OED	B C	C	261	I	3.4	257	285
1OED	B C	C	272	L	1.2	257	285
1OED	D C	D	244	T	1.1	243	271
1OED	D C	C	270	F	1.1	257	285
1OED	D E	D	238	D	51.7	213	239
1OEY	A J	J	301	E	1.4	300	305
1OEY	C L	L	301	E	1.2	300	305
1OEY	D M	M	301	E	1.5	300	305
1OFU	X A	X	89	H	1.4	89	95
1OFU	X A	X	93	R	1.1	89	95
1OFU	X A	A	273	L	2.4	273	287
1OFU	Y B	Y	93	R	3.9	89	95
1OFU	Y B	B	273	L	2.0	273	287
1OFU	Y B	B	276	Y	1.0	273	287
1OHZ	A B	B	45	S	1.8	45	56
1OHZ	A B	B	46	T	1.2	45	56
1OHZ	A B	B	49	L	1.8	45	56
1OHZ	A B	B	53	R	1.9	45	56
1OIJ	A B	B	65	D	1.0	65	76
1OJ5	A B	A	293	R	1.4	288	300
1OJ5	A B	B	805	L	1.6	799	808
1OL5	A B	A	183	E	2.8	175	187
1OL5	A B	A	246	Y	1.5	230	250
1OL5	A B	B	34	W	2.8	33	41
1OL5	A B	B	35	F	3.2	33	41
1ONK	A B	A	174	W	4.7	170	183
1ONK	A B	A	191	Y	1.0	190	197
1ONV	A B	A	471	K	1.1	470	477
1ONV	A B	A	498	K	1.2	486	501
1ONV	A B	B	953	L	1.9	944	961
1OO0	A B	A	57	V	1.1	55	69
1OO0	A B	A	125	Y	1.9	117	142

1OO0	A B	A	129	D	1.8	117	142
1OO0	A B	A	133	L	1.2	117	142
1OO0	A B	A	136	S	1.7	117	142
1OO0	A B	A	140	L	2.5	117	142
1OO0	A B	A	141	H	3.9	117	142
1OOK	A B	A	14	E	1.9	14	14
1OOK	A B	A	14	E	2.3	14	14
1OOK	A B	A	14	L	2.0	14	14
1OOP	A B	B	146	L	1.1	143	147
1OOP	A C	A	67	F	1.3	64	69
1OOP	A D	A	65	E	1.7	64	69
1OOP	B C	C	99	L	1.0	99	105
1OOP	C D	C	45	E	2.5	43	48
1OQD	B L	L	19	L	1.1	17	23
1OQD	B L	L	20	R	1.8	17	23
1OQD	B L	L	22	S	1.2	17	23
1OQO	A C	C	14	F	3.4	8	19
1OQO	A C	C	15	Y	2.6	8	19
1OQO	A C	C	36	R	1.1	25	38
1OQO	B D	D	14	F	2.9	8	19
1OQO	B D	D	15	Y	2.0	8	19
1OQO	B D	D	36	R	1.0	25	38
1OQP	A B	A	110	F	2.3	99	111
1OQP	A B	A	130	L	1.2	120	131
1OQP	A B	A	142	M	2.8	136	147
1OQP	A B	A	145	E	1.4	136	147
1OQP	A B	A	163	M	9.1	156	166
1OQP	A B	B	245	E	1.4	240	253
1OQP	A B	B	247	K	1.0	240	253
1OQP	A B	B	248	W	5.7	240	253
1OQP	A B	B	251	L	2.4	240	253
1OQP	A B	B	252	L	2.2	240	253
1OQS	A B	A	3	F	4.4	2	14
1OQS	A B	A	9	I	1.5	2	14
1OQS	A B	B	20	W	3.4	18	22
1OQS	A F	F	105	C	1.0	91	109
1OQS	C D	C	2	L	11.1	2	14
1OQS	C D	C	3	F	3.9	2	14
1OQS	C D	C	9	I	1.3	2	14
1OQS	C D	C	49	D	1.1	40	55
1OQS	C D	D	2	L	1.0	2	14
1OQS	E F	E	9	I	1.4	2	14
1OQS	E F	E	49	D	1.6	40	53
1OQS	E F	E	52	Y	2.5	40	53
1OQS	E F	F	2	L	2.7	2	14
1OQS	E F	F	3	F	2.8	2	14
1OQS	G D	D	43	R	1.0	40	55
1OQS	G H	G	3	F	1.8	2	14
1OQS	G H	H	5	F	1.0	2	14
1OQS	G H	H	20	W	3.5	18	22
1OR0	A B	A	36	P	1.3	35	50
1OR0	A B	A	39	F	1.7	35	50
1OR0	A B	A	40	Y	2.8	35	50
1OR0	A B	A	41	G	22.6	35	50
1OR0	A B	A	42	Y	2.5	35	50
1OR0	A B	A	46	Q	2.5	35	50
1OR0	A B	A	54	I	1.2	51	63
1OR0	A B	A	57	L	4.3	51	63
1OR0	A B	A	58	Y	1.5	51	63
1OR0	A B	A	74	E	2.5	74	83

1OR0	A B	A	79	W	1.2	74	83
1OR0	A B	A	92	W	4.3	85	95
1OR0	A B	A	100	F	3.8	98	118
1OR0	A B	A	107	F	4.1	98	118
1OR0	A B	A	156	T	1.6	153	157
1OR0	A B	B	151	E	1.0	151	155
1OR0	A B	B	154	F	1.2	151	155
1OR0	A B	B	492	R	1.2	489	495
1OR0	A B	B	505	R	2.6	505	511
1OR0	A B	B	508	V	1.0	505	511
1OR0	C D	C	39	F	1.6	35	50
1OR0	C D	C	40	Y	4.7	35	50
1OR0	C D	C	41	G	7.8	35	50
1OR0	C D	C	42	Y	2.3	35	50
1OR0	C D	C	46	Q	2.2	35	50
1OR0	C D	C	48	R	1.3	35	50
1OR0	C D	C	54	I	1.3	51	63
1OR0	C D	C	57	L	2.0	51	63
1OR0	C D	C	58	Y	1.2	51	63
1OR0	C D	C	74	E	1.8	74	83
1OR0	C D	C	78	V	1.0	74	83
1OR0	C D	C	79	W	6.9	74	83
1OR0	C D	C	92	W	4.6	85	95
1OR0	C D	C	100	F	3.8	98	118
1OR0	C D	C	107	F	3.7	98	118
1OR0	C D	C	140	H	1.9	134	144
1OR0	C D	C	155	R	5.7	153	157
1OR0	C D	C	156	T	6.9	153	157
1OR0	C D	D	154	F	1.1	151	155
1OR0	C D	D	492	R	1.4	489	495
1OR0	C D	D	505	R	2.4	505	511
1OR0	C D	D	508	V	1.3	505	511
1OR7	A C	A	22	F	1.3	19	29
1OR7	A C	A	24	L	2.7	19	29
1OR7	A C	A	31	H	1.9	30	41
1OR7	A C	A	58	Y	1.1	46	60
1OR7	A C	A	132	F	1.2	124	137
1OR7	A C	A	171	R	1.3	167	186
1OR7	A C	A	175	F	3.1	167	186
1OR7	A C	C	4	E	1.6	3	11
1OR7	A C	C	33	W	2.8	27	44
1OR7	A C	C	37	H	2.4	27	44
1OR7	A C	C	38	L	1.2	27	44
1OR7	A C	C	39	I	2.4	27	44
1OR7	A C	C	43	M	2.3	27	44
1OR7	A C	C	55	I	1.9	55	65
1OR7	A C	C	59	V	1.9	55	65
1OR7	A C	C	63	I	2.1	55	65
1OR7	B F	B	24	L	3.2	19	29
1OR7	B F	B	26	V	1.0	19	29
1OR7	B F	B	31	H	1.7	30	41
1OR7	B F	B	58	Y	1.8	46	60
1OR7	B F	B	132	F	1.1	124	137
1OR7	B F	B	151	L	1.0	140	152
1OR7	B F	B	156	Y	1.6	156	163
1OR7	B F	B	171	R	1.1	167	190
1OR7	B F	B	175	F	3.2	167	190
1OR7	B F	F	4	E	1.7	3	11
1OR7	B F	F	23	L	1.0	17	25
1OR7	B F	F	38	L	1.5	27	44

1OR7	B F	F	43	M	2.6	27	44
1OR7	B F	F	55	I	1.6	55	64
1OR7	B F	F	59	V	1.9	55	64
1OR7	B F	F	60	M	1.6	55	64
1OR7	B F	F	63	I	1.9	55	64
1ORQ	A B	A	125	Q	1.2	123	128
1ORQ	B C	C	116	F	4.7	116	125
1ORS	A B	A	123	E	1.3	122	127
1ORS	A B	A	124	Q	1.8	122	127
1ORS	B C	C	107	E	1.1	100	113
1ORS	B C	C	116	F	3.6	116	149
1OSP	L H	L	124	Q	1.5	122	127
1OSV	A C	A	296	V	1.0	277	301
1OSV	A C	A	300	K	1.0	277	301
1OSV	A C	A	461	L	1.2	460	466
1OSV	A C	C	4	L	1.1	3	10
1OSV	A C	C	5	L	2.0	3	10
1OSV	A C	C	9	L	1.8	3	10
1OSV	B D	B	314	I	1.5	310	319
1OSV	B D	B	317	L	2.1	310	319
1OSV	B D	B	461	L	1.2	460	467
1OSV	B D	D	5	L	3.3	3	10
1OSV	B D	D	6	R	1.3	3	10
1OSV	B E	B	460	P	1.0	460	467
1OTR	A B	A	15	I	2.5	9	20
1OUU	A B	A	31	R	2.3	21	36
1OUU	A B	A	104	H	1.4	98	114
1OUU	A B	A	108	V	1.0	98	114
1OUU	A B	A	112	I	1.4	98	114
1OUU	A B	A	123	H	1.4	120	138
1OUU	A B	B	30	R	1.0	20	35
1OUU	A B	B	34	V	1.1	20	35
1OUU	A B	B	112	I	1.2	101	119
1OUU	A D	D	36	P	1.0	36	42
1OUU	A D	D	37	W	2.1	36	42
1OUU	A D	D	41	Y	1.9	36	42
1OUU	C D	C	31	R	3.8	21	36
1OUU	C D	C	112	I	1.4	97	114
1OUU	C D	C	123	H	1.7	120	138
1OUU	C D	D	34	V	1.1	20	35
1OUU	C D	D	108	D	1.0	101	119
1OUU	C D	D	112	I	1.1	101	119
1OUU	C D	D	127	Q	1.4	124	142
1OVA	A B	A	156	L	1.1	150	165
1OVA	A B	B	156	L	1.1	150	165
1OVA	A B	B	160	W	1.6	150	165
1OVL	A B	A	370	R	2.1	364	375
1OVL	A B	A	373	V	1.1	364	375
1OVL	A B	A	500	I	1.3	500	510
1OVL	A B	A	538	H	1.1	521	540
1OVL	A B	B	370	R	1.6	364	375
1OVL	A B	B	373	V	2.2	364	375
1OVL	A B	B	500	I	1.0	500	510
1OVL	D E	D	370	R	1.0	364	375
1OVL	D E	E	373	V	1.0	364	375
1OVL	D F	F	590	K	1.3	586	596
1OW3	A B	A	126	R	1.3	114	127
1OW3	A B	A	197	V	1.1	192	204
1OW3	A B	A	202	N	2.7	192	204
1OW3	A B	A	213	L	2.8	209	215

1OW3	A B	A	216	I	1.1	216	229
1OW3	A B	B	68	R	1.2	67	75
1OW3	A B	B	69	L	2.6	67	75
1OW3	A B	B	72	L	1.6	67	75
1OW3	A B	B	93	E	1.0	89	94
1OW7	A D	A	925	Y	1.3	923	941
1OW7	A D	A	1032	K	2.8	1013	1047
1OW7	A D	D	9	M	2.0	3	12
1OW7	B E	B	962	R	1.2	947	970
1OW7	B E	E	5	L	1.5	3	12
1OW7	B E	E	8	L	1.0	3	12
1OW7	B E	E	9	M	1.3	3	12
1OW7	C F	C	962	R	1.0	949	975
1OW7	C F	C	998	I	1.3	980	1007
1OW7	C F	F	8	L	1.0	3	12
1OW7	C F	F	9	M	1.3	3	12
1OWS	A B	A	116	K	1.9	115	119
1OXK	A B	A	16	E	4.7	11	20
1OXK	A B	A	27	F	2.3	27	52
1OXK	A B	A	31	L	1.3	27	52
1OXK	A B	A	64	H	1.4	56	73
1OXK	A B	B	1098	V	1.7	1097	1110
1OXK	A B	B	1105	R	2.9	1097	1110
1OXK	A B	B	1106	M	3.6	1097	1110
1OXK	A B	B	1199	R	3.5	1199	1210
1OXK	A D	A	109	K	1.2	109	113
1OXK	A D	D	1154	L	1.3	1152	1163
1OXK	C D	C	31	L	1.1	27	52
1OXK	C D	C	64	H	1.1	56	73
1OXK	C D	D	1098	V	1.4	1097	1110
1OXK	C D	D	1102	V	1.1	1097	1110
1OXK	C F	C	109	K	1.0	109	113
1OXK	C F	F	1154	L	1.2	1152	1163
1OXK	E B	B	1154	L	1.2	1152	1163
1OXK	E F	E	16	E	1.7	11	20
1OXK	E F	E	31	L	1.1	27	52
1OXK	E F	E	64	H	1.6	56	73
1OXK	E F	E	68	G	1.3	56	73
1OXK	E F	F	1098	V	1.4	1097	1110
1OXK	E F	F	1102	V	1.4	1097	1110
1OXK	G H	G	27	F	2.6	27	52
1OXK	G H	G	31	L	2.1	27	52
1OXK	G H	G	34	Q	1.0	27	52
1OXK	G H	G	38	Q	1.1	27	52
1OXK	G H	G	64	H	1.4	56	73
1OXK	G H	G	68	G	1.0	56	73
1OXK	G H	H	1098	V	2.4	1097	1110
1OXK	G H	H	1102	V	1.4	1097	1110
1OXK	G H	H	1105	R	3.6	1097	1110
1OXK	I J	I	16	E	1.0	11	20
1OXK	I J	I	31	L	1.0	27	52
1OXK	I J	I	64	H	1.2	56	73
1OXK	I J	J	1098	V	1.4	1097	1110
1OXK	I J	J	1102	V	1.7	1097	1110
1OXK	I J	J	1105	R	1.4	1097	1110
1OXK	I J	J	1106	M	1.1	1097	1110
1OXK	K L	K	16	E	1.4	11	20
1OXK	K L	K	31	L	1.2	27	52
1OXK	K L	K	64	H	1.1	56	73
1OXK	K L	L	1098	V	1.4	1097	1110

1OYV	A I	A	136	K	1.0	133	145
1OYV	B I	B	104	Y	1.5	104	117
1OZS	A B	A	104	F	2.6	93	105
1P0S	L H	H	127	W	4.1	125	133
1P16	B D	B	164	G	95.1	159	170
1P16	B D	B	165	Y	1.4	159	170
1P22	A B	A	160	I	1.8	154	163
1P22	A B	A	179	W	2.8	177	185
1P22	A B	B	48	I	1.3	46	54
1P22	A B	B	80	F	1.1	78	84
1P22	A B	B	102	V	1.4	92	105
1P22	A B	B	111	P	1.1	111	118
1P22	A B	B	114	I	1.1	111	118
1P22	A B	B	115	R	1.3	111	118
1P27	A B	A	56	V	1.2	54	68
1P27	A B	A	59	E	1.5	54	68
1P27	A B	A	124	Y	2.6	116	141
1P27	A B	A	135	S	2.2	116	141
1P27	A B	A	140	H	2.2	116	141
1P27	C D	C	56	V	1.0	54	68
1P27	C D	C	124	Y	2.5	116	141
1P27	C D	C	128	D	1.4	116	141
1P27	C D	C	135	S	2.1	116	141
1P27	C D	C	139	L	2.6	116	141
1P27	C D	C	140	H	1.9	116	141
1P3Q	R V	R	440	G	1.9	439	443
1P4B	H P	P	2	H	2.5	2	11
1P4B	L P	P	10	L	1.0	2	11
1P4E	A C	A	12	P	1.4	12	23
1P4E	A C	C	119	I	1.9	116	129
1P4E	A C	C	123	L	1.0	116	129
1P4E	A C	C	127	F	2.5	116	129
1P4E	A D	A	119	I	1.3	116	136
1P4E	A D	A	127	F	3.5	116	136
1P4E	A D	A	309	H	1.1	303	318
1P4E	A D	A	312	T	1.4	303	318
1P4E	A D	D	12	P	1.4	12	23
1P4E	A D	D	353	H	1.1	352	360
1P4E	B C	B	119	I	1.4	116	129
1P4E	B C	B	120	V	1.2	116	129
1P4E	B C	B	123	L	1.2	116	129
1P4E	B C	B	124	Q	1.2	116	129
1P4E	B C	B	127	F	3.0	116	129
1P4E	B C	B	309	H	1.5	304	318
1P4E	B C	B	313	S	1.0	304	318
1P4E	B C	B	325	N	1.1	321	328
1P4E	B C	C	12	P	1.7	12	23
1P4E	B C	C	13	K	1.1	12	23
1P4E	B C	C	353	H	1.1	352	360
1P4E	B D	B	12	P	1.5	12	23
1P4E	B D	D	119	I	1.8	116	129
1P4E	B D	D	123	L	1.1	116	129
1P4E	B D	D	124	Q	1.0	116	129
1P4E	B D	D	126	Q	2.6	116	129
1P4E	B D	D	127	F	3.6	116	129
1P4E	B D	D	141	K	2.4	138	149
1P4Q	A B	A	18	E	1.1	18	29
1P4Q	A B	B	110	P	13.7	110	135
1P4Q	A B	B	177	I	1.2	171	184
1P4Q	A B	B	180	H	1.2	171	184

1P7T	A B	A	558	A	1.8	553	562
1P7T	A B	B	69	R	4.9	32	71
1P7T	A B	B	647	R	1.5	632	648
1P8D	A C	A	456	I	1.9	451	458
1P8D	A C	C	8	L	1.7	3	12
1P8D	B D	B	287	K	1.0	261	288
1P8D	B D	B	455	E	1.5	451	458
1P8D	B D	D	5	L	1.9	3	11
1P8D	B D	D	9	L	1.5	3	11
1P8V	B C	B	22	E	1.1	20	27
1P8V	B C	B	23	L	1.1	20	27
1P8V	B C	B	24	L	3.0	20	27
1P9D	S U	S	289	Y	2.3	283	293
1P9M	A B	B	30	R	1.0	27	44
1P9M	A B	B	31	Y	1.3	27	44
1P9M	A B	B	124	Q	2.5	111	126
1P9M	A B	B	125	F	1.8	111	126
1P9M	B C	B	182	R	1.0	156	183
1PC8	A B	A	168	W	1.3	164	177
1PC8	A B	A	185	Y	1.1	184	192
1PCQ	A O	A	234	L	1.1	230	242
1PCQ	B P	B	234	L	1.1	230	242
1PCQ	D R	D	261	T	1.0	257	269
1PCQ	E S	E	234	L	1.0	230	242
1PCQ	F T	F	230	I	1.2	230	242
1PCQ	F T	F	234	L	1.2	230	242
1PCQ	F T	F	237	L	1.5	230	242
1PCQ	G U	G	268	R	3.0	257	269
1PD7	A B	A	7	F	1.7	5	21
1PD7	A B	A	14	V	1.3	5	21
1PD7	A B	A	18	K	1.5	5	21
1PD7	A B	B	203	Q	1.3	202	221
1PD7	A B	B	205	L	2.2	202	221
1PD7	A B	B	211	Y	1.5	202	221
1PD7	A B	B	212	L	1.4	202	221
1PG7	I M	M	124	Q	1.1	122	127
1PG7	W X	W	125	E	1.4	123	128
1PG7	Y Z	Y	125	E	1.3	123	128
1PGR	A B	A	17	K	1.3	12	40
1PGR	A B	A	20	E	2.3	12	40
1PGR	A B	A	23	R	1.1	12	40
1PGR	C D	C	17	K	1.1	12	40
1PGR	C D	C	20	E	1.6	12	40
1PGR	C D	C	24	K	1.2	12	40
1PGR	C D	C	106	T	1.0	98	125
1PGR	E F	E	17	K	1.3	12	40
1PGR	E F	E	20	E	3.4	12	40
1PGR	E F	E	23	R	1.8	12	40
1PGR	E F	E	109	L	1.4	101	125
1PGR	G H	G	17	K	2.0	12	40
1PGR	G H	G	20	E	1.9	12	40
1PGR	G H	G	24	K	1.1	12	40
1PH1	A B	B	143	E	1.8	142	161
1PH1	A B	B	150	H	1.2	142	161
1PH1	A B	B	153	H	1.8	142	161
1PH1	A B	B	160	I	1.2	142	161
1PH1	A B	B	172	I	2.3	172	177
1PHN	A B	A	5	I	1.2	4	15
1PHN	A B	A	6	T	1.1	4	15
1PHN	A B	A	9	I	2.7	4	15

1PHN	A B	A	13	D	1.4	4	15
1PHN	A B	A	24	L	1.6	21	47
1PHN	A B	A	31	Y	1.6	21	47
1PHN	A B	A	38	L	1.1	21	47
1PHN	A B	A	93	R	3.1	78	102
1PHN	A B	A	97	Y	3.3	78	102
1PHN	A B	B	9	V	1.6	4	15
1PHN	A B	B	31	V	1.1	21	33
1PHN	A B	B	34	G	34.3	34	47
1PHN	A B	B	38	L	1.9	34	47
1PHN	A B	B	93	R	1.6	78	102
1PHN	A B	B	97	Y	4.3	78	102
1PHN	A B	B	100	I	1.5	78	102
1PID	A B	B	11	L	1.4	9	20
1PID	C D	C	2	I	2.6	2	9
1PID	C D	C	6	C	1.6	2	9
1PID	C D	C	16	L	1.9	13	19
1PID	C D	D	11	L	2.3	9	20
1PID	C D	D	15	L	1.4	9	20
1PK1	A B	A	51	L	1.2	46	52
1PK1	A B	B	66	L	1.4	66	79
1PK1	A B	B	67	G	39.2	66	79
1PK1	A B	B	70	L	1.3	66	79
1PK1	A B	B	71	K	2.3	66	79
1PK1	C D	C	51	L	1.2	46	52
1PK1	C D	D	66	L	1.8	66	79
1PK1	C D	D	67	G	14.0	66	79
1PK1	C D	D	70	L	1.2	66	79
1PK1	C D	D	71	K	1.0	66	79
1PLG	L H	L	129	Q	1.9	127	133
1PMA	A B	B	68	L	1.1	49	70
1PMA	C P	P	65	L	1.5	49	70
1PMA	C P	P	68	L	1.4	49	70
1PMA	D Q	Q	67	R	1.0	49	70
1PMA	D Q	Q	68	L	1.4	49	70
1PMA	E R	E	93	R	1.0	82	104
1PMA	E R	R	65	L	1.5	49	70
1PMA	E R	R	68	L	1.2	49	70
1PMA	E S	E	99	E	17.6	82	104
1PMA	F S	S	64	E	1.0	49	70
1PMA	F S	S	65	L	1.4	49	70
1PMA	F S	S	68	L	1.0	49	70
1PMA	G T	T	65	L	1.3	49	70
1PMA	G T	T	67	R	1.0	49	70
1PMA	G T	T	68	L	1.4	49	70
1PMA	G U	G	99	E	1.0	82	104
1PMA	H U	U	65	L	1.5	49	70
1PMA	H U	U	67	R	1.0	49	70
1PMA	H U	U	68	L	1.4	49	70
1PMA	I V	V	67	R	1.0	49	70
1PMA	I V	V	68	L	1.3	49	70
1PMA	I W	I	111	N	1.4	109	123
1PMA	J W	W	65	L	1.4	49	70
1PMA	J W	W	68	L	1.4	49	70
1PMA	K X	X	65	L	1.5	49	70
1PMA	K X	X	68	L	1.1	49	70
1PMA	L Y	L	93	R	1.3	82	104
1PMA	L Y	Y	65	L	1.5	49	70
1PMA	L Y	Y	68	L	1.2	49	70
1PMA	M Z	Z	65	L	1.1	49	70

1PMA	M Z	Z	68	L	1.3	49	70
1PMX	A B	A	16	F	1.9	8	19
1PMX	A B	B	114	M	1.2	107	115
1PNB	A B	A	16	R	2.9	16	27
1PNB	A B	A	17	A	2.7	16	27
1PNB	A B	A	18	C	2.7	16	27
1PNS	C N	C	9	G	126.3	7	11
1PNS	D E	E	107	R	1.2	104	114
1PNS	E H	E	151	L	1.2	145	152
1PNS	F R	R	65	I	1.0	60	77
1PNS	F R	R	76	L	1.2	60	77
1PNS	G K	K	59	Y	1.0	58	75
1PNS	J N	N	41	R	2.3	41	51
1PNS	J N	N	45	R	1.2	41	51
1POI	A B	A	91	F	1.3	85	94
1POI	A B	B	75	M	1.7	72	76
1POI	A D	A	203	E	1.0	198	205
1POI	A D	A	223	R	1.0	219	225
1POI	A D	D	89	G	146.5	84	98
1POI	A D	D	90	F	3.1	84	98
1POI	A D	D	93	N	1.9	84	98
1POI	A D	D	97	H	2.3	84	98
1POI	C B	B	89	G	100.4	84	98
1POI	C B	B	90	F	1.7	84	98
1POI	C B	B	97	H	1.7	84	98
1POI	C D	C	88	R	2.2	85	93
1POI	C D	C	92	E	1.7	85	93
1POI	C D	C	129	G	152.7	129	133
1POI	C D	D	72	L	1.6	72	76
1POI	C D	D	75	M	1.3	72	76
1POI	C D	D	85	V	1.4	84	98
1POI	C D	D	140	G	20.0	138	144
1PON	A B	A	24	I	1.8	24	31
1PON	A B	B	43	I	1.1	41	51
1PQ1	A B	A	97	F	1.7	83	101
1PQ1	A B	A	126	V	1.4	119	131
1PQ1	A B	A	130	L	1.0	119	131
1PQ1	A B	A	138	G	138.8	137	157
1PQ1	A B	A	139	R	2.8	137	157
1PQ1	A B	A	195	Y	2.5	188	196
1PQ1	A B	B	87	E	1.7	86	112
1PQ1	A B	B	90	I	1.5	86	112
1PQ1	A B	B	93	E	1.0	86	112
1PQ1	A B	B	94	L	1.9	86	112
1PQ1	A B	B	95	R	1.6	86	112
1PQ1	A B	B	97	I	2.0	86	112
1PQ1	A B	B	98	G	6.6	86	112
1PQ1	A B	B	99	D	3.6	86	112
1PQ1	A B	B	101	F	4.3	86	112
1PQ1	A B	B	105	Y	2.8	86	112
1PRC	C L	C	234	M	1.8	223	240
1PRC	C L	L	159	N	1.7	150	164
1PRC	C L	L	163	Q	2.1	150	164
1PRC	C L	L	262	W	1.1	259	263
1PRC	C M	C	173	V	2.0	172	180
1PRC	C M	C	223	L	3.0	223	240
1PRC	C M	C	227	Y	1.9	223	240
1PRC	C M	C	262	P	1.6	262	280
1PRC	C M	C	268	W	5.2	262	280
1PRC	C M	C	269	W	1.5	262	280

1PRC	C M	M	189	I	1.4	177	191
1PRC	C M	M	190	R	1.7	177	191
1PRC	L H	L	109	R	1.3	84	111
1PRC	L M	L	6	E	1.8	6	10
1PRC	L M	L	9	Y	2.6	6	10
1PRC	L M	L	116	H	1.8	116	140
1PRC	L M	L	117	V	2.1	116	140
1PRC	L M	L	151	L	1.2	150	164
1PRC	L M	L	180	L	1.1	171	199
1PRC	L M	L	187	L	3.1	171	199
1PRC	L M	L	188	G	3.9	171	199
1PRC	L M	L	190	H	1.4	171	199
1PRC	L M	L	191	G	10.8	171	199
1PRC	L M	L	192	G	6.8	171	199
1PRC	L M	L	194	I	1.4	171	199
1PRC	L M	L	195	L	1.8	171	199
1PRC	L M	L	214	Q	1.5	209	220
1PRC	L M	L	215	Y	2.4	209	220
1PRC	L M	L	218	D	2.4	209	220
1PRC	L M	L	219	V	1.0	209	220
1PRC	L M	L	231	R	1.9	226	239
1PRC	L M	L	233	G	226.1	226	239
1PRC	L M	L	234	L	1.3	226	239
1PRC	L M	L	266	W	1.5	264	268
1PRC	L M	L	267	L	1.5	264	268
1PRC	L M	M	82	L	1.6	81	87
1PRC	L M	M	86	R	3.3	81	87
1PRC	L M	M	143	H	2.6	143	158
1PRC	L M	M	144	I	1.6	143	158
1PRC	L M	M	178	W	2.1	177	191
1PRC	L M	M	214	F	2.4	198	224
1PRC	L M	M	217	H	1.2	198	224
1PRC	L M	M	218	G	10.4	198	224
1PRC	L M	M	233	I	1.3	232	238
1PRC	L M	M	244	E	1.4	241	254
1PRC	L M	M	245	R	1.0	241	254
1PRC	L M	M	248	L	1.8	241	254
1PRC	L M	M	249	F	2.1	241	254
1PRC	L M	M	252	W	5.4	241	254
1PRC	L M	M	261	E	1.4	260	285
1PRC	L M	M	264	H	1.1	260	285
1PRC	L M	M	267	G	4.2	260	285
1PRC	M H	M	199	W	2.1	198	224
1PRC	M H	M	202	F	3.1	198	224
1PRC	M H	M	206	F	1.1	198	224
1PRC	M H	M	265	R	1.1	260	285
1PRC	M H	M	266	W	2.0	260	285
1PRC	M H	M	269	F	1.2	260	285
1PRC	M H	M	284	L	1.0	260	285
1PRC	M H	M	295	W	2.8	292	299
1PRC	M H	H	17	W	1.2	12	37
1PRC	M H	H	20	Q	1.0	12	37
1PRC	M H	H	21	W	2.0	12	37
1PRC	M H	H	32	L	1.6	12	37
1PRC	M H	H	35	E	1.4	12	37
1PSB	A C	A	51	E	1.2	50	61
1PSB	A C	A	52	V	1.3	50	61
1PSB	A C	A	55	K	1.8	50	61
1PSB	A C	C	72	K	1.5	72	87
1PSB	A C	C	73	E	1.8	72	87

1PSB	A C	C	76	F	2.5	72	87
1PSB	B D	B	52	V	1.2	50	61
1PSB	B D	B	87	F	2.2	70	90
1PSB	B D	D	72	K	1.2	72	87
1PSB	B D	D	73	E	1.2	72	87
1PSB	B D	D	76	F	4.0	72	87
1PSB	B D	D	83	R	1.6	72	87
1PSB	B D	D	86	L	1.1	72	87
1PSK	L H	L	123	Q	1.0	121	127
1PSS	L M	L	103	R	1.7	84	111
1PSS	L M	L	107	I	1.7	84	111
1PSS	L M	L	116	H	1.1	116	139
1PSS	L M	L	117	I	2.5	116	139
1PSS	L M	L	151	W	1.6	150	162
1PSS	L M	L	187	L	3.7	171	199
1PSS	L M	L	189	L	1.4	171	199
1PSS	L M	L	190	H	1.6	171	199
1PSS	L M	L	191	G	2.7	171	199
1PSS	L M	L	194	V	1.1	171	199
1PSS	L M	L	195	L	2.6	171	199
1PSS	L M	L	211	H	2.0	209	220
1PSS	L M	L	215	F	3.8	209	220
1PSS	L M	L	217	R	2.2	209	220
1PSS	L M	L	219	L	1.6	209	220
1PSS	L M	L	228	G	2.7	226	254
1PSS	L M	L	230	H	5.7	226	254
1PSS	L M	L	233	G	107.9	226	254
1PSS	L M	L	234	L	2.0	226	254
1PSS	L M	L	235	L	1.8	226	254
1PSS	L M	L	263	W	1.0	262	268
1PSS	L M	M	42	F	1.8	36	43
1PSS	L M	M	87	R	1.1	82	88
1PSS	L M	M	129	W	1.0	113	140
1PSS	L M	M	132	R	1.4	113	140
1PSS	L M	M	136	R	1.6	113	140
1PSS	L M	M	146	T	1.3	145	160
1PSS	L M	M	180	F	2.3	179	192
1PSS	L M	M	183	L	1.3	179	192
1PSS	L M	M	209	L	1.7	200	224
1PSS	L M	M	216	F	5.9	200	224
1PSS	L M	M	219	H	2.2	200	224
1PSS	L M	M	220	G	1.3	200	224
1PSS	L M	M	235	L	2.7	235	239
1PSS	L M	M	246	E	1.3	245	256
1PSS	L M	M	251	F	2.8	245	256
1PSS	L M	M	252	W	2.2	245	256
1PSS	L M	M	254	W	2.1	245	256
1PSS	L M	M	266	H	1.9	262	275
1PSS	M H	M	41	W	1.4	36	43
1PSS	M H	M	201	F	2.4	200	224
1PSS	M H	M	264	G	13.6	262	275
1PSS	M H	M	268	W	1.6	262	275
1PSS	M H	M	297	W	1.0	294	300
1PTO	A D	D	72	F	1.2	63	74
1PTO	A E	A	76	R	1.0	57	78
1PTO	B D	B	146	Y	1.4	143	160
1PTO	B D	B	154	Y	1.0	143	160
1PTO	B D	D	63	P	28.1	63	74
1PTO	B D	D	66	V	1.3	63	74
1PTO	B F	B	152	M	1.4	143	160

1PTO	B F	B	155	L	1.2	143	160
1PTO	B F	F	61	I	1.3	51	67
1PTO	B F	F	64	Y	1.8	51	67
1PTO	C E	E	63	P	9.3	63	75
1PTO	E F	E	72	F	1.3	63	75
1PTO	E F	F	52	W	2.5	51	67
1PTO	G H	H	154	Y	1.4	143	160
1PTO	G H	H	155	L	1.4	143	160
1PTO	G I	I	154	Y	1.4	146	159
1PTO	G I	I	155	M	1.3	146	159
1PTO	G I	I	158	M	1.4	146	159
1PTO	G J	G	118	I	1.8	118	127
1PTO	G K	K	73	M	1.1	63	74
1PTO	I J	I	151	R	1.0	146	159
1PTO	I J	J	65	E	1.3	63	74
1PTO	I K	K	63	P	21.2	63	74
1PTO	I K	K	66	V	5.6	63	74
1PTO	J H	J	63	P	22.7	63	74
1PTO	J H	H	146	Y	1.2	143	160
1PTO	J H	H	157	Y	1.4	143	160
1PTO	J H	H	158	V	1.3	143	160
1PTO	K L	K	72	F	1.3	63	74
1PTO	K L	L	59	F	2.5	51	67
1PTO	L H	L	61	I	1.1	51	67
1PTO	L H	L	64	Y	1.8	51	67
1PTO	L H	H	152	M	1.5	143	160
1PTO	L H	H	155	L	1.2	143	160
1PUM	A B	A	174	W	4.7	170	182
1PUM	A B	A	191	Y	1.0	190	197
1PVH	A B	B	124	G	72.2	109	137
1PVH	A B	B	128	N	1.2	109	137
1PVH	C D	D	25	Q	1.1	22	35
1PVH	C D	D	124	G	92.2	109	137
1PYT	A B	A	93	M	1.3	82	96
1PYT	A C	A	66	V	1.7	61	71
1PYT	A D	A	94	F	2.8	82	96
1PYT	B D	B	81	W	1.3	73	90
1PYU	A B	B	95	D	2.0	95	100
1PYU	C D	D	95	D	1.7	95	100
1PZ5	A B	A	124	Q	1.3	122	128
1PZL	A B	A	190	V	1.3	175	195
1PZL	A B	A	204	L	2.4	204	214
1PZL	A B	A	205	D	1.9	204	214
1PZL	A B	A	207	Q	1.3	204	214
1PZL	A B	A	211	L	1.8	204	214
1PZL	A B	B	10	L	2.3	8	18
1PZL	A B	B	11	H	1.1	8	18
1PZL	A B	B	14	L	3.5	8	18
1PZL	A B	B	15	Q	1.8	8	18
1Q16	A B	A	2	K	1.7	2	7
1Q16	A B	A	30	D	1.2	30	40
1Q16	A B	A	31	W	5.2	30	40
1Q16	A B	A	32	E	2.7	30	40
1Q16	A B	A	35	Y	3.0	30	40
1Q16	A B	A	36	R	3.9	30	40
1Q16	A B	A	39	W	2.8	30	40
1Q16	A B	A	115	K	1.3	115	128
1Q16	A B	A	244	Y	1.8	240	245
1Q16	A B	A	265	H	1.6	261	273
1Q16	A B	A	269	E	3.1	261	273

1Q16	A B	A	272	Y	3.2	261	273
1Q16	A B	A	289	K	2.3	286	290
1Q16	A B	A	520	R	1.3	515	532
1Q16	A B	A	780	L	1.3	777	781
1Q16	A B	A	1105	L	1.5	1105	1111
1Q16	A B	A	1121	E	1.1	1121	1127
1Q16	A B	A	1125	K	1.7	1121	1127
1Q16	A B	B	24	V	1.1	21	31
1Q16	A B	B	29	V	1.6	21	31
1Q16	A B	B	108	Y	3.1	108	113
1Q16	A B	B	111	L	1.4	108	113
1Q16	A B	B	112	H	3.0	108	113
1Q16	A B	B	248	Y	1.2	248	253
1Q16	A B	B	250	R	1.5	248	253
1Q16	A B	B	252	E	2.0	248	253
1Q16	A B	B	261	E	1.0	258	262
1Q16	A B	B	281	E	1.2	280	285
1Q16	A B	B	413	R	3.2	399	423
1Q16	A B	B	417	R	1.5	399	423
1Q16	A B	B	444	Y	1.9	437	450
1Q16	A B	B	449	I	1.9	437	450
1Q16	A B	B	455	R	3.2	452	456
1Q16	A C	A	3	F	1.6	2	7
1Q16	A C	C	25	W	1.3	10	30
1Q16	A C	C	28	Y	1.7	10	30
1Q16	A C	C	29	D	1.1	10	30
1Q16	B C	B	81	R	2.6	81	87
1Q16	B C	B	98	D	1.3	97	101
1Q16	B C	C	117	R	2.5	116	121
1Q16	B C	C	213	Y	4.7	211	215
1Q1J	L H	L	124	E	1.3	122	126
1Q1J	L I	L	123	E	1.7	122	126
1Q1J	M H	M	123	E	1.8	122	126
1Q1J	M I	M	124	E	1.4	122	126
1Q5Q	A H	A	75	R	1.4	68	89
1Q5Q	A H	A	87	Y	2.6	68	89
1Q5Q	A H	H	58	L	1.0	49	71
1Q5Q	A H	H	64	E	2.3	49	71
1Q5Q	A H	H	67	E	1.1	49	71
1Q5Q	A H	H	68	K	2.3	49	71
1Q5Q	A H	H	69	I	1.3	49	71
1Q5Q	A I	I	66	Y	2.1	49	71
1Q5Q	A I	I	78	G	7.7	76	89
1Q5Q	B I	B	75	R	1.7	68	89
1Q5Q	B I	B	87	Y	2.6	68	89
1Q5Q	B I	I	58	L	1.0	49	71
1Q5Q	B I	I	64	E	3.2	49	71
1Q5Q	B I	I	68	K	1.9	49	71
1Q5Q	B I	I	69	I	1.1	49	71
1Q5Q	D L	L	78	G	16.2	76	89
1Q5Q	E L	E	75	R	1.2	68	89
1Q5Q	E L	E	87	Y	2.1	68	89
1Q5Q	E L	L	64	E	1.3	49	71
1Q5Q	E L	L	65	H	1.0	49	71
1Q5Q	E L	L	69	I	1.3	49	71
1Q5Q	E M	M	62	E	1.4	49	71
1Q5Q	E M	M	66	Y	1.9	49	71
1Q5Q	E M	M	78	G	7.4	76	89
1Q5Q	E M	M	82	R	1.3	76	89
1Q5Q	F M	F	75	R	1.3	68	89

1Q5Q	F M	F	79	I	1.6	68	89
1Q5Q	F M	F	87	Y	2.5	68	89
1Q5Q	F M	M	64	E	1.3	49	71
1Q5Q	F M	M	69	I	1.8	49	71
1Q5Q	F N	F	85	R	1.0	68	89
1Q5Q	F N	N	78	G	7.8	76	89
1Q5Q	G H	H	78	G	16.3	76	89
1Q5Q	G N	G	75	R	1.7	68	89
1Q5Q	G N	G	87	Y	2.6	68	89
1Q5Q	G N	N	64	E	2.3	49	71
1Q5Q	G N	N	68	K	3.2	49	71
1Q5Q	G N	N	69	I	1.3	49	71
1Q5R	A H	A	79	I	1.5	68	89
1Q5R	A H	A	87	Y	3.2	68	89
1Q5R	A H	H	-40	F	1.2	-40	-34
1Q5R	A H	H	64	E	1.0	49	71
1Q5R	A H	H	69	I	1.4	49	71
1Q5R	A I	I	70	E	1.3	49	71
1Q5R	A I	I	78	G	13.3	76	90
1Q5R	B I	B	75	R	2.7	68	89
1Q5R	B I	B	79	I	1.5	68	89
1Q5R	B I	B	87	Y	3.0	68	89
1Q5R	B I	I	-40	F	1.6	-40	-34
1Q5R	B I	I	64	E	2.1	49	71
1Q5R	B I	I	68	K	1.6	49	71
1Q5R	B I	I	69	I	1.6	49	71
1Q5R	B J	J	62	E	1.0	49	71
1Q5R	B J	J	66	Y	1.4	49	71
1Q5R	B J	J	70	E	1.5	49	71
1Q5R	B J	J	78	G	24.8	76	90
1Q5R	C J	C	79	I	1.4	68	89
1Q5R	C J	C	87	Y	3.2	68	89
1Q5R	C J	J	-40	F	2.0	-40	-34
1Q5R	C J	J	64	E	1.5	49	71
1Q5R	C J	J	68	K	1.1	49	71
1Q5R	C J	J	69	I	1.3	49	71
1Q5R	C K	C	98	S	1.1	96	114
1Q5R	C K	K	70	E	2.0	49	71
1Q5R	C K	K	78	G	20.6	76	90
1Q5R	D K	D	79	I	2.9	68	89
1Q5R	D K	D	84	M	1.0	68	89
1Q5R	D K	D	87	Y	3.1	68	89
1Q5R	D K	K	-40	F	2.1	-40	-34
1Q5R	D K	K	61	V	1.4	49	71
1Q5R	D K	K	64	E	3.0	49	71
1Q5R	D K	K	65	H	1.3	49	71
1Q5R	D K	K	68	K	1.7	49	71
1Q5R	D K	K	69	I	1.4	49	71
1Q5R	D L	D	98	S	1.2	96	114
1Q5R	D L	L	70	E	1.8	49	71
1Q5R	D L	L	78	G	10.2	76	90
1Q5R	E L	E	75	R	2.2	68	89
1Q5R	E L	E	79	I	1.5	68	89
1Q5R	E L	E	87	Y	3.4	68	89
1Q5R	E L	L	-40	F	1.3	-40	-34
1Q5R	E L	L	64	E	1.1	49	71
1Q5R	E L	L	69	I	3.2	49	71
1Q5R	E M	E	98	S	1.3	96	114
1Q5R	E M	M	70	E	2.0	49	71
1Q5R	E M	M	78	G	11.5	76	90

1Q5R	F M	F	79	I	1.4	68	89
1Q5R	F M	F	87	Y	3.2	68	89
1Q5R	F M	M	-40	F	1.7	-40	-34
1Q5R	F M	M	64	E	1.1	49	71
1Q5R	F M	M	69	I	1.5	49	71
1Q5R	F N	F	98	S	1.2	96	114
1Q5R	F N	N	70	E	2.0	49	71
1Q5R	F N	N	78	G	11.2	76	90
1Q5R	G H	G	98	S	1.1	96	114
1Q5R	G H	H	70	E	1.9	49	71
1Q5R	G H	H	78	G	24.0	76	90
1Q5R	G N	G	79	I	1.5	68	89
1Q5R	G N	G	87	Y	3.5	68	89
1Q5R	G N	N	-40	F	2.3	-40	-34
1Q5R	G N	N	64	E	1.0	49	71
1Q5R	G N	N	69	I	1.5	49	71
1Q68	A B	A	410	I	1.6	407	416
1Q72	L H	L	124	Q	1.7	122	127
1Q7L	A B	A	13	V	1.8	11	22
1Q7L	A B	A	16	F	2.5	11	22
1Q7L	A B	A	121	Y	1.1	115	131
1Q7L	A B	A	127	R	1.4	115	131
1Q7L	A B	A	128	L	2.3	115	131
1Q7L	A B	A	155	M	1.3	155	159
1Q7L	A B	B	323	W	3.0	322	334
1Q7L	A B	B	324	W	2.2	322	334
1Q7L	A B	B	351	Y	2.0	348	355
1Q7L	A B	B	352	I	1.4	348	355
1Q7L	A B	B	353	R	4.9	348	355
1Q7L	A B	B	381	E	1.1	381	399
1Q7L	A B	B	384	F	5.6	381	399
1Q7L	A B	B	385	L	1.7	381	399
1Q7L	A B	B	387	G	63.7	381	399
1Q7L	A B	B	388	V	1.0	381	399
1Q7L	A B	B	389	D	1.1	381	399
1Q7L	A B	B	391	Y	2.0	381	399
1Q7L	A B	B	395	L	2.2	381	399
1Q7L	A B	B	396	P	1.2	381	399
1Q7L	A B	B	398	L	1.3	381	399
1Q7L	C B	B	350	R	1.1	348	355
1Q7L	C D	C	16	F	1.7	11	21
1Q7L	C D	C	121	Y	1.1	115	131
1Q7L	C D	C	128	L	2.3	115	131
1Q7L	C D	C	155	M	1.3	155	159
1Q7L	C D	C	164	F	1.1	162	168
1Q7L	C D	D	323	W	3.6	322	334
1Q7L	C D	D	324	W	2.3	322	334
1Q7L	C D	D	351	Y	2.2	348	355
1Q7L	C D	D	352	I	1.4	348	355
1Q7L	C D	D	353	R	4.5	348	355
1Q7L	C D	D	381	E	1.5	381	399
1Q7L	C D	D	384	F	3.7	381	399
1Q7L	C D	D	387	G	40.5	381	399
1Q7L	C D	D	391	Y	1.5	381	399
1Q7L	C D	D	395	L	2.4	381	399
1Q7L	C D	D	396	P	1.2	381	399
1Q7L	C D	D	398	L	1.4	381	399
1Q86	H N	H	34	N	1.0	33	43
1Q86	H N	H	37	T	1.0	33	43
1Q86	H N	H	38	K	1.2	33	43

1Q86	H N	H	62	H	2.1	58	69
1Q86	H N	N	7	Y	2.8	4	12
1Q86	H N	N	8	I	2.1	4	12
1Q86	O R	O	24	L	1.1	20	30
1Q90	A B	B	80	W	1.1	79	106
1Q90	A D	A	255	L	1.6	249	283
1Q90	A D	A	269	L	1.9	249	283
1Q90	A D	A	273	K	1.6	249	283
1Q90	A D	D	38	Y	1.3	34	58
1Q90	A D	D	42	V	1.4	34	58
1Q90	A D	D	56	V	1.5	34	58
1Q90	A L	A	267	V	4.9	249	283
1Q90	A L	A	271	L	2.2	249	283
1Q90	A N	A	259	F	1.8	249	283
1Q90	A N	A	263	L	1.0	249	283
1Q90	A N	N	73	V	1.1	71	95
1Q90	A N	N	76	G	1.3	71	95
1Q90	A N	N	83	M	2.1	71	95
1Q90	A N	N	94	G	6.7	71	95
1Q90	A R	A	258	F	1.6	249	283
1Q90	A R	A	261	F	2.0	249	283
1Q90	A R	A	268	L	1.2	249	283
1Q90	A R	A	276	F	1.4	249	283
1Q90	A R	R	45	M	1.5	39	69
1Q90	A R	R	49	L	1.6	39	69
1Q90	A R	R	52	G	17.0	39	69
1Q90	A R	R	55	L	1.3	39	69
1Q90	B C	B	150	I	1.5	142	158
1Q90	B D	B	42	T	1.0	35	56
1Q90	B D	B	66	F	2.2	65	76
1Q90	B D	B	88	W	3.5	79	106
1Q90	B D	B	105	Y	1.8	79	106
1Q90	B D	B	118	W	1.2	115	139
1Q90	B D	B	145	Y	1.5	142	158
1Q90	B D	B	146	W	3.9	142	158
1Q90	B D	D	54	L	1.0	34	58
1Q90	B D	D	80	Y	1.8	79	91
1Q90	B D	D	111	V	1.7	110	114
1Q90	B D	D	112	P	2.9	110	114
1Q90	B D	D	133	F	3.0	127	148
1Q90	B G	B	88	W	1.3	79	106
1Q90	B G	B	91	S	1.1	79	106
1Q90	B G	B	92	M	1.4	79	106
1Q90	B G	B	95	L	2.1	79	106
1Q90	B G	B	99	L	1.3	79	106
1Q90	B G	G	6	L	1.6	4	30
1Q90	B G	G	18	I	1.2	4	30
1Q90	B G	G	20	G	72.8	4	30
1Q90	B G	G	21	L	2.4	4	30
1Q90	B R	R	67	F	2.8	39	69
1Q90	B R	R	68	F	1.9	39	69
1Q90	D G	D	79	W	1.7	79	91
1Q90	D G	D	133	F	1.3	127	148
1Q90	D G	G	18	I	1.0	4	30
1Q90	D G	G	26	Y	1.3	4	30
1Q90	D G	G	29	Y	2.7	4	30
1Q90	D N	D	46	G	1.6	34	58
1Q90	D N	D	53	G	39.3	34	58
1Q95	F L	F	114	L	1.1	111	118
1Q9O	B A	A	123	Q	1.8	121	125

1Q9O	D C	C	123	Q	1.6	121	127
1Q9W	A B	A	123	Q	1.6	121	126
1QD6	A C	A	18	I	1.6	18	24
1QD6	A C	A	19	I	1.0	18	24
1QD6	A C	A	22	M	2.7	18	24
1QD6	A C	A	23	L	2.2	18	24
1QD6	B D	B	18	I	1.6	18	24
1QD6	B D	B	19	I	1.2	18	24
1QD6	B D	B	22	M	2.9	18	24
1QD6	B D	B	23	L	2.2	18	24
1QDL	A B	A	275	D	2.0	264	284
1QDL	A B	A	278	R	1.9	264	284
1QDL	A B	A	282	G	1.9	264	284
1QDL	A B	B	15	Y	2.0	13	24
1QDL	A B	B	19	Q	1.1	13	24
1QDL	A B	B	22	G	1.8	13	24
1QFN	A B	A	72	Y	1.1	72	84
1QFU	L H	L	123	Q	1.3	121	127
1QGW	A B	A	53	D	1.6	51	62
1QGW	A B	A	56	K	1.7	51	62
1QGW	A C	A	57	K	1.2	51	62
1QGW	A C	A	61	F	3.1	51	62
1QGW	A C	C	5	F	1.9	4	9
1QGW	A C	C	24	L	1.6	22	30
1QGW	A C	C	28	K	1.9	22	30
1QGW	A C	C	62	E	1.2	48	63
1QGW	A C	C	83	L	1.5	76	100
1QGW	A C	C	88	I	1.4	76	100
1QGW	A C	C	92	Y	2.7	76	100
1QGW	A C	C	95	Y	1.4	76	100
1QGW	A C	C	98	L	1.6	76	100
1QGW	A C	C	108	R	1.0	103	111
1QGW	A D	A	60	E	1.8	51	62
1QGW	A D	D	141	F	1.1	124	143
1QGW	B D	B	57	V	1.7	51	65
1QGW	B D	D	8	V	1.6	6	10
1QGW	B D	D	24	L	1.5	22	31
1QGW	B D	D	28	K	1.1	22	31
1QGW	B D	D	38	L	1.5	34	47
1QGW	B D	D	41	V	1.5	34	47
1QGW	B D	D	79	M	1.2	76	100
1QGW	B D	D	83	L	1.9	76	100
1QGW	B D	D	84	R	1.1	76	100
1QGW	B D	D	87	E	1.0	76	100
1QGW	B D	D	88	I	1.4	76	100
1QGW	B D	D	91	R	1.7	76	100
1QGW	B D	D	92	Y	2.7	76	100
1QGW	B D	D	95	Y	1.6	76	100
1QGW	B D	D	98	L	2.6	76	100
1QHH	A C	A	142	R	1.1	141	154
1QHH	B C	B	365	R	2.3	362	374
1QHH	B C	B	392	I	1.6	390	404
1QHH	B C	B	395	I	2.6	390	404
1QHH	B C	B	396	L	1.2	390	404
1QHH	B C	B	398	Y	1.9	390	404
1QHH	B C	B	399	L	1.2	390	404
1QHH	B C	B	402	I	2.8	390	404
1QHH	B C	B	411	L	1.4	408	414
1QHH	B C	C	487	V	1.1	480	491
1QHH	B C	C	493	Y	2.2	493	501

1QHH	B C	C	503	I	1.1	503	523
1QHH	B C	C	512	L	1.4	503	523
1QHH	B C	C	514	E	2.9	503	523
1QHH	B C	C	515	F	2.7	503	523
1QHH	B C	C	535	L	1.5	531	539
1QHH	B C	C	538	L	1.2	531	539
1QHH	B D	B	292	I	2.5	290	301
1QHH	B D	B	299	V	1.7	290	301
1QHH	B D	B	300	I	1.8	290	301
1QHH	B D	B	332	E	2.7	329	345
1QHH	B D	B	336	V	1.3	329	345
1QHH	B D	B	339	R	1.0	329	345
1QHH	B D	B	340	I	1.1	329	345
1QHH	B D	D	564	L	1.3	564	568
1QHH	B D	D	565	H	1.6	564	568
1QHH	B D	D	595	D	1.8	594	609
1QHH	B D	D	596	E	1.8	594	609
1QHH	B D	D	598	E	2.7	594	609
1QHH	B D	D	599	E	1.5	594	609
1QHH	B D	D	600	E	2.3	594	609
1QHH	B D	D	601	R	1.9	594	609
1QHH	B D	D	602	R	2.9	594	609
1QHH	B D	D	605	Y	3.4	594	609
1QHH	B D	D	608	I	1.8	594	609
1QLE	A B	A	84	G	134.4	84	101
1QLE	A B	A	170	L	1.5	170	174
1QLE	A B	A	334	L	1.0	334	361
1QLE	A B	A	337	Q	1.0	334	361
1QLE	A B	A	341	M	1.0	334	361
1QLE	A B	A	359	I	2.1	334	361
1QLE	A B	A	397	P	1.1	396	401
1QLE	A B	A	400	R	1.2	396	401
1QLE	A B	A	468	R	1.1	443	469
1QLE	A B	B	38	V	3.4	26	58
1QLE	A B	B	49	V	1.1	26	58
1QLE	A B	B	89	L	1.7	82	104
1QLE	A B	B	97	L	1.2	82	104
1QLE	A B	B	100	L	1.7	82	104
1QLE	A C	A	136	W	2.2	128	151
1QLE	A C	A	184	F	2.3	178	207
1QLE	A C	A	198	I	1.5	178	207
1QLE	A C	A	236	P	2.0	219	248
1QLE	A C	A	240	G	13.9	219	248
1QLE	A C	C	18	F	1.2	16	23
1QLE	A C	C	28	L	1.6	24	36
1QLE	A C	C	88	Y	1.4	80	107
1QLE	A C	C	89	G	24.0	80	107
1QLE	A C	C	92	L	1.8	80	107
1QLE	A C	C	104	W	2.8	80	107
1QLE	B L	B	29	H	2.0	26	58
1QLE	C D	C	91	I	1.3	80	107
1QLE	C D	D	23	F	2.2	17	47
1QLS	A D	A	48	F	1.6	46	52
1QLS	A D	D	6	F	1.0	2	10
1QLS	A D	D	7	L	14.5	2	10
1QO0	A D	A	64	R	1.2	60	73
1QO0	A D	A	154	R	1.1	151	166
1QO0	A D	A	158	H	1.0	151	166
1QO0	A D	D	91	P	1.0	91	101
1QO0	A E	E	34	R	2.5	23	36

1QO0	B D	D	34	R	2.2	23	36
1QO0	B D	D	113	H	1.0	112	160
1QO0	B E	B	151	I	2.0	151	167
1QO0	B E	B	158	H	1.5	151	167
1QO0	B E	E	91	P	1.2	91	101
1QO3	A C	A	173	K	2.3	152	175
1QPW	A B	A	31	R	2.5	21	36
1QPW	A B	A	122	H	1.4	119	136
1QPW	A B	B	34	V	1.4	20	35
1QPW	A B	B	108	N	1.0	100	119
1QPW	A B	B	111	V	1.0	100	119
1QPW	A B	B	124	P	3.9	124	142
1QPW	A B	B	131	Q	1.2	124	142
1QPW	A D	A	95	P	1.2	95	113
1QPW	A D	D	37	W	1.6	36	41
1QPW	C B	B	37	W	3.8	36	41
1QPW	C B	B	102	N	1.0	100	119
1QPW	C D	C	31	R	4.4	21	36
1QPW	C D	C	103	H	2.7	95	112
1QPW	C D	C	119	P	1.1	119	137
1QPW	C D	C	122	H	2.4	119	137
1QPW	C D	D	30	R	1.1	22	35
1QPW	C D	D	34	V	1.2	22	35
1QPW	C D	D	112	V	1.3	100	119
1QPW	C D	D	116	R	2.4	100	119
1QPW	C D	D	124	P	1.3	124	142
1QPW	C D	D	131	Q	2.1	124	142
1QRJ	A B	B	17	M	1.2	17	30
1QS7	A B	A	19	F	1.6	6	20
1QS7	A B	A	51	M	1.6	45	55
1QS7	A B	A	71	L	2.1	65	74
1QS7	A B	A	72	M	1.4	65	74
1QS7	A B	A	84	E	1.5	78	93
1QS7	A B	A	92	F	1.3	78	93
1QS7	A B	A	112	L	1.6	102	113
1QS7	A B	A	120	E	1.0	118	129
1QS7	A B	B	8	G	8.0	6	19
1QS7	A B	B	9	H	1.5	6	19
1QS7	A B	B	11	V	2.1	6	19
1QS7	A B	B	12	R	1.1	6	19
1QS7	A B	B	14	I	2.0	6	19
1QS7	A B	B	16	R	2.0	6	19
1QS7	A B	B	17	L	2.7	6	19
1QTY	S T	S	17	F	1.4	17	25
1QTY	S T	S	21	Y	1.9	17	25
1QTY	V Y	V	17	F	1.8	17	25
1QTY	V Y	V	21	Y	1.7	17	25
1QUQ	A B	A	52	S	1.0	51	55
1QUQ	A B	A	152	M	2.1	152	164
1QUQ	A B	A	153	N	2.1	152	164
1QUQ	A B	A	156	T	1.0	152	164
1QUQ	A B	A	159	I	2.1	152	164
1QUQ	A B	A	163	I	1.3	152	164
1QUQ	A B	B	106	I	2.2	96	109
1QUQ	C D	C	152	M	2.2	152	166
1QUQ	C D	C	153	N	2.0	152	166
1QUQ	C D	C	156	T	1.0	152	166
1QUQ	C D	C	159	I	1.6	152	166
1QUQ	C D	C	163	I	1.7	152	166
1QUQ	C D	D	99	Y	1.4	96	109

1QVF	A Y	Y	76	G	3.3	74	82
1QVF	A Y	Y	79	V	1.6	74	82
1QVF	F L	F	34	N	1.2	33	42
1QVF	F L	F	37	T	1.0	33	42
1QVF	F L	F	57	E	1.7	57	69
1QVF	F L	F	62	H	2.0	57	69
1QVF	F L	L	7	Y	3.7	4	12
1QVF	F L	L	8	I	1.1	4	12
1QVF	F L	L	27	R	1.5	19	33
1QVF	R U	U	28	L	1.5	13	36
1QVI	A Y	A	804	Q	1.2	798	823
1QVI	A Y	A	808	L	1.9	798	823
1QVI	A Y	A	811	I	2.9	798	823
1QVI	A Y	A	812	Q	2.6	798	823
1QVI	A Y	A	815	I	2.1	798	823
1QVI	A Y	A	818	W	1.9	798	823
1QVI	A Y	A	819	L	1.2	798	823
1QVI	A Y	A	829	L	1.6	829	836
1QVI	A Y	A	830	Y	1.5	829	836
1QVI	A Y	A	833	V	1.1	829	836
1QVI	A Y	Y	27	I	1.2	14	28
1QVI	A Y	Y	59	M	2.1	53	60
1QVI	A Y	Y	75	I	1.0	69	79
1QVI	A Y	Y	76	F	3.6	69	79
1QVI	A Y	Y	93	F	1.9	86	96
1QVI	A Y	Y	113	L	1.1	106	115
1QVI	A Z	A	777	R	1.4	766	797
1QVI	A Z	A	782	I	1.9	766	797
1QVI	A Z	A	785	F	2.7	766	797
1QVI	A Z	A	786	Q	1.3	766	797
1QVI	A Z	A	789	I	2.0	766	797
1QVI	A Z	A	791	G	62.1	766	797
1QVI	A Z	A	792	Y	4.9	766	797
1QVI	A Z	A	793	L	1.6	766	797
1QVI	A Z	A	794	I	1.1	766	797
1QVI	A Z	A	801	L	2.1	798	823
1QVI	A Z	Z	86	Y	3.4	83	92
1QVI	A Z	Z	125	I	1.9	119	129
1QVI	A Z	Z	144	F	1.0	141	151
1QVI	A Z	Z	148	V	2.0	141	151
1QZ7	A B	A	260	H	2.3	249	265
1QZ7	A B	A	292	K	2.0	291	306
1QZ7	A B	A	293	F	2.3	291	306
1QZ7	A B	A	296	I	2.7	291	306
1QZ7	A B	B	470	E	1.0	470	481
1QZ7	A B	B	473	L	2.9	470	481
1QZ7	A B	B	474	D	2.3	470	481
1QZ7	A B	B	476	H	2.9	470	481
1QZ7	A B	B	480	V	1.0	470	481
1R0N	A B	B	247	M	1.1	247	251
1R0N	A B	B	248	Y	1.4	247	251
1R1K	D A	D	422	H	1.6	414	431
1R1K	D A	D	489	K	1.9	481	510
1R1K	D A	D	496	E	1.5	481	510
1R1K	D A	A	389	E	1.6	385	406
1R1K	D A	A	396	F	1.9	385	406
1R1K	D A	A	397	L	1.3	385	406
1R1K	D A	A	425	R	1.5	420	438
1R1R	A D	A	348	L	1.1	341	349
1R1R	A D	A	716	K	1.0	711	724

1R1R	A D	A	719	L	2.5	711	724
1R1R	A D	A	722	Y	1.1	711	724
1R1R	A D	D	370	L	1.3	367	373
1R1R	B E	B	348	L	1.1	341	349
1R1R	B E	B	719	L	1.4	711	724
1R1R	B E	B	722	Y	1.0	711	724
1R1R	C F	C	344	Y	1.2	341	349
1R1R	C F	C	348	L	1.1	341	349
1R1R	C F	C	716	K	1.0	711	724
1R1R	C F	C	719	L	2.5	711	724
1R1R	C F	C	722	Y	1.0	711	724
1R1R	C F	F	370	L	1.3	367	373
1R20	A D	A	396	F	1.8	385	405
1R20	A D	A	414	F	1.3	413	418
1R20	A D	A	425	R	2.2	420	438
1R20	A D	D	422	H	1.1	414	430
1R20	A D	D	470	R	4.2	455	477
1R20	A D	D	487	F	3.4	481	513
1R20	A D	D	488	G	22.5	481	513
1R20	A D	D	489	K	1.3	481	513
1R20	A D	D	491	L	1.3	481	513
1R20	A D	D	496	E	2.7	481	513
1R24	C D	C	127	S	1.0	122	128
1R27	A B	A	31	W	5.6	30	40
1R27	A B	A	32	E	2.5	30	40
1R27	A B	A	35	Y	3.1	30	40
1R27	A B	A	36	R	3.0	30	40
1R27	A B	A	38	R	2.0	30	40
1R27	A B	A	39	W	2.5	30	40
1R27	A B	A	244	Y	2.0	240	245
1R27	A B	A	269	E	1.7	261	273
1R27	A B	A	272	Y	3.1	261	273
1R27	A B	A	289	K	2.2	286	290
1R27	A B	A	520	R	1.5	515	532
1R27	A B	A	780	L	1.6	777	781
1R27	A B	A	1105	L	1.4	1105	1111
1R27	A B	A	1110	L	2.2	1105	1111
1R27	A B	A	1121	E	1.8	1121	1127
1R27	A B	B	24	V	1.6	21	31
1R27	A B	B	29	V	1.6	21	31
1R27	A B	B	30	W	2.5	21	31
1R27	A B	B	108	Y	2.9	108	113
1R27	A B	B	111	L	1.7	108	113
1R27	A B	B	112	H	2.5	108	113
1R27	A B	B	248	Y	1.3	248	253
1R27	A B	B	250	R	1.3	248	253
1R27	A B	B	252	E	1.9	248	253
1R27	A B	B	412	M	1.5	399	423
1R27	A B	B	413	R	2.6	399	423
1R27	A B	B	417	R	1.1	399	423
1R27	A B	B	444	Y	1.9	437	450
1R27	A B	B	449	I	1.8	437	450
1R27	A B	B	455	R	2.9	452	456
1R27	C D	C	31	W	5.5	30	40
1R27	C D	C	32	E	3.0	30	40
1R27	C D	C	35	Y	3.1	30	40
1R27	C D	C	36	R	2.5	30	40
1R27	C D	C	38	R	2.2	30	40
1R27	C D	C	39	W	1.8	30	40
1R27	C D	C	244	Y	1.9	240	245

1R27	C D	C	269	E	1.6	264	273
1R27	C D	C	272	Y	3.1	264	273
1R27	C D	C	289	K	1.6	286	290
1R27	C D	C	520	R	1.3	515	532
1R27	C D	C	780	L	1.7	777	781
1R27	C D	C	1105	L	1.0	1105	1111
1R27	C D	C	1110	L	2.8	1105	1111
1R27	C D	C	1121	E	2.7	1121	1127
1R27	C D	D	24	V	1.4	21	31
1R27	C D	D	29	V	1.6	21	31
1R27	C D	D	30	W	2.3	21	31
1R27	C D	D	108	Y	2.7	108	113
1R27	C D	D	111	L	1.5	108	113
1R27	C D	D	112	H	2.6	108	113
1R27	C D	D	248	Y	1.4	248	253
1R27	C D	D	250	R	1.2	248	253
1R27	C D	D	252	E	1.4	248	253
1R27	C D	D	412	M	1.4	400	423
1R27	C D	D	413	R	2.6	400	423
1R27	C D	D	417	R	1.3	400	423
1R27	C D	D	444	Y	1.6	437	450
1R27	C D	D	449	I	1.9	437	450
1R27	C D	D	455	R	2.7	452	456
1R2B	A C	A	58	Y	1.0	55	61
1R2B	A C	A	116	H	1.7	115	127
1R2B	A D	A	17	D	1.4	14	28
1R2B	B C	B	24	R	1.9	14	28
1R2B	B D	B	58	Y	1.1	55	61
1R2B	B D	B	116	H	2.3	115	128
1R3I	H C	C	45	Y	2.6	24	52
1R3I	H C	C	49	L	3.1	24	52
1R3I	H C	C	62	Y	1.3	62	71
1R3I	L H	L	123	E	1.1	122	127
1R3I	L H	L	124	Q	1.9	122	127
1R4A	A E	A	74	I	1.0	72	77
1R4A	A E	E	2174	E	1.3	2173	2187
1R4A	A E	E	2177	Y	2.9	2173	2187
1R4A	A E	E	2193	T	1.7	2191	2202
1R4A	B F	F	2177	Y	3.3	2173	2187
1R4A	B F	F	2193	T	1.3	2191	2202
1R4A	C G	G	2177	Y	1.8	2173	2186
1R4A	D H	H	2177	Y	2.8	2173	2187
1R4A	D H	H	2196	K	1.0	2191	2202
1R4M	A B	A	14	D	1.3	14	18
1R4M	A B	A	51	L	1.4	49	53
1R4M	A B	A	67	G	76.6	67	72
1R4M	A B	A	71	G	107.9	67	72
1R4M	A B	A	339	Y	2.1	336	367
1R4M	A B	A	478	Y	1.0	476	486
1R4M	A B	A	484	R	1.6	476	486
1R4M	A B	A	492	T	1.3	491	511
1R4M	A B	A	496	F	1.5	491	511
1R4M	A B	A	499	G	65.5	491	511
1R4M	A B	A	503	Q	3.5	491	511
1R4M	A B	B	23	F	3.4	20	26
1R4M	A B	B	114	R	4.6	103	115
1R4M	A B	B	279	R	1.2	278	286
1R4M	A B	B	283	G	1.5	278	286
1R4M	A B	B	302	V	1.5	293	313
1R4M	A B	B	309	K	1.2	293	313

1R4M	A I	A	244	R	1.1	237	249
1R4M	A I	I	129	R	1.2	123	135
1R4M	A I	I	132	E	1.7	123	135
1R4M	B I	B	151	R	1.4	148	162
1R4M	C D	C	14	D	1.2	14	18
1R4M	C D	C	22	D	1.4	22	29
1R4M	C D	C	51	L	1.5	49	53
1R4M	C D	C	67	G	108.7	67	72
1R4M	C D	C	71	G	150.7	67	72
1R4M	C D	C	339	Y	3.0	336	367
1R4M	C D	C	340	I	1.0	336	367
1R4M	C D	C	478	Y	1.0	476	486
1R4M	C D	C	484	R	1.5	476	486
1R4M	C D	C	492	T	1.4	491	511
1R4M	C D	C	496	F	1.5	491	511
1R4M	C D	C	499	G	58.4	491	511
1R4M	C D	C	503	Q	2.3	491	511
1R4M	C D	D	23	F	3.8	20	26
1R4M	C D	D	114	R	1.7	103	115
1R4M	C D	D	279	R	1.5	278	286
1R4M	C D	D	283	G	1.6	278	286
1R4M	C D	D	298	V	1.0	293	313
1R4M	C D	D	302	V	1.2	293	313
1R4M	C D	D	306	E	2.9	293	313
1R4M	C H	C	448	Y	1.0	447	468
1R4M	E B	E	448	Y	1.2	447	468
1R4M	E F	E	14	D	1.2	14	18
1R4M	E F	E	44	E	1.1	40	48
1R4M	E F	E	51	L	1.5	49	53
1R4M	E F	E	67	G	134.1	67	72
1R4M	E F	E	71	G	186.8	67	72
1R4M	E F	E	340	I	1.0	336	367
1R4M	E F	E	478	Y	1.0	476	486
1R4M	E F	E	480	H	1.0	476	486
1R4M	E F	E	484	R	1.6	476	486
1R4M	E F	E	492	T	1.5	491	511
1R4M	E F	E	493	I	2.0	491	511
1R4M	E F	E	496	F	1.4	491	511
1R4M	E F	E	499	G	63.3	491	511
1R4M	E F	E	503	Q	3.3	491	511
1R4M	E F	F	23	F	2.2	20	26
1R4M	E F	F	114	R	2.2	103	115
1R4M	E F	F	279	R	1.4	278	286
1R4M	E F	F	283	G	1.7	278	286
1R4M	E F	F	298	V	1.0	293	313
1R4M	E F	F	302	V	1.4	293	313
1R4M	E F	F	306	E	3.1	293	313
1R4M	E F	F	309	K	1.2	293	313
1R4M	E K	K	132	E	1.0	123	135
1R4M	F K	F	148	I	1.2	148	162
1R4M	F K	F	151	R	1.3	148	162
1R4M	G H	G	14	D	1.2	14	18
1R4M	G H	G	22	D	1.4	22	29
1R4M	G H	G	51	L	1.5	49	53
1R4M	G H	G	67	G	108.9	67	72
1R4M	G H	G	71	G	159.4	67	72
1R4M	G H	G	340	I	1.0	336	367
1R4M	G H	G	478	Y	1.0	476	486
1R4M	G H	G	484	R	1.7	476	486
1R4M	G H	G	492	T	1.3	491	511

1R4M	G H	G	496	F	1.5	491	511
1R4M	G H	G	499	G	58.8	491	511
1R4M	G H	G	503	Q	2.2	491	511
1R4M	G H	H	23	F	1.6	20	26
1R4M	G H	H	114	R	1.7	103	115
1R4M	G H	H	279	R	1.5	278	286
1R4M	G H	H	283	G	1.5	278	286
1R4M	G H	H	294	S	1.0	293	313
1R4M	G H	H	298	V	1.1	293	313
1R4M	G H	H	302	V	1.7	293	313
1R4M	G H	H	306	E	2.8	293	313
1R4M	G H	H	309	K	1.2	293	313
1R4M	G L	G	244	R	1.2	237	249
1R4M	H L	H	148	I	1.4	148	162
1R4M	H L	H	151	R	1.4	148	162
1R4P	A B	B	33	W	1.1	33	45
1R4P	A D	A	293	Y	1.3	290	296
1R4P	A D	D	44	L	1.5	33	45
1R4P	A E	A	293	Y	2.3	290	296
1R4P	A E	E	33	W	4.5	33	45
1R4P	A F	A	290	Q	1.4	290	296
1R4P	A F	F	33	W	1.0	33	45
1R4Q	A B	B	45	I	1.0	34	46
1R4Q	A C	A	283	G	49.7	279	285
1R4Q	A D	A	205	R	1.2	203	212
1R4Q	A D	D	45	I	1.2	34	46
1R4Q	A E	E	45	I	1.2	34	46
1R4Q	L G	G	45	I	1.1	34	46
1R4Q	L I	I	45	I	1.0	37	47
1R4Q	L J	J	45	I	1.1	36	47
1R5V	A B	A	48	F	2.6	46	50
1R5V	A B	A	70	L	1.9	56	78
1R5V	A B	A	74	K	1.2	56	78
1R5V	A B	A	76	R	3.1	56	78
1R5V	A B	B	84	D	1.7	82	90
1R5V	A B	B	113	F	1.2	92	119
1R5V	A B	B	116	F	3.2	92	119
1R5V	A B	B	117	L	4.3	92	119
1R5V	A E	A	58	G	136.8	56	78
1R5V	A E	A	65	V	1.3	56	78
1R5V	A E	A	69	N	1.2	56	78
1R5V	C D	C	48	F	2.8	46	50
1R5V	C D	C	70	L	1.6	56	78
1R5V	C D	C	74	K	1.3	56	78
1R5V	C D	C	76	R	2.0	56	78
1R5V	C D	D	84	D	1.8	82	90
1R5V	C D	D	110	Y	1.0	92	119
1R5V	C D	D	113	F	1.0	92	119
1R5V	C D	D	116	F	3.1	92	119
1R5V	C D	D	117	L	2.8	92	119
1R5V	C F	C	58	G	199.2	56	78
1R5V	C F	C	65	V	1.3	56	78
1R5V	C F	C	69	N	1.0	56	78
1R5V	E B	B	88	W	2.8	82	90
1R5V	E B	B	105	V	1.7	92	119
1R5V	E B	B	108	H	1.0	92	119
1R5V	E B	B	112	I	1.1	92	119
1R5V	F D	D	88	W	2.1	82	90
1R5V	F D	D	94	F	1.0	92	119
1R5V	F D	D	105	V	1.7	92	119

1R5V	F D	D	108	H	1.0	92	119
1R5V	F D	D	109	N	1.1	92	119
1R5V	F D	D	112	I	1.4	92	119
1R5W	A B	A	48	F	2.0	46	50
1R5W	A B	A	74	K	19.5	56	78
1R5W	A B	B	113	F	1.3	92	119
1R5W	A B	B	116	F	3.4	92	119
1R5W	A B	B	117	L	2.8	92	119
1R5W	A E	A	58	G	26.4	56	78
1R5W	A E	A	62	N	1.0	56	78
1R5W	A F	A	57	Q	1.4	56	78
1R5W	B E	B	88	W	3.8	82	90
1R5W	B E	B	108	H	1.0	92	119
1R5W	C D	C	48	F	2.1	46	50
1R5W	C D	C	74	K	2.9	56	78
1R5W	C D	C	76	R	2.3	56	78
1R5W	C D	D	113	F	1.3	92	119
1R5W	C D	D	116	F	3.4	92	119
1R5W	C D	D	117	L	2.8	92	119
1R5W	C F	C	58	G	25.9	56	78
1R5W	D F	D	88	W	2.9	82	90
1R5W	D F	D	108	H	1.0	92	119
1R6O	A C	A	14	F	1.3	4	20
1R6O	A C	A	84	F	1.2	82	98
1R6O	A C	A	86	R	1.9	82	98
1R6O	A C	A	122	Y	3.8	119	127
1R6O	A C	C	49	K	1.4	40	50
1R6O	A C	C	79	E	1.6	78	95
1R6O	A C	C	80	V	1.0	78	95
1R6O	A C	C	82	E	1.9	78	95
1R6O	A C	C	83	T	1.0	78	95
1R6O	A C	C	84	K	1.1	78	95
1R6O	A D	A	8	L	1.0	4	20
1R6O	A D	A	18	R	1.2	4	20
1R6O	A D	D	40	M	1.3	40	50
1R6O	A D	D	55	V	1.4	55	69
1R6O	A D	D	63	L	1.3	55	69
1R6O	A D	D	66	H	1.1	55	69
1R6O	B D	B	85	Q	1.2	82	98
1R6O	B D	B	86	R	2.1	82	98
1R6O	B D	B	122	Y	3.2	119	127
1R6O	B D	D	79	E	2.4	78	95
1R6O	B D	D	80	V	1.1	78	95
1R6O	B D	D	82	E	2.3	78	95
1R6O	B D	D	83	T	1.5	78	95
1R8Q	A E	A	77	L	3.0	75	82
1R8Q	A E	A	81	Y	1.9	75	82
1R8Q	A E	E	160	I	1.6	157	175
1R8Q	A E	E	186	Y	1.4	182	200
1R8Q	A E	E	187	V	1.5	182	200
1R8Q	A E	E	190	Y	3.1	182	200
1R8Q	A E	E	194	M	1.3	182	200
1R8Q	A E	E	197	T	1.4	182	200
1R8Q	A E	E	198	D	1.3	182	200
1R8Q	A F	F	232	R	1.9	228	241
1R8Q	A F	F	236	D	1.0	228	241
1R8Q	B F	B	77	L	2.4	75	83
1R8Q	B F	F	160	I	1.3	157	175
1R8Q	B F	F	186	Y	1.2	182	200
1R8Q	B F	F	187	V	1.2	182	200

1R8Q	B F	F	190	Y	2.5	182	200
1R8Q	B F	F	194	M	1.4	182	200
1R8Q	B F	F	197	T	1.4	182	200
1R8Q	B F	F	212	R	1.1	210	217
1R8U	A B	A	225	E	1.7	225	236
1R8U	A B	A	228	L	2.1	225	236
1R8U	A B	A	231	L	2.4	225	236
1R8U	A B	B	349	K	2.3	348	374
1R8U	A B	B	350	R	1.6	348	374
1R8U	A B	B	353	I	1.1	348	374
1R8U	A B	B	358	V	2.2	348	374
1R8U	A B	B	361	L	1.7	348	374
1R8U	A B	B	365	K	1.8	348	374
1R8U	A B	B	383	H	1.5	382	397
1R8U	A B	B	387	M	1.1	382	397
1R8U	A B	B	413	Q	1.5	406	424
1RCO	B C	B	194	R	2.3	182	195
1RCO	B C	B	418	V	1.2	413	433
1RCO	B C	B	421	R	2.5	413	433
1RCO	B C	C	28	R	1.2	23	36
1RCO	B F	B	70	W	1.3	70	75
1RCO	B F	B	73	G	91.8	70	75
1RCO	B F	B	74	L	1.3	70	75
1RCO	B W	B	184	N	2.1	182	195
1RCO	B W	B	186	G	31.2	182	195
1RCO	B W	B	187	R	2.8	182	195
1RCO	B W	B	190	Y	3.2	182	195
1RCO	B W	B	191	E	1.1	182	195
1RCO	B W	B	219	L	1.5	214	233
1RCO	B W	B	223	E	5.4	214	233
1RCO	B W	B	226	Y	2.0	214	233
1RCO	B W	B	227	K	1.5	214	233
1RCO	B W	B	256	F	1.3	247	261
1RCO	E C	E	70	W	1.4	70	75
1RCO	E C	E	73	G	95.7	70	75
1RCO	E C	E	74	L	1.3	70	75
1RCO	E F	E	194	R	2.3	182	195
1RCO	E F	E	418	V	1.2	413	433
1RCO	E F	E	421	R	2.5	413	433
1RCO	E F	F	28	R	1.2	23	36
1RCO	E M	E	183	K	3.0	182	195
1RCO	E M	E	184	N	1.8	182	195
1RCO	E M	E	186	G	18.2	182	195
1RCO	E M	E	187	R	2.5	182	195
1RCO	E M	E	219	L	1.6	214	233
1RCO	E M	E	223	E	4.4	214	233
1RCO	E M	E	226	Y	2.0	214	233
1RCO	E M	E	227	K	1.5	214	233
1RCO	E M	E	256	F	1.4	247	261
1RCO	H C	H	186	G	29.0	182	195
1RCO	H C	H	187	R	3.2	182	195
1RCO	H C	H	191	E	1.2	182	195
1RCO	H C	H	219	L	1.6	214	233
1RCO	H C	H	223	E	3.7	214	233
1RCO	H C	H	226	Y	2.0	214	233
1RCO	H C	H	227	K	1.5	214	233
1RCO	H C	H	256	F	1.4	247	261
1RCO	H I	H	194	R	2.3	182	195
1RCO	H I	H	418	V	1.2	413	433
1RCO	H I	H	421	R	2.5	413	433

1RCO	H I	I	28	R	1.2	23	36
1RCO	H M	H	70	W	1.4	70	75
1RCO	H M	H	73	G	23.6	70	75
1RCO	H M	H	74	L	1.2	70	75
1RCO	K I	K	70	W	1.5	70	75
1RCO	K I	K	73	G	33.5	70	75
1RCO	K I	K	74	L	1.2	70	75
1RCO	K M	K	194	R	2.3	182	195
1RCO	K M	K	418	V	1.2	413	433
1RCO	K M	K	421	R	2.5	413	433
1RCO	K M	K	431	R	1.4	413	433
1RCO	K M	M	28	R	2.4	23	36
1RCO	K M	M	32	Y	1.1	23	36
1RCO	K T	K	186	G	20.8	182	195
1RCO	K T	K	191	E	1.6	182	195
1RCO	K T	K	219	L	1.6	214	233
1RCO	K T	K	223	E	2.0	214	233
1RCO	K T	K	226	Y	2.0	214	233
1RCO	K T	K	256	F	1.4	247	261
1RCO	L F	L	186	G	25.3	182	195
1RCO	L F	L	187	R	1.0	182	195
1RCO	L F	L	191	E	1.1	182	195
1RCO	L F	L	219	L	1.5	214	233
1RCO	L F	L	223	E	3.7	214	233
1RCO	L F	L	226	Y	2.0	214	233
1RCO	L F	L	227	K	1.4	214	233
1RCO	L F	L	256	F	1.3	247	261
1RCO	L S	L	194	R	2.3	182	195
1RCO	L S	L	418	V	1.2	413	433
1RCO	L S	L	421	R	2.5	413	433
1RCO	L S	S	28	R	1.2	23	36
1RCO	L W	L	70	W	1.6	70	75
1RCO	L W	L	73	G	78.4	70	75
1RCO	L W	L	74	L	1.4	70	75
1RCO	O I	O	184	N	1.6	182	195
1RCO	O I	O	186	G	19.9	182	195
1RCO	O I	O	187	R	2.3	182	195
1RCO	O I	O	191	E	1.1	182	195
1RCO	O I	O	219	L	3.1	214	233
1RCO	O I	O	223	E	1.3	214	233
1RCO	O I	O	256	F	1.4	247	261
1RCO	O P	O	194	R	2.3	182	195
1RCO	O P	O	418	V	1.2	413	433
1RCO	O P	O	421	R	2.5	413	433
1RCO	O P	P	28	R	1.1	23	36
1RCO	O T	O	70	W	1.2	70	75
1RCO	O T	O	73	G	40.7	70	75
1RCO	O T	O	74	L	1.2	70	75
1RCO	R P	R	70	W	1.4	70	75
1RCO	R P	R	73	G	115.0	70	75
1RCO	R P	R	74	L	1.4	70	75
1RCO	R S	R	186	G	14.4	182	195
1RCO	R S	R	219	L	1.5	214	233
1RCO	R S	R	223	E	3.3	214	233
1RCO	R S	R	226	Y	2.0	214	233
1RCO	R S	R	227	K	1.6	214	233
1RCO	R S	R	256	F	1.4	247	261
1RCO	R T	R	194	R	2.3	182	195
1RCO	R T	R	418	V	1.2	413	433
1RCO	R T	R	421	R	2.5	413	433

1RCO	R T	R	428	V	2.4	413	433
1RCO	R T	R	431	R	2.4	413	433
1RCO	R T	R	432	N	1.2	413	433
1RCO	R T	T	25	Q	1.6	23	36
1RCO	R T	T	28	R	2.0	23	36
1RCO	R T	T	29	Q	1.4	23	36
1RCO	R T	T	32	Y	2.1	23	36
1RCO	V P	V	183	K	1.2	182	195
1RCO	V P	V	186	G	44.2	182	195
1RCO	V P	V	191	E	1.1	182	195
1RCO	V P	V	219	L	1.3	214	233
1RCO	V P	V	220	F	2.1	214	233
1RCO	V P	V	223	E	12.8	214	233
1RCO	V P	V	226	Y	3.5	214	233
1RCO	V P	V	227	K	8.8	214	233
1RCO	V P	V	256	F	1.0	247	261
1RCO	V S	V	70	W	1.2	70	75
1RCO	V S	V	73	G	20.6	70	75
1RCO	V S	V	74	L	1.2	70	75
1RCO	V W	V	194	R	2.3	182	195
1RCO	V W	V	418	V	1.2	413	433
1RCO	V W	V	421	R	2.5	413	433
1RCO	V W	W	28	R	1.2	23	36
1RD8	A B	B	56	I	1.3	38	60
1RD8	A B	B	59	M	2.5	38	60
1RD8	A B	B	92	W	2.5	75	103
1RD8	A B	B	93	T	1.2	75	103
1RD8	A B	B	100	V	1.4	75	103
1RD8	A B	B	101	L	1.0	75	103
1RD8	A B	B	104	N	2.1	104	127
1RD8	A B	B	108	L	2.6	104	127
1RD8	A B	B	111	H	1.3	104	127
1RD8	A B	B	115	V	1.2	104	127
1RD8	A B	B	122	V	1.7	104	127
1RD8	A D	A	107	E	1.3	105	112
1RD8	A D	A	110	E	2.6	105	112
1RD8	A D	D	75	R	1.5	75	103
1RD8	A D	D	76	R	2.2	75	103
1RD8	A D	D	79	N	1.0	75	103
1RD8	C B	B	47	G	61.6	38	60
1RD8	C B	B	51	K	1.8	38	60
1RD8	C D	D	48	I	2.3	38	60
1RD8	C D	D	56	I	1.3	38	60
1RD8	C D	D	59	M	1.5	38	60
1RD8	C D	D	92	W	2.2	75	103
1RD8	C D	D	93	T	1.1	75	103
1RD8	C D	D	100	V	1.6	75	103
1RD8	C D	D	104	N	1.5	104	127
1RD8	C D	D	111	H	1.3	104	127
1RD8	C D	D	112	D	1.0	104	127
1RD8	C D	D	115	V	1.4	104	127
1RD8	C D	D	122	V	1.1	104	127
1RD8	E B	E	110	E	1.5	105	112
1RD8	E B	B	76	R	1.0	75	103
1RD8	E D	D	47	G	62.9	38	60
1RD8	E D	D	50	N	1.0	38	60
1RD8	E D	D	51	K	1.8	38	60
1RDT	A D	A	394	E	1.1	386	408
1RDT	A D	A	397	Y	2.7	386	408
1RDT	A D	A	417	K	1.0	414	420

1RDT	A D	A	423	P	1.1	421	441
1RDT	A D	D	407	E	1.1	403	425
1RDT	A D	D	414	L	1.0	403	425
1RDT	A D	D	434	K	1.9	431	459
1RDT	A D	D	436	L	1.2	431	459
1RDT	A D	D	443	R	1.3	431	459
1RE0	A B	A	79	R	1.4	78	83
1RE0	A B	A	80	H	1.5	78	83
1RE0	A B	A	81	Y	2.0	78	83
1RE0	A B	B	201	I	1.7	198	216
1RE0	A B	B	256	Y	2.4	248	266
1RE0	A B	B	260	M	1.2	248	266
1RE0	A B	B	262	N	1.5	248	266
1RE0	A B	B	264	D	1.4	248	266
1RF8	A B	A	74	F	11.8	71	81
1RF8	A B	A	75	W	44.7	71	81
1RF8	A B	A	135	L	11.3	126	140
1RF8	A B	A	139	G	1.1	126	140
1RF8	A B	B	244	L	1.2	237	246
1RF8	A B	B	280	P	1.5	280	291
1RF8	A B	B	282	F	6.6	280	291
1RF8	A B	B	287	K	2.5	280	291
1RF8	A B	B	289	K	2.4	280	291
1RFN	A B	A	128	Y	4.6	126	133
1RGI	G A	G	95	Q	1.3	95	112
1RGI	G A	G	99	G	35.6	95	112
1RGI	G A	A	143	Y	1.3	137	145
1RGI	G A	A	345	I	2.6	338	349
1RH5	A B	A	38	F	1.9	23	41
1RH5	A B	A	183	F	2.2	169	185
1RH5	A B	A	184	V	1.6	169	185
1RH5	A B	A	224	V	1.5	209	227
1RH5	A B	A	376	P	1.0	363	396
1RH5	A B	A	380	M	1.4	363	396
1RH5	A B	A	408	V	1.9	402	420
1RH5	A B	A	411	V	1.3	402	420
1RH5	A B	A	412	Y	1.3	402	420
1RH5	A B	B	14	F	1.6	12	24
1RH5	A B	B	17	E	1.2	12	24
1RH5	A B	B	21	V	1.3	12	24
1RH5	A B	B	36	V	1.0	30	66
1RH5	A B	B	43	G	74.8	30	66
1RH5	A B	B	44	I	1.9	30	66
1RH5	A B	B	47	L	1.0	30	66
1RH5	A B	B	48	G	37.2	30	66
1RH5	A B	B	51	G	82.3	30	66
1RH5	A B	B	52	Y	1.3	30	66
1RH5	A B	B	54	I	2.0	30	66
1RH5	A B	B	55	H	1.0	30	66
1RH5	A C	A	36	L	1.4	23	41
1RH5	A C	A	153	I	1.0	137	164
1RH5	A C	C	33	V	1.3	30	49
1RH5	A C	C	34	I	1.3	30	49
1RH5	A C	C	40	F	3.2	30	49
1RHH	A B	A	123	Q	1.7	121	126
1RHH	C D	C	123	Q	1.0	121	126
1RI8	A B	B	35	E	1.2	25	36
1RI8	A B	B	114	R	1.5	109	116
1RIH	L H	L	123	E	1.1	122	127
1RIO	H B	H	413	R	1.9	409	423

1RIO	H B	H	417	N	1.0	409	423
1RIO	H B	B	35	E	2.4	34	40
1RIO	H B	B	45	Q	1.0	45	53
1RIW	A C	A	25	E	1.5	25	32
1RIW	B C	B	161	T	1.6	159	166
1RIW	B C	B	165	L	1.5	159	166
1RIW	B C	C	279	W	6.0	277	286
1RIW	B C	C	280	I	1.6	277	286
1RIW	B C	C	283	V	1.7	277	286
1RIW	B C	C	284	I	1.9	277	286
1RJ9	A B	A	46	L	1.1	46	60
1RJ9	A B	A	235	N	1.1	234	247
1RJC	A B	B	112	R	1.6	109	116
1RJC	A B	B	113	N	1.3	109	116
1RJC	A B	B	114	R	1.9	109	116
1RJL	A B	A	123	E	1.1	122	126
1RJL	A B	A	124	Q	1.6	122	126
1RK8	A B	B	57	V	1.2	55	69
1RK8	A B	B	60	E	2.0	55	69
1RK8	A B	B	63	R	1.4	55	69
1RK8	A B	B	133	L	1.0	117	142
1RK8	A B	B	136	S	2.0	117	142
1RK8	A B	B	140	L	2.7	117	142
1RK8	A B	B	141	H	4.3	117	142
1RK8	B C	B	119	G	2.2	117	142
1RKE	A B	A	24	V	1.3	7	34
1RKE	A B	A	25	I	1.0	7	34
1RKE	A B	A	28	E	2.6	7	34
1RKE	A B	A	113	R	3.1	102	149
1RKE	A B	A	116	L	1.2	102	149
1RKE	A B	B	945	R	1.3	944	971
1RKE	A B	B	948	I	1.5	944	971
1RKE	A B	B	997	I	2.5	986	1005
1RKE	A B	B	998	L	1.5	986	1005
1RKE	A B	B	1000	T	1.0	986	1005
1RKE	A B	B	1025	H	3.3	1014	1045
1RLD	A S	A	418	V	1.7	413	433
1RLD	A S	A	425	E	1.9	413	433
1RLD	B T	B	194	R	1.0	182	195
1RLD	B T	B	425	E	1.7	413	433
1RLD	B T	T	532	Y	1.1	523	535
1RM1	A C	A	142	I	1.0	129	147
1RM1	B C	B	14	T	1.2	14	29
1RM1	B C	B	15	I	4.0	14	29
1RM1	B C	B	23	L	1.2	14	29
1RM1	B C	B	26	L	2.1	14	29
1RM1	B C	B	36	L	3.0	34	55
1RM1	B C	B	39	R	1.6	34	55
1RM1	B C	B	40	V	1.3	34	55
1RM1	B C	B	47	V	1.9	34	55
1RM1	B C	B	52	L	2.0	34	55
1RM1	B C	C	5	E	1.2	4	21
1RM1	B C	C	10	Y	2.5	4	21
1RM1	B C	C	13	I	2.7	4	21
1RM1	B C	C	17	V	1.9	4	21
1RM1	B C	C	20	E	1.0	4	21
1RM1	B C	C	24	D	1.4	22	28
1RM1	B C	C	25	F	1.9	22	28
1RM1	B C	C	38	L	2.3	32	50
1RM1	B C	C	45	K	1.3	32	50

1RM6	A B	A	276	E	1.2	275	282
1RM6	A B	A	760	E	1.7	755	768
1RM6	A B	B	130	W	1.7	129	135
1RM6	A B	B	131	W	2.4	129	135
1RM6	A B	B	134	G	1.3	129	135
1RM6	A B	B	304	Y	2.8	302	323
1RM6	A B	B	307	R	1.6	302	323
1RM6	A C	A	20	G	152.0	20	25
1RM6	A C	A	23	K	1.2	20	25
1RM6	A C	A	24	V	2.2	20	25
1RM6	A C	A	275	R	3.0	275	282
1RM6	A C	A	660	E	1.6	656	677
1RM6	A C	A	661	G	7.9	656	677
1RM6	A C	A	665	G	66.3	656	677
1RM6	A C	A	668	W	1.8	656	677
1RM6	A C	A	672	G	2.6	656	677
1RM6	A C	C	29	R	1.9	24	33
1RM6	A C	C	89	Q	1.3	87	95
1RM6	A C	C	93	H	1.0	87	95
1RM6	A C	C	127	K	1.0	123	130
1RM6	A C	C	142	K	1.6	141	156
1RM6	B C	B	37	L	1.7	34	42
1RM6	B C	B	79	E	1.4	78	83
1RM6	B C	B	106	H	1.7	104	110
1RM6	B C	C	117	K	1.2	104	118
1RM6	D E	D	280	I	1.1	275	282
1RM6	D E	D	755	P	4.1	755	768
1RM6	D E	D	760	E	1.6	755	768
1RM6	D E	E	130	W	1.6	129	135
1RM6	D E	E	131	W	2.5	129	135
1RM6	D E	E	134	G	3.6	129	135
1RM6	D E	E	307	R	1.4	302	323
1RM6	D F	D	20	G	154.8	20	25
1RM6	D F	D	23	K	1.5	20	25
1RM6	D F	D	24	V	2.2	20	25
1RM6	D F	D	275	R	2.9	275	282
1RM6	D F	D	660	E	2.3	656	677
1RM6	D F	D	661	G	10.2	656	677
1RM6	D F	D	665	G	89.1	656	677
1RM6	D F	D	668	W	1.7	656	677
1RM6	D F	D	672	G	2.6	656	677
1RM6	D F	F	29	R	1.8	24	33
1RM6	D F	F	89	Q	1.3	87	95
1RM6	D F	F	127	K	1.3	123	130
1RM6	D F	F	142	K	1.8	141	156
1RM6	E F	E	37	L	1.7	34	42
1RM6	E F	E	38	P	1.5	34	42
1RM6	E F	E	41	R	1.6	34	42
1RM6	E F	E	105	T	1.0	104	110
1RM6	E F	E	106	H	1.6	104	110
1RP3	A B	A	11	R	1.3	4	18
1RP3	A B	A	15	I	1.9	4	18
1RP3	A B	A	16	L	1.4	4	18
1RP3	A B	A	19	L	2.0	19	32
1RP3	A B	A	23	K	1.6	19	32
1RP3	A B	A	40	R	1.6	39	56
1RP3	A B	A	43	I	1.4	39	56
1RP3	A B	A	74	K	1.4	63	83
1RP3	A B	A	148	F	3.1	126	156
1RP3	A B	A	179	K	1.6	164	184

1RP3	A B	A	182	V	1.4	164	184
1RP3	A B	A	183	S	1.2	164	184
1RP3	A B	A	190	K	1.6	187	200
1RP3	A B	A	195	L	1.0	187	200
1RP3	A B	A	197	F	2.5	187	200
1RP3	A B	A	198	Y	2.5	187	200
1RP3	A B	B	7	L	1.2	5	15
1RP3	A B	B	11	I	1.8	5	15
1RP3	A B	B	39	L	1.6	32	47
1RP3	A B	B	42	I	1.1	32	47
1RP3	A B	B	46	L	2.0	32	47
1RP3	A B	B	60	V	1.6	56	69
1RP3	A B	B	64	K	2.8	56	69
1RP3	A B	B	76	D	1.8	76	88
1RP3	A B	B	78	K	1.5	76	88
1RP3	A B	B	79	V	1.4	76	88
1RP3	A B	B	80	V	1.7	76	88
1RP3	A B	B	82	G	10.6	76	88
1RP3	A B	B	83	L	2.3	76	88
1RP3	A B	B	84	I	1.7	76	88
1RP3	A B	B	86	F	2.5	76	88
1RP3	A B	B	87	F	4.8	76	88
1RP3	C D	C	15	I	1.2	4	18
1RP3	C D	C	16	L	1.6	4	18
1RP3	C D	C	19	L	1.1	19	32
1RP3	C D	C	31	K	1.3	19	32
1RP3	C D	C	40	R	1.5	39	56
1RP3	C D	C	43	I	1.6	39	56
1RP3	C D	C	47	V	1.0	39	56
1RP3	C D	C	144	L	1.0	126	152
1RP3	C D	C	148	F	2.4	126	152
1RP3	C D	C	178	V	1.1	165	184
1RP3	C D	C	182	V	1.1	165	184
1RP3	C D	C	194	Q	1.8	187	199
1RP3	C D	C	197	F	2.4	187	199
1RP3	C D	C	198	Y	2.5	187	199
1RP3	C D	C	209	I	1.8	203	210
1RP3	C D	D	11	I	2.0	4	18
1RP3	C D	D	15	L	1.3	4	18
1RP3	C D	D	39	L	1.8	36	48
1RP3	C D	D	46	L	1.3	36	48
1RP3	C D	D	56	L	1.0	51	69
1RP3	C D	D	60	V	1.2	51	69
1RP3	C D	D	64	K	2.0	51	69
1RP3	C D	D	78	K	1.3	76	88
1RP3	C D	D	79	V	1.0	76	88
1RP3	C D	D	80	V	1.9	76	88
1RP3	C D	D	82	G	62.8	76	88
1RP3	C D	D	83	L	2.0	76	88
1RP3	C D	D	84	I	1.6	76	88
1RP3	C D	D	85	E	1.2	76	88
1RP3	C D	D	86	F	2.5	76	88
1RP3	C D	D	87	F	4.7	76	88
1RP3	E F	E	15	I	1.2	4	18
1RP3	E F	E	40	R	1.5	39	55
1RP3	E F	E	43	I	1.6	39	55
1RP3	E F	E	71	L	1.0	62	82
1RP3	E F	E	148	F	2.6	126	157
1RP3	E F	E	179	K	1.4	165	184
1RP3	E F	E	182	V	1.6	165	184

1RP3	E F	E	183	S	1.8	165	184
1RP3	E F	E	190	K	1.8	187	199
1RP3	E F	E	194	Q	2.1	187	199
1RP3	E F	E	195	L	1.2	187	199
1RP3	E F	E	197	F	2.4	187	199
1RP3	E F	E	198	Y	2.5	187	199
1RP3	E F	E	209	I	1.2	203	210
1RP3	E F	F	11	I	1.9	5	17
1RP3	E F	F	15	L	1.3	5	17
1RP3	E F	F	39	L	1.7	36	47
1RP3	E F	F	46	L	1.5	36	47
1RP3	E F	F	60	V	1.0	56	69
1RP3	E F	F	64	K	1.9	56	69
1RP3	E F	F	76	D	2.2	76	88
1RP3	E F	F	78	K	1.4	76	88
1RP3	E F	F	79	V	1.1	76	88
1RP3	E F	F	80	V	1.3	76	88
1RP3	E F	F	82	G	30.9	76	88
1RP3	E F	F	83	L	2.4	76	88
1RP3	E F	F	84	I	1.4	76	88
1RP3	E F	F	86	F	2.4	76	88
1RP3	E F	F	87	F	4.6	76	88
1RP3	G D	G	190	K	1.0	187	200
1RP3	G D	G	227	R	1.1	214	234
1RP3	G D	D	76	D	1.3	76	88
1RP3	G H	G	16	L	2.2	4	18
1RP3	G H	G	19	L	1.0	19	32
1RP3	G H	G	23	K	2.4	19	32
1RP3	G H	G	40	R	1.7	39	56
1RP3	G H	G	43	I	1.7	39	56
1RP3	G H	G	74	K	1.4	62	83
1RP3	G H	G	148	F	2.4	126	155
1RP3	G H	G	178	V	1.5	167	184
1RP3	G H	G	179	K	1.5	167	184
1RP3	G H	G	182	V	1.0	167	184
1RP3	G H	G	183	S	1.3	167	184
1RP3	G H	G	194	Q	2.0	187	200
1RP3	G H	G	195	L	1.1	187	200
1RP3	G H	G	197	F	1.9	187	200
1RP3	G H	G	198	Y	2.6	187	200
1RP3	G H	G	199	E	1.9	187	200
1RP3	G H	G	209	I	1.8	203	210
1RP3	G H	H	11	I	2.5	4	15
1RP3	G H	H	39	L	2.3	38	47
1RP3	G H	H	46	L	1.4	38	47
1RP3	G H	H	64	K	1.8	56	70
1RP3	G H	H	67	I	1.2	56	70
1RP3	G H	H	76	D	1.0	76	88
1RP3	G H	H	78	K	1.5	76	88
1RP3	G H	H	79	V	1.2	76	88
1RP3	G H	H	80	V	2.0	76	88
1RP3	G H	H	82	G	33.4	76	88
1RP3	G H	H	83	L	2.4	76	88
1RP3	G H	H	84	I	1.7	76	88
1RP3	G H	H	85	E	1.4	76	88
1RP3	G H	H	86	F	2.4	76	88
1RP3	G H	H	87	F	4.2	76	88
1RPQ	A W	W	6	F	2.3	5	10
1RSO	A B	A	17	L	1.1	8	24
1RSO	A B	A	43	I	1.0	31	45

1RSO	A B	A	52	L	1.1	47	58
1RSO	A D	A	51	A	3.1	47	58
1RSO	A D	D	135	K	1.2	120	136
1RSO	C B	C	54	D	5.3	47	58
1RSO	C D	C	39	R	1.1	31	45
1RSO	C D	C	43	I	1.6	31	45
1RSO	C D	C	48	L	1.0	47	58
1RSO	C D	C	49	F	2.2	47	58
1RSO	C D	D	113	L	1.7	107	119
1RSO	C D	D	121	H	1.2	120	136
1RSO	C D	D	122	L	1.1	120	136
1RSO	C D	D	125	L	1.6	120	136
1RSO	C D	D	126	L	1.5	120	136
1RSO	C D	D	133	N	2.1	120	136
1RTD	A B	A	373	Q	2.2	364	378
1RTD	A B	A	380	I	1.1	379	383
1RTD	A B	B	258	Q	1.0	254	271
1RTD	A B	B	396	E	1.2	395	401
1RTD	A B	B	397	T	1.9	395	401
1RTD	C D	C	380	I	1.2	364	383
1RTD	C D	D	258	Q	1.2	254	271
1RU7	A B	A	103	E	1.1	102	111
1RU7	A B	B	556	I	1.1	538	559
1RU7	A B	B	589	L	1.7	575	627
1RU7	A B	B	593	T	1.3	575	627
1RU7	A B	B	600	V	1.6	575	627
1RU7	A B	B	604	N	2.2	575	627
1RU7	A B	B	608	L	2.0	575	627
1RU7	A B	B	611	H	3.7	575	627
1RU7	A B	B	615	V	1.0	575	627
1RU7	A D	D	547	G	2.2	538	559
1RU7	A F	A	104	E	3.4	102	111
1RU7	A F	F	575	K	3.4	575	627
1RU7	A F	F	576	R	2.8	575	627
1RU7	C B	C	104	E	3.1	102	111
1RU7	C B	C	107	E	3.0	102	111
1RU7	C B	B	575	K	1.9	575	627
1RU7	C B	B	576	R	3.1	575	627
1RU7	C B	B	579	N	1.7	575	627
1RU7	C D	D	556	I	1.1	538	559
1RU7	C D	D	589	L	2.0	575	626
1RU7	C D	D	593	T	1.3	575	626
1RU7	C D	D	600	V	1.6	575	626
1RU7	C D	D	608	L	2.0	575	626
1RU7	C D	D	611	H	3.2	575	626
1RU7	C D	D	649	M	1.0	646	654
1RU7	C F	F	547	G	13.6	538	559
1RU7	C F	F	550	N	1.4	538	559
1RU7	C F	F	610	F	1.0	575	627
1RU7	E B	B	547	G	62.2	538	559
1RU7	E B	B	550	N	1.3	538	559
1RU7	E B	B	610	F	1.0	575	627
1RU7	E D	E	104	E	1.2	102	111
1RU7	E D	D	575	K	1.4	575	626
1RU7	E F	F	556	I	1.1	538	559
1RU7	E F	F	589	L	1.6	575	627
1RU7	E F	F	592	W	6.1	575	627
1RU7	E F	F	593	T	1.4	575	627
1RU7	E F	F	596	A	5.4	575	627
1RU7	E F	F	600	V	1.4	575	627

1RU7	E F	F	604	N	1.4	575	627
1RU7	E F	F	608	L	1.9	575	627
1RU7	E F	F	611	H	2.4	575	627
1RU7	E F	F	615	V	1.0	575	627
1RU7	G H	G	103	E	1.4	102	111
1RU7	G H	G	106	R	1.1	102	111
1RU7	G H	H	556	I	1.0	538	559
1RU7	G H	H	589	L	2.1	575	627
1RU7	G H	H	593	T	1.3	575	627
1RU7	G H	H	600	V	1.3	575	627
1RU7	G H	H	604	N	1.2	575	627
1RU7	G H	H	608	L	2.1	575	627
1RU7	G H	H	611	H	2.7	575	627
1RU7	G H	H	615	V	1.0	575	627
1RU7	G H	H	619	Y	5.9	575	627
1RU7	G H	H	622	V	5.4	575	627
1RU7	G H	H	652	V	5.7	646	654
1RU7	G H	H	653	R	5.3	646	654
1RU7	G J	J	547	G	16.0	538	559
1RU7	G J	J	550	N	1.0	538	559
1RU7	G J	J	610	F	1.0	575	626
1RU7	I H	I	104	E	1.9	102	111
1RU7	I H	H	575	K	2.8	575	627
1RU7	I H	H	576	R	1.9	575	627
1RU7	I J	J	556	I	1.1	538	559
1RU7	I J	J	589	L	1.6	575	626
1RU7	I J	J	593	T	1.3	575	626
1RU7	I J	J	600	V	1.5	575	626
1RU7	I J	J	608	L	2.1	575	626
1RU7	I J	J	611	H	2.4	575	626
1RU7	I J	J	615	V	1.0	575	626
1RU7	I J	J	649	M	1.7	646	654
1RU7	I L	L	547	G	1.6	538	559
1RU7	I L	L	550	N	1.3	538	559
1RU7	I L	L	551	K	1.2	538	559
1RU7	I L	L	610	F	1.0	575	627
1RU7	K H	H	547	G	39.0	538	559
1RU7	K H	H	550	N	1.0	538	559
1RU7	K H	H	610	F	1.1	575	627
1RU7	K J	K	104	E	1.2	102	111
1RU7	K J	J	575	K	1.5	575	626
1RU7	K L	L	555	V	1.0	538	559
1RU7	K L	L	556	I	1.0	538	559
1RU7	K L	L	589	L	1.8	575	627
1RU7	K L	L	593	T	1.4	575	627
1RU7	K L	L	600	V	1.5	575	627
1RU7	K L	L	604	N	2.4	575	627
1RU7	K L	L	608	L	2.1	575	627
1RU7	K L	L	611	H	1.1	575	627
1RUY	H I	I	593	T	5.4	575	624
1RUY	H I	I	597	E	1.0	575	624
1RUY	H I	I	601	L	1.1	575	624
1RUY	H I	I	604	N	1.6	575	624
1RUY	H I	I	608	L	1.6	575	624
1RUY	H I	I	611	H	2.4	575	624
1RUY	H K	K	547	G	33.8	538	559
1RUY	H K	K	610	F	1.3	575	624
1RUY	H M	H	104	E	1.6	102	111
1RUY	H M	H	107	E	2.5	102	111
1RUY	H M	M	575	K	1.2	575	624

1RUY	H M	M	576	R	1.8	575	624
1RUY	J I	J	104	E	1.9	102	111
1RUY	J I	J	107	E	2.2	102	111
1RUY	J I	I	575	K	1.7	575	624
1RUY	J I	I	579	N	1.3	575	624
1RUY	J K	K	589	L	1.4	575	624
1RUY	J K	K	601	L	1.1	575	624
1RUY	J K	K	604	N	1.6	575	624
1RUY	J K	K	608	L	1.6	575	624
1RUY	J K	K	611	H	2.4	575	624
1RUY	J K	K	649	M	1.0	646	654
1RUY	J M	M	547	G	6.1	538	559
1RUY	J M	M	610	F	1.0	575	624
1RUY	L I	I	547	G	34.2	538	559
1RUY	L I	I	610	F	1.4	575	624
1RUY	L K	L	104	E	2.6	102	111
1RUY	L K	L	107	E	1.4	102	111
1RUY	L K	K	575	K	2.3	575	624
1RUY	L K	K	576	R	2.2	575	624
1RUY	L K	K	579	N	1.4	575	624
1RUY	L M	M	556	I	1.0	538	559
1RUY	L M	M	593	T	5.3	575	624
1RUY	L M	M	601	L	1.1	575	624
1RUY	L M	M	604	N	1.6	575	624
1RUY	L M	M	608	L	1.6	575	624
1RUY	L M	M	611	H	2.4	575	624
1RUZ	H I	H	106	R	1.1	102	111
1RUZ	H I	I	556	I	1.0	538	559
1RUZ	H I	I	589	L	2.0	575	620
1RUZ	H I	I	593	T	1.1	575	620
1RUZ	H I	I	600	V	1.9	575	620
1RUZ	H I	I	604	N	2.8	575	620
1RUZ	H I	I	608	L	1.7	575	620
1RUZ	H I	I	611	H	2.6	575	620
1RUZ	H I	I	615	V	1.4	575	620
1RUZ	H I	I	622	V	1.8	621	627
1RUZ	H K	K	547	G	4.1	538	559
1RUZ	H M	H	104	E	1.3	102	111
1RUZ	J I	J	104	E	1.2	102	111
1RUZ	J I	I	576	R	1.0	575	620
1RUZ	J K	K	556	I	1.0	538	559
1RUZ	J K	K	589	L	1.4	575	620
1RUZ	J K	K	600	V	1.9	575	620
1RUZ	J K	K	604	N	2.7	575	620
1RUZ	J K	K	608	L	1.8	575	620
1RUZ	J K	K	611	H	2.7	575	620
1RUZ	J K	K	615	V	1.5	575	620
1RUZ	J K	K	622	V	1.3	621	627
1RUZ	J M	M	547	G	1.8	538	559
1RUZ	L I	I	547	G	1.6	538	559
1RUZ	L K	L	104	E	2.9	102	111
1RUZ	L K	L	107	E	2.0	102	111
1RUZ	L K	K	576	R	2.5	575	620
1RUZ	L M	L	106	R	1.0	102	111
1RUZ	L M	M	556	I	1.0	538	559
1RUZ	L M	M	600	V	1.3	575	620
1RUZ	L M	M	604	N	2.7	575	620
1RUZ	L M	M	608	L	1.8	575	620
1RUZ	L M	M	611	H	2.8	575	620
1RUZ	L M	M	615	V	1.5	575	620

1RUZ	L M	M	622	V	1.5	621	627
1RV6	V Y	V	25	F	1.4	25	32
1RV6	V Y	V	29	W	2.6	25	32
1RV6	W X	W	25	F	1.3	25	32
1RY1	C D	C	59	V	1.2	59	75
1RY1	C D	C	70	M	1.8	59	75
1RY1	C D	C	73	M	1.2	59	75
1RY1	U W	U	289	G	935.3	284	292
1RY1	W S	W	369	M	1.7	365	381
1RY1	W S	S	57	L	1.0	51	65
1RYP	A B	A	126	Q	1.2	114	131
1RYP	A B	B	20	Q	1.7	19	30
1RYP	A B	B	23	Y	3.3	19	30
1RYP	A B	B	83	R	2.7	79	96
1RYP	A G	A	27	Q	2.8	26	36
1RYP	A G	A	30	Y	3.6	26	36
1RYP	A G	A	87	I	1.2	87	108
1RYP	A G	A	88	P	1.1	87	108
1RYP	A G	A	91	R	1.7	87	108
1RYP	A G	G	120	Q	1.7	108	122
1RYP	A H	A	106	Y	1.0	87	108
1RYP	A H	H	61	Y	1.3	49	70
1RYP	A I	A	115	D	2.9	114	131
1RYP	A I	I	66	H	2.6	49	70
1RYP	B C	B	119	Q	2.7	107	121
1RYP	B C	C	21	Q	1.7	20	30
1RYP	B C	C	24	Y	3.2	20	30
1RYP	B C	C	85	E	1.7	81	102
1RYP	B I	B	90	R	2.8	79	96
1RYP	B I	B	91	K	2.6	79	96
1RYP	B I	B	94	H	2.7	79	96
1RYP	B I	I	61	S	1.8	49	70
1RYP	B I	I	65	L	3.8	49	70
1RYP	B I	I	68	L	1.1	49	70
1RYP	C D	C	117	D	2.0	108	125
1RYP	C D	C	120	Q	1.8	108	125
1RYP	C D	D	19	Q	1.0	18	30
1RYP	C D	D	22	Y	5.1	18	30
1RYP	C D	D	29	R	1.1	18	30
1RYP	C D	D	81	D	1.8	79	100
1RYP	C D	D	83	R	3.4	79	100
1RYP	C J	C	92	R	1.6	81	102
1RYP	C J	C	96	Q	1.7	81	102
1RYP	C J	J	60	Y	1.5	48	70
1RYP	C J	J	63	N	6.2	48	70
1RYP	C J	J	64	L	1.6	48	70
1RYP	C J	J	67	L	1.7	48	70
1RYP	C K	K	66	Y	1.8	49	71
1RYP	D E	E	23	Q	2.0	22	32
1RYP	D E	E	26	Y	3.5	22	32
1RYP	D K	K	65	L	1.6	49	71
1RYP	D L	L	81	K	1.1	76	90
1RYP	E F	E	184	L	1.6	176	187
1RYP	E F	F	21	Q	2.1	20	31
1RYP	E F	F	24	Y	2.7	20	31
1RYP	E F	F	79	P	1.2	78	99
1RYP	E L	E	93	R	1.0	82	103
1RYP	E L	E	101	L	1.3	82	103
1RYP	E L	L	68	L	1.7	49	70
1RYP	E M	E	111	S	1.0	109	121

1RYP	E M	M	66	Y	1.2	49	70
1RYP	E M	M	82	R	2.1	77	91
1RYP	E M	M	86	H	1.6	77	91
1RYP	F G	F	117	Q	2.4	105	119
1RYP	F G	G	22	Q	2.6	21	32
1RYP	F G	G	25	Y	4.0	21	32
1RYP	F G	G	83	D	2.1	81	102
1RYP	F G	G	85	R	1.2	81	102
1RYP	F G	G	86	H	2.1	81	102
1RYP	F M	F	89	R	2.7	78	99
1RYP	F M	M	65	W	1.2	49	70
1RYP	F M	M	68	F	2.6	49	70
1RYP	F N	F	110	H	1.0	105	119
1RYP	F N	N	66	N	1.3	49	68
1RYP	G H	G	98	F	1.5	81	102
1RYP	G H	H	66	Y	1.4	49	70
1RYP	G H	H	77	T	1.6	75	89
1RYP	G N	G	85	R	1.5	81	102
1RYP	G N	G	92	R	1.1	81	102
1RYP	H I	H	53	Q	2.5	49	70
1RYP	H I	I	88	F	2.0	76	90
1RYP	H N	H	87	Y	3.0	75	89
1RYP	H N	N	51	D	1.2	49	68
1RYP	H N	N	53	Q	2.1	49	68
1RYP	I J	I	51	D	3.2	49	70
1RYP	I J	J	87	Y	2.1	75	89
1RYP	I J	J	144	L	1.1	134	145
1RYP	I J	J	153	D	1.5	151	167
1RYP	I J	J	156	E	2.6	151	167
1RYP	I J	J	160	Q	1.5	151	167
1RYP	J K	K	84	R	1.2	76	92
1RYP	J K	K	137	F	1.5	134	147
1RYP	J Z	Z	166	H	2.0	150	168
1RYP	J Z	Z	197	F	1.2	193	205
1RYP	J Z	Z	198	W	1.6	193	205
1RYP	K L	K	50	G	29.2	49	71
1RYP	K L	L	88	Y	1.7	76	90
1RYP	K Z	K	144	D	3.6	134	147
1RYP	K Z	K	170	R	2.1	153	171
1RYP	K Z	Z	135	F	2.6	133	143
1RYP	K Z	Z	138	G	6.4	133	143
1RYP	K Z	Z	167	R	3.3	150	168
1RYP	L M	L	51	D	4.0	49	70
1RYP	L M	L	54	F	3.6	49	70
1RYP	L M	L	55	W	2.7	49	70
1RYP	L M	M	89	Y	6.7	77	91
1RYP	M N	M	51	D	1.3	49	70
1RYP	M N	N	93	Y	2.4	81	98
1RYP	O P	O	126	Q	1.8	114	131
1RYP	O P	O	130	Q	1.0	114	131
1RYP	O P	P	20	Q	1.9	19	30
1RYP	O P	P	23	Y	3.5	19	30
1RYP	O P	P	80	P	1.8	79	96
1RYP	O P	P	81	D	1.3	79	96
1RYP	O P	P	83	R	3.2	79	96
1RYP	O U	O	27	Q	3.2	26	36
1RYP	O U	O	30	Y	3.9	26	36
1RYP	O U	O	87	I	1.2	87	108
1RYP	O U	O	88	P	2.0	87	108
1RYP	O U	O	89	D	1.7	87	108

1RYP	O U	O	91	R	2.0	87	108
1RYP	O U	U	120	Q	1.2	108	122
1RYP	O V	O	98	K	1.0	87	108
1RYP	O V	O	105	R	1.1	87	108
1RYP	O V	O	106	Y	1.6	87	108
1RYP	O V	V	61	Y	1.8	49	70
1RYP	O V	V	65	L	1.2	49	70
1RYP	O W	O	115	D	2.2	114	131
1RYP	O W	W	66	H	2.2	49	70
1RYP	O W	W	69	Y	1.0	49	70
1RYP	P Q	Q	21	Q	1.9	20	30
1RYP	P Q	Q	24	Y	3.1	20	30
1RYP	P Q	Q	85	E	1.6	81	102
1RYP	P W	W	61	S	1.2	49	70
1RYP	P W	W	64	E	1.1	49	70
1RYP	P X	P	108	K	1.8	107	122
1RYP	P X	P	109	L	1.1	107	122
1RYP	P X	X	77	T	1.6	75	89
1RYP	Q R	Q	117	D	1.5	108	122
1RYP	Q R	Q	120	Q	2.2	108	122
1RYP	Q R	R	19	Q	1.4	18	29
1RYP	Q R	R	22	Y	2.8	18	29
1RYP	Q R	R	81	D	1.6	79	101
1RYP	Q R	R	83	R	3.8	79	101
1RYP	Q X	Q	96	Q	1.7	81	102
1RYP	Q X	X	60	Y	1.4	48	70
1RYP	Q X	X	63	N	1.6	48	70
1RYP	Q X	X	64	L	1.5	48	70
1RYP	Q X	X	67	L	1.5	48	70
1RYP	Q Y	Y	66	Y	1.4	50	71
1RYP	R S	S	26	Y	3.2	22	32
1RYP	R Y	R	94	Q	1.9	79	101
1RYP	R Y	R	97	R	1.3	79	101
1RYP	R Y	Y	65	L	1.7	50	71
1RYP	R Y	Y	68	I	1.6	50	71
1RYP	S T	T	21	Q	1.7	20	31
1RYP	S T	T	24	Y	3.5	20	31
1RYP	S T	T	79	P	1.3	78	99
1RYP	S Z	S	101	L	1.1	82	103
1RYP	S Z	Z	65	L	1.0	49	70
1RYP	T U	T	110	H	1.6	105	119
1RYP	T U	T	117	Q	2.3	105	119
1RYP	T U	T	173	E	1.4	165	175
1RYP	T U	T	176	L	1.2	176	181
1RYP	T U	U	22	Q	2.6	21	32
1RYP	T U	U	25	Y	3.8	21	32
1RYP	T U	U	83	D	2.3	81	102
1RYP	T U	U	85	R	1.0	81	102
1RYP	U V	U	98	F	1.6	81	102
1RYP	U V	V	66	Y	1.4	49	70
1RYP	U V	V	84	E	1.1	75	89
1RYP	V N	V	165	W	1.0	148	166
1RYP	V N	V	190	P	1.1	190	195
1RYP	V N	V	191	D	1.1	190	195
1RYP	V N	V	194	E	1.4	190	195
1RYP	V N	N	211	W	2.7	211	216
1RYP	V W	V	53	Q	2.2	49	70
1RYP	V W	W	88	F	2.0	76	90
1RYP	W M	W	164	W	1.2	148	165
1RYP	W M	M	173	K	1.2	168	185

1RYP	W M	M	177	D	1.5	168	185
1RYP	W M	M	184	E	1.0	168	185
1RYP	W N	N	142	M	1.0	138	151
1RYP	W N	N	146	L	1.5	138	151
1RYP	W N	N	175	V	1.2	162	179
1RYP	W X	W	51	D	3.7	49	70
1RYP	W X	X	87	Y	2.2	75	89
1RYP	W X	X	142	E	1.4	134	145
1RYP	W X	X	144	L	1.0	134	145
1RYP	W X	X	153	D	1.6	151	168
1RYP	W X	X	155	F	1.1	151	168
1RYP	W X	X	156	E	2.7	151	168
1RYP	W X	X	160	Q	1.7	151	168
1RYP	X L	L	166	H	1.3	150	168
1RYP	X L	L	198	W	1.4	193	205
1RYP	X M	X	138	F	1.3	134	145
1RYP	X M	X	139	G	153.8	134	145
1RYP	X M	X	140	M	1.0	134	145
1RYP	X M	M	136	L	1.3	134	146
1RYP	X Y	Y	84	R	1.4	76	92
1RYP	X Y	Y	137	F	1.5	134	146
1RYP	Y L	Y	144	D	2.9	134	146
1RYP	Y L	Y	170	R	2.6	153	171
1RYP	Y L	L	135	F	2.5	133	143
1RYP	Y L	L	138	G	4.5	133	143
1RYP	Y L	L	141	D	1.9	133	143
1RYP	Y L	L	167	R	3.0	150	168
1RYP	Y Z	Y	50	G	51.1	50	71
1RYP	Y Z	Y	57	E	1.1	50	71
1RYP	Y Z	Z	88	Y	2.8	76	90
1RZ7	L H	L	124	Q	1.4	122	127
1RZF	L H	L	125	E	2.3	123	128
1RZG	A B	B	124	Q	1.2	122	127
1RZG	C D	D	124	Q	1.6	122	128
1RZI	C D	C	124	Q	1.0	122	128
1RZI	I J	I	124	Q	1.0	122	128
1RZI	K F	K	123	E	1.0	122	128
1RZI	K F	K	126	K	1.1	122	128
1RZI	M N	M	123	E	1.4	122	126
1RZI	O P	O	124	Q	1.1	122	128
1RZO	A B	A	1182	Y	3.2	1181	1193
1RZO	A B	A	1245	S	8.0	1244	1249
1RZO	A B	A	1246	I	7.7	1244	1249
1RZO	C D	C	1182	Y	2.1	1181	1193
1RZO	C D	C	1185	G	23.5	1181	1193
1RZO	C D	C	1192	R	1.0	1181	1193
1RZO	C D	C	1245	S	1.9	1244	1249
1RZO	C D	C	1248	I	1.6	1244	1249
1RZR	A D	A	51	V	1.1	50	57
1RZR	A D	D	51	V	1.4	51	57
1RZR	A D	D	76	A	1.3	73	87
1RZR	A D	D	80	R	1.5	73	87
1RZR	A D	D	83	E	1.9	73	87
1RZR	A S	A	85	I	1.0	73	87
1RZR	A S	S	20	T	1.5	17	26
1RZR	A S	S	47	I	2.6	47	51
1RZR	C T	C	85	I	1.0	73	87
1RZR	C T	T	48	M	2.1	47	51
1RZR	G L	G	80	R	1.1	73	87
1S0Y	A D	A	23	G	8.8	14	33

1S0Y	A D	A	27	V	1.3	14	33
1S0Y	C F	C	20	L	1.4	14	33
1S0Y	C F	C	23	G	6.6	14	33
1S0Y	C F	C	24	L	1.2	14	33
1S0Y	C F	C	27	V	1.2	14	33
1S0Y	C F	F	32	I	2.4	14	33
1S0Y	E B	E	23	G	41.1	14	33
1S0Y	E B	E	24	L	1.3	14	33
1S0Y	E B	B	20	L	1.2	14	33
1S0Y	E B	B	27	V	1.2	14	33
1S0Y	E B	B	32	I	1.0	14	33
1S0Y	G J	G	20	L	1.6	14	33
1S0Y	G J	J	23	D	1.1	14	33
1S0Y	G J	J	32	I	2.3	14	33
1S0Y	I L	I	23	G	2.5	19	32
1S0Y	I L	I	24	L	1.2	19	32
1S0Y	I L	I	27	V	1.2	19	32
1S0Y	I L	L	20	L	1.0	14	33
1S0Y	K H	K	20	L	1.1	14	33
1S0Y	K H	K	23	G	99.8	14	33
1S0Y	K H	H	20	L	1.6	14	32
1S0Y	K H	H	27	V	1.3	14	32
1S1C	A X	X	998	L	1.1	983	1012
1S1C	A X	X	1005	K	1.9	983	1012
1S1C	A Y	A	69	L	1.7	67	75
1S1C	A Y	Y	1003	V	1.0	991	1011
1S1C	A Y	Y	1010	M	1.3	991	1011
1S1C	B X	B	72	L	1.2	67	75
1S1C	B Y	Y	1005	K	1.3	991	1011
1S1H	C N	C	10	L	2.1	10	28
1S1H	C N	C	14	G	1.9	10	28
1S1H	J N	N	40	Q	9.3	39	48
1S1H	J N	N	42	F	13.5	39	48
1S3K	L H	L	129	Q	1.8	127	131
1S4Z	A C	A	163	F	2.8	157	167
1S4Z	B C	B	164	Y	1.1	157	167
1S5E	A D	A	223	F	1.7	198	227
1S5E	A E	A	220	R	1.0	198	227
1S5E	A E	E	73	R	1.0	59	78
1S5E	A F	A	220	R	2.3	198	227
1S5E	A F	F	74	I	1.7	59	78
1S5E	A G	A	225	G	2.3	198	227
1S5E	A G	G	73	R	2.5	59	78
1S5E	A G	G	74	I	1.1	59	78
1S5E	A H	A	17	K	1.6	13	19
1S5E	B J	B	223	F	1.7	199	227
1S5E	B K	B	220	R	1.0	199	227
1S5E	B K	K	70	D	1.3	59	78
1S5E	B K	K	73	R	1.0	59	78
1S5E	B L	B	220	R	1.3	199	227
1S5E	B L	L	70	D	1.5	59	78
1S5E	B L	L	74	I	1.6	59	78
1S5E	B M	B	225	G	2.0	199	227
1S5E	B M	M	73	R	2.8	59	78
1S5E	B M	M	74	I	1.2	59	78
1S5E	B N	B	17	K	1.0	13	19
1S5E	B N	B	226	Y	1.4	199	227
1S5L	a c	c	2317	F	1.1	2306	2324
1S5L	a c	c	2442	L	1.0	2422	2447
1S5L	a c	c	2446	G	37.6	2422	2447

1S5L	A C	A	288	L	20.4	282	293
1S5L	A C	C	317	F	1.4	306	324
1S5L	A C	C	431	F	11.6	422	454
1S5L	A C	C	432	V	19.4	422	454
1S5L	A C	C	435	F	14.2	422	454
1S5L	A C	C	439	V	1.1	422	454
1S5L	A C	C	446	G	41.8	422	454
1S5L	a d	a	2178	G	4.1	2176	2187
1S5L	a d	a	2208	G	76.5	2196	2222
1S5L	a d	a	2216	G	94.5	2196	2222
1S5L	a d	a	2254	Y	3.4	2248	2259
1S5L	a d	a	2257	R	1.1	2248	2259
1S5L	a d	a	2258	L	3.3	2248	2259
1S5L	a d	a	2269	R	1.3	2268	2281
1S5L	a d	a	2327	G	271.4	2317	2331
1S5L	a d	d	2142	N	1.0	2141	2157
1S5L	a d	d	2179	F	2.7	2175	2190
1S5L	a d	d	2183	L	1.0	2175	2190
1S5L	a d	d	2207	G	3.1	2195	2221
1S5L	a d	d	2215	G	55.1	2195	2221
1S5L	a d	d	2315	Y	5.5	2314	2334
1S5L	a d	d	2321	L	1.3	2314	2334
1S5L	a d	d	2324	G	31.0	2314	2334
1S5L	A D	A	126	Y	1.7	110	136
1S5L	A D	A	143	I	1.0	142	166
1S5L	A D	A	178	G	1.7	176	187
1S5L	A D	A	208	G	74.0	196	222
1S5L	A D	A	216	G	117.2	196	222
1S5L	A D	A	254	Y	4.0	248	259
1S5L	A D	A	258	L	2.4	248	259
1S5L	A D	A	269	R	1.2	268	276
1S5L	A D	A	272	H	1.2	268	276
1S5L	A D	A	321	I	1.6	321	331
1S5L	A D	A	327	G	315.0	321	331
1S5L	A D	D	125	F	1.0	110	134
1S5L	A D	D	179	F	1.4	175	190
1S5L	A D	D	207	G	3.9	195	221
1S5L	A D	D	214	H	1.7	195	221
1S5L	A D	D	215	G	51.9	195	221
1S5L	A D	D	252	F	2.7	246	258
1S5L	A D	D	255	Q	34.1	246	258
1S5L	A D	D	257	F	1.1	246	258
1S5L	A D	D	265	R	1.0	265	271
1S5L	A D	D	301	Q	1.2	299	307
1S5L	A D	D	314	F	2.0	314	334
1S5L	A D	D	321	L	2.5	314	334
1S5L	A D	D	324	G	29.7	314	334
1S5L	A D	D	328	W	1.0	314	334
1S5L	a i	a	2022	T	1.1	2013	2023
1S5L	a i	a	2036	I	1.0	2035	2055
1S5L	A I	A	36	I	1.0	35	55
1S5L	a t	t	2006	Y	1.4	2002	2009
1S5L	A T	T	6	Y	2.1	2	9
1S5L	b d	b	2257	W	1.7	2236	2259
1S5L	b d	b	2453	F	1.5	2447	2462
1S5L	b d	b	2457	V	1.0	2447	2462
1S5L	b d	b	2460	L	1.7	2447	2462
1S5L	b d	b	2463	F	1.1	2463	2474
1S5L	b d	b	2464	F	2.2	2463	2474
1S5L	b d	b	2467	I	1.0	2463	2474

1S5L	b d	b	2468	W	1.6	2463	2474
1S5L	b d	d	2188	F	1.3	2175	2190
1S5L	b d	d	2280	W	4.0	2272	2291
1S5L	b d	d	2284	I	1.0	2272	2291
1S5L	b d	d	2287	V	1.3	2272	2291
1S5L	B D	B	257	W	1.1	236	259
1S5L	B D	B	453	F	1.5	447	462
1S5L	B D	B	457	V	1.1	447	462
1S5L	B D	B	460	L	1.7	447	462
1S5L	B D	B	464	F	1.9	463	474
1S5L	B D	B	468	W	1.8	463	474
1S5L	B D	B	471	A	1.5	463	474
1S5L	B D	D	140	P	1.2	140	157
1S5L	B D	D	144	I	1.0	140	157
1S5L	B D	D	147	S	1.1	140	157
1S5L	B D	D	284	I	1.0	272	291
1S5L	B D	D	287	V	1.1	272	291
1S5L	B L	L	34	Y	1.1	14	37
1S5L	b o	b	2418	K	1.0	2414	2426
1S5L	B O	B	418	K	1.2	414	423
1S5L	B U	U	45	E	1.0	43	48
1S5L	c k	c	2062	F	1.0	2055	2072
1S5L	c k	c	2070	F	1.4	2055	2072
1S5L	c k	k	2016	L	1.5	2016	2034
1S5L	c k	k	2017	P	1.2	2016	2034
1S5L	C K	C	62	F	1.7	55	72
1S5L	C K	C	70	F	1.6	55	72
1S5L	c o	c	2381	K	1.1	2377	2383
1S5L	C O	C	381	K	1.1	377	383
1S5L	C O	O	7	Y	1.1	7	11
1S5L	c v	v	2102	P	14.9	2102	2107
1S5L	C V	V	102	P	17.0	102	107
1S5L	d e	e	2043	Y	1.3	2041	2047
1S5L	d e	e	2046	F	2.6	2041	2047
1S5L	d e	e	2072	K	1.3	2071	2083
1S5L	d e	e	2075	V	1.4	2071	2083
1S5L	D E	E	46	F	2.6	41	47
1S5L	D E	E	78	F	1.0	71	83
1S5L	d f	f	2036	I	1.0	2016	2042
1S5L	D F	F	39	M	2.2	16	42
1S5L	d l	d	2195	P	1.0	2195	2221
1S5L	d l	l	2030	L	1.1	2014	2037
1S5L	d l	l	2031	F	1.0	2014	2037
1S5L	d l	l	2034	Y	1.7	2014	2037
1S5L	D L	D	195	P	1.0	195	221
1S5L	D L	L	19	L	1.2	14	37
1S5L	D L	L	30	L	1.2	14	37
1S5L	D L	L	31	F	1.1	14	37
1S5L	D L	L	34	Y	2.4	14	37
1S5L	D M	D	304	R	1.4	299	307
1S5L	d o	o	2182	L	1.0	2179	2186
1S5L	D O	O	182	L	1.0	179	186
1S5L	d v	d	2328	W	1.0	2314	2334
1S5L	d x	d	2018	L	1.4	2015	2023
1S5L	d x	d	2021	W	3.0	2015	2023
1S5L	d x	x	2037	L	1.1	2015	2044
1S5L	D X	D	18	L	1.7	15	23
1S5L	e f	e	2030	F	1.1	2028	2040
1S5L	e f	e	2033	G	51.5	2028	2040
1S5L	e f	e	2034	W	2.2	2028	2040

1S5L	e f	f	2030	I	1.5	2016	2042
1S5L	e f	f	2031	F	2.4	2016	2042
1S5L	e f	f	2034	G	83.2	2016	2042
1S5L	E F	E	30	F	1.1	28	40
1S5L	E F	E	33	G	36.8	28	40
1S5L	E F	E	34	W	2.6	28	40
1S5L	E F	F	30	I	1.4	16	42
1S5L	E F	F	31	F	2.4	16	42
1S5L	E F	F	34	G	56.3	16	42
1S5L	f j	j	2031	G	121.0	2012	2032
1S5L	F J	J	28	F	1.2	12	32
1S5L	F J	J	31	G	79.4	12	32
1S5L	h x	x	2016	L	1.5	2015	2044
1S5L	H X	X	16	L	1.5	15	44
1S5L	k z	z	2005	F	2.2	2002	2027
1S5L	k z	z	2009	L	1.1	2002	2027
1S5L	K Z	Z	54	V	2.6	33	58
1S5L	l m	l	2017	L	1.4	2014	2037
1S5L	l m	l	2020	G	3.3	2014	2037
1S5L	l m	l	2024	I	1.0	2014	2037
1S5L	l m	l	2035	F	3.0	2014	2037
1S5L	l m	m	2007	G	314.7	2005	2030
1S5L	l m	m	2015	V	1.0	2005	2030
1S5L	L M	L	17	L	1.3	14	37
1S5L	L M	L	20	G	19.4	14	37
1S5L	L M	L	24	I	1.1	14	37
1S5L	L M	L	35	F	3.3	14	37
1S5L	L M	M	7	G	175.3	5	30
1S5L	L M	M	11	T	1.1	5	30
1S5L	L M	M	14	F	2.3	5	30
1S5L	l t	l	2018	Y	2.5	2014	2037
1S5L	l t	l	2025	L	1.8	2014	2037
1S5L	l t	l	2029	L	1.5	2014	2037
1S5L	l t	t	2013	I	1.8	2010	2022
1S5L	l t	t	2016	L	1.8	2010	2022
1S5L	L T	L	18	Y	2.3	14	37
1S5L	L T	L	25	L	1.3	14	37
1S5L	L T	L	29	L	1.7	14	37
1S5L	L T	T	6	Y	1.4	2	9
1S5L	L T	T	13	I	2.0	10	23
1S5L	L T	T	16	L	2.0	10	23
1S5L	O U	U	121	L	1.6	119	123
1S5R	A B	A	368	Y	1.1	366	377
1S5R	A B	A	369	V	1.2	366	377
1S5R	A B	A	370	L	1.9	366	377
1S5R	A B	A	373	M	1.1	366	377
1S5R	A B	B	307	A	1.2	302	318
1S5R	A B	B	308	I	1.3	302	318
1S5R	A B	B	310	Y	2.0	302	318
1S5R	A B	B	332	L	1.0	322	346
1S5R	A B	B	379	F	1.0	370	380
1S6C	A B	A	59	G	5.2	50	63
1S6C	A B	A	77	I	2.0	71	82
1S6C	A B	A	78	Y	1.7	71	82
1S6C	A B	A	81	F	2.5	71	82
1S6C	A B	A	111	F	1.7	108	120
1S6C	A B	B	227	F	2.9	225	235
1S70	A B	B	10	R	1.8	6	12
1S70	A B	B	14	L	2.0	13	20
1S70	A B	B	205	V	1.1	202	209

1S78	C D	C	123	E	1.3	122	126
1S9K	D E	D	165	L	1.4	141	191
1S9K	D E	D	173	E	1.0	141	191
1S9K	D E	D	176	K	1.4	141	191
1S9K	D E	D	183	I	1.8	141	191
1S9K	D E	D	186	L	1.5	141	191
1S9K	D E	E	290	L	1.2	269	316
1S9K	D E	E	293	K	2.4	269	316
1S9K	D E	E	297	L	1.6	269	316
1S9K	D E	E	311	L	2.1	269	316
1S9K	D E	E	315	V	1.2	269	316
1S9V	A B	A	66	L	1.3	56	77
1S9V	A B	A	70	L	1.9	56	77
1S9V	A B	A	73	L	1.1	56	77
1S9V	A B	A	74	I	1.5	56	77
1S9V	A B	B	82	N	2.3	65	88
1S9V	A B	B	85	L	1.0	65	88
1S9V	A B	B	86	E	1.0	65	88
1S9V	A E	E	69	E	1.1	65	88
1S9V	A E	E	72	R	1.5	65	88
1S9V	A E	E	76	D	1.2	65	88
1S9V	D E	D	70	L	2.1	56	76
1S9V	D E	D	74	I	1.7	56	76
1S9V	D E	E	85	L	1.0	65	88
1S9V	D E	E	86	E	2.1	65	88
1SA0	A B	A	406	H	2.1	405	412
1SA0	A B	A	407	W	4.8	405	412
1SA0	A B	B	257	V	1.6	253	260
1SA0	A E	A	112	K	1.8	103	128
1SA0	B E	B	108	Y	1.7	108	115
1SA0	C B	B	407	W	3.1	405	411
1SA0	C D	C	406	H	2.1	405	412
1SA0	C D	C	407	W	4.5	405	412
1SA0	C D	C	411	E	1.2	405	412
1SA0	C D	D	253	R	1.1	253	260
1SA0	C D	D	257	V	1.8	253	260
1SA0	D E	E	123	L	1.2	106	124
1SB0	A B	A	18	L	1.0	12	27
1SB0	A B	A	21	K	1.6	12	27
1SB0	A B	A	65	Y	1.4	61	80
1SB0	A B	B	95	L	2.0	89	109
1SB0	A B	B	99	L	3.4	89	109
1SB0	A B	B	105	E	1.1	89	109
1SB2	A B	A	27	E	1.0	23	32
1SB3	A B	A	760	E	1.0	755	768
1SB3	A B	B	130	W	4.4	129	135
1SB3	A B	B	131	W	2.2	129	135
1SB3	A B	B	134	G	1.9	129	135
1SB3	A B	B	304	Y	1.5	302	322
1SB3	A B	B	307	R	1.4	302	322
1SB3	A C	A	20	G	245.5	20	25
1SB3	A C	A	23	K	1.3	20	25
1SB3	A C	A	24	V	2.1	20	25
1SB3	A C	A	275	R	2.9	275	282
1SB3	A C	A	657	L	2.9	656	677
1SB3	A C	A	660	E	2.5	656	677
1SB3	A C	A	661	G	9.7	656	677
1SB3	A C	A	665	G	86.6	656	677
1SB3	A C	A	668	W	1.3	656	677
1SB3	A C	A	672	G	2.6	656	677

1SB3	A C	C	29	R	2.1	24	33
1SB3	A C	C	89	Q	1.2	87	95
1SB3	A C	C	127	K	1.1	123	130
1SB3	A C	C	142	K	1.8	141	155
1SB3	B C	B	37	L	1.6	34	42
1SB3	B C	B	105	T	1.0	104	110
1SB3	B C	B	106	H	1.2	104	110
1SB3	B C	C	26	D	1.0	24	33
1SB3	D E	D	755	P	1.3	755	768
1SB3	D E	D	760	E	1.0	755	768
1SB3	D E	E	130	W	4.7	129	135
1SB3	D E	E	131	W	2.4	129	135
1SB3	D E	E	134	G	1.1	129	135
1SB3	D E	E	304	Y	1.7	302	322
1SB3	D E	E	307	R	1.5	302	322
1SB3	D F	D	20	G	242.7	20	25
1SB3	D F	D	23	K	1.4	20	25
1SB3	D F	D	24	V	2.1	20	25
1SB3	D F	D	275	R	3.0	275	282
1SB3	D F	D	660	E	2.2	656	677
1SB3	D F	D	661	G	6.7	656	677
1SB3	D F	D	665	G	109.7	656	677
1SB3	D F	D	668	W	2.0	656	677
1SB3	D F	D	672	G	2.6	656	677
1SB3	D F	F	29	R	2.1	24	33
1SB3	D F	F	89	Q	1.3	87	95
1SB3	D F	F	127	K	1.1	123	130
1SB3	D F	F	142	K	1.3	141	156
1SB3	E F	E	37	L	1.7	34	42
1SB3	E F	E	79	E	1.8	78	84
1SB3	E F	E	83	E	1.7	78	84
1SB3	E F	E	105	T	1.0	104	110
1SB3	E F	F	117	K	1.8	104	118
1SBN	E I	E	64	H	1.3	64	73
1SBN	E I	E	104	Y	1.3	104	116
1SBS	H L	L	129	E	1.2	128	133
1SCJ	A B	A	104	Y	1.9	104	117
1SCJ	A B	A	108	I	1.0	104	117
1SCJ	A B	A	112	E	2.4	104	117
1SCJ	A B	A	141	K	1.3	133	145
1SCJ	A B	A	221	C	6.1	220	238
1SCT	A B	A	68	G	2.7	64	83
1SCT	A B	A	75	Y	5.3	64	83
1SCT	A B	A	89	R	2.3	87	104
1SCT	A B	B	32	E	1.8	31	46
1SCT	A B	B	69	R	1.0	66	85
1SCT	A B	B	70	G	1.3	66	85
1SCT	A B	B	77	Y	3.6	66	85
1SCT	A D	D	21	R	1.6	14	28
1SCT	A D	D	25	G	7.6	14	28
1SCT	A D	D	26	V	1.2	14	28
1SCT	C B	B	25	G	3.7	14	28
1SCT	C B	B	26	V	1.5	14	28
1SCT	C D	C	30	E	1.0	29	44
1SCT	C D	C	67	R	1.0	64	82
1SCT	C D	C	75	Y	3.1	64	82
1SCT	C D	C	89	R	2.5	87	104
1SCT	C D	D	32	E	2.2	31	46
1SCT	C D	D	69	R	3.4	66	84
1SCT	C D	D	77	Y	3.5	66	84

1SCT	C D	D	91	R	1.0	89	106
1SCT	E F	E	68	G	5.5	64	82
1SCT	E F	E	75	Y	2.7	64	82
1SCT	E F	E	88	S	1.7	87	104
1SCT	E F	E	89	R	1.4	87	104
1SCT	E F	F	32	E	1.3	31	46
1SCT	E F	F	69	R	1.7	66	85
1SCT	E F	F	70	G	2.7	66	85
1SCT	E F	F	77	Y	3.0	66	85
1SCT	E H	E	30	E	1.2	29	44
1SCT	E H	H	21	R	1.8	14	28
1SCT	E H	H	25	G	13.9	14	28
1SCT	G F	F	26	V	1.1	14	28
1SCT	G H	G	68	G	1.5	64	82
1SCT	G H	G	75	Y	3.0	64	82
1SCT	G H	G	89	R	1.6	87	103
1SCT	G H	G	93	V	1.0	87	103
1SCT	G H	H	32	E	1.6	31	46
1SCT	G H	H	69	R	2.4	66	85
1SCT	G H	H	77	Y	4.4	66	85
1SDD	A B	B	1850	I	1.4	1849	1853
1SDD	A B	B	1851	Q	3.1	1849	1853
1SEB	A B	A	48	F	2.6	46	52
1SEB	A B	A	51	F	1.1	46	52
1SEB	A B	A	70	L	1.6	56	77
1SEB	A D	A	60	L	1.0	56	77
1SEB	A D	A	67	K	1.0	56	77
1SEB	E F	E	48	F	2.2	46	52
1SEB	E F	E	51	F	1.1	46	52
1SEB	E F	E	70	L	1.4	56	77
1SEB	E H	E	60	L	1.6	56	77
1SEB	E H	E	67	K	1.1	56	77
1SEQ	L H	L	122	E	1.0	121	126
1SEQ	L H	L	123	Q	1.6	121	126
1SFC	A B	A	36	Q	1.4	30	92
1SFC	A B	A	39	V	1.6	30	92
1SFC	A B	A	46	M	1.2	30	92
1SFC	A B	A	53	V	1.8	30	92
1SFC	A B	A	61	S	1.2	30	92
1SFC	A B	A	67	A	1.2	30	92
1SFC	A B	A	68	D	1.4	30	92
1SFC	A B	A	78	E	1.2	30	92
1SFC	A B	A	85	K	2.1	30	92
1SFC	A B	B	204	K	1.7	190	257
1SFC	A B	B	205	L	1.3	190	257
1SFC	A B	B	212	L	1.8	190	257
1SFC	A B	B	215	M	1.2	190	257
1SFC	A B	B	216	F	1.8	190	257
1SFC	A B	B	230	I	1.9	190	257
1SFC	A B	B	232	R	1.2	190	257
1SFC	A B	B	236	N	1.7	190	257
1SFC	A B	B	243	Y	2.3	190	257
1SFC	A D	A	45	I	1.7	30	92
1SFC	A D	A	52	K	1.3	30	92
1SFC	A D	A	63	L	1.7	30	92
1SFC	A D	A	66	R	1.0	30	92
1SFC	A D	A	70	L	1.3	30	92
1SFC	A D	A	77	F	1.2	30	92
1SFC	A D	D	161	R	1.5	144	202
1SFC	A D	D	172	D	1.4	144	202

1SFC	A D	D	178	I	2.1	144	202
1SFC	A D	D	182	M	1.1	144	202
1SFC	A D	D	189	K	1.4	144	202
1SFC	A D	D	192	I	1.2	144	202
1SFC	B C	B	192	L	1.8	190	257
1SFC	B C	B	199	H	2.8	190	257
1SFC	B C	B	206	E	2.0	190	257
1SFC	B C	B	210	R	1.3	190	257
1SFC	B C	B	216	F	1.2	190	257
1SFC	B C	B	227	G	1.6	190	257
1SFC	B C	B	237	V	1.0	190	257
1SFC	B C	B	244	V	1.4	190	257
1SFC	B C	B	248	V	1.0	190	257
1SFC	B C	B	255	V	1.0	190	257
1SFC	B C	C	11	L	1.0	10	82
1SFC	B C	C	21	L	2.2	10	82
1SFC	B C	C	31	R	1.4	10	82
1SFC	B C	C	49	M	1.0	10	82
1SFC	B C	C	59	R	1.6	10	82
1SFC	B C	C	60	V	1.3	10	82
1SFC	B C	C	63	G	14.6	10	82
1SFC	B C	C	67	I	1.6	10	82
1SFC	C D	C	29	T	1.7	10	82
1SFC	C D	C	36	V	1.0	10	82
1SFC	C D	C	46	T	1.3	10	82
1SFC	C D	C	50	L	1.3	10	82
1SFC	C D	C	57	L	1.2	10	82
1SFC	C D	C	61	E	1.6	10	82
1SFC	C D	C	78	L	1.5	10	82
1SFC	C D	D	153	V	1.2	144	202
1SFC	C D	D	160	L	1.2	144	202
1SFC	C D	D	167	M	1.4	144	202
1SFC	C D	D	181	I	2.0	144	202
1SFC	C D	D	184	K	1.1	144	202
1SFC	C D	D	191	R	1.0	144	202
1SFC	E C	E	86	R	1.4	32	95
1SFC	E C	E	93	L	1.7	32	95
1SFC	E F	E	32	L	1.4	32	95
1SFC	E F	E	33	Q	1.3	32	95
1SFC	E F	E	36	Q	1.3	32	95
1SFC	E F	E	60	L	1.5	32	95
1SFC	E F	E	78	E	1.1	32	95
1SFC	E F	E	85	K	2.2	32	95
1SFC	E F	E	88	Y	1.1	32	95
1SFC	E F	E	89	W	1.6	32	95
1SFC	E F	F	205	L	2.7	190	231
1SFC	E F	F	215	M	1.5	190	231
1SFC	E F	F	222	L	1.0	190	231
1SFC	E F	F	233	I	2.1	232	261
1SFC	E F	F	243	Y	1.0	232	261
1SFC	E H	E	45	I	1.4	32	95
1SFC	E H	E	52	K	2.0	32	95
1SFC	E H	E	53	V	1.0	32	95
1SFC	E H	E	63	L	1.6	32	95
1SFC	E H	E	77	F	2.2	32	95
1SFC	E H	E	84	L	1.0	32	95
1SFC	E H	H	178	I	1.9	157	203
1SFC	E H	H	182	M	1.1	157	203
1SFC	E H	H	189	K	1.4	157	203
1SFC	F H	F	194	E	3.9	190	231

1SFC	F H	H	146	M	2.5	144	156
1SFC	F H	H	150	L	1.6	144	156
1SFC	G H	G	29	T	1.3	19	37
1SFC	G H	G	47	L	1.6	38	82
1SFC	G H	G	57	L	1.4	38	82
1SFC	G H	G	61	E	1.5	38	82
1SFC	G H	G	64	M	1.1	38	82
1SFC	G H	G	78	L	1.3	38	82
1SFC	G H	H	181	I	2.8	157	203
1SFC	G H	H	184	K	1.3	157	203
1SFC	G H	H	202	M	1.1	157	203
1SFC	I J	I	36	Q	1.1	30	92
1SFC	I J	I	43	V	1.3	30	92
1SFC	I J	I	46	M	2.6	30	92
1SFC	I J	I	47	R	1.9	30	92
1SFC	I J	I	78	E	1.2	30	92
1SFC	I J	I	85	K	1.1	30	92
1SFC	I J	I	89	W	1.1	30	92
1SFC	I J	J	212	L	1.6	194	258
1SFC	I J	J	215	M	3.0	194	258
1SFC	I J	J	216	F	1.7	194	258
1SFC	I J	J	233	I	1.6	194	258
1SFC	I J	J	243	Y	1.1	194	258
1SFC	I J	J	257	Y	2.1	194	258
1SFC	I L	I	31	R	1.0	30	92
1SFC	I L	I	42	V	1.0	30	92
1SFC	I L	I	45	I	1.2	30	92
1SFC	I L	I	52	K	1.2	30	92
1SFC	I L	I	63	L	1.9	30	92
1SFC	I L	I	66	R	1.0	30	92
1SFC	I L	I	70	L	1.7	30	92
1SFC	I L	I	77	F	1.3	30	92
1SFC	I L	I	84	L	1.3	30	92
1SFC	I L	L	157	I	2.0	144	204
1SFC	I L	L	161	R	1.1	144	204
1SFC	I L	L	168	G	2.7	144	204
1SFC	I L	L	171	I	1.3	144	204
1SFC	I L	L	178	I	2.0	144	204
1SFC	I L	L	179	D	1.1	144	204
1SFC	I L	L	182	M	1.3	144	204
1SFC	I L	L	189	K	1.9	144	204
1SFC	I L	L	192	I	1.4	144	204
1SFC	I L	L	203	L	1.1	144	204
1SFC	J K	J	195	I	1.2	194	258
1SFC	J K	J	202	I	1.8	194	258
1SFC	J K	J	206	E	3.4	194	258
1SFC	J K	J	213	H	1.3	194	258
1SFC	J K	J	227	G	2.8	194	258
1SFC	J K	J	230	I	2.4	194	258
1SFC	J K	J	231	D	1.9	194	258
1SFC	J K	J	234	E	1.4	194	258
1SFC	J K	J	244	V	1.1	194	258
1SFC	J K	J	255	V	1.1	194	258
1SFC	J K	K	31	R	1.9	22	34
1SFC	J K	K	32	M	1.6	22	34
1SFC	J K	K	35	L	1.5	35	82
1SFC	J K	K	43	G	1.3	35	82
1SFC	J K	K	59	R	1.1	35	82
1SFC	J K	K	63	G	16.7	35	82
1SFC	J K	K	67	I	1.5	35	82

1SFC	J K	K	81	L	2.0	35	82
1SFC	J L	J	198	R	2.7	194	258
1SFC	J L	J	202	I	2.3	194	258
1SFC	J L	J	216	F	1.7	194	258
1SFC	J L	L	150	L	1.7	144	204
1SFC	K L	K	26	L	1.1	22	34
1SFC	K L	K	30	R	1.4	22	34
1SFC	K L	K	33	L	1.1	22	34
1SFC	K L	K	40	K	1.5	35	82
1SFC	K L	K	47	L	2.1	35	82
1SFC	K L	K	50	L	1.1	35	82
1SFC	K L	K	57	L	1.0	35	82
1SFC	K L	K	61	E	2.0	35	82
1SFC	K L	K	71	M	1.1	35	82
1SFC	K L	K	75	E	1.0	35	82
1SFC	K L	K	78	L	1.1	35	82
1SFC	K L	L	145	E	1.2	144	204
1SFC	K L	L	156	I	3.1	144	204
1SFC	K L	L	160	L	1.2	144	204
1SFC	K L	L	163	M	1.3	144	204
1SFC	K L	L	177	Q	1.2	144	204
1SFC	K L	L	181	I	2.3	144	204
1SFC	K L	L	184	K	1.7	144	204
1SFC	K L	L	191	R	1.0	144	204
1SFC	K L	L	192	I	1.4	144	204
1SHZ	A C	A	98	V	1.0	85	106
1SHZ	A C	A	230	R	1.0	227	232
1SHZ	A C	C	68	L	1.2	56	70
1SHZ	A F	A	104	E	1.4	85	106
1SHZ	A F	F	155	E	1.3	145	163
1SHZ	A F	F	158	R	2.6	145	163
1SHZ	A F	F	159	S	1.4	145	163
1SHZ	D C	D	104	E	1.9	78	106
1SHZ	D C	D	116	Q	1.0	113	124
1SHZ	D C	D	117	L	1.2	113	124
1SHZ	D C	C	158	R	1.3	147	164
1SKR	A B	B	33	G	212.9	33	38
1SKR	A B	B	34	P	1.9	33	38
1SKR	A B	B	37	M	1.0	33	38
1SKY	B E	B	207	T	1.0	202	215
1SKY	B E	B	272	Q	1.1	263	277
1SKY	B E	E	286	G	38.7	281	290
1SM3	L H	L	124	E	1.9	122	127
1SMP	A I	A	169	Y	3.1	168	183
1SMP	A I	A	176	H	1.3	168	183
1SMP	A I	A	177	E	1.2	168	183
1SP4	A B	A	8	R	1.9	7	11
1SP4	A B	A	18	K	1.7	15	19
1SP4	A B	A	30	W	3.8	29	45
1SP4	A B	A	32	F	1.6	29	45
1SP4	A B	A	33	G	60.8	29	45
1SP4	A B	A	35	V	2.0	29	45
1SP4	A B	A	38	I	2.7	29	45
1SP4	A B	A	40	D	2.1	29	45
1SP4	A B	A	41	R	5.5	29	45
1SP4	A B	A	42	I	1.6	29	45
1SP4	A B	B	59	M	1.3	56	64
1SP4	A B	B	80	W	3.3	76	87
1SP4	A B	B	83	W	1.7	76	87
1SP4	A B	B	165	Y	2.2	157	167

1SPB	P S	S	104	Y	4.4	104	117
1SPB	P S	S	105	S	1.2	104	117
1SPB	P S	S	112	E	2.7	104	117
1SQ0	A B	A	596	E	1.1	594	606
1SQ0	A B	A	599	K	1.4	594	606
1SQ0	A B	A	603	F	1.8	594	606
1SQ0	A B	A	604	Q	1.0	594	606
1SQB	A B	A	4	Y	1.8	4	11
1SQB	A B	A	73	N	1.0	73	82
1SQB	A B	A	76	E	1.9	73	82
1SQB	A B	A	80	E	1.7	73	82
1SQB	A B	A	137	E	1.3	124	144
1SQB	A B	A	359	N	1.0	351	369
1SQB	A B	A	366	V	1.4	351	369
1SQB	A B	A	367	S	1.6	351	369
1SQB	A B	B	83	F	1.7	82	92
1SQB	A B	B	90	E	2.7	82	92
1SQB	A B	B	375	S	1.2	375	390
1SQB	A C	A	336	F	1.7	331	348
1SQB	A C	A	436	R	1.5	434	440
1SQB	A E	A	151	N	1.0	145	158
1SQB	A J	J	15	R	3.4	5	16
1SQB	A K	K	12	Q	1.0	8	17
1SQB	B I	B	160	I	1.1	155	168
1SQB	B I	B	368	Y	1.5	354	372
1SQB	C D	C	67	T	1.4	62	73
1SQB	C D	C	72	D	3.3	62	73
1SQB	C D	C	226	I	1.1	225	244
1SQB	C D	C	230	L	2.1	225	244
1SQB	C D	C	233	L	2.3	225	244
1SQB	C D	C	237	L	1.2	225	244
1SQB	C D	D	49	R	2.9	48	52
1SQB	C D	D	196	P	1.2	196	232
1SQB	C D	D	197	E	3.3	196	232
1SQB	C D	D	201	R	2.3	196	232
1SQB	C D	D	205	G	8.6	196	232
1SQB	C D	D	208	M	1.6	196	232
1SQB	C D	D	212	M	1.1	196	232
1SQB	C D	D	216	L	1.6	196	232
1SQB	C D	D	223	K	1.1	196	232
1SQB	C D	D	227	W	3.2	196	232
1SQB	C D	D	230	L	2.1	196	232
1SQB	C E	C	50	F	1.2	32	55
1SQB	C E	C	54	H	1.2	32	55
1SQB	C E	C	79	I	2.3	76	104
1SQB	C E	E	58	F	3.1	29	61
1SQB	C F	C	319	P	1.3	319	340
1SQB	C F	F	20	Y	3.4	8	25
1SQB	C F	F	66	L	1.1	52	71
1SQB	C F	F	69	S	1.4	52	71
1SQB	C F	F	70	M	1.0	52	71
1SQB	C G	C	322	Q	1.7	319	340
1SQB	C G	C	326	W	3.4	319	340
1SQB	C G	C	330	A	1.5	319	340
1SQB	C G	C	333	L	1.3	319	340
1SQB	C G	C	337	W	3.1	319	340
1SQB	C G	G	51	P	2.1	29	68
1SQB	C G	G	52	F	3.1	29	68
1SQB	C G	G	55	F	2.5	29	68
1SQB	C G	G	59	Y	1.0	29	68

1SQB	C G	G	62	G	35.1	29	68
1SQB	C G	G	66	F	1.2	29	68
1SQB	D E	D	211	M	1.1	196	232
1SQB	D E	D	215	L	1.7	196	232
1SQB	D E	D	218	L	1.0	196	232
1SQB	D E	E	39	V	1.0	29	61
1SQB	D F	F	60	F	2.4	52	71
1SQB	D F	F	63	K	1.7	52	71
1SQB	D H	H	59	L	1.5	55	74
1SQB	D J	D	23	H	2.3	23	39
1SQB	D J	D	203	R	1.4	196	232
1SQB	D J	D	206	L	1.5	196	232
1SQB	D J	D	207	K	2.2	196	232
1SQB	D J	J	35	F	2.4	17	47
1SQB	D J	J	43	Y	1.3	17	47
1SQB	D J	J	52	W	3.7	52	56
1SQB	E G	E	32	R	2.3	29	61
1SQB	E J	E	33	K	1.0	29	61
1SQB	E J	E	34	G	50.3	29	61
1SQB	E J	E	45	V	2.1	29	61
1SQB	E J	E	49	Y	1.7	29	61
1SQB	E J	E	52	K	1.0	29	61
1SQB	E J	J	10	Y	2.7	5	16
1SQB	E J	J	14	F	1.7	5	16
1SQB	E J	J	31	F	1.6	17	47
1SQB	E J	J	32	E	1.1	17	47
1SQB	E K	E	52	K	1.2	29	61
1SQB	E K	K	34	W	1.3	18	37
1SQB	F G	F	55	Y	1.0	52	71
1SQB	J K	J	22	L	1.1	17	47
1SQB	J K	J	29	L	2.3	17	47
1SQB	J K	J	33	R	1.0	17	47
1SQB	J K	K	24	W	1.8	18	37
1SQB	J K	K	27	V	1.5	18	37
1SQB	J K	K	34	W	1.8	18	37
1SQB	J K	K	48	I	2.2	46	50
1SQK	A B	A	345	I	2.0	338	347
1SQK	A B	A	346	L	1.9	338	347
1SQK	A B	B	19	K	1.0	12	24
1SQK	A B	B	22	L	2.5	12	24
1SQX	A B	A	4	Y	2.3	4	11
1SQX	A B	A	76	E	2.1	74	82
1SQX	A B	A	80	E	1.4	74	82
1SQX	A B	A	137	E	1.6	124	144
1SQX	A B	A	356	R	1.1	351	369
1SQX	A B	A	366	V	1.2	351	369
1SQX	A B	B	90	E	1.2	82	92
1SQX	A C	A	332	D	1.2	331	348
1SQX	A C	A	436	R	1.4	434	440
1SQX	A E	A	142	D	1.1	124	144
1SQX	A E	A	152	Y	1.0	145	158
1SQX	A G	A	434	Y	1.0	434	440
1SQX	A I	A	140	E	1.4	124	144
1SQX	A I	A	395	W	1.1	392	402
1SQX	A K	K	24	W	1.1	18	36
1SQX	C D	C	71	R	2.3	59	73
1SQX	C D	C	77	W	2.3	76	104
1SQX	C D	C	81	Y	8.4	76	104
1SQX	C D	C	223	Y	4.0	223	246
1SQX	C D	C	226	I	1.3	223	246

1SQX	C D	C	233	L	2.2	223	246
1SQX	C D	C	237	L	1.0	223	246
1SQX	C D	C	244	L	1.9	223	246
1SQX	C D	C	245	F	2.3	223	246
1SQX	C D	D	115	Y	1.5	114	119
1SQX	C D	D	205	G	25.7	196	232
1SQX	C D	D	208	M	1.7	196	232
1SQX	C D	D	216	L	1.7	196	232
1SQX	C D	D	219	V	1.3	196	232
1SQX	C D	D	227	W	3.0	196	232
1SQX	C D	D	230	L	1.8	196	232
1SQX	C E	C	50	F	2.6	32	55
1SQX	C E	C	79	I	1.5	76	104
1SQX	C E	E	54	V	2.6	29	63
1SQX	C E	E	58	F	5.2	29	63
1SQX	C F	C	319	P	1.3	319	341
1SQX	C F	C	376	L	1.2	345	377
1SQX	C F	F	20	Y	3.4	8	25
1SQX	C F	F	33	R	3.0	33	37
1SQX	C G	C	322	Q	2.0	319	341
1SQX	C G	C	326	W	1.9	319	341
1SQX	C G	C	333	L	1.8	319	341
1SQX	C G	C	337	W	3.4	319	341
1SQX	C G	C	346	P	1.1	345	377
1SQX	C G	C	347	Y	1.9	345	377
1SQX	C G	G	52	F	2.8	29	70
1SQX	C G	G	55	F	3.1	29	70
1SQX	C G	G	62	G	30.7	29	70
1SQX	C G	G	66	F	2.1	29	70
1SQX	D F	F	60	F	1.7	52	71
1SQX	D F	F	70	M	1.0	52	71
1SQX	D G	D	220	Y	1.6	196	232
1SQX	D G	D	221	A	3.4	196	232
1SQX	D G	D	224	R	2.5	196	232
1SQX	D G	D	225	H	1.1	196	232
1SQX	D G	G	29	Y	4.2	29	70
1SQX	D H	D	128	F	1.0	124	133
1SQX	D H	H	44	V	1.2	28	47
1SQX	D H	H	59	L	1.8	55	77
1SQX	D H	H	74	F	3.4	55	77
1SQX	D J	D	203	R	1.1	196	232
1SQX	D J	D	206	L	1.4	196	232
1SQX	D J	D	207	K	1.8	196	232
1SQX	D J	D	211	M	1.0	196	232
1SQX	D J	J	35	F	2.7	17	47
1SQX	D J	J	40	D	1.1	17	47
1SQX	D J	J	43	Y	2.7	17	47
1SQX	E D	E	39	V	1.4	29	63
1SQX	E D	D	215	L	1.1	196	232
1SQX	E G	E	32	R	2.4	29	63
1SQX	E J	E	33	K	1.1	29	63
1SQX	E J	E	34	G	46.0	29	63
1SQX	E J	E	45	V	1.9	29	63
1SQX	E J	E	49	Y	2.4	29	63
1SQX	E J	J	10	Y	2.1	5	16
1SQX	E J	J	14	F	2.0	5	16
1SQX	E J	J	20	F	2.4	17	47
1SQX	E J	J	24	I	2.8	17	47
1SQX	E J	J	31	F	1.5	17	47
1SQX	E K	E	52	K	1.2	29	63

1SQX	E K	K	34	W	2.1	18	36
1SQX	G F	F	55	Y	1.2	52	71
1SQX	K J	K	24	W	2.2	18	36
1SQX	K J	K	27	V	1.4	18	36
1SQX	K J	K	34	W	2.0	18	36
1SQX	K J	J	22	L	1.1	17	47
1SQX	K J	J	29	L	2.3	17	47
1SQX	K J	J	30	F	1.4	17	47
1SR4	B C	B	42	E	1.1	41	54
1SR4	B C	B	47	I	1.7	41	54
1SR5	B C	B	14	E	1.6	14	14
1SSE	A B	A	302	F	1.0	301	310
1SUV	A C	A	670	V	5.0	668	684
1SUV	A E	A	622	V	4.0	612	627
1SUV	A E	A	646	R	1.8	640	663
1SUV	A E	E	356	D	2.7	349	363
1SUV	C E	C	314	Y	1.1	311	316
1SUV	D F	D	314	Y	1.1	311	316
1SUY	A C	A	57	L	24.9	53	74
1SUY	A D	A	79	D	3.2	79	102
1SUY	A D	A	80	I	1.1	79	102
1SUY	A D	A	90	D	1.9	79	102
1SUY	B C	B	279	D	3.3	279	302
1SUY	B C	B	280	I	1.1	279	302
1SUY	B C	B	290	D	1.7	279	302
1SUY	B D	B	257	L	24.6	253	274
1SUY	B D	B	265	D	1.1	253	274
1SV0	A C	A	105	V	1.3	103	119
1SV0	B D	B	105	V	1.2	103	119
1SV0	B D	D	109	R	1.4	109	123
1SV0	B D	D	140	K	1.0	139	145
1SV0	B D	D	153	R	1.3	147	154
1SVD	A M	A	187	R	1.1	175	189
1SVD	A M	A	414	R	1.2	406	426
1SVD	A M	A	422	E	2.5	406	426
1SVD	A M	M	26	R	2.6	24	37
1SVD	A M	M	30	Q	1.1	24	37
1SVD	A M	M	33	Y	1.1	24	37
1SVF	A B	A	146	K	1.3	123	183
1SVF	A B	A	171	H	1.9	123	183
1SVF	A B	B	473	Y	2.2	450	476
1SVF	C D	C	146	K	1.1	123	181
1SVF	C D	C	171	H	2.2	123	181
1SVF	C D	D	473	Y	2.4	450	475
1SVX	A B	A	56	Y	2.3	50	58
1SVX	A B	A	89	Y	2.6	83	90
1SVX	A B	B	137	K	1.1	129	142
1SVX	A B	B	140	K	1.0	129	142
1SVX	A B	B	200	K	2.5	186	201
1SXJ	B C	B	204	Q	1.0	202	216
1SXJ	B C	B	253	R	1.3	245	259
1SXJ	B C	B	298	R	1.2	282	301
1SXJ	B C	B	307	L	1.8	306	320
1SXJ	B C	C	94	R	1.5	90	95
1SXJ	B C	C	132	R	1.1	124	137
1SXJ	B C	C	293	E	1.0	293	311
1SXJ	B C	C	297	V	1.1	293	311
1SXJ	B C	C	300	L	1.7	293	311
1SXJ	B C	C	308	Y	1.2	293	311
1SXJ	C D	C	256	W	1.8	256	270

1SXJ	C D	C	302	K	1.0	293	311
1SXJ	C D	C	306	I	1.1	293	311
1SXJ	C D	C	318	I	2.5	316	331
1SXJ	C D	C	321	S	2.1	316	331
1SXJ	C D	C	325	G	1.6	316	331
1SXJ	C D	D	51	K	1.1	43	54
1SXJ	C D	D	155	R	3.2	147	157
1SXJ	C D	D	316	T	1.0	316	334
1SXJ	C D	D	319	K	1.6	316	334
1SXJ	C D	D	324	W	3.1	316	334
1SXJ	C D	D	327	F	2.8	316	334
1SXJ	C D	D	331	S	1.1	316	334
1SXJ	D E	D	280	F	2.8	280	294
1SXJ	D E	D	284	K	1.3	280	294
1SXJ	D E	D	341	I	2.4	339	353
1SXJ	D E	D	344	L	9.4	339	353
1SXJ	D E	E	305	F	1.6	296	306
1SXJ	D E	E	318	K	1.3	315	333
1SXJ	D E	E	323	E	1.0	315	333
1SXJ	D E	E	326	S	1.3	315	333
1SXJ	D E	E	329	D	1.5	315	333
1SY9	A B	A	11	E	1.5	6	20
1SY9	A B	A	39	L	1.5	29	40
1SY9	A B	A	51	M	1.1	45	55
1SY9	A B	A	84	E	1.3	81	93
1SY9	A B	B	162	R	2.1	157	173
1SY9	A B	B	165	G	105.8	157	173
1SYQ	A B	A	12	I	2.1	7	27
1SYQ	A B	A	16	V	1.4	7	27
1SYQ	A B	A	19	Q	1.0	7	27
1SYQ	A B	A	22	H	1.0	7	27
1SYQ	A B	A	23	L	1.9	7	27
1SYQ	A B	A	47	V	1.5	41	63
1SYQ	A B	A	51	V	1.2	41	63
1SYQ	A B	A	54	L	1.7	41	63
1SYQ	A B	A	57	V	1.1	41	63
1SYQ	A B	A	115	I	1.0	102	150
1SYQ	A B	A	119	T	1.1	102	150
1SYQ	A B	A	122	L	1.2	102	150
1SYQ	A B	A	126	F	1.8	102	150
1SYQ	A B	B	608	L	2.2	608	627
1SYQ	A B	B	609	L	1.1	608	627
1SYQ	A B	B	613	K	1.1	608	627
1SYQ	A B	B	615	L	3.0	608	627
1SYQ	A B	B	622	L	3.0	608	627
1SYQ	A B	B	623	L	2.5	608	627
1SYQ	A B	B	624	R	1.2	608	627
1SYX	A B	A	114	D	1.5	109	125
1SYX	C D	C	114	D	1.4	109	125
1T03	A B	A	380	I	1.2	364	383
1T03	A B	A	504	G	9.4	500	508
1T03	A B	B	396	E	1.2	395	401
1T03	L H	L	124	Q	1.4	122	128
1T0F	A C	A	66	V	1.1	61	73
1T0F	A C	A	70	L	1.6	61	73
1T0F	A C	A	143	L	1.6	140	156
1T0F	A C	A	147	E	2.2	140	156
1T0F	A C	A	151	R	1.3	140	156
1T0F	A C	C	521	L	1.5	521	527
1T0F	A C	C	522	R	3.3	521	527

1T0F	A C	C	525	Y	1.0	521	527
1T0F	A C	C	535	H	3.1	534	541
1T0F	B D	B	143	L	1.2	140	156
1T0F	B D	B	147	E	1.9	140	156
1T0F	B D	B	151	R	1.2	140	156
1T0F	B D	D	521	L	1.5	521	527
1T0F	B D	D	522	R	2.9	521	527
1T0F	B D	D	535	H	1.5	534	541
1T0F	B D	D	539	K	2.0	534	541
1T0F	B D	D	547	M	1.9	547	551
1T0F	B D	D	550	L	1.9	547	551
1T0J	B C	B	245	M	2.1	240	257
1T0J	B C	B	348	V	4.2	346	363
1T0J	B C	B	351	R	1.4	346	363
1T0J	B C	B	352	L	2.7	346	363
1T0J	B C	B	392	L	1.0	392	411
1T0J	B C	C	433	D	1.8	429	443
1T0J	B C	C	434	L	1.3	429	443
1T0J	B C	C	436	G	82.7	429	443
1T0J	B C	C	437	Y	4.1	429	443
1T0J	B C	C	440	W	6.0	429	443
1T0J	B C	C	441	I	1.5	429	443
1T0K	A B	B	53	K	1.0	50	64
1T0Q	A B	A	12	L	3.1	10	14
1T0Q	A B	A	28	L	1.0	25	29
1T0Q	A B	A	55	Y	2.8	55	76
1T0Q	A B	A	62	Q	1.2	55	76
1T0Q	A B	A	63	R	1.4	55	76
1T0Q	A B	A	102	L	1.0	87	118
1T0Q	A B	A	105	Y	1.7	87	118
1T0Q	A B	A	113	R	2.3	87	118
1T0Q	A B	A	116	R	2.1	87	118
1T0Q	A B	A	117	F	1.1	87	118
1T0Q	A B	A	128	T	1.7	121	141
1T0Q	A B	A	131	M	1.4	121	141
1T0Q	A B	A	132	M	1.9	121	141
1T0Q	A B	A	142	L	1.2	142	148
1T0Q	A B	A	146	Y	4.2	142	148
1T0Q	A B	A	153	R	1.0	153	157
1T0Q	A B	A	156	D	1.5	153	157
1T0Q	A B	A	159	H	4.3	158	162
1T0Q	A B	A	173	R	2.7	167	182
1T0Q	A B	A	177	D	1.4	167	182
1T0Q	A B	A	443	R	1.4	441	446
1T0Q	A B	B	30	V	1.6	27	33
1T0Q	A B	B	31	V	1.1	27	33
1T0Q	A B	B	54	M	1.7	53	64
1T0Q	A B	B	58	Y	11.2	53	64
1T0Q	A B	B	83	Y	3.4	83	107
1T0Q	A B	B	84	R	1.8	83	107
1T0Q	A B	B	86	Y	1.4	83	107
1T0Q	A B	B	91	D	1.1	83	107
1T0Q	A B	B	94	E	1.0	83	107
1T0Q	A B	B	129	R	1.2	128	144
1T0Q	A B	B	130	Y	1.8	128	144
1T0Q	A B	B	136	Q	1.6	128	144
1T0Q	A B	B	143	H	2.2	128	144
1T0Q	A B	B	153	N	1.0	149	180
1T0Q	A B	B	161	D	1.3	149	180
1T0Q	A B	B	163	L	1.5	149	180

1T0Q	A B	B	166	L	1.0	149	180
1T0Q	A B	B	171	Y	2.6	149	180
1T0Q	A B	B	174	R	1.6	149	180
1T0Q	A B	B	190	R	1.5	187	196
1T0Q	A B	B	194	E	1.7	187	196
1T0Q	A B	B	207	E	2.5	197	210
1T0Q	A C	A	333	L	3.9	317	338
1T0Q	A C	A	374	D	1.2	365	382
1T0Q	A C	A	375	V	1.9	365	382
1T0Q	A C	A	379	N	1.0	365	382
1T0Q	A C	C	36	Y	1.3	27	37
1T1K	A B	B	11	L	1.5	9	20
1T1K	A B	B	15	L	3.3	9	20
1T2K	C D	C	280	L	1.5	254	314
1T2K	C D	C	284	V	1.0	254	314
1T2K	C D	C	287	L	1.4	254	314
1T2K	C D	C	294	L	1.0	254	314
1T2K	C D	C	301	L	1.8	254	314
1T2K	C D	C	302	R	1.0	254	314
1T2K	C D	D	362	L	1.3	337	396
1T2K	C D	D	369	L	1.5	337	396
1T2K	C D	D	376	L	1.1	337	396
1T2K	C D	D	380	V	1.0	337	396
1T2K	C D	D	383	L	1.4	337	396
1T2V	A F	A	1704	F	1.0	1701	1710
1T2V	B G	B	1659	P	1.1	1659	1672
1T2V	B G	B	1704	F	3.7	1701	1709
1T2V	C H	C	1659	P	1.0	1659	1672
1T34	A H	A	113	G	1.4	112	116
1T34	A H	A	172	Y	1.0	163	179
1T34	B H	B	92	P	1.3	89	101
1T3L	A B	A	246	M	2.0	241	258
1T3L	A B	A	252	D	1.1	241	258
1T3L	A B	A	353	L	2.0	347	357
1T3L	A B	A	392	L	1.3	392	412
1T3L	A B	B	363	L	1.2	359	373
1T3L	A B	B	365	G	16.4	359	373
1T3L	A B	B	366	Y	3.8	359	373
1T3L	A B	B	369	W	6.3	359	373
1T3L	A B	B	370	I	1.4	359	373
1T3M	A B	A	27	Y	2.1	21	44
1T3M	A B	A	31	L	2.0	21	44
1T3M	A B	A	35	V	1.4	21	44
1T3M	A B	A	42	L	1.0	21	44
1T3M	A B	A	52	V	2.0	48	62
1T3M	A B	A	56	V	1.8	48	62
1T3M	A B	A	60	E	1.3	48	62
1T3M	A D	A	125	G	125.0	124	133
1T3M	A D	D	237	R	2.4	232	238
1T3M	C B	C	125	G	130.5	124	133
1T3M	C B	B	233	E	2.0	232	238
1T3M	C B	B	237	R	2.0	232	238
1T3M	C D	C	27	Y	2.1	21	44
1T3M	C D	C	31	L	2.1	21	44
1T3M	C D	C	35	V	1.3	21	44
1T3M	C D	C	42	L	1.0	21	44
1T3M	C D	C	52	V	1.9	48	62
1T3M	C D	C	56	V	1.9	48	62
1T3M	C D	C	60	E	1.1	48	62
1T3Q	A B	A	36	R	1.7	31	40

1T3Q	A B	A	96	Q	1.3	94	102
1T3Q	A B	A	134	R	2.3	130	137
1T3Q	A B	A	148	E	2.9	148	155
1T3Q	A B	A	149	T	1.5	148	155
1T3Q	A B	A	152	D	1.4	148	155
1T3Q	A B	B	129	D	2.0	124	132
1T3Q	A B	B	285	R	2.9	285	291
1T3Q	A B	B	673	M	1.1	672	693
1T3Q	A B	B	677	G	5.3	672	693
1T3Q	A B	B	680	R	1.0	672	693
1T3Q	A B	B	681	G	168.2	672	693
1T3Q	A B	B	688	G	3.1	672	693
1T3Q	A C	C	107	N	1.0	103	109
1T3Q	B C	B	128	E	1.3	124	132
1T3Q	B C	B	779	F	2.5	775	784
1T3Q	B C	C	263	L	2.2	261	285
1T3Q	D E	D	36	R	1.7	31	40
1T3Q	D E	D	96	Q	1.1	94	102
1T3Q	D E	D	109	F	3.6	109	125
1T3Q	D E	D	130	R	1.2	130	137
1T3Q	D E	D	134	R	3.5	130	137
1T3Q	D E	D	148	E	3.3	148	155
1T3Q	D E	D	149	T	1.6	148	155
1T3Q	D E	D	152	D	1.3	148	155
1T3Q	D E	E	27	L	3.2	21	28
1T3Q	D E	E	129	D	2.0	124	132
1T3Q	D E	E	285	R	2.9	285	291
1T3Q	D E	E	673	M	2.2	672	693
1T3Q	D E	E	677	G	6.5	672	693
1T3Q	D E	E	680	R	1.6	672	693
1T3Q	D E	E	681	G	165.1	672	693
1T3Q	D E	E	688	G	2.4	672	693
1T3Q	D F	D	33	D	1.2	31	40
1T3Q	D F	F	107	N	1.3	103	109
1T3Q	E F	E	129	D	1.2	124	132
1T3Q	E F	E	775	P	1.4	775	784
1T3Q	E F	E	779	F	2.0	775	784
1T3Q	E F	F	263	L	2.1	261	285
1T4K	A B	A	124	Q	1.8	122	127
1T4K	A D	A	185	E	2.2	183	187
1T4K	C D	C	124	Q	1.9	122	127
1T60	H I	H	102	R	1.0	99	105
1T66	C D	C	129	Q	1.2	127	132
1T66	L H	L	128	E	1.1	127	133
1T6O	A B	A	484	L	1.6	475	488
1T6O	A B	A	500	M	1.2	491	506
1T6O	A B	A	504	I	1.3	491	506
1T6O	A B	B	495	L	2.4	487	503
1T6O	A B	B	498	L	2.3	487	503
1T6O	A B	B	501	M	1.0	487	503
1T6V	L N	L	112	R	1.2	109	116
1T6V	L N	N	96	L	1.8	94	98
1T6V	M N	M	96	K	1.2	89	100
1T6V	M O	M	112	R	1.0	109	116
1T9G	D S	D	21	K	1.4	18	38
1T9G	D S	D	23	F	2.0	18	38
1T9G	D S	D	29	K	1.1	18	38
1T9G	D S	D	59	L	1.2	50	60
1T9G	D S	S	198	I	1.2	195	204
1T9G	R S	R	90	E	2.0	89	104

1T9G	R S	R	118	N	1.0	114	128
1T9G	R S	R	121	P	1.0	114	128
1T9G	R S	R	122	R	2.2	114	128
1T9G	R S	S	133	Q	1.1	133	142
1T9G	R S	S	136	Q	1.2	133	142
1T9G	R S	S	140	G	12.2	133	142
1TA3	A B	A	234	K	1.1	233	245
1TA3	A B	A	235	N	1.6	233	245
1TA3	A B	A	237	Y	1.1	233	245
1TA3	A B	A	238	Y	2.7	233	245
1TA3	A B	A	269	L	1.0	266	274
1TA3	A B	A	273	Y	1.0	266	274
1TB6	L H	L	1	F	3.6	1	1
1TB6	L H	L	14	E	1.9	14	14
1TB6	L H	L	14	E	1.4	14	14
1TB6	L H	L	14	L	1.4	14	14
1TB6	L H	H	242	I	1.5	235	243
1TBA	A B	A	62	L	1.0	62	67
1TBG	A E	A	7	L	1.3	3	26
1TBG	A E	A	14	L	2.1	3	26
1TBG	A E	A	15	K	1.2	3	26
1TBG	A E	A	18	I	1.5	3	26
1TBG	A E	A	30	L	1.4	30	34
1TBG	A E	A	33	I	1.5	30	34
1TBG	A E	E	522	L	2.3	512	527
1TBG	A E	E	523	K	3.1	512	527
1TBG	A E	E	526	V	1.1	512	527
1TBG	A E	E	540	F	4.0	533	546
1TBG	A E	E	541	R	2.8	533	546
1TBG	A E	E	543	Y	2.3	533	546
1TBG	A E	E	544	V	1.8	533	546
1TBG	B F	B	10	E	1.2	4	26
1TBG	B F	B	11	A	1.0	4	26
1TBG	B F	B	14	L	2.6	4	26
1TBG	B F	B	15	K	1.7	4	26
1TBG	B F	B	30	L	1.5	30	34
1TBG	B F	B	33	I	1.1	30	34
1TBG	B F	F	516	K	1.0	511	527
1TBG	B F	F	521	Q	1.0	511	527
1TBG	B F	F	522	L	2.1	511	527
1TBG	B F	F	523	K	1.0	511	527
1TBG	B F	F	533	V	1.1	533	546
1TBG	B F	F	540	F	3.8	533	546
1TBG	B F	F	541	R	2.1	533	546
1TBG	B F	F	543	Y	2.8	533	546
1TBG	B F	F	544	V	1.8	533	546
1TBG	B F	F	552	P	1.2	552	556
1TBG	B F	F	553	L	3.5	552	556
1TBG	C G	C	7	L	1.6	6	25
1TBG	C G	C	14	L	2.2	6	25
1TBG	C G	C	15	K	1.3	6	25
1TBG	C G	C	18	I	2.2	6	25
1TBG	C G	C	22	R	1.1	6	25
1TBG	C G	C	30	L	1.1	30	34
1TBG	C G	G	518	E	1.0	511	527
1TBG	C G	G	519	V	1.4	511	527
1TBG	C G	G	522	L	1.7	511	527
1TBG	C G	G	525	E	2.7	511	527
1TBG	C G	G	533	V	2.1	533	546
1TBG	C G	G	540	F	2.4	533	546

1TBG	C G	G	541	R	1.6	533	546
1TBG	C G	G	543	Y	2.6	533	546
1TBG	C G	G	544	V	1.7	533	546
1TBG	C G	G	552	P	1.0	552	556
1TBG	C G	G	553	L	2.9	552	556
1TBG	D H	D	7	L	1.1	4	25
1TBG	D H	D	14	L	2.6	4	25
1TBG	D H	D	15	K	1.5	4	25
1TBG	D H	D	18	I	1.6	4	25
1TBG	D H	D	30	L	1.4	30	34
1TBG	D H	D	33	I	1.2	30	34
1TBG	D H	H	512	K	1.1	511	527
1TBG	D H	H	521	Q	1.1	511	527
1TBG	D H	H	522	L	2.2	511	527
1TBG	D H	H	523	K	1.0	511	527
1TBG	D H	H	525	E	1.6	511	527
1TBG	D H	H	533	V	1.1	533	546
1TBG	D H	H	540	F	3.4	533	546
1TBG	D H	H	541	R	1.8	533	546
1TBG	D H	H	543	Y	2.1	533	546
1TBG	D H	H	544	V	1.4	533	546
1TBG	D H	H	553	L	3.4	552	556
1TBG	D H	H	554	V	1.2	552	556
1TBQ	H R	R	26	P	1.7	26	34
1TBQ	K S	S	26	P	1.0	26	35
1TBQ	K S	S	84	C	1.6	79	87
1TCE	A B	A	80	H	2.5	73	83
1TCO	A B	A	349	V	1.3	349	370
1TCO	A B	A	350	F	5.1	349	370
1TCO	A B	A	354	L	1.8	349	370
1TCO	A B	A	356	F	3.0	349	370
1TCO	A B	A	360	K	1.0	349	370
1TCO	A B	A	364	M	1.6	349	370
1TCO	A B	A	369	L	2.3	349	370
1TCO	A B	B	29	L	2.8	16	31
1TCO	A B	B	42	F	7.1	39	45
1TCO	A B	B	98	Y	2.5	87	99
1TCO	A B	B	111	L	1.5	108	120
1TCO	A B	B	131	I	1.6	125	140
1TCO	A B	B	135	T	1.4	125	140
1TCO	A B	B	137	I	1.1	125	140
1TCO	A B	B	152	F	1.5	149	158
1TCO	A B	B	156	V	2.1	149	158
1TEC	E I	E	71	H	1.3	71	80
1TEC	E I	E	112	W	3.8	112	125
1TET	L H	L	124	Q	1.3	122	127
1TFC	A C	A	280	I	1.3	261	286
1TFC	A C	A	298	M	2.0	294	304
1TFC	A C	A	452	E	1.9	448	456
1TFC	A C	C	690	L	1.8	688	697
1TFC	A C	C	693	L	1.3	688	697
1TFC	A C	C	694	L	1.8	688	697
1TFC	B D	B	298	M	2.0	294	304
1TFC	B D	B	452	E	2.8	448	456
1TFC	B D	D	690	L	2.2	688	696
1TFO	A B	A	607	K	1.5	602	608
1TFO	A B	B	31	R	1.4	20	34
1TFO	A B	B	56	E	3.9	42	58
1TH1	A C	A	176	H	1.4	166	181
1TH1	A C	A	219	H	1.1	208	222

1TH1	A C	A	225	R	1.4	225	234
1TH1	A C	A	254	Y	1.7	249	266
1TH1	A C	A	265	H	1.2	249	266
1TH1	A C	A	349	V	1.0	334	350
1TH1	A C	A	383	W	1.8	375	390
1TH1	A C	A	386	R	1.5	375	390
1TH1	A C	A	387	N	1.9	375	390
1TH1	A C	A	426	N	2.2	414	428
1TH1	A C	A	435	K	1.7	432	441
1TH1	A C	A	469	R	1.4	458	471
1TH1	A C	A	654	Y	1.8	649	664
1TH1	A C	A	660	F	1.4	649	664
1TH1	B D	B	220	N	1.2	208	222
1TH1	B D	B	253	F	1.3	249	265
1TH1	B D	B	254	Y	1.2	249	265
1TH1	B D	B	349	V	1.1	334	350
1TH1	B D	B	387	N	1.5	375	390
1TH1	B D	B	426	N	2.4	414	429
1TH1	B D	B	619	C	1.0	608	624
1TH1	B D	B	620	E	1.2	608	624
1TH1	B D	B	654	Y	1.2	649	664
1TH1	B D	B	657	A	1.1	649	664
1TH1	B D	B	660	F	1.1	649	664
1TH1	B D	D	1477	Q	1.0	1471	1480
1TH1	B D	D	1522	L	1.2	1520	1524
1TI2	A B	A	220	E	1.4	219	223
1TI2	A B	A	254	H	2.4	254	259
1TI2	A B	A	257	R	1.1	254	259
1TI2	A B	A	258	L	1.3	254	259
1TI2	A B	A	331	E	1.1	329	341
1TI2	A B	B	18	N	1.4	18	29
1TI2	A B	B	25	D	1.5	18	29
1TI2	A B	B	26	E	3.4	18	29
1TI2	A B	B	147	H	1.9	144	149
1TI2	C D	C	220	E	1.0	219	223
1TI2	C D	C	258	L	1.2	254	259
1TI2	C D	C	331	E	1.1	329	342
1TI2	C D	C	341	K	1.4	329	342
1TI2	C D	D	18	N	1.6	18	29
1TI2	C D	D	20	F	1.3	18	29
1TI2	C D	D	21	M	1.8	18	29
1TI2	C D	D	25	D	1.5	18	29
1TI2	C D	D	26	E	1.7	18	29
1TI2	C D	D	147	H	1.7	144	148
1TI2	E F	E	254	H	1.2	254	259
1TI2	E F	E	258	L	1.2	254	259
1TI2	E F	E	334	A	2.1	329	341
1TI2	E F	F	20	F	1.4	18	29
1TI2	E F	F	21	M	1.0	18	29
1TI2	E F	F	28	E	1.3	18	29
1TI2	E F	F	147	H	2.3	144	149
1TI2	G H	G	254	H	2.5	254	259
1TI2	G H	G	258	L	1.3	254	259
1TI2	G H	G	337	R	1.0	329	342
1TI2	G H	H	20	F	2.9	18	29
1TI2	G H	H	21	M	1.4	18	29
1TI2	G H	H	26	E	1.7	18	29
1TI2	G H	H	147	H	2.1	144	149
1TI2	I J	I	254	H	1.6	254	259
1TI2	I J	I	331	E	1.5	329	342

1TI2	I J	J	18	N	1.5	18	29
1TI2	I J	J	20	F	1.2	18	29
1TI2	I J	J	21	M	1.8	18	29
1TI2	I J	J	25	D	1.6	18	29
1TI2	I J	J	26	E	2.5	18	29
1TI2	I J	J	147	H	1.5	144	149
1TI2	K L	K	67	K	2.4	66	71
1TI2	K L	K	254	H	1.8	254	259
1TI2	K L	K	258	L	1.1	254	259
1TI2	K L	L	18	N	1.3	18	30
1TI2	K L	L	25	D	1.6	18	30
1TI2	K L	L	26	E	2.2	18	30
1TI2	K L	L	28	E	1.1	18	30
1TI2	K L	L	147	H	1.7	144	148
1TI8	A B	B	48	I	1.0	38	56
1TI8	A B	B	51	K	1.0	38	56
1TI8	A B	B	55	L	1.8	38	56
1TI8	A B	B	89	T	1.1	75	126
1TI8	A B	B	92	W	2.0	75	126
1TI8	A B	B	100	V	1.4	75	126
1TI8	A B	B	104	N	1.4	75	126
1TI8	A B	B	108	I	1.7	75	126
1TI8	A B	B	115	M	1.2	75	126
1TI8	A B	B	122	V	1.1	75	126
1TII	A C	C	202	N	1.2	197	228
1TII	A C	C	204	L	1.2	197	228
1TII	A C	C	209	L	1.7	197	228
1TII	A C	C	212	F	2.4	197	228
1TII	D C	D	66	K	2.0	56	75
1TII	E C	C	225	L	1.3	197	228
1TII	F C	C	222	L	1.6	197	228
1TII	G C	G	73	L	1.9	57	75
1TII	G C	C	226	L	1.3	197	228
1TII	H C	H	66	K	1.3	57	75
1TIL	A B	A	16	E	1.0	16	27
1TIL	A B	A	20	R	4.4	16	27
1TIL	A B	A	49	T	2.1	34	56
1TIL	A B	A	108	M	1.0	108	116
1TIL	A B	A	112	I	1.1	108	116
1TIL	A B	B	24	H	1.2	24	40
1TIL	A B	B	25	H	7.2	24	40
1TIL	A B	B	62	G	108.8	58	73
1TIL	A B	B	89	R	2.2	85	95
1TIL	A B	B	90	L	1.1	85	95
1TIL	A F	A	114	E	1.4	108	116
1TIL	A F	F	108	F	1.8	106	113
1TIL	C D	C	20	R	4.1	16	30
1TIL	C D	C	49	T	2.6	34	56
1TIL	C D	D	24	H	1.4	24	41
1TIL	C D	D	25	H	2.2	24	41
1TIL	C D	D	62	G	33.1	58	73
1TIL	C D	D	89	R	1.7	85	92
1TIL	C D	D	90	L	1.2	85	92
1TIL	E F	E	20	R	3.8	16	29
1TIL	E F	E	39	E	1.5	34	56
1TIL	E F	E	109	G	1.0	109	116
1TIL	E F	F	62	G	59.7	58	73
1TIL	E F	F	89	R	1.8	85	92
1TN6	A B	A	96	F	1.1	94	110
1TN6	A B	A	131	Y	4.4	131	144

1TN6	A B	A	132	T	3.4	131	144
1TN6	A B	A	166	Y	1.6	166	180
1TN6	A B	A	170	H	1.9	166	180
1TN6	A B	A	200	Y	4.7	200	213
1TN6	A B	A	234	N	3.0	234	246
1TN6	A B	A	235	S	1.1	234	246
1TN6	A B	A	238	N	1.8	234	246
1TN6	A B	A	241	Y	1.5	234	246
1TN6	A B	A	274	E	1.5	274	283
1TN6	A B	A	275	S	2.8	274	283
1TN6	A B	A	282	G	82.5	274	283
1TN6	A B	A	317	D	1.1	309	325
1TN6	A B	A	355	Y	1.8	353	367
1TN6	A B	A	358	Y	2.6	353	367
1TN6	A B	A	361	R	1.6	353	367
1TN6	A B	B	544	T	1.2	543	562
1TN6	A B	B	600	R	2.8	600	614
1TN6	A B	B	629	F	3.8	620	634
1TN6	A B	B	751	Y	1.7	749	762
1TN6	A B	B	774	L	1.0	770	780
1TO9	A B	A	110	Y	1.6	107	115
1TO9	A B	A	118	R	1.2	118	123
1TO9	A B	A	121	L	1.4	118	123
1TO9	A B	A	200	I	1.8	196	210
1TO9	A B	A	203	Y	2.1	196	210
1TO9	A B	B	110	Y	2.9	107	115
1TO9	A B	B	203	Y	2.2	196	210
1TO9	A B	B	206	Y	1.3	196	210
1TOC	A B	A	7	F	2.0	7	11
1TOC	B R	R	108	E	1.0	106	113
1TOC	C D	C	7	F	2.0	7	11
1TOC	C D	C	14	E	1.4	14	14
1TOC	C D	C	14	E	1.1	14	14
1TOC	D S	S	107	V	3.1	106	113
1TOC	D S	S	108	E	1.2	106	113
1TOC	D T	D	127	Q	1.2	126	130
1TOC	E F	E	7	F	1.9	7	11
1TOC	H U	U	107	V	1.3	106	113
1TPX	A C	A	197	K	1.5	175	198
1TQE	P X	P	66	L	1.0	62	69
1TQE	P X	X	113	V	1.7	111	124
1TQE	P X	X	117	L	1.0	111	124
1TQE	P X	X	120	F	1.4	111	124
1TQE	Q X	X	121	L	1.8	111	124
1TQE	R Y	Y	120	F	1.5	111	124
1TQE	S Y	Y	114	K	1.2	111	124
1TQE	S Y	Y	121	L	1.8	111	124
1TQY	A B	A	114	L	1.1	111	122
1TQY	A B	A	118	Y	3.3	111	122
1TQY	A B	A	119	L	1.3	111	122
1TQY	A B	A	154	W	2.9	146	156
1TQY	A B	A	178	N	1.0	171	185
1TQY	A B	A	184	E	1.0	171	185
1TQY	A B	A	203	I	2.6	202	211
1TQY	A B	B	109	F	1.0	109	123
1TQY	A B	B	116	F	3.8	109	123
1TQY	A B	B	119	L	1.7	109	123
1TQY	A B	B	120	W	2.3	109	123
1TQY	A B	B	137	Y	1.5	137	148
1TQY	A B	B	142	G	9.1	137	148

1TQY	A B	B	146	I	1.7	137	148
1TQY	A B	B	173	R	2.4	162	177
1TQY	A B	B	193	P	1.0	193	203
1TQY	A B	B	194	W	2.5	193	203
1TQY	C D	C	114	L	1.2	111	122
1TQY	C D	C	115	E	2.3	111	122
1TQY	C D	C	118	Y	3.9	111	122
1TQY	C D	C	119	L	1.5	111	122
1TQY	C D	C	149	P	1.1	145	156
1TQY	C D	C	154	W	2.8	145	156
1TQY	C D	C	202	P	1.0	202	211
1TQY	C D	C	203	I	2.5	202	211
1TQY	C D	D	109	F	1.3	109	123
1TQY	C D	D	113	H	1.6	109	123
1TQY	C D	D	115	E	1.9	109	123
1TQY	C D	D	116	F	5.0	109	123
1TQY	C D	D	120	W	3.1	109	123
1TQY	C D	D	142	G	11.3	139	148
1TQY	C D	D	146	I	1.6	139	148
1TQY	C D	D	173	R	2.1	161	177
1TQY	C D	D	194	W	3.2	193	203
1TQY	E F	E	114	L	1.1	111	122
1TQY	E F	E	118	Y	3.8	111	122
1TQY	E F	E	119	L	1.0	111	122
1TQY	E F	E	154	W	2.7	146	157
1TQY	E F	E	203	I	2.5	202	211
1TQY	E F	F	116	F	4.2	109	123
1TQY	E F	F	119	L	1.2	109	123
1TQY	E F	F	120	W	1.6	109	123
1TQY	E F	F	142	G	10.0	139	148
1TQY	E F	F	146	I	1.8	139	148
1TQY	E F	F	173	R	1.6	162	177
1TQY	E F	F	193	P	1.1	193	203
1TQY	E F	F	194	W	2.7	193	203
1TQY	G H	G	114	L	1.1	111	122
1TQY	G H	G	118	Y	3.7	111	122
1TQY	G H	G	119	L	1.2	111	122
1TQY	G H	G	154	W	3.1	146	156
1TQY	G H	G	203	I	2.3	202	211
1TQY	G H	H	109	F	1.1	109	123
1TQY	G H	H	113	H	1.2	109	123
1TQY	G H	H	116	F	4.2	109	123
1TQY	G H	H	120	W	1.7	109	123
1TQY	G H	H	142	G	16.1	139	148
1TQY	G H	H	146	I	1.9	139	148
1TQY	G H	H	173	R	1.0	161	178
1TQY	G H	H	177	R	2.1	161	178
1TQY	G H	H	193	P	1.0	193	203
1TQY	G H	H	194	W	2.8	193	203
1TQY	G H	H	275	R	1.7	273	284
1TTW	A B	B	45	F	1.9	44	50
1TTW	A B	B	49	V	2.4	44	50
1TU3	A F	A	88	M	1.5	83	90
1TU3	A F	F	822	V	1.0	805	837
1TU3	A F	F	830	V	1.0	805	837
1TU3	A F	F	833	E	1.7	805	837
1TU3	A G	G	821	F	1.4	805	837
1TU3	B F	F	817	V	1.1	805	837
1TU3	B F	F	821	F	1.0	805	837
1TU3	B G	B	85	L	1.0	83	88

1TU3	B G	G	833	E	2.8	805	837
1TU3	B H	H	812	D	1.2	807	837
1TU3	C G	C	116	K	2.0	105	122
1TU3	C G	G	812	D	1.3	805	837
1TU3	C G	G	815	E	1.1	805	837
1TU3	C H	C	88	M	1.5	86	90
1TU3	C H	H	822	V	1.2	807	837
1TU3	C H	H	826	Q	1.2	807	837
1TU3	C I	I	821	F	1.9	805	836
1TU3	D H	D	82	Y	1.2	80	84
1TU3	D H	H	821	F	1.6	807	837
1TU3	D I	D	85	L	1.0	85	90
1TU3	D I	D	88	M	1.1	85	90
1TU3	D I	I	822	V	1.1	805	836
1TU3	D I	I	833	E	2.4	805	836
1TU3	E J	E	85	L	1.5	83	90
1TU3	E J	E	88	M	1.5	83	90
1TU3	E J	J	822	V	1.1	807	837
1TU3	E J	J	823	K	1.2	807	837
1TU3	E J	J	833	E	2.4	807	837
1TUE	A B	A	446	W	1.7	446	456
1TUE	A B	A	447	R	1.9	446	456
1TUE	A B	A	450	V	2.7	446	456
1TUE	A B	A	454	R	2.7	446	456
1TUE	A B	A	455	Y	1.1	446	456
1TUE	A B	A	460	F	2.0	460	473
1TUE	A B	B	20	I	1.7	4	26
1TUE	A B	B	23	Y	4.9	4	26
1TUE	A B	B	24	E	1.5	4	26
1TUE	A B	B	43	E	2.3	30	53
1TUE	D E	D	446	W	1.5	446	456
1TUE	D E	D	447	R	1.3	446	456
1TUE	D E	D	454	R	1.3	446	456
1TUE	D E	D	455	Y	1.7	446	456
1TUE	D E	D	460	F	1.6	460	472
1TUE	D E	D	461	I	1.2	460	472
1TUE	D E	D	626	R	2.4	624	628
1TUE	D E	E	23	Y	1.9	4	26
1TUE	D E	E	24	E	1.7	4	26
1TUE	F G	F	446	W	2.1	446	456
1TUE	F G	F	447	R	1.8	446	456
1TUE	F G	F	454	R	1.3	446	456
1TUE	F G	F	455	Y	1.1	446	456
1TUE	F G	F	460	F	2.1	460	472
1TUE	F G	F	461	I	1.7	460	472
1TUE	F G	F	626	R	2.6	624	628
1TUE	F G	G	23	Y	3.7	5	26
1TUE	F G	G	24	E	1.7	5	26
1TUE	F G	G	43	E	1.6	30	53
1TUE	H G	G	85	G	1.2	66	87
1TUE	H J	H	446	W	1.5	446	456
1TUE	H J	H	447	R	2.3	446	456
1TUE	H J	H	450	V	1.6	446	456
1TUE	H J	H	454	R	2.9	446	456
1TUE	H J	H	455	Y	1.2	446	456
1TUE	H J	H	460	F	2.8	460	473
1TUE	H J	H	461	I	2.2	460	473
1TUE	H J	J	19	I	2.4	5	26
1TUE	H J	J	23	Y	5.5	5	26
1TUE	H J	J	24	E	2.1	5	26

1TUE	H J	J	43	E	3.1	30	53
1TUE	K L	K	446	W	1.4	446	456
1TUE	K L	K	447	R	2.2	446	456
1TUE	K L	K	454	R	2.7	446	456
1TUE	K L	K	455	Y	1.3	446	456
1TUE	K L	K	460	F	1.6	460	473
1TUE	K L	K	461	I	2.2	460	473
1TUE	K L	L	23	Y	5.0	5	26
1TUE	K L	L	24	E	1.9	5	26
1TUE	K L	L	43	E	2.6	30	52
1TUE	M Q	M	446	W	1.1	446	456
1TUE	M Q	M	447	R	2.5	446	456
1TUE	M Q	M	454	R	2.2	446	456
1TUE	M Q	M	460	F	2.8	460	473
1TUE	M Q	M	461	I	2.7	460	473
1TUE	M Q	M	464	L	1.5	460	473
1TUE	M Q	Q	20	I	2.4	5	26
1TUE	M Q	Q	23	Y	2.5	5	26
1TUE	M Q	Q	24	E	1.7	5	26
1TX4	A B	A	197	V	1.4	192	201
1TX4	A B	A	216	I	1.1	216	229
1TX4	A B	B	69	L	1.9	67	75
1TX4	A B	B	72	L	1.4	67	75
1TX4	A B	B	90	D	1.0	89	94
1TY4	A C	A	123	F	1.5	121	127
1TY4	A C	A	134	F	4.0	128	140
1TY4	A C	A	152	V	1.7	146	158
1TY4	A C	A	169	G	196.7	168	184
1TY4	A C	A	170	R	2.5	168	184
1TY4	A C	A	172	I	1.3	168	184
1TY4	A C	A	173	G	25.4	168	184
1TY4	A C	C	50	I	1.5	50	60
1TY4	A C	C	51	G	96.9	50	60
1TY4	A C	C	54	I	3.3	50	60
1TY4	A C	C	55	G	94.5	50	60
1TY4	A C	C	57	K	1.1	50	60
1TY4	A C	C	58	L	2.5	50	60
1TY4	A C	C	63	D	2.5	63	68
1TY4	A C	C	65	F	2.5	63	68
1TY4	A C	C	66	D	1.0	63	68
1TY4	B D	B	123	F	1.4	121	127
1TY4	B D	B	134	F	2.5	128	140
1TY4	B D	B	151	D	1.3	146	158
1TY4	B D	B	152	V	1.6	146	158
1TY4	B D	B	156	V	1.4	146	158
1TY4	B D	B	169	G	160.2	168	184
1TY4	B D	B	170	R	1.9	168	184
1TY4	B D	B	173	G	67.6	168	184
1TY4	B D	D	50	I	1.1	50	60
1TY4	B D	D	51	G	84.9	50	60
1TY4	B D	D	54	I	2.7	50	60
1TY4	B D	D	55	G	129.8	50	60
1TY4	B D	D	58	L	2.7	50	60
1TY4	B D	D	63	D	1.6	63	68
1TY4	B D	D	65	F	2.6	63	68
1TYE	A B	B	262	L	1.6	259	263
1TYE	A B	B	321	Y	1.3	315	324
1TYE	C D	D	262	L	2.3	259	263
1TYE	C D	D	321	Y	1.1	315	323
1TYE	E F	F	321	Y	1.9	315	325

1TYE	E F	F	324	L	1.6	315	325
1TYG	B A	A	187	L	1.4	178	192
1TZH	L H	L	124	Q	1.0	122	128
1TZI	B V	V	17	F	1.5	17	24
1TZN	A a	a	1121	H	1.0	1120	1135
1TZN	A a	a	1154	L	1.2	1154	1167
1TZN	C c	c	1154	L	1.2	1154	1167
1TZN	E e	e	1154	L	1.2	1154	1167
1TZN	F f	f	1122	E	1.3	1120	1135
1TZN	F f	f	1154	L	1.2	1154	1167
1TZN	G g	g	1154	L	1.2	1154	1167
1TZN	H h	H	348	E	1.6	346	351
1TZN	H h	h	1121	H	1.4	1120	1135
1TZN	H h	h	1154	L	1.2	1154	1167
1TZN	H h	h	1158	Y	1.7	1154	1167
1TZN	I i	I	348	E	1.6	346	351
1TZN	I i	i	1121	H	1.4	1120	1135
1TZN	I i	i	1154	L	1.2	1154	1167
1TZN	I i	i	1158	Y	1.7	1154	1167
1TZN	I i	i	1161	K	1.6	1154	1167
1TZN	K k	k	1154	L	1.2	1154	1167
1TZN	L l	l	1154	L	1.2	1154	1167
1TZN	M m	m	1154	L	1.8	1154	1167
1TZN	M m	m	1161	K	1.0	1154	1167
1TZN	O o	o	1122	E	1.3	1120	1135
1TZN	O o	o	1154	L	1.2	1154	1167
1TZN	O o	o	1158	Y	1.2	1154	1167
1U0N	A B	A	636	R	1.4	634	644
1U0N	A D	A	603	F	1.6	594	606
1U0N	C D	D	218	R	1.0	214	223
1U0S	Y A	Y	91	I	2.2	87	96
1U0S	Y A	Y	94	I	1.9	87	96
1U0S	Y A	Y	110	R	1.5	108	119
1U0S	Y A	Y	113	E	1.5	108	119
1U0S	Y A	Y	117	K	1.3	108	119
1U0S	Y A	A	195	R	2.5	192	206
1U0S	Y A	A	197	Y	2.9	192	206
1U0S	Y A	A	198	L	2.0	192	206
1U2U	A B	B	12	L	1.8	4	29
1U35	A B	A	451	I	1.2	445	455
1U35	A B	A	454	Y	1.3	445	455
1U35	A B	A	467	F	5.2	464	477
1U35	A B	A	470	L	2.1	464	477
1U35	A B	A	474	I	1.3	464	477
1U35	A B	A	475	A	4.4	464	477
1U35	A B	A	492	L	1.4	486	514
1U35	A B	A	496	C	2.1	486	514
1U35	A B	A	499	Y	2.4	486	514
1U35	A B	A	500	L	1.6	486	514
1U35	A B	A	501	V	1.6	486	514
1U35	A B	A	504	F	2.8	486	514
1U35	A B	A	521	P	1.4	521	532
1U35	A B	A	524	I	1.4	521	532
1U35	A B	B	37	L	1.9	31	41
1U35	A B	B	40	R	4.3	31	41
1U35	A B	B	50	I	1.8	48	76
1U35	A B	B	57	V	1.1	48	76
1U35	A B	B	61	F	3.0	48	76
1U35	A B	B	62	L	1.0	48	76
1U35	A B	B	66	I	1.2	48	76

1U35	A B	B	70	V	1.2	48	76
1U35	A B	B	86	V	1.5	83	93
1U35	A G	A	448	L	1.5	445	455
1U35	B D	B	68	D	1.3	48	76
1U35	B D	B	71	T	2.1	48	76
1U35	B D	B	72	Y	3.7	48	76
1U35	B D	B	88	Y	4.1	83	93
1U35	B D	B	92	R	2.1	83	93
1U35	B D	D	1273	E	2.4	1253	1281
1U35	B D	D	1276	R	1.4	1253	1281
1U35	B D	D	1280	Y	3.3	1253	1281
1U35	B D	D	1296	R	2.1	1288	1299
1U35	B D	D	1297	L	2.0	1288	1299
1U35	B D	D	1298	L	1.4	1288	1299
1U35	C D	C	820	K	1.0	817	821
1U35	C D	C	834	I	1.3	827	838
1U35	C D	C	849	V	1.8	845	873
1U35	C D	C	850	Y	2.3	845	873
1U35	C D	C	851	M	1.5	845	873
1U35	C D	C	854	V	1.4	845	873
1U35	C D	C	855	L	1.8	845	873
1U35	C D	C	858	L	2.0	845	873
1U35	C D	C	863	L	1.1	845	873
1U35	C D	C	867	V	1.1	845	873
1U35	C D	C	880	P	1.2	880	889
1U35	C D	C	883	I	1.7	880	889
1U35	C D	D	1241	V	1.4	1235	1246
1U35	C D	D	1245	V	1.0	1235	1246
1U35	C D	D	1258	I	2.0	1253	1281
1U35	C D	D	1262	F	3.0	1253	1281
1U35	C D	D	1267	F	3.0	1253	1281
1U35	C D	D	1270	I	1.3	1253	1281
1U35	C D	D	1291	V	5.6	1288	1299
1U35	C D	D	1303	L	2.2	1302	1319
1U35	C D	D	1306	H	1.6	1302	1319
1U35	C D	D	1311	G	96.4	1302	1319
1U35	C D	D	1315	V	1.2	1302	1319
1U35	C D	D	1318	Y	3.0	1302	1319
1U35	E C	E	648	L	2.0	645	657
1U35	E C	E	712	I	1.1	686	714
1U35	E F	E	650	E	1.2	645	657
1U35	E F	E	651	I	2.0	645	657
1U35	E F	E	669	R	1.0	664	677
1U35	E F	E	670	L	2.0	664	677
1U35	E F	E	692	L	1.8	686	714
1U35	E F	E	699	Y	2.4	686	714
1U35	E F	E	700	L	2.2	686	714
1U35	E F	E	701	V	1.8	686	714
1U35	E F	E	704	F	3.1	686	714
1U35	E F	E	721	P	1.5	721	732
1U35	E F	E	724	I	1.5	721	732
1U35	E F	F	236	R	1.7	231	241
1U35	E F	F	237	L	2.1	231	241
1U35	E F	F	239	R	2.1	231	241
1U35	E F	F	240	R	3.9	231	241
1U35	E F	F	250	I	1.8	250	276
1U35	E F	F	258	L	2.0	250	276
1U35	E F	F	261	F	3.5	250	276
1U35	E F	F	262	L	1.3	250	276
1U35	E F	F	266	I	2.7	250	276

1U35	E F	F	270	V	1.7	250	276
1U35	E F	F	286	V	1.8	283	293
1U35	F H	F	272	Y	3.4	250	276
1U35	F H	F	275	H	1.9	250	276
1U35	F H	F	288	Y	1.5	283	293
1U35	F H	H	1480	Y	2.9	1453	1481
1U35	F H	H	1489	R	1.0	1488	1499
1U35	F H	H	1497	L	1.1	1488	1499
1U35	G H	G	1046	G	21.6	1045	1073
1U35	G H	G	1049	V	1.5	1045	1073
1U35	G H	G	1050	Y	2.5	1045	1073
1U35	G H	G	1051	M	1.1	1045	1073
1U35	G H	G	1054	V	1.0	1045	1073
1U35	G H	G	1055	L	2.0	1045	1073
1U35	G H	G	1057	Y	1.5	1045	1073
1U35	G H	G	1058	L	1.4	1045	1073
1U35	G H	G	1063	L	3.1	1045	1073
1U35	G H	G	1064	E	1.7	1045	1073
1U35	G H	G	1067	V	1.1	1045	1073
1U35	G H	G	1080	P	1.3	1080	1090
1U35	G H	G	1083	I	1.4	1080	1090
1U35	G H	G	1092	E	1.7	1091	1097
1U35	G H	H	1437	Y	1.3	1435	1445
1U35	G H	H	1441	V	1.6	1435	1445
1U35	G H	H	1458	I	2.0	1453	1481
1U35	G H	H	1459	M	1.8	1453	1481
1U35	G H	H	1462	F	3.4	1453	1481
1U35	G H	H	1463	V	1.0	1453	1481
1U35	G H	H	1465	D	1.1	1453	1481
1U35	G H	H	1466	I	1.0	1453	1481
1U35	G H	H	1469	R	1.0	1453	1481
1U35	G H	H	1470	I	2.3	1453	1481
1U35	G H	H	1511	G	142.5	1502	1520
1U35	G H	H	1515	V	1.2	1502	1520
1U35	G H	H	1518	Y	1.4	1502	1520
1U3H	A C	C	58	G	1.2	56	70
1U3H	B D	D	70	R	1.0	57	91
1U3H	C D	C	74	T	1.0	72	77
1U3H	C D	C	76	R	3.0	72	77
1U3H	C D	D	57	D	1.3	57	91
1U3H	C D	D	89	T	1.1	57	91
1U3H	C P	C	66	G	1.3	56	70
1U3H	D P	D	61	Y	1.7	57	91
1U3H	D P	D	67	Y	2.5	57	91
1U3H	D P	D	74	E	1.9	57	91
1U3H	D P	D	78	V	1.1	57	91
1U3H	D P	D	82	N	1.6	57	91
1U3H	G H	G	48	F	3.2	46	52
1U3H	G H	G	73	L	1.4	72	77
1U3H	G H	G	74	T	1.0	72	77
1U3H	G H	G	76	R	2.8	72	77
1U3H	G H	H	57	D	1.3	55	88
1U3H	G H	H	86	E	2.4	55	88
1U3H	H I	H	74	E	1.8	55	88
1U3H	H I	H	78	V	1.1	55	88
1U3H	H I	H	82	N	1.7	55	88
1U54	A B	A	218	R	3.1	213	220
1U54	A B	B	302	L	1.0	299	304
1U54	A B	B	303	K	1.8	299	304
1U54	A B	B	336	G	12.2	336	347

1U5T	A B	A	97	L	1.5	88	105
1U5T	A B	A	140	M	1.1	131	144
1U5T	A B	B	457	P	1.9	457	465
1U5T	A B	B	461	R	1.2	457	465
1U5T	A C	C	22	T	1.2	20	39
1U6G	A B	A	558	L	2.6	558	573
1U6G	A B	A	604	T	1.5	604	613
1U6G	A B	A	611	L	2.6	604	613
1U6G	A C	A	42	Y	1.5	39	54
1U6G	A C	A	128	F	2.6	114	137
1U6G	A C	A	135	G	113.7	114	137
1U6G	A C	A	160	Y	1.3	158	169
1U6G	A C	A	199	R	1.3	198	211
1U6G	A C	A	438	E	2.5	438	455
1U6G	A C	A	497	F	3.4	497	526
1U6G	A C	A	719	K	1.2	688	720
1U6G	A C	C	22	F	1.5	20	34
1U6G	A C	C	105	I	1.2	100	117
1U6G	A C	C	193	K	1.1	189	205
1U6G	A C	C	348	K	1.4	348	362
1U6G	A C	C	351	R	1.2	348	362
1U6G	A C	C	1080	D	1.6	1077	1095
1U6G	A C	C	1087	E	1.2	1077	1095
1U6G	A C	C	1165	E	1.5	1163	1174
1U6G	B C	C	20	K	1.0	20	34
1U6H	A B	A	11	I	1.4	6	23
1U6H	A B	A	46	V	1.2	40	63
1U6H	A B	A	53	L	1.2	40	63
1U6H	A B	A	122	L	1.0	101	146
1U6H	A B	A	125	F	1.1	101	146
1U6H	A B	B	856	L	2.3	854	874
1U6H	A B	B	857	L	1.6	854	874
1U6H	A B	B	863	L	2.5	854	874
1U6H	A B	B	870	M	1.1	854	874
1U7B	A B	B	340	L	2.8	340	344
1U7B	A B	B	343	F	3.2	340	344
1U7F	C B	C	284	E	6.4	281	289
1U7F	C B	B	496	R	1.1	492	499
1U7F	C B	B	533	L	1.2	530	542
1U7F	C B	B	537	D	1.5	530	542
1U7F	C B	B	541	H	1.0	530	542
1U8T	A E	E	8	Q	1.1	8	16
1U8T	A E	E	11	I	2.0	8	16
1U8T	B F	F	8	Q	2.4	8	14
1U8T	B F	F	11	I	2.0	8	14
1U8T	B F	F	12	D	1.5	8	14
1U9I	B C	B	82	D	2.0	80	90
1U9I	B C	B	88	R	1.1	80	90
1U9I	B C	B	89	S	1.3	80	90
1U9I	B C	B	326	R	3.1	321	331
1U9I	B C	C	165	F	1.7	157	175
1U9I	B C	C	172	K	1.3	157	175
1U9I	B C	C	393	R	2.1	389	405
1U9I	E D	E	161	R	1.2	157	175
1U9I	E D	E	162	R	1.2	157	175
1U9I	E D	E	165	F	2.9	157	175
1U9I	E D	E	169	A	1.1	157	175
1U9I	E D	E	200	V	1.1	196	201
1U9I	E D	E	397	I	1.5	389	406
1U9I	E D	D	82	D	1.1	80	90

1U9I	E D	D	88	R	1.8	80	90
1U9I	E D	D	89	S	4.4	80	90
1U9I	E D	D	326	R	2.5	321	331
1UB4	A C	A	86	R	2.2	83	87
1UB4	A C	A	105	K	2.0	96	110
1UB4	A C	A	108	V	1.0	96	110
1UB4	A C	C	458	L	2.3	455	461
1UB4	B C	C	455	L	1.3	455	461
1UCY	H E	H	57	H	22.6	56	60
1UCY	H E	E	237	W	4.6	235	243
1UCY	H E	E	238	I	1.4	235	243
1UCY	H E	E	241	V	1.6	235	243
1UCY	H E	E	242	I	2.2	235	243
1UCY	J K	J	14	E	2.9	14	14
1UCY	J K	J	14	E	1.4	14	14
1UCY	J K	J	14	F	1.3	14	14
1UCY	J K	J	14	Y	3.6	14	14
1UCY	L E	L	14	E	1.4	14	14
1UCY	L H	L	14	L	1.0	14	14
1UCY	M N	M	14	E	1.7	14	14
1UCY	M N	M	14	E	1.0	14	14
1UCY	M N	M	14	L	1.5	14	14
1UCY	M N	M	14	F	1.3	14	14
1UCY	M N	M	14	Y	3.2	14	14
1UDI	E I	E	111	P	1.1	111	124
1UDI	E I	I	31	E	1.1	26	34
1UDI	E I	I	33	I	1.6	26	34
1UEA	A B	A	205	H	1.1	195	208
1UEA	C D	C	202	E	1.1	195	207
1UEA	C D	C	205	H	1.9	195	207
1UEL	A B	B	287	I	1.0	283	298
1UEL	A B	B	289	Y	2.0	283	298
1UEL	A B	B	291	M	1.0	283	298
1UEL	A B	B	293	M	1.0	283	298
1UEL	A B	B	297	G	58.2	283	298
1UEX	A C	C	635	V	1.4	634	644
1UEX	B C	C	663	R	1.9	660	666
1UF2	A D	A	460	N	1.6	454	461
1UF2	A D	D	36	F	1.7	34	47
1UF2	A D	D	37	N	1.1	34	47
1UF2	A D	D	40	S	1.7	34	47
1UF2	A E	E	101	T	1.3	98	104
1UF2	A I	A	188	I	1.5	176	190
1UF2	A J	J	41	N	1.1	34	47
1UF2	B E	E	34	G	1.7	34	47
1UF2	B E	E	41	N	1.0	34	47
1UF2	B F	F	34	G	4.2	34	45
1UGH	E I	E	168	P	1.2	168	179
1UGH	E I	I	28	E	1.2	26	34
1UHE	B A	A	32	L	1.0	30	36
1UHL	A B	A	465	E	1.5	457	473
1UHL	A B	A	468	Y	1.8	457	473
1UHL	A B	A	486	F	1.0	485	491
1UHL	A B	B	406	R	1.5	403	414
1UJ3	A B	A	124	Q	1.4	122	127
1UJW	A B	B	372	I	1.4	344	375
1UJW	A B	B	389	M	1.2	386	417
1UJW	A B	B	390	W	2.1	386	417
1UJW	A B	B	394	G	6.3	386	417
1UKL	A C	A	755	V	13.0	755	778

1UKL	A C	C	371	R	1.7	371	391
1UKL	A C	C	376	Y	2.2	371	391
1UKL	A D	A	295	I	1.6	273	302
1UKL	A D	A	296	E	2.8	273	302
1UKL	A D	D	379	Y	2.7	369	389
1UKL	A D	D	386	K	1.0	369	389
1UKL	B E	E	371	R	1.2	369	391
1UKL	B E	E	376	Y	1.7	369	391
1UKL	B E	E	379	Y	2.3	369	391
1UKL	B F	B	437	E	2.1	428	439
1UKL	B F	F	367	S	1.2	366	371
1UKV	G Y	G	226	R	2.0	210	227
1UKV	G Y	G	241	E	1.9	239	253
1UKV	G Y	G	244	Q	2.2	239	253
1UKV	G Y	G	248	R	3.9	239	253
1UKV	G Y	G	252	I	1.0	239	253
1ULI	A B	A	361	R	3.2	354	368
1ULI	A B	A	365	L	2.1	354	368
1ULI	A B	A	377	D	1.0	373	389
1ULI	A B	A	380	E	2.4	373	389
1ULI	A B	B	87	M	1.5	85	96
1ULI	A B	B	90	G	9.9	85	96
1ULI	A B	B	91	R	1.6	85	96
1ULI	A B	B	93	R	1.2	85	96
1ULI	C D	C	361	R	2.6	354	368
1ULI	C D	C	365	L	2.1	354	368
1ULI	C D	C	376	Q	1.4	373	389
1ULI	C D	C	377	D	2.4	373	389
1ULI	C D	C	380	E	2.7	373	389
1ULI	C D	D	87	M	1.8	85	95
1ULI	C D	D	90	G	16.3	85	95
1ULI	C D	D	91	R	1.4	85	95
1ULI	E F	E	361	R	3.3	354	368
1ULI	E F	E	365	L	2.0	354	368
1ULI	E F	E	376	Q	1.6	373	389
1ULI	E F	E	377	D	2.5	373	389
1ULI	E F	E	380	E	1.0	373	389
1ULI	E F	E	383	V	1.2	373	389
1ULI	E F	E	384	E	1.3	373	389
1ULI	E F	F	87	M	1.3	85	95
1ULI	E F	F	90	G	7.8	85	95
1ULI	E F	F	91	R	1.2	85	95
1ULI	E F	F	94	K	3.9	85	95
1UM4	L H	L	125	E	1.5	124	130
1UM9	A B	A	152	P	1.0	150	163
1UM9	A B	A	155	G	340.7	150	163
1UM9	A B	A	158	I	5.8	150	163
1UM9	A B	A	162	L	1.1	150	163
1UM9	A B	A	189	F	2.2	181	193
1UM9	A B	B	65	G	106.1	60	74
1UM9	A B	B	69	G	211.4	60	74
1UM9	A B	B	73	H	3.8	60	74
1UM9	A B	B	93	Q	1.4	91	100
1UM9	A B	B	97	Q	1.8	91	100
1UM9	A B	B	103	Y	3.6	101	105
1UM9	A B	B	104	R	9.0	101	105
1UM9	A D	A	344	M	2.3	341	345
1UM9	A D	A	355	H	1.1	354	367
1UM9	A D	A	359	Q	1.6	354	367
1UM9	A D	A	363	L	1.5	354	367

1UM9	A D	D	306	L	1.5	304	308
1UM9	C B	C	355	H	1.0	354	365
1UM9	C B	C	359	Q	2.6	354	365
1UM9	C B	C	363	L	1.2	354	365
1UM9	C D	C	152	P	1.1	150	163
1UM9	C D	C	155	G	274.6	150	163
1UM9	C D	C	189	F	2.3	181	193
1UM9	C D	C	354	W	2.8	354	365
1UM9	C D	D	65	G	103.4	60	75
1UM9	C D	D	69	G	182.0	60	75
1UM9	C D	D	73	H	4.3	60	75
1UM9	C D	D	74	G	2.2	60	75
1UM9	C D	D	93	Q	1.4	91	100
1UM9	C D	D	97	Q	2.2	91	100
1UM9	C D	D	102	R	1.1	101	105
1UM9	C D	D	103	Y	3.5	101	105
1UM9	C D	D	104	R	3.7	101	105
1UM9	C D	D	244	Y	2.6	244	255
1UPT	B A	B	2177	Y	3.9	2173	2185
1UPT	B A	B	2180	K	1.1	2173	2185
1UPT	B A	B	2196	K	1.0	2196	2202
1UPT	B A	A	77	Y	2.7	75	81
1UPT	D C	D	2177	Y	4.0	2173	2185
1UPT	D E	E	104	K	1.0	100	109
1UPT	F E	F	2177	Y	3.8	2173	2185
1UPT	F E	F	2180	K	1.2	2173	2185
1UPT	F E	F	2196	K	1.0	2196	2202
1UPT	F E	E	77	Y	3.0	75	81
1UPT	H G	H	2177	Y	2.6	2173	2185
1UR6	A B	A	5	R	3.8	2	13
1UR6	A B	B	44	R	1.0	41	46
1URQ	A C	A	1097	F	1.0	1053	1108
1URQ	A D	A	1083	L	1.4	1053	1108
1URQ	A D	A	1086	R	1.3	1053	1108
1URQ	A D	A	1097	F	1.4	1053	1108
1URQ	A D	D	156	I	1.6	140	199
1URQ	A D	D	170	I	1.5	140	199
1URQ	A D	D	177	I	1.9	140	199
1URQ	A D	D	178	D	1.2	140	199
1URQ	A D	D	181	M	1.0	140	199
1URQ	A D	D	188	K	1.8	140	199
1URQ	A D	D	191	I	1.7	140	199
1URQ	B C	B	199	H	1.8	197	257
1URQ	B C	B	206	E	2.4	197	257
1URQ	B C	B	209	I	2.0	197	257
1URQ	B C	B	213	H	2.0	197	257
1URQ	B C	B	223	V	1.5	197	257
1URQ	B C	B	230	I	1.0	197	257
1URQ	B C	B	234	E	2.7	197	257
1URQ	B C	B	244	V	1.2	197	257
1URQ	B C	B	251	T	1.2	197	257
1URQ	B C	B	255	V	1.1	197	257
1URQ	B C	C	31	R	2.0	17	81
1URQ	B C	C	32	M	2.4	17	81
1URQ	B C	C	35	L	1.9	17	81
1URQ	B C	C	49	M	1.4	17	81
1URQ	B C	C	56	Q	1.7	17	81
1URQ	B C	C	59	R	2.8	17	81
1URQ	B C	C	63	G	15.9	17	81
1URQ	B C	C	67	I	2.5	17	81

1URQ	B C	C	77	N	1.1	17	81
1URQ	B D	B	216	F	2.3	197	257
1URQ	B D	D	159	L	1.1	140	199
1URQ	C D	C	26	L	1.6	17	81
1URQ	C D	C	29	T	1.4	17	81
1URQ	C D	C	33	L	1.1	17	81
1URQ	C D	C	36	V	1.5	17	81
1URQ	C D	C	57	L	1.2	17	81
1URQ	C D	C	61	E	4.9	17	81
1URQ	C D	C	64	M	1.3	17	81
1URQ	C D	C	65	N	1.2	17	81
1URQ	C D	C	71	M	1.6	17	81
1URQ	C D	C	78	L	1.1	17	81
1URQ	C D	D	152	V	1.8	140	199
1URQ	C D	D	155	I	1.8	140	199
1URQ	C D	D	159	L	1.5	140	199
1URQ	C D	D	176	Q	1.3	140	199
1URQ	C D	D	179	R	2.6	140	199
1URQ	C D	D	180	I	2.6	140	199
1URQ	C D	D	183	K	2.1	140	199
1URQ	C D	D	190	R	1.5	140	199
1USP	A B	A	49	L	1.8	46	69
1USP	A B	A	53	G	15.0	46	69
1USP	A B	B	49	L	1.4	46	69
1USP	A B	B	53	G	11.4	46	69
1USP	A B	B	57	C	3.5	46	69
1USP	A B	B	123	Y	3.3	122	127
1USV	A B	B	128	R	1.3	123	149
1USV	C D	C	387	K	1.2	387	410
1USV	C D	C	398	K	1.2	387	410
1USV	G H	G	387	K	1.8	387	408
1USV	G H	G	391	V	1.1	387	408
1USV	G H	G	398	K	1.3	387	408
1UTB	A B	A	109	M	1.1	105	123
1UTB	A B	A	116	M	1.4	105	123
1UTB	A B	A	235	I	1.3	232	238
1UTB	A B	B	109	M	1.0	105	123
1UTB	A B	B	116	M	1.4	105	123
1UTB	A B	B	235	I	1.1	232	238
1UUZ	A D	A	95	M	2.0	93	97
1UUZ	A D	D	123	W	2.9	120	125
1UVQ	A B	A	73	L	2.0	59	80
1UVQ	A B	A	76	M	1.8	59	80
1UVQ	A B	A	77	I	1.7	59	80
1UVQ	A B	A	79	R	2.1	59	80
1UVQ	A B	B	57	D	1.1	55	63
1UVQ	A B	B	87	F	1.3	65	92
1UVQ	A B	B	89	G	10.3	65	92
1UVQ	A B	B	91	L	1.7	65	92
1UVQ	A C	A	71	H	2.4	59	80
1UVQ	A C	A	72	N	4.5	59	80
1UVQ	A C	A	75	I	1.0	59	80
1UVQ	B C	B	57	D	1.1	55	63
1UVQ	B C	B	60	Y	1.6	55	63
1UVQ	B C	B	61	W	2.8	55	63
1UVQ	B C	B	78	V	1.3	65	92
1UW4	B C	B	998	R	1.3	993	1012
1UW4	B C	C	111	R	1.3	104	115
1UW4	D C	D	843	I	1.6	839	860
1UW4	D C	D	847	D	1.4	839	860

1UW4	D C	D	850	L	1.0	839	860
1UW4	D C	D	855	L	1.7	839	860
1UW4	D C	D	858	E	1.9	839	860
1UW4	D C	D	867	R	1.1	865	881
1UWE	L H	L	124	Q	1.2	122	127
1UWE	U V	U	124	Q	1.5	122	128
1UWE	X Y	X	124	Q	1.1	122	127
1UWX	K M	K	125	Q	1.3	123	128
1UWX	L H	L	125	Q	1.3	123	128
1UWX	M B	B	38	Y	1.7	28	42
1UYW	L H	L	124	Q	1.6	122	127
1UYW	N M	N	123	E	1.1	122	127
1UYW	N M	N	124	Q	1.5	122	127
1UZD	A F	A	70	W	2.4	70	75
1UZD	A F	A	73	G	2.0	70	75
1UZD	A F	A	74	L	1.2	70	75
1UZD	A I	A	194	R	2.5	182	196
1UZD	A I	A	421	R	1.9	413	433
1UZD	A I	A	425	E	1.1	413	433
1UZD	A I	I	29	Q	1.4	23	36
1UZD	A T	A	186	G	39.3	182	196
1UZD	A T	A	190	Y	1.9	182	196
1UZD	A T	A	191	E	1.6	182	196
1UZD	A T	A	223	E	3.7	214	233
1UZD	A T	A	226	Y	1.7	214	233
1UZD	B C	B	194	R	2.2	182	195
1UZD	B C	B	421	R	1.5	413	433
1UZD	B C	B	454	E	1.5	453	462
1UZD	B C	C	32	Y	2.4	23	36
1UZD	B T	B	70	W	2.8	70	75
1UZD	B T	B	73	G	2.6	70	75
1UZD	B T	B	74	L	1.3	70	75
1UZD	E F	E	194	R	1.9	182	195
1UZD	E F	E	421	R	1.7	413	433
1UZD	E F	E	425	E	1.1	413	433
1UZD	E F	F	29	Q	2.0	23	36
1UZD	E F	F	32	Y	3.1	23	36
1UZD	E I	E	70	W	2.7	70	75
1UZD	E I	E	73	G	5.1	70	75
1UZD	E I	E	74	L	1.2	70	75
1UZD	E I	E	80	Y	1.2	77	81
1UZD	E J	E	186	G	69.7	182	195
1UZD	E J	E	190	Y	1.8	182	195
1UZD	E J	E	191	E	1.6	182	195
1UZD	E J	E	223	E	4.0	214	233
1UZD	E J	E	226	Y	1.8	214	233
1UZD	H J	H	194	R	2.3	182	196
1UZD	H J	H	421	R	1.6	413	433
1UZD	H J	H	425	E	1.3	413	433
1UZD	H J	J	32	Y	2.9	23	36
1UZD	H P	H	70	W	2.7	70	75
1UZD	H P	H	73	G	3.8	70	75
1UZD	H P	H	74	L	1.3	70	75
1UZD	H W	H	186	G	55.9	182	196
1UZD	H W	H	187	R	1.1	182	196
1UZD	H W	H	190	Y	1.7	182	196
1UZD	H W	H	191	E	1.2	182	196
1UZD	H W	H	223	E	7.3	214	233
1UZD	H W	H	226	Y	1.3	214	233
1UZD	H W	H	227	K	3.9	214	233

1UZD	H W	H	230	A	3.7	214	233
1UZD	K I	K	186	G	30.3	182	196
1UZD	K I	K	187	R	2.0	182	196
1UZD	K I	K	190	Y	1.8	182	196
1UZD	K I	K	191	E	1.3	182	196
1UZD	K I	K	222	A	1.2	214	233
1UZD	K I	K	223	E	4.9	214	233
1UZD	K I	K	226	Y	1.4	214	233
1UZD	K I	K	227	K	1.3	214	233
1UZD	K I	K	230	A	1.1	214	233
1UZD	K J	K	70	W	2.6	70	75
1UZD	K J	K	74	L	1.3	70	75
1UZD	K P	K	194	R	2.3	182	196
1UZD	K P	K	421	R	1.3	413	433
1UZD	K P	K	425	E	1.0	413	433
1UZD	K P	K	432	N	1.0	413	433
1UZD	K P	P	32	Y	2.2	23	36
1UZD	O C	O	70	W	2.6	70	75
1UZD	O C	O	73	G	2.4	70	75
1UZD	O C	O	74	L	1.2	70	75
1UZD	O M	O	186	G	65.7	182	195
1UZD	O M	O	187	R	1.4	182	195
1UZD	O M	O	190	Y	1.7	182	195
1UZD	O M	O	191	E	1.5	182	195
1UZD	O M	O	223	E	4.2	214	233
1UZD	O M	O	226	Y	1.7	214	233
1UZD	O T	O	194	R	2.4	182	195
1UZD	O T	T	32	Y	1.4	23	36
1UZD	R M	R	194	R	1.7	182	196
1UZD	R M	R	421	R	2.5	413	433
1UZD	R M	R	432	N	1.1	413	433
1UZD	R M	M	29	Q	2.1	23	36
1UZD	R M	M	32	Y	2.2	23	36
1UZD	R P	R	186	G	37.5	182	196
1UZD	R P	R	187	R	2.0	182	196
1UZD	R P	R	190	Y	1.5	182	196
1UZD	R P	R	191	E	1.4	182	196
1UZD	R P	R	223	E	3.5	214	233
1UZD	R P	R	226	Y	2.3	214	233
1UZD	R W	R	70	W	2.6	70	75
1UZD	R W	R	73	G	1.6	70	75
1UZD	R W	R	74	L	1.2	70	75
1UZD	V C	V	186	G	44.4	182	195
1UZD	V C	V	190	Y	1.8	182	195
1UZD	V C	V	191	E	1.5	182	195
1UZD	V C	V	219	L	6.1	214	233
1UZD	V C	V	223	E	3.9	214	233
1UZD	V C	V	226	Y	1.6	214	233
1UZD	V M	V	70	W	2.6	70	75
1UZD	V M	V	73	G	2.3	70	75
1UZD	V M	V	74	L	1.2	70	75
1UZD	V W	V	194	R	1.9	182	195
1UZD	V W	V	421	R	1.4	413	433
1UZD	V W	W	32	Y	1.7	23	36
1UZH	A F	A	70	W	2.5	70	75
1UZH	A F	A	74	L	1.3	70	75
1UZH	A T	A	184	N	2.0	182	195
1UZH	A T	A	186	G	112.0	182	195
1UZH	A T	A	187	R	2.4	182	195
1UZH	A T	A	190	Y	1.2	182	195

1UZH	A T	A	191	E	2.1	182	195
1UZH	B C	B	194	R	2.8	182	195
1UZH	B C	B	421	R	2.2	413	433
1UZH	B C	B	425	E	1.2	413	433
1UZH	B C	B	451	W	1.2	441	452
1UZH	B C	B	454	E	1.5	453	462
1UZH	B C	C	29	Q	1.8	23	36
1UZH	B C	C	32	Y	2.8	23	36
1UZH	B F	B	186	G	144.7	182	195
1UZH	B F	B	191	E	1.5	182	195
1UZH	E F	E	194	R	2.8	182	195
1UZH	E F	E	421	R	1.3	413	433
1UZH	E F	E	425	E	1.2	413	433
1UZH	E F	E	451	W	1.3	441	452
1UZH	E F	E	454	E	1.1	453	462
1UZH	E F	F	32	Y	2.0	23	36
1UZH	E I	E	70	W	2.6	70	75
1UZH	E I	E	73	G	1.2	70	75
1UZH	E I	E	74	L	1.2	70	75
1UZH	H P	H	70	W	2.6	70	75
1UZH	H P	H	74	L	1.3	70	75
1UZH	H W	H	184	N	2.0	182	195
1UZH	H W	H	186	G	111.5	182	195
1UZH	H W	H	190	Y	1.0	182	195
1UZH	H W	H	191	E	1.8	182	195
1UZH	H W	H	227	K	1.0	214	233
1UZH	K I	K	184	N	1.5	182	195
1UZH	K I	K	186	G	99.9	182	195
1UZH	K I	K	187	R	1.0	182	195
1UZH	K I	K	190	Y	1.1	182	195
1UZH	K I	K	191	E	1.4	182	195
1UZH	K I	K	227	K	1.2	214	233
1UZH	K J	K	70	W	2.7	70	75
1UZH	K J	K	74	L	1.2	70	75
1UZH	K P	K	194	R	2.5	182	195
1UZH	K P	K	421	R	1.9	413	433
1UZH	K P	K	425	E	1.2	413	433
1UZH	K P	K	451	W	1.3	441	452
1UZH	K P	K	454	E	1.0	453	462
1UZH	K P	P	32	Y	3.2	23	36
1UZH	O C	O	70	W	2.6	70	75
1UZH	O C	O	74	L	1.3	70	75
1UZH	O M	O	186	G	157.6	182	195
1UZH	O M	O	191	E	1.5	182	195
1UZH	O T	O	194	R	2.2	182	195
1UZH	O T	O	421	R	2.2	413	433
1UZH	O T	O	451	W	1.1	441	452
1UZH	O T	O	454	E	1.1	453	462
1UZH	O T	T	32	Y	1.9	23	36
1UZH	R M	R	194	R	1.7	182	195
1UZH	R M	R	421	R	1.5	413	433
1UZH	R M	R	425	E	1.1	413	433
1UZH	R M	R	451	W	1.2	441	452
1UZH	R M	R	454	E	1.4	453	462
1UZH	R M	M	32	Y	2.1	23	36
1UZH	R P	R	186	G	98.4	182	195
1UZH	R P	R	190	Y	4.1	182	195
1UZH	R P	R	191	E	1.0	182	195
1UZH	R W	R	70	W	2.7	70	75
1UZH	R W	R	74	L	1.8	70	75

1UZH	V C	V	186	G	132.0	182	195
1UZH	V C	V	190	Y	1.9	182	195
1UZH	V C	V	191	E	1.6	182	195
1UZH	V C	V	220	F	1.0	214	233
1UZH	V M	V	70	W	2.7	70	75
1UZH	V M	V	74	L	1.2	70	75
1UZH	V W	V	194	R	1.0	182	195
1UZH	V W	V	421	R	1.2	413	433
1UZH	V W	V	425	E	1.1	413	433
1UZH	V W	V	451	W	1.2	441	452
1UZH	V W	V	454	E	1.1	453	462
1UZH	V W	W	32	Y	3.0	23	36
1V02	B E	B	270	F	1.1	270	293
1V02	B E	B	271	L	1.4	270	293
1V02	B E	E	270	F	1.4	270	293
1V02	F E	F	270	F	1.8	270	293
1V02	F E	F	298	F	2.8	298	305
1V02	F E	F	301	R	1.0	298	305
1V02	F E	F	302	V	1.2	298	305
1V02	F E	E	270	F	2.2	270	293
1V02	F E	E	298	F	2.2	298	305
1V02	F E	E	301	R	1.3	298	305
1V02	F E	E	302	V	1.2	298	305
1V29	A B	A	28	F	1.5	26	43
1V29	A B	A	29	W	2.5	26	43
1V29	A B	A	32	R	2.1	26	43
1V29	A B	A	34	K	1.3	26	43
1V29	A B	A	36	L	2.4	26	43
1V29	A B	A	39	L	1.6	26	43
1V29	A B	A	40	L	1.4	26	43
1V29	A B	A	51	I	1.1	48	62
1V29	A B	A	53	R	1.6	48	62
1V29	A B	A	54	V	1.6	48	62
1V29	A B	A	55	I	1.6	48	62
1V29	A B	A	58	Y	1.0	48	62
1V29	A B	A	144	R	1.3	141	150
1V29	A B	A	148	V	1.3	141	150
1V29	A B	A	149	K	1.5	141	150
1V29	A B	B	33	R	1.1	30	45
1V29	A B	B	34	L	1.3	30	45
1V29	A B	B	36	F	4.6	30	45
1V29	A B	B	37	G	2.4	30	45
1V29	A B	B	38	L	2.5	30	45
1V29	A B	B	41	G	5.5	30	45
1V29	A B	B	56	R	1.3	53	61
1V29	A B	B	66	D	1.6	64	70
1V29	A B	B	95	L	1.3	92	105
1V29	A B	B	96	E	1.5	92	105
1V29	A B	B	98	R	1.1	92	105
1V29	A B	B	99	T	1.4	92	105
1V29	A B	B	102	F	2.6	92	105
1V29	A B	B	126	L	1.1	116	129
1V4U	A B	A	32	R	1.3	22	37
1V4U	A B	A	105	H	1.2	97	115
1V4U	A B	A	109	V	1.2	97	115
1V4U	A B	A	124	H	4.1	121	139
1V4U	A B	B	30	R	2.4	20	35
1V4U	A B	B	34	V	1.7	20	35
1V4U	A B	B	124	V	1.2	124	142
1V4U	A D	A	97	P	1.3	97	115

1V4U	A D	D	36	P	1.0	36	41
1V4U	A D	D	37	W	3.8	36	41
1V4U	A D	D	102	N	1.7	100	119
1V4U	C B	B	37	W	3.0	36	41
1V4U	C D	C	32	R	2.8	22	37
1V4U	C D	C	36	V	1.2	22	37
1V4U	C D	C	105	H	1.3	97	115
1V4U	C D	C	109	V	1.0	97	115
1V4U	C D	C	124	H	3.9	121	141
1V4U	C D	D	30	R	3.0	20	35
1V4U	C D	D	34	V	1.1	20	35
1V4U	C D	D	55	K	1.2	51	56
1V4U	C D	D	124	V	1.1	124	142
1V4U	C D	D	127	Q	2.8	124	142
1V54	A B	A	51	D	3.1	51	87
1V54	A B	A	299	V	1.7	299	328
1V54	A B	A	306	T	1.1	299	328
1V54	A B	A	314	I	1.3	299	328
1V54	A B	A	321	F	3.3	299	328
1V54	A B	A	324	L	1.1	299	328
1V54	A B	A	327	L	1.0	299	328
1V54	A B	A	342	L	1.4	336	360
1V54	A B	A	346	F	2.3	336	360
1V54	A B	A	353	L	2.4	336	360
1V54	A B	A	357	V	3.8	336	360
1V54	A B	A	363	L	2.7	361	368
1V54	A B	A	366	V	1.2	361	368
1V54	A B	A	367	L	2.0	361	368
1V54	A B	A	430	F	1.0	407	434
1V54	A B	A	433	L	1.4	407	434
1V54	A B	A	450	W	2.6	448	479
1V54	A B	B	20	L	1.1	15	46
1V54	A B	B	23	F	2.1	15	46
1V54	A B	B	24	H	1.4	15	46
1V54	A B	B	31	V	1.2	15	46
1V54	A B	B	38	V	1.6	15	46
1V54	A B	B	39	L	1.4	15	46
1V54	A B	B	42	I	1.1	15	46
1V54	A B	B	73	L	2.2	66	88
1V54	A B	B	84	L	1.5	66	88
1V54	A B	B	85	Y	1.2	66	88
1V54	A C	A	96	R	3.5	95	103
1V54	A C	A	100	M	1.0	95	103
1V54	A C	A	107	P	2.0	104	118
1V54	A C	A	148	F	2.8	141	171
1V54	A C	A	152	L	1.5	141	171
1V54	A C	A	162	I	1.8	141	171
1V54	A C	A	196	L	1.4	183	215
1V54	A C	A	208	M	1.0	183	215
1V54	A C	A	230	L	2.0	228	261
1V54	A C	A	234	L	1.7	228	261
1V54	A C	C	15	P	1.0	15	37
1V54	A C	C	17	P	1.4	15	37
1V54	A C	C	18	L	1.1	15	37
1V54	A C	C	20	G	3.2	15	37
1V54	A C	C	25	L	2.0	15	37
1V54	A C	C	35	F	1.5	15	37
1V54	A C	C	57	W	2.6	41	69
1V54	A C	C	64	E	2.3	41	69
1V54	A C	C	81	Y	1.5	73	107

1V54	A C	C	82	G	18.1	73	107
1V54	A C	C	85	L	1.5	73	107
1V54	A C	C	92	L	1.1	73	107
1V54	A C	C	93	F	1.8	73	107
1V54	A C	C	96	G	57.3	73	107
1V54	A C	C	97	F	3.7	73	107
1V54	A C	C	99	W	4.2	73	107
1V54	A C	C	103	H	3.0	73	107
1V54	A D	A	408	T	1.1	407	434
1V54	A D	A	411	K	2.3	407	434
1V54	A D	A	412	I	1.5	407	434
1V54	A D	A	416	I	1.4	407	434
1V54	A D	A	459	F	1.9	448	479
1V54	A D	A	463	T	1.5	448	479
1V54	A D	D	77	E	1.9	77	104
1V54	A D	D	81	V	1.6	77	104
1V54	A D	D	88	F	2.2	77	104
1V54	A D	D	89	I	1.4	77	104
1V54	A D	D	92	T	1.2	77	104
1V54	A D	D	96	L	2.5	77	104
1V54	A F	A	270	Y	1.2	270	285
1V54	A F	A	492	L	2.3	492	496
1V54	A F	A	495	L	1.9	492	496
1V54	A L	A	5	R	1.3	3	8
1V54	A L	A	6	W	3.8	3	8
1V54	A L	A	25	W	2.3	12	41
1V54	A L	A	36	L	2.3	12	41
1V54	A L	A	469	V	1.4	448	479
1V54	A L	A	473	W	3.2	448	479
1V54	A L	A	476	F	1.9	448	479
1V54	A L	L	21	L	1.0	18	45
1V54	A L	L	22	L	1.0	18	45
1V54	A L	L	25	M	1.4	18	45
1V54	A L	L	28	F	2.2	18	45
1V54	A L	L	29	F	1.3	18	45
1V54	A L	L	32	G	1.9	18	45
1V54	A L	L	33	F	2.7	18	45
1V54	A L	L	36	P	1.4	18	45
1V54	A L	L	37	F	2.2	18	45
1V54	A L	L	39	I	1.3	18	45
1V54	A L	L	40	V	1.2	18	45
1V54	A L	L	43	Q	1.7	18	45
1V54	A M	A	409	W	1.6	407	434
1V54	A M	A	466	M	2.0	448	479
1V54	A M	A	469	V	1.1	448	479
1V54	A M	A	470	F	3.0	448	479
1V54	A M	A	473	W	1.4	448	479
1V54	A M	A	474	E	1.9	448	479
1V54	A M	A	478	S	1.0	448	479
1V54	A M	M	15	Q	1.8	12	36
1V54	A M	M	19	L	3.5	12	36
1V54	A M	M	23	F	2.9	12	36
1V54	A M	M	26	F	2.7	12	36
1V54	A T	A	186	W	1.7	183	215
1V54	A T	A	197	L	1.7	183	215
1V54	A T	A	271	M	2.3	270	285
1V54	A T	A	274	V	1.6	270	285
1V54	A T	A	275	W	1.3	270	285
1V54	A T	A	278	M	2.4	270	285
1V54	A T	A	281	G	5.2	270	285

1V54	A T	T	18	F	2.8	13	36
1V54	A T	T	22	G	20.3	13	36
1V54	B D	D	115	W	4.1	113	126
1V54	B D	D	133	G	5.5	130	137
1V54	B H	H	68	W	1.9	66	79
1V54	B I	B	22	H	1.6	15	46
1V54	B I	B	29	M	2.3	15	46
1V54	B I	B	32	F	1.1	15	46
1V54	B I	B	40	Y	1.3	15	46
1V54	B I	B	44	L	1.5	15	46
1V54	B I	B	218	Y	1.8	216	226
1V54	B I	I	13	L	1.4	12	36
1V54	B I	I	31	F	1.2	12	36
1V54	B I	I	35	Y	1.2	12	36
1V54	B I	I	47	Y	2.8	37	53
1V54	B I	I	60	F	3.0	56	67
1V54	C F	F	9	D	1.1	9	13
1V54	C F	F	16	L	1.1	16	26
1V54	C G	C	34	W	1.5	15	37
1V54	C G	C	132	L	1.4	129	153
1V54	C G	C	142	V	1.2	129	153
1V54	C G	C	149	H	1.5	129	153
1V54	C G	C	165	I	1.0	156	184
1V54	C G	C	172	Y	1.1	156	184
1V54	C G	C	182	Y	1.0	156	184
1V54	C G	G	16	W	2.5	13	36
1V54	C G	G	25	L	1.0	13	36
1V54	C G	G	28	V	1.7	13	36
1V54	C H	H	30	W	2.7	26	46
1V54	C J	C	15	P	1.0	15	37
1V54	C J	C	16	W	2.3	15	37
1V54	C J	C	56	Q	1.0	41	69
1V54	C J	C	59	R	1.0	41	69
1V54	C J	C	60	D	2.1	41	69
1V54	C J	C	63	R	1.4	41	69
1V54	C J	C	67	F	2.9	41	69
1V54	C J	C	68	Q	1.2	41	69
1V54	C J	C	223	L	1.1	192	224
1V54	C J	J	5	V	1.4	5	12
1V54	C J	J	28	D	1.2	26	55
1V54	C J	J	32	Y	1.3	26	55
1V54	C J	J	35	T	1.5	26	55
1V54	C J	J	42	G	24.4	26	55
1V54	D E	D	44	E	1.5	35	46
1V54	D E	D	56	K	2.8	53	64
1V54	D E	D	60	Y	2.9	53	64
1V54	D E	D	68	F	3.3	68	72
1V54	D E	E	34	N	1.9	26	37
1V54	D E	E	56	R	1.0	45	58
1V54	D E	E	61	F	2.7	61	76
1V54	D E	E	66	R	4.8	61	76
1V54	D E	E	69	E	2.3	61	76
1V54	D I	D	131	I	3.8	130	137
1V54	D I	I	46	A	2.0	37	53
1V54	D I	I	47	Y	2.0	37	53
1V54	D I	I	50	F	2.6	37	53
1V54	D I	I	51	Y	2.0	37	53
1V54	D I	I	62	E	1.1	56	67
1V54	D K	D	79	K	1.0	77	104
1V54	D K	D	80	T	1.1	77	104

1V54	D K	D	83	G	196.5	77	104
1V54	D K	D	87	F	1.3	77	104
1V54	D K	D	90	G	35.2	77	104
1V54	D K	D	97	I	2.1	77	104
1V54	D K	D	118	K	1.4	113	126
1V54	D K	D	121	K	1.3	113	126
1V54	D K	D	122	R	1.1	113	126
1V54	D K	D	125	D	1.2	113	126
1V54	D K	K	10	H	2.9	9	13
1V54	D K	K	14	G	2.3	14	35
1V54	D K	K	17	V	1.1	14	35
1V54	D K	K	18	L	2.2	14	35
1V54	D K	K	21	G	63.2	14	35
1V54	D K	K	24	F	2.9	14	35
1V54	D K	K	28	V	1.2	14	35
1V54	D K	K	32	M	1.1	14	35
1V54	D M	D	103	V	1.5	77	104
1V54	D M	M	27	L	1.1	12	36
1V54	D M	M	35	Y	1.6	12	36
1V54	E F	E	27	W	2.2	26	37
1V54	E I	E	81	I	2.0	79	89
1V54	E I	E	84	Y	3.8	79	89
1V54	E I	I	12	L	1.6	12	36
1V54	G H	H	75	R	1.2	66	79
1V54	J L	L	42	H	1.1	18	45
1V54	L M	L	19	W	1.7	18	45
1V54	L M	L	22	L	1.7	18	45
1V54	L M	L	33	F	1.4	18	45
1V54	L M	L	37	F	1.9	18	45
1V54	L M	L	38	F	1.8	18	45
1V54	L M	M	26	F	1.5	12	36
1V54	L M	M	33	V	1.9	12	36
1V54	L M	M	40	Y	1.1	37	42
1V54	N G	N	186	W	1.0	183	215
1V54	N G	N	197	L	1.6	183	215
1V54	N G	N	275	W	1.2	270	285
1V54	N G	N	278	M	2.0	270	285
1V54	N G	N	281	G	1.5	270	285
1V54	N G	G	18	F	2.8	13	36
1V54	N G	G	22	G	13.5	13	36
1V54	N O	N	51	D	3.3	51	87
1V54	N O	N	299	V	2.0	299	328
1V54	N O	N	300	D	1.1	299	328
1V54	N O	N	314	I	1.6	299	328
1V54	N O	N	321	F	4.0	299	328
1V54	N O	N	346	F	2.3	336	360
1V54	N O	N	353	L	2.2	336	360
1V54	N O	N	363	L	1.3	361	368
1V54	N O	N	365	I	1.1	361	368
1V54	N O	N	430	F	1.5	407	434
1V54	N O	N	433	L	1.0	407	434
1V54	N O	N	450	W	1.7	448	479
1V54	N O	O	20	L	1.2	15	46
1V54	N O	O	31	V	1.1	15	46
1V54	N O	O	38	V	1.4	15	46
1V54	N O	O	39	L	1.5	15	46
1V54	N O	O	73	L	2.0	66	89
1V54	N O	O	80	S	1.0	66	89
1V54	N O	O	81	L	1.9	66	89
1V54	N O	O	84	L	1.5	66	89

1V54	N O	O	85	Y	1.9	66	89
1V54	N P	N	96	R	4.4	95	118
1V54	N P	N	100	M	1.1	95	118
1V54	N P	N	103	W	1.2	95	118
1V54	N P	N	107	P	4.0	95	118
1V54	N P	N	148	F	2.8	141	171
1V54	N P	N	152	L	1.5	141	171
1V54	N P	N	162	I	1.8	141	171
1V54	N P	N	196	L	1.5	183	215
1V54	N P	N	208	M	1.3	183	215
1V54	N P	N	230	L	1.6	228	261
1V54	N P	N	234	L	1.8	228	261
1V54	N P	P	15	P	1.0	15	37
1V54	N P	P	16	W	1.6	15	37
1V54	N P	P	17	P	1.6	15	37
1V54	N P	P	18	L	1.2	15	37
1V54	N P	P	20	G	2.5	15	37
1V54	N P	P	25	L	2.2	15	37
1V54	N P	P	35	F	1.4	15	37
1V54	N P	P	57	W	2.4	41	69
1V54	N P	P	64	E	2.3	41	69
1V54	N P	P	81	Y	1.7	73	107
1V54	N P	P	82	G	18.7	73	107
1V54	N P	P	85	L	1.8	73	107
1V54	N P	P	92	L	1.1	73	107
1V54	N P	P	93	F	1.7	73	107
1V54	N P	P	96	G	40.4	73	107
1V54	N P	P	97	F	3.3	73	107
1V54	N P	P	99	W	4.3	73	107
1V54	N P	P	103	H	3.0	73	107
1V54	N P	P	199	V	1.5	192	224
1V54	N Q	N	408	T	1.3	407	434
1V54	N Q	N	411	K	2.8	407	434
1V54	N Q	N	412	I	2.0	407	434
1V54	N Q	N	416	I	1.5	407	434
1V54	N Q	N	459	F	2.1	448	479
1V54	N Q	N	460	I	3.1	448	479
1V54	N Q	N	463	T	1.4	448	479
1V54	N Q	Q	77	E	2.3	77	104
1V54	N Q	Q	81	V	1.9	77	104
1V54	N Q	Q	88	F	2.0	77	104
1V54	N Q	Q	89	I	1.7	77	104
1V54	N Q	Q	92	T	3.2	77	104
1V54	N Q	Q	96	L	2.9	77	104
1V54	N S	N	492	L	2.3	492	496
1V54	N S	N	495	L	1.7	492	496
1V54	N W	W	50	L	1.3	26	55
1V54	N X	N	449	M	1.1	448	479
1V54	N Y	N	5	R	1.9	3	8
1V54	N Y	N	6	W	4.0	3	8
1V54	N Y	N	25	W	2.4	12	41
1V54	N Y	N	36	L	2.3	12	41
1V54	N Y	N	469	V	1.5	448	479
1V54	N Y	N	473	W	3.9	448	479
1V54	N Y	N	476	F	2.0	448	479
1V54	N Y	N	477	A	1.0	448	479
1V54	N Y	Y	19	W	1.1	18	45
1V54	N Y	Y	21	L	2.0	18	45
1V54	N Y	Y	22	L	1.0	18	45
1V54	N Y	Y	25	M	1.3	18	45

1V54	N Y	Y	28	F	2.3	18	45
1V54	N Y	Y	29	F	1.7	18	45
1V54	N Y	Y	32	G	2.3	18	45
1V54	N Y	Y	33	F	2.5	18	45
1V54	N Y	Y	36	P	1.4	18	45
1V54	N Y	Y	37	F	2.7	18	45
1V54	N Y	Y	39	I	1.3	18	45
1V54	N Y	Y	40	V	1.3	18	45
1V54	N Z	N	409	W	1.1	407	434
1V54	N Z	N	462	L	1.2	448	479
1V54	N Z	N	466	M	1.7	448	479
1V54	N Z	N	469	V	1.2	448	479
1V54	N Z	N	470	F	3.5	448	479
1V54	N Z	N	473	W	1.7	448	479
1V54	N Z	N	474	E	1.3	448	479
1V54	N Z	Z	15	Q	2.0	12	36
1V54	N Z	Z	18	G	1.2	12	36
1V54	N Z	Z	19	L	1.2	12	36
1V54	N Z	Z	22	T	4.5	12	36
1V54	N Z	Z	26	F	2.8	12	36
1V54	O Q	Q	115	W	4.0	113	126
1V54	O Q	Q	133	G	13.8	130	137
1V54	O U	U	62	S	1.2	54	64
1V54	O V	O	22	H	1.2	15	46
1V54	O V	O	25	D	1.0	15	46
1V54	O V	O	29	M	1.2	15	46
1V54	O V	O	33	L	1.3	15	46
1V54	O V	O	218	Y	1.8	216	226
1V54	O V	V	13	L	1.2	12	36
1V54	O V	V	35	Y	1.1	12	36
1V54	O V	V	47	Y	2.6	37	51
1V54	O V	V	50	F	1.1	37	51
1V54	O V	V	60	F	3.2	56	67
1V54	P S	S	17	E	1.3	16	26
1V54	P T	P	34	W	1.7	15	37
1V54	P T	P	132	L	1.5	129	153
1V54	P T	P	142	V	1.2	129	153
1V54	P T	P	149	H	1.3	129	153
1V54	P T	P	165	I	1.0	156	184
1V54	P T	P	172	Y	1.1	156	184
1V54	P T	T	16	W	2.6	13	36
1V54	P T	T	28	V	1.6	13	36
1V54	P U	U	30	W	2.7	26	46
1V54	P W	P	16	W	2.4	15	37
1V54	P W	P	56	Q	1.2	41	69
1V54	P W	P	59	R	1.2	41	69
1V54	P W	P	60	D	1.4	41	69
1V54	P W	P	63	R	2.5	41	69
1V54	P W	P	67	F	3.6	41	69
1V54	P W	P	68	Q	1.4	41	69
1V54	P W	W	5	V	1.4	5	12
1V54	P W	W	28	D	2.3	26	55
1V54	P W	W	32	Y	1.3	26	55
1V54	P W	W	35	T	1.8	26	55
1V54	P W	W	42	G	25.2	26	55
1V54	Q R	Q	44	E	2.3	35	46
1V54	Q R	Q	56	K	1.8	53	64
1V54	Q R	Q	60	Y	3.0	53	64
1V54	Q R	Q	68	F	4.8	68	72
1V54	Q R	R	34	N	2.0	26	37

1V54	Q R	R	56	R	1.1	45	58
1V54	Q R	R	61	F	2.3	61	76
1V54	Q R	R	66	R	4.7	61	76
1V54	Q R	R	69	E	1.8	61	76
1V54	Q V	Q	131	I	1.8	130	137
1V54	Q V	V	50	F	1.3	37	51
1V54	Q V	V	62	E	1.1	56	67
1V54	Q X	Q	79	K	1.3	77	104
1V54	Q X	Q	83	G	200.0	77	104
1V54	Q X	Q	87	F	1.3	77	104
1V54	Q X	Q	90	G	32.2	77	104
1V54	Q X	Q	97	I	1.7	77	104
1V54	Q X	Q	114	E	1.0	113	126
1V54	Q X	Q	118	K	2.4	113	126
1V54	Q X	Q	121	K	1.1	113	126
1V54	Q X	Q	122	R	1.1	113	126
1V54	Q X	Q	125	D	1.1	113	126
1V54	Q X	X	10	H	2.7	9	13
1V54	Q X	X	14	G	1.2	14	35
1V54	Q X	X	17	V	1.0	14	35
1V54	Q X	X	18	L	2.1	14	35
1V54	Q X	X	21	G	66.4	14	35
1V54	Q X	X	24	F	2.4	14	35
1V54	Q X	X	32	M	1.0	14	35
1V54	Q Z	Q	98	W	1.3	77	104
1V54	Q Z	Q	103	V	1.0	77	104
1V54	R V	R	81	I	1.7	81	89
1V54	R V	R	84	Y	2.7	81	89
1V54	R V	V	12	L	1.3	12	36
1V54	T U	U	75	R	1.4	66	79
1V54	W Y	Y	42	H	1.2	18	45
1V54	Y Z	Y	19	W	1.2	18	45
1V54	Y Z	Y	22	L	1.5	18	45
1V54	Y Z	Y	33	F	1.6	18	45
1V54	Y Z	Y	37	F	2.0	18	45
1V54	Y Z	Y	38	F	2.4	18	45
1V54	Y Z	Y	41	R	2.0	18	45
1V54	Y Z	Z	26	F	1.4	12	36
1V54	Y Z	Z	29	P	1.3	12	36
1V54	Y Z	Z	32	W	1.0	12	36
1V54	Y Z	Z	33	V	2.0	12	36
1V54	Y Z	Z	40	Y	1.2	37	42
1V5I	A B	A	104	Y	3.4	104	117
1V5I	A B	A	108	I	1.4	104	117
1V5I	A B	A	112	E	1.5	104	117
1V75	A B	A	31	R	2.6	21	36
1V75	A B	A	35	V	1.0	21	36
1V75	A B	A	110	G	74.1	95	114
1V75	A B	B	30	R	3.7	20	35
1V75	A B	B	112	I	1.2	100	118
1V7M	H V	V	102	G	1.0	91	109
1V7N	I X	X	98	R	1.5	89	103
1V7N	I X	X	105	Q	2.0	104	109
1V7N	K Z	Z	101	L	1.1	95	108
1V7N	L H	L	123	Q	1.5	121	127
1V7N	M Z	M	186	E	1.0	182	187
1V7N	O K	O	123	Q	1.1	121	126
1VCB	B C	B	76	Y	3.8	67	84
1VCB	B C	B	101	L	1.5	97	111
1VCB	B C	B	104	L	2.6	97	111

1VCB	B C	C	161	R	2.2	158	170
1VCB	B C	C	164	Q	1.2	158	170
1VCB	E F	E	76	Y	2.5	67	84
1VCB	E F	E	80	K	1.2	67	84
1VCB	E F	E	101	L	1.6	97	111
1VCB	E F	E	104	L	2.7	97	111
1VCB	E F	F	158	L	1.5	158	170
1VCB	E F	F	161	R	1.5	158	170
1VCB	G H	G	34	I	1.2	24	35
1VCB	G H	H	67	S	1.0	67	84
1VCB	G H	H	68	H	1.7	67	84
1VCB	G H	H	75	M	1.2	67	84
1VCB	G H	H	82	R	1.4	67	84
1VCB	H F	H	41	T	1.4	40	46
1VCB	H F	H	109	F	1.1	97	111
1VCB	H I	H	76	Y	3.4	67	84
1VCB	H I	H	101	L	1.5	97	111
1VCB	H I	H	104	L	2.1	97	111
1VCB	H I	I	158	L	2.4	158	170
1VCB	H I	I	161	R	2.4	158	170
1VCB	H I	I	166	V	1.1	158	170
1VCB	H I	I	169	L	1.0	158	170
1VCB	J K	K	68	H	2.3	67	84
1VCB	J K	K	75	M	1.3	67	84
1VCB	J K	K	82	R	1.6	67	84
1VCB	K L	K	76	Y	3.4	67	84
1VCB	K L	K	101	L	1.5	97	111
1VCB	K L	K	104	L	2.4	97	111
1VCB	K L	L	158	L	3.4	158	170
1VCB	K L	L	161	R	2.4	158	170
1VCB	K L	L	166	V	1.0	158	170
1VCB	K L	L	169	L	1.0	158	170
1VF5	A B	A	46	I	1.0	35	55
1VF5	A B	A	66	Y	1.2	65	74
1VF5	A B	A	80	W	1.0	79	107
1VF5	A B	A	84	S	1.1	79	107
1VF5	A B	A	85	I	1.0	79	107
1VF5	A B	A	87	R	1.9	79	107
1VF5	A B	A	105	Y	2.5	79	107
1VF5	A B	A	115	E	4.9	115	139
1VF5	A B	A	122	V	1.5	115	139
1VF5	A B	A	132	G	1.0	115	139
1VF5	A B	A	145	Y	1.5	142	151
1VF5	A B	A	146	W	3.5	142	151
1VF5	A B	B	51	I	1.7	39	58
1VF5	A B	B	111	V	1.1	96	112
1VF5	A B	B	133	F	4.5	129	137
1VF5	A C	A	80	W	1.9	79	107
1VF5	A C	C	254	R	1.7	252	276
1VF5	A D	A	79	G	5.4	79	107
1VF5	A D	A	82	I	1.0	79	107
1VF5	A D	D	37	P	5.2	22	43
1VF5	A E	E	17	G	263.1	2	24
1VF5	A Q	A	168	L	1.0	162	171
1VF5	B C	B	52	V	1.2	39	58
1VF5	B C	B	56	V	1.4	39	58
1VF5	B C	C	258	M	1.4	252	276
1VF5	B C	C	265	V	1.2	252	276
1VF5	B G	B	46	G	93.8	39	58
1VF5	C D	C	264	L	1.3	252	276

1VF5	C G	C	259	I	1.0	252	276
1VF5	C G	G	11	L	1.4	10	16
1VF5	C H	C	270	L	1.1	252	276
1VF5	E F	F	5	M	9.5	4	29
1VF5	F G	F	15	L	1.4	4	29
1VF5	F G	F	19	G	117.1	4	29
1VF5	F G	F	23	G	102.3	4	29
1VF5	F G	F	27	L	1.2	4	29
1VF5	F H	F	22	L	1.4	4	29
1VF5	F H	H	17	W	1.3	8	28
1VF5	G H	G	13	L	1.1	10	16
1VF5	G H	H	8	W	1.1	8	28
1VF5	N D	N	146	W	1.0	142	151
1VF5	N O	N	66	Y	2.2	62	76
1VF5	N O	N	88	W	3.2	79	106
1VF5	N O	N	105	Y	3.3	79	106
1VF5	N O	N	122	V	1.2	115	139
1VF5	N O	N	145	Y	5.8	142	151
1VF5	N O	O	51	I	1.8	39	58
1VF5	N O	O	111	V	1.7	96	112
1VF5	N O	O	133	F	3.1	129	137
1VF5	N P	N	80	W	1.8	79	106
1VF5	N P	P	254	R	1.4	252	276
1VF5	N Q	Q	42	F	2.4	22	43
1VF5	N R	R	14	L	2.0	2	26
1VF5	N R	R	17	G	1.4	2	26
1VF5	O P	O	42	V	1.0	39	58
1VF5	O P	O	52	V	2.7	39	58
1VF5	O P	P	272	L	1.2	252	276
1VF5	O R	R	15	F	1.0	2	26
1VF5	O T	O	46	G	120.7	39	58
1VF5	O T	T	18	L	1.0	17	22
1VF5	P Q	P	261	F	1.4	252	276
1VF5	P Q	P	264	L	1.2	252	276
1VF5	P T	P	259	I	1.0	252	276
1VF5	P T	P	266	M	1.1	252	276
1VF5	P T	T	23	Y	1.0	23	32
1VF5	P U	P	270	L	1.1	252	276
1VF5	P U	P	274	L	1.0	252	276
1VF5	P U	U	23	V	1.2	5	28
1VF5	R S	R	12	I	3.2	2	26
1VF5	R S	R	13	A	3.1	2	26
1VF5	R S	S	5	M	7.4	4	29
1VF5	S T	S	15	L	1.4	4	29
1VF5	S T	S	19	G	95.8	4	29
1VF5	S T	S	23	G	97.5	4	29
1VF5	S T	T	26	Y	1.0	23	32
1VF5	S T	T	30	K	1.4	23	32
1VF5	S U	S	22	L	1.9	4	29
1VF5	S U	U	17	W	1.3	5	28
1VF5	T U	T	13	L	1.2	10	16
1VF5	T U	U	8	W	1.2	5	28
1VF6	A C	A	19	L	1.8	13	27
1VF6	A C	A	22	K	1.0	13	27
1VF6	A C	A	23	L	1.4	13	27
1VF6	A C	A	38	F	3.3	32	44
1VF6	A C	A	47	F	2.3	45	68
1VF6	A C	A	50	I	1.8	45	68
1VF6	A C	C	127	L	1.8	122	136
1VF6	A C	C	134	I	1.5	122	136

1VF6	A C	C	146	D	8.9	141	156
1VF6	A C	C	150	L	1.5	141	156
1VF6	A C	C	159	F	1.4	157	169
1VF6	A C	C	166	H	2.5	157	169
1VF6	B D	B	19	L	1.0	11	26
1VF6	B D	B	22	K	1.0	11	26
1VF6	B D	B	23	L	1.1	11	26
1VF6	B D	B	38	F	2.9	32	44
1VF6	B D	B	47	F	2.4	45	68
1VF6	B D	B	50	I	1.6	45	68
1VF6	B D	B	51	L	1.1	45	68
1VF6	B D	D	127	L	1.8	124	136
1VF6	B D	D	134	I	2.0	124	136
1VF6	B D	D	146	D	1.7	141	156
1VF6	B D	D	150	L	1.8	141	156
1VF6	B D	D	154	V	1.6	141	156
1VF6	B D	D	159	F	1.3	157	170
1VF6	B D	D	163	F	1.0	157	170
1VF6	B D	D	166	H	2.2	157	170
1VG0	A B	A	240	I	1.0	238	247
1VG0	A B	A	382	Q	1.1	377	391
1VG0	A B	A	386	R	3.6	377	391
1VG0	A B	A	390	V	1.1	377	391
1VG9	A B	A	386	R	2.0	377	391
1VG9	A B	A	390	V	1.4	377	391
1VG9	C D	C	386	R	2.7	379	391
1VG9	C D	C	390	V	2.9	379	391
1VG9	E F	E	379	E	1.4	377	391
1VG9	E F	E	382	Q	1.1	377	391
1VG9	E F	E	386	R	3.2	377	391
1VG9	E F	E	390	V	1.0	377	391
1VG9	G H	G	382	Q	1.0	377	391
1VG9	G H	G	386	R	3.0	377	391
1VG9	G H	G	390	V	2.6	377	391
1VGE	L H	L	124	Q	1.3	122	127
1VKT	A B	A	13	L	8.4	13	17
1VOQ	B H	B	50	E	1.0	47	52
1VOQ	C N	C	29	Y	1.3	27	47
1VOQ	G K	K	59	Y	1.1	59	63
1VOQ	M S	M	90	L	11.6	87	91
1VQN	F M	F	34	N	1.2	33	43
1VQN	F M	F	62	H	1.7	61	69
1VQN	F M	M	7	Y	2.6	4	12
1VQN	F M	M	8	I	1.2	4	12
1VQN	N Q	N	24	L	1.2	20	28
1VQN	S V	V	28	L	1.2	13	36
1VQP	A Z	Z	29	I	3.0	24	34
1VQP	A Z	Z	30	E	3.3	24	34
1VQP	A Z	Z	33	M	1.3	24	34
1VQP	A Z	Z	76	G	1.2	74	81
1VQP	A Z	Z	79	V	1.2	74	81
1VQP	F M	F	37	T	1.1	33	43
1VQP	F M	F	41	E	1.1	33	43
1VQP	F M	F	62	H	2.2	61	69
1VQP	F M	M	7	Y	3.2	4	12
1VQP	F M	M	8	I	1.0	4	12
1VQP	F M	M	23	L	1.3	19	33
1VQP	N Q	N	24	L	1.0	20	30
1VQP	S V	V	28	L	1.0	13	36
1VRA	A B	A	65	L	1.0	63	75

1VRA	A B	B	213	L	1.1	210	223
1VRA	A B	B	214	Q	2.2	210	223
1VRA	A B	B	217	L	1.7	210	223
1VRA	A B	B	262	N	2.1	260	281
1VRA	A B	B	274	L	3.0	260	281
1VRA	A B	B	277	Q	1.3	260	281
1VRA	A B	B	278	I	1.8	260	281
1VRQ	A B	A	496	R	1.2	491	500
1VRQ	A B	A	507	H	3.7	505	513
1VRQ	A B	A	511	Y	4.3	505	513
1VRQ	A B	A	558	F	5.5	558	563
1VRQ	A B	A	561	L	1.1	558	563
1VRQ	A B	B	117	R	1.3	113	128
1VRQ	A B	B	121	R	4.4	113	128
1VRQ	A B	B	177	W	2.2	172	186
1VRQ	A B	B	298	F	2.4	298	312
1VRQ	A B	B	305	M	1.5	298	312
1VRQ	A B	B	309	V	1.1	298	312
1VRQ	A C	C	182	H	3.1	180	195
1VRQ	A C	C	193	E	3.5	180	195
1VRQ	A D	A	706	W	1.6	696	711
1VRQ	A D	A	856	R	4.1	855	859
1VRQ	A D	A	857	S	1.3	855	859
1VRQ	A D	D	36	D	1.2	36	44
1VRQ	A D	D	39	W	3.9	36	44
1VRQ	B D	B	230	S	1.4	229	237
1VRQ	B D	B	231	V	1.9	229	237
1VRQ	B D	B	299	H	2.0	298	312
1VRQ	B D	B	388	F	1.8	385	391
1VRS	B E	E	462	V	1.5	462	474
1VS5	C N	C	28	F	1.8	25	45
1VS5	C N	C	32	L	1.9	25	45
1VS5	D E	D	49	D	1.6	49	64
1VS5	D E	D	86	G	1.2	85	96
1VS5	J N	N	81	I	1.4	81	89
1VS6	D P	P	8	E	1.6	7	11
1VS6	T X	X	19	L	3.5	17	21
1VSA	D J	D	26	H	49.8	25	30
1VSA	D J	D	33	R	4.7	31	40
1VSA	G V	V	71	Y	1.1	71	75
1VSA	H O	O	60	L	3.0	50	62
1VSA	I N	I	107	R	1.6	105	110
1VSA	O P	O	43	G	1.1	38	49
1VSA	O P	O	47	Y	2.1	38	49
1VSA	R W	W	26	R	1.0	17	30
1VSP	C N	N	7	I	1.3	4	8
1VSP	D J	D	26	H	1.0	25	38
1VSP	D J	D	29	W	1.6	25	38
1VSP	G V	V	71	Y	1.1	67	75
1VSP	I N	I	107	R	1.8	105	109
1VSP	O P	O	47	Y	1.1	43	48
1VSP	R W	W	26	R	1.4	17	32
1VYJ	I J	J	8	I	3.4	8	12
1VYJ	I J	J	11	Y	1.8	8	12
1VYJ	K L	L	11	Y	2.8	8	12
1VYT	A E	A	196	M	1.7	191	208
1VYT	A E	A	303	L	2.4	297	308
1VYT	A E	A	307	R	1.6	297	308
1VYT	A E	A	342	L	1.1	342	360
1VYT	A E	E	430	L	1.0	424	445

1VYT	A E	E	434	L	1.1	424	445
1VYT	A E	E	436	G	63.3	424	445
1VYT	A E	E	437	Y	4.8	424	445
1VYT	A E	E	440	W	5.9	424	445
1VYT	A E	E	441	I	1.7	424	445
1VYW	A B	A	49	I	1.5	46	58
1VYW	A B	A	56	K	1.3	46	58
1VYW	A B	B	182	I	1.6	179	193
1VYW	A B	B	185	Y	3.3	179	193
1VYW	A B	B	186	L	1.7	179	193
1VYW	A B	B	266	K	2.7	252	269
1VYW	A B	B	267	F	1.9	252	269
1VYW	A B	B	296	H	1.1	288	302
1VYW	A B	B	299	L	1.5	288	302
1VYW	A D	A	2	E	1.0	-1	3
1VYW	A D	D	293	R	1.2	288	302
1VYW	C D	C	49	I	1.9	46	56
1VYW	C D	D	182	I	1.1	179	191
1VYW	C D	D	185	Y	3.6	179	191
1VYW	C D	D	266	K	2.2	253	269
1VYW	C D	D	267	F	2.4	253	269
1VYW	C D	D	295	E	1.0	288	302
1VYW	C D	D	296	H	2.0	288	302
1VYW	C D	D	299	L	1.3	288	302
1VZJ	A I	A	17	W	3.2	8	20
1VZJ	A I	A	24	W	3.3	23	27
1VZJ	B I	B	10	W	4.8	2	20
1VZJ	B I	B	17	W	3.5	2	20
1VZJ	B I	B	24	W	4.3	23	31
1VZJ	C I	C	3	L	2.4	2	20
1VZJ	C I	C	10	W	4.0	2	20
1VZJ	C I	C	14	F	1.1	2	20
1VZJ	C I	C	17	W	3.8	2	20
1VZJ	C I	C	24	W	2.8	23	32
1VZJ	D I	D	10	W	4.0	2	20
1VZJ	D I	D	17	W	4.1	2	20
1VZJ	D I	D	24	W	4.5	23	32
1VZJ	E J	E	10	W	3.8	7	20
1VZJ	E J	E	17	W	4.4	7	20
1VZJ	E J	E	24	W	2.1	23	28
1VZJ	F J	F	10	W	4.1	2	20
1VZJ	F J	F	17	W	3.5	2	20
1VZJ	F J	F	24	W	2.5	23	34
1VZJ	G J	G	3	L	1.9	2	20
1VZJ	G J	G	10	W	4.4	2	20
1VZJ	G J	G	17	W	3.9	2	20
1VZJ	G J	G	24	W	2.4	23	30
1VZJ	H J	H	10	W	4.8	2	20
1VZJ	H J	H	17	W	4.0	2	20
1VZJ	H J	H	24	W	4.6	23	31
1W0Y	H L	H	128	F	1.3	126	129
1W1I	A F	F	81	R	1.1	76	93
1W1I	A F	F	84	Y	2.7	76	93
1W1I	A F	F	128	E	1.5	126	144
1W1I	A F	F	131	S	1.4	126	144
1W1I	A F	F	132	L	1.3	126	144
1W1I	B E	E	81	R	1.7	76	93
1W1I	B E	E	84	Y	2.0	76	93
1W1I	B E	E	127	D	1.2	126	144
1W1I	B E	E	128	E	1.3	126	144

1W1I	B E	E	132	L	3.1	126	144
1W1I	B E	E	142	R	1.0	126	144
1W1I	B E	E	143	D	1.4	126	144
1W1I	C G	G	84	Y	2.8	76	93
1W1I	C G	G	127	D	1.0	126	144
1W1I	C G	G	142	R	1.4	126	144
1W1I	D H	H	84	Y	1.5	76	93
1W1I	D H	H	139	E	1.9	126	144
1W1I	D H	H	142	R	1.3	126	144
1W1I	D H	H	143	D	1.0	126	144
1W2B	A Y	Y	79	V	1.1	77	82
1W2B	F L	F	34	N	3.2	33	42
1W2B	F L	F	37	T	2.5	33	42
1W2B	F L	F	41	E	1.5	33	42
1W2B	F L	F	62	H	2.0	58	69
1W2B	F L	F	66	L	1.1	58	69
1W2B	F L	L	4	A	1.8	4	12
1W2B	F L	L	7	Y	3.0	4	12
1W2B	F L	L	8	I	1.9	4	12
1W2B	K N	K	71	E	1.5	66	72
1W2B	M P	M	24	L	1.1	20	30
1W2W	A B	A	110	V	1.1	110	125
1W2W	A B	A	114	N	2.2	110	125
1W2W	A B	A	158	G	48.5	156	169
1W2W	A B	A	161	Y	2.6	156	169
1W2W	A B	A	162	L	2.2	156	169
1W2W	A B	A	195	L	1.0	193	211
1W2W	A B	A	197	V	1.6	193	211
1W2W	A B	A	198	I	1.4	193	211
1W2W	A B	A	199	R	2.4	193	211
1W2W	A B	A	202	W	1.8	193	211
1W2W	A B	B	240	R	3.9	237	249
1W2W	A B	B	241	L	1.6	237	249
1W2W	A B	B	242	T	1.8	237	249
1W2W	A B	B	244	Y	2.4	237	249
1W2W	A B	B	245	E	5.8	237	249
1W2W	A B	B	297	L	1.1	294	304
1W2W	E F	E	114	N	2.6	110	125
1W2W	E F	E	158	G	37.2	156	169
1W2W	E F	E	161	Y	2.3	156	169
1W2W	E F	E	162	L	1.6	156	169
1W2W	E F	E	195	L	1.1	193	211
1W2W	E F	E	197	V	1.1	193	211
1W2W	E F	E	198	I	1.5	193	211
1W2W	E F	E	199	R	3.2	193	211
1W2W	E F	E	202	W	1.4	193	211
1W2W	E F	F	240	R	3.5	237	249
1W2W	E F	F	241	L	1.4	237	249
1W2W	E F	F	242	T	2.1	237	249
1W2W	E F	F	244	Y	2.2	237	249
1W2W	E F	F	245	E	5.7	237	249
1W2W	E F	F	297	L	1.2	294	304
1W2W	I J	I	110	V	1.3	110	125
1W2W	I J	I	114	N	2.4	110	125
1W2W	I J	I	158	G	40.7	156	169
1W2W	I J	I	161	Y	2.2	156	169
1W2W	I J	I	162	L	1.5	156	169
1W2W	I J	I	197	V	1.2	193	207
1W2W	I J	I	198	I	1.4	193	207
1W2W	I J	I	199	R	3.8	193	207

1W2W	I J	I	202	W	2.1	193	207
1W2W	I J	J	240	R	3.6	237	250
1W2W	I J	J	242	T	2.0	237	250
1W2W	I J	J	244	Y	2.2	237	250
1W2W	I J	J	245	E	5.7	237	250
1W2W	I J	J	249	D	2.2	237	250
1W2W	I J	J	297	L	1.2	294	304
1W2W	M N	M	110	V	1.2	110	125
1W2W	M N	M	114	N	2.1	110	125
1W2W	M N	M	158	G	41.8	156	169
1W2W	M N	M	161	Y	1.8	156	169
1W2W	M N	M	195	L	1.2	193	209
1W2W	M N	M	198	I	1.5	193	209
1W2W	M N	M	199	R	2.6	193	209
1W2W	M N	M	202	W	1.6	193	209
1W2W	M N	N	240	R	3.7	237	249
1W2W	M N	N	241	L	1.5	237	249
1W2W	M N	N	242	T	1.0	237	249
1W2W	M N	N	244	Y	1.9	237	249
1W2W	M N	N	245	E	5.6	237	249
1W2W	M N	N	297	L	1.0	294	304
1W5C	A D	A	130	Q	1.4	110	133
1W5C	A D	A	143	I	3.1	143	147
1W5C	A D	A	181	N	1.2	176	182
1W5C	A D	A	205	V	1.4	196	221
1W5C	A D	A	208	G	20.1	196	221
1W5C	A D	A	216	G	104.9	196	221
1W5C	A D	A	319	D	21.9	317	327
1W5C	A D	A	320	I	22.4	317	327
1W5C	A D	A	321	I	1.2	317	327
1W5C	A D	A	323	R	20.6	317	327
1W5C	A D	A	324	A	21.5	317	327
1W5C	A D	D	136	V	1.0	129	137
1W5C	A D	D	186	Q	20.6	178	189
1W5C	A D	D	198	M	1.4	195	212
1W5C	A D	D	207	G	2.0	195	212
1W5C	A D	D	214	H	2.0	213	222
1W5C	A D	D	215	G	52.0	213	222
1W5C	A D	D	321	L	1.8	315	330
1W5C	A D	D	324	G	132.1	315	330
1W5C	B D	B	450	W	1.0	447	452
1W5C	B D	B	453	F	1.4	453	462
1W5C	B D	B	460	L	1.4	453	462
1W5C	B D	B	467	I	1.1	463	475
1W5C	B D	B	478	V	1.0	476	481
1W5C	C V	V	103	K	1.0	102	106
1W5C	D E	D	54	F	1.8	37	55
1W5C	D E	D	102	T	1.2	101	108
1W5C	D E	D	103	R	2.0	101	108
1W5C	D E	E	44	Y	1.8	42	47
1W5C	D E	E	81	E	1.0	73	84
1W5C	D F	F	37	I	1.1	18	42
1W5C	E F	E	34	G	31.4	18	41
1W5C	E F	F	31	I	2.0	18	42
1W5C	E F	F	32	F	1.9	18	42
1W5C	E F	F	35	G	40.2	18	42
1W5C	G J	G	143	I	2.2	143	147
1W5C	G J	G	205	V	1.4	196	221
1W5C	G J	G	208	G	20.3	196	221
1W5C	G J	G	216	G	122.2	196	221

1W5C	G J	G	319	D	21.1	317	327
1W5C	G J	G	320	I	21.0	317	327
1W5C	G J	G	321	I	1.3	317	327
1W5C	G J	G	323	R	19.6	317	327
1W5C	G J	G	324	A	20.5	317	327
1W5C	G J	J	136	V	1.0	129	137
1W5C	G J	J	186	Q	20.4	178	189
1W5C	G J	J	198	M	1.4	195	212
1W5C	G J	J	207	G	1.7	195	212
1W5C	G J	J	214	H	2.2	213	222
1W5C	G J	J	215	G	35.8	213	222
1W5C	G J	J	301	Q	1.2	300	306
1W5C	G J	J	321	L	1.6	315	330
1W5C	G J	J	324	G	143.4	315	330
1W5C	H J	H	226	Y	1.0	223	229
1W5C	H J	H	276	D	1.2	272	277
1W5C	H J	H	450	W	1.0	447	452
1W5C	H J	H	453	F	1.4	453	462
1W5C	H J	H	460	L	1.5	453	462
1W5C	H J	H	467	I	1.1	463	475
1W5C	H J	H	478	V	1.0	476	481
1W5C	I T	T	103	K	1.3	102	106
1W5C	J K	J	54	F	1.8	42	55
1W5C	J K	J	102	T	1.0	101	108
1W5C	J K	J	103	R	1.4	101	108
1W5C	J K	K	44	Y	1.4	42	47
1W5C	J K	K	81	E	1.0	73	84
1W5C	J L	L	37	I	1.1	18	42
1W5C	K L	K	34	G	36.8	18	41
1W5C	K L	L	31	I	2.0	18	42
1W5C	K L	L	32	F	1.9	18	42
1W5C	K L	L	35	G	52.1	18	42
1W63	B M	B	35	K	1.2	27	44
1W63	B M	B	71	L	1.3	65	76
1W63	B M	B	136	Y	7.7	135	145
1W63	B M	B	150	D	1.2	146	151
1W63	B M	B	175	M	2.3	175	189
1W63	B M	B	179	N	4.1	175	189
1W63	B M	B	186	E	1.0	175	189
1W63	B M	B	217	W	7.5	217	226
1W63	B M	B	405	Y	1.2	405	421
1W63	B M	M	81	F	1.0	78	95
1W63	B M	M	83	F	2.1	78	95
1W63	B M	M	86	K	1.0	78	95
1W63	B M	M	108	V	1.0	107	118
1W63	D N	D	35	K	1.2	27	44
1W63	D N	D	68	L	1.5	65	76
1W63	D N	D	71	L	1.3	65	76
1W63	D N	D	150	D	1.2	146	151
1W63	D N	D	186	E	1.0	175	189
1W63	D N	D	221	F	1.0	217	226
1W63	D N	D	367	V	1.2	367	384
1W63	D N	D	368	D	1.5	367	384
1W63	D N	D	405	Y	2.0	405	421
1W63	D N	N	81	F	1.0	78	95
1W63	D N	N	108	V	1.0	107	118
1W63	E M	E	7	L	1.0	7	17
1W63	F O	F	35	K	1.2	27	44
1W63	F O	F	71	L	1.3	65	76
1W63	F O	F	150	D	1.2	146	151

1W63	F O	F	186	E	1.0	175	189
1W63	F O	O	81	F	1.0	78	95
1W63	F O	O	83	F	2.1	78	95
1W63	F O	O	86	K	1.0	78	95
1W63	F O	O	108	V	1.0	107	118
1W63	G P	G	399	D	1.0	394	410
1W63	G P	P	101	E	1.1	100	106
1W63	H P	H	35	K	1.2	27	44
1W63	H P	H	71	L	1.3	65	76
1W63	H P	H	150	D	1.2	146	151
1W63	H P	H	186	E	1.0	175	189
1W63	H P	P	81	F	1.0	78	95
1W63	H P	P	83	F	1.7	78	95
1W63	H P	P	86	K	1.0	78	95
1W63	H P	P	108	V	1.0	107	118
1W63	J R	J	35	K	1.2	27	44
1W63	J R	J	71	L	1.3	65	76
1W63	J R	J	108	R	2.0	100	112
1W63	J R	J	136	Y	4.5	135	145
1W63	J R	J	140	T	1.5	135	145
1W63	J R	J	143	V	1.1	135	145
1W63	J R	J	150	D	1.2	146	151
1W63	J R	J	186	E	1.0	175	189
1W63	J R	J	217	W	2.8	217	226
1W63	J R	J	221	F	1.6	217	226
1W63	J R	J	368	D	1.0	367	384
1W63	J R	J	405	Y	1.3	405	421
1W63	J R	R	81	F	1.0	78	95
1W63	J R	R	108	V	1.2	107	118
1W63	J R	R	134	F	2.8	131	135
1W63	K V	V	101	E	1.0	100	106
1W63	L V	L	35	K	1.0	27	44
1W63	L V	L	71	L	1.3	65	76
1W63	L V	L	150	D	1.2	146	151
1W63	L V	L	186	E	1.0	175	189
1W63	L V	L	367	V	1.4	367	384
1W63	L V	L	368	D	1.6	367	384
1W63	L V	V	81	F	1.0	78	95
1W63	L V	V	83	F	1.7	78	95
1W63	L V	V	86	K	1.0	78	95
1W63	L V	V	108	V	1.0	107	118
1W72	A H	A	65	R	1.4	57	85
1W72	A H	A	72	Q	1.6	57	85
1W72	A L	A	84	Y	1.0	57	85
1W72	D I	D	65	R	1.5	57	85
1W7P	A D	A	93	Y	2.4	87	110
1W7P	A D	A	97	L	1.4	87	110
1W7P	A D	A	100	I	1.4	87	110
1W7P	A D	D	441	Y	2.0	437	449
1W7P	A D	D	457	P	1.3	457	466
1W7P	A D	D	533	M	1.0	529	542
1W7P	C D	C	22	T	1.4	20	41
1W98	A B	B	149	E	1.5	148	165
1WA8	A B	A	17	F	1.9	7	40
1WA8	A B	A	23	D	1.0	7	40
1WA8	A B	A	24	L	9.7	7	40
1WA8	A B	A	56	R	1.2	46	79
1WA8	A B	A	57	F	20.6	46	79
1WA8	A B	A	74	N	14.4	46	79
1WA8	A B	B	625	I	7.5	610	643

1WA8	A B	B	632	G	23.3	610	643
1WA8	A B	B	636	L	1.2	610	643
1WA8	A B	B	664	E	1.2	649	680
1WCM	A B	A	370	I	1.1	368	374
1WCM	A B	A	497	T	1.5	495	506
1WCM	A B	A	658	L	1.3	639	660
1WCM	A B	A	761	M	1.2	755	764
1WCM	A B	A	810	P	6.4	810	828
1WCM	A B	A	813	F	2.4	810	828
1WCM	A B	A	820	G	8.0	810	828
1WCM	A B	A	821	R	1.2	810	828
1WCM	A B	A	1406	V	4.7	1406	1411
1WCM	A B	B	1023	V	3.7	1023	1035
1WCM	A B	B	1141	H	1.1	1132	1142
1WCM	A B	B	1146	F	1.9	1144	1152
1WCM	A B	B	1149	E	6.5	1144	1152
1WCM	A B	B	1150	R	2.1	1144	1152
1WCM	A B	B	1202	L	2.0	1198	1210
1WCM	A B	B	1203	L	1.9	1198	1210
1WCM	A B	B	1206	E	2.7	1198	1210
1WCM	A B	B	1207	L	1.0	1198	1210
1WCM	A B	B	1208	M	1.4	1198	1210
1WCM	A E	A	942	F	1.0	935	944
1WCM	A E	A	1017	L	5.5	1017	1026
1WCM	A E	A	1338	V	2.0	1332	1340
1WCM	A E	A	1339	L	1.1	1332	1340
1WCM	A F	A	504	L	1.9	495	506
1WCM	A F	F	88	Y	3.1	87	103
1WCM	A F	F	92	R	1.2	87	103
1WCM	A F	F	95	G	21.3	87	103
1WCM	A G	G	23	K	1.8	22	33
1WCM	B C	B	847	D	2.5	843	848
1WCM	B C	C	27	L	1.6	27	40
1WCM	B C	C	38	I	1.0	27	40
1WCM	B C	C	61	E	3.4	60	70
1WCM	B C	C	62	F	4.0	60	70
1WCM	B C	C	69	L	3.0	60	70
1WCM	B I	B	308	W	1.3	308	321
1WCM	B J	B	190	Y	2.4	186	191
1WCM	B J	J	33	G	80.2	33	40
1WCM	B J	J	59	K	1.3	56	62
1WCM	C J	J	57	I	1.5	56	62
1WCM	C J	J	58	E	1.0	56	62
1WCM	C J	J	61	L	2.0	56	62
1WCM	C L	C	68	G	9.4	60	70
1WDC	A B	A	804	Q	1.1	775	823
1WDC	A B	A	808	L	2.4	775	823
1WDC	A B	A	811	I	8.9	775	823
1WDC	A B	A	812	Q	1.4	775	823
1WDC	A B	A	814	N	1.2	775	823
1WDC	A B	A	815	I	2.1	775	823
1WDC	A B	A	816	R	2.1	775	823
1WDC	A B	A	817	K	6.0	775	823
1WDC	A B	A	818	W	3.0	775	823
1WDC	A B	A	819	L	1.6	775	823
1WDC	A B	A	826	W	3.1	825	837
1WDC	A B	A	829	L	2.1	825	837
1WDC	A B	A	832	K	1.0	825	837
1WDC	A B	B	59	M	1.4	53	61
1WDC	A B	B	75	I	1.2	69	80

1WDC	A B	B	76	F	2.0	69	80
1WDC	A B	B	79	K	1.6	69	80
1WDC	A B	B	89	I	1.0	86	96
1WDC	A B	B	93	F	1.8	86	96
1WDC	A B	B	113	L	1.3	106	116
1WDC	A B	B	124	E	1.1	122	132
1WDC	A B	B	148	I	1.0	141	149
1WDC	A C	A	781	I	2.0	775	823
1WDC	A C	A	782	I	1.6	775	823
1WDC	A C	A	785	F	5.0	775	823
1WDC	A C	A	786	Q	1.9	775	823
1WDC	A C	A	788	H	3.0	775	823
1WDC	A C	A	789	I	2.2	775	823
1WDC	A C	A	790	R	1.2	775	823
1WDC	A C	A	791	G	23.9	775	823
1WDC	A C	A	792	Y	3.7	775	823
1WDC	A C	A	793	L	1.4	775	823
1WDC	A C	A	795	R	1.4	775	823
1WDC	A C	A	798	Y	1.0	775	823
1WDC	A C	A	799	K	1.0	775	823
1WDC	A C	A	801	L	1.0	775	823
1WDC	A C	A	805	R	2.3	775	823
1WDC	A C	C	17	L	1.8	5	22
1WDC	A C	C	20	F	4.0	5	22
1WDC	A C	C	21	W	2.5	5	22
1WDC	A C	C	86	Y	4.1	83	93
1WDC	A C	C	90	F	1.0	83	93
1WDC	A C	C	125	I	1.8	119	130
1WDC	A C	C	148	V	1.8	141	151
1WDC	B C	C	20	F	1.7	5	22
1WDD	A S	A	194	R	2.2	182	195
1WDD	A S	A	226	Y	2.0	214	233
1WDD	A S	A	421	R	1.6	413	433
1WDD	A S	A	432	N	1.4	413	433
1WDD	A S	A	451	W	4.3	441	452
1WDD	A S	S	28	K	1.2	23	36
1WDD	A S	S	29	Q	1.1	23	36
1WDD	A S	S	32	Y	1.0	23	36
1WDD	E W	E	194	R	2.5	182	195
1WDD	E W	E	226	Y	1.9	214	233
1WDD	E W	E	421	R	1.3	413	433
1WDD	E W	E	425	E	1.2	413	433
1WDD	E W	E	432	N	1.6	413	433
1WDD	E W	W	28	K	1.2	23	36
1WDD	E W	W	29	Q	1.3	23	36
1WDK	A C	A	229	E	5.0	227	243
1WDK	A C	A	232	M	1.8	227	243
1WDK	A C	C	157	M	1.2	151	162
1WDK	B D	B	228	I	1.4	227	243
1WDK	B D	B	229	E	4.3	227	243
1WDW	A B	A	93	Y	1.6	89	96
1WDW	A B	B	170	R	1.1	161	175
1WDW	C D	C	52	Q	1.5	49	61
1WDW	C D	C	89	Y	1.2	89	96
1WDW	C D	C	93	Y	1.7	89	96
1WDW	C D	D	16	I	1.3	16	31
1WDW	C D	D	170	R	1.5	161	175
1WDW	E D	E	30	E	1.0	18	32
1WDW	E F	E	52	Q	1.5	49	61
1WDW	E F	E	89	Y	1.1	89	96

1WDW	E F	E	93	Y	1.6	89	96
1WDW	E F	E	94	R	1.3	89	96
1WDW	E F	F	166	N	1.8	161	175
1WDW	E F	F	170	R	2.3	161	175
1WDW	G H	G	89	Y	1.6	89	96
1WDW	G H	G	90	N	1.4	89	96
1WDW	G H	G	93	Y	1.6	89	96
1WDW	G H	H	13	E	1.0	13	31
1WDW	G H	H	16	I	1.4	13	31
1WDW	I J	I	89	Y	1.1	89	96
1WDW	I J	I	93	Y	1.1	89	96
1WDW	I J	J	16	I	1.1	16	31
1WDW	K L	K	89	Y	1.4	89	96
1WDW	K L	K	90	N	1.6	89	96
1WDW	K L	K	93	Y	1.7	89	96
1WDW	K L	L	16	I	3.0	13	31
1WDW	K L	L	20	K	1.0	13	31
1WE3	B P	B	233	L	1.0	229	243
1WE3	C Q	C	237	E	8.4	229	243
1WE3	D R	D	233	L	1.1	229	243
1WEJ	H F	F	62	E	2.8	61	70
1WEJ	L F	F	99	K	3.0	88	102
1WEJ	L H	L	123	E	1.1	122	128
1WEJ	L H	L	124	Q	1.3	122	128
1WKW	A B	B	58	F	1.1	56	62
1WMH	A B	A	75	L	1.6	74	87
1WMH	A B	A	76	E	1.0	74	87
1WMH	A B	A	79	E	2.2	74	87
1WMH	A B	A	82	R	1.8	74	87
1WMI	A B	A	23	Y	1.0	20	36
1WMI	A B	B	18	V	1.9	8	27
1WMI	A B	B	40	E	1.3	38	49
1WMI	A B	B	44	L	1.6	38	49
1WMI	C D	C	27	L	1.3	20	36
1WMI	C D	C	30	R	1.3	20	36
1WMI	C D	D	44	L	1.1	38	50
1WPX	A B	A	220	L	1.7	214	228
1WPX	A B	A	231	W	3.5	230	251
1WPX	A B	A	239	Y	1.2	230	251
1WPX	A B	A	301	D	1.5	301	308
1WPX	A B	A	307	L	1.2	301	308
1WPX	A B	B	507	F	4.0	507	518
1WPX	A B	B	514	S	1.2	507	518
1WQ1	R G	R	88	K	1.3	87	104
1WQ1	R G	R	92	D	1.3	87	104
1WQ1	R G	G	795	S	1.5	793	806
1WQ1	R G	G	796	T	1.3	793	806
1WQ9	A B	A	5	F	2.9	5	13
1WQ9	A B	B	5	F	1.8	5	13
1WQL	A B	A	246	S	1.1	241	248
1WQL	A B	A	371	R	2.6	364	378
1WQL	A B	A	375	I	2.2	364	378
1WQL	A B	A	376	F	1.6	364	378
1WQL	A B	A	387	D	2.4	384	399
1WQL	A B	B	90	R	1.0	84	95
1WQL	A B	B	92	R	1.2	84	95
1WR1	A B	B	338	Q	1.1	333	343
1WR6	A E	A	227	L	1.8	218	229
1WR6	A E	A	244	D	1.4	242	247
1WR6	A E	A	251	L	1.2	250	268

1WR6	B F	B	227	L	1.7	218	230
1WR6	B F	B	243	G	1.3	242	247
1WR6	B F	B	246	E	1.4	242	247
1WR6	C G	C	227	L	1.6	218	230
1WR6	C G	C	244	D	1.1	242	247
1WR6	C G	C	251	L	1.1	250	268
1WR6	D H	D	227	L	2.0	218	230
1WR6	D H	D	250	E	2.0	250	269
1WRD	A B	A	236	E	1.1	217	241
1WRD	A B	A	237	M	1.3	217	241
1WRD	A B	A	253	L	1.0	248	275
1WRD	A B	A	256	E	1.9	248	275
1WRD	A B	A	257	L	1.8	248	275
1WWW	V Y	V	7	F	1.1	5	9
1WX5	A B	A	190	H	1.8	189	198
1WX5	A B	A	194	H	1.2	189	198
1WX5	A B	B	114	E	1.8	104	116
1WX5	C D	C	42	I	1.0	30	45
1WYU	A B	A	14	M	2.6	8	18
1WYU	A B	A	23	L	1.1	23	27
1WYU	A B	A	26	L	1.9	23	27
1WYU	A B	A	50	V	1.4	47	61
1WYU	A B	A	57	L	1.6	47	61
1WYU	A B	A	81	V	1.1	80	88
1WYU	A B	A	85	L	2.9	80	88
1WYU	A B	A	89	G	18.3	89	93
1WYU	A B	A	91	F	2.4	89	93
1WYU	A B	A	105	G	150.5	104	122
1WYU	A B	A	111	F	2.3	104	122
1WYU	A B	A	112	E	3.0	104	122
1WYU	A B	A	115	T	1.7	104	122
1WYU	A B	A	116	M	1.4	104	122
1WYU	A B	A	119	E	3.6	104	122
1WYU	A B	A	166	V	1.2	161	174
1WYU	A B	A	170	Y	1.8	161	174
1WYU	A B	A	309	Y	1.9	308	312
1WYU	A B	A	333	Y	1.2	324	338
1WYU	A B	A	336	A	1.2	324	338
1WYU	A B	A	337	L	1.5	324	338
1WYU	A B	A	341	G	1.4	339	363
1WYU	A B	A	344	E	1.6	339	363
1WYU	A B	A	347	L	1.1	339	363
1WYU	A B	A	390	R	1.9	386	396
1WYU	A B	A	391	R	1.0	386	396
1WYU	A B	B	7	F	2.1	6	10
1WYU	A B	B	8	E	1.2	6	10
1WYU	A B	B	29	L	1.5	26	30
1WYU	A B	B	50	L	3.3	47	60
1WYU	A B	B	53	H	1.1	47	60
1WYU	A B	B	54	Y	6.1	47	60
1WYU	A B	B	57	L	1.4	47	60
1WYU	A B	B	58	S	1.4	47	60
1WYU	A B	B	89	L	1.0	81	90
1WYU	A B	B	104	G	172.4	103	121
1WYU	A B	B	115	Y	1.3	103	121
1WYU	A B	B	119	L	1.2	103	121
1WYU	A B	B	134	H	2.5	132	150
1WYU	A B	B	144	R	1.4	132	150
1WYU	A B	B	167	G	50.8	167	176
1WYU	A B	B	172	T	1.2	167	176

1WYU	A B	B	175	M	1.0	167	176
1WYU	A B	B	324	F	1.6	324	338
1WYU	A B	B	331	W	1.8	324	338
1WYU	A B	B	337	L	1.1	324	338
1WYU	A B	B	339	L	1.4	339	363
1WYU	A B	B	348	L	1.0	339	363
1WYU	A B	B	351	L	3.9	339	363
1WYU	A B	B	354	R	1.8	339	363
1WYU	A B	B	355	Y	2.5	339	363
1WYU	A B	B	392	K	1.2	387	397
1WYU	A B	B	424	K	2.8	424	439
1WYU	A D	A	10	E	1.6	8	18
1WYU	C B	C	10	E	1.0	8	18
1WYU	C D	C	14	M	2.6	8	18
1WYU	C D	C	17	R	1.0	8	18
1WYU	C D	C	23	L	1.2	23	27
1WYU	C D	C	26	L	1.9	23	27
1WYU	C D	C	50	V	1.7	47	61
1WYU	C D	C	57	L	1.6	47	61
1WYU	C D	C	81	V	1.1	80	87
1WYU	C D	C	85	L	2.4	80	87
1WYU	C D	C	89	G	6.6	89	93
1WYU	C D	C	91	F	2.1	89	93
1WYU	C D	C	105	G	122.3	104	121
1WYU	C D	C	108	Q	1.7	104	121
1WYU	C D	C	111	F	2.3	104	121
1WYU	C D	C	112	E	3.9	104	121
1WYU	C D	C	115	T	1.9	104	121
1WYU	C D	C	116	M	1.3	104	121
1WYU	C D	C	119	E	3.3	104	121
1WYU	C D	C	166	V	1.1	161	174
1WYU	C D	C	170	Y	1.8	161	174
1WYU	C D	C	332	M	1.0	324	338
1WYU	C D	C	334	L	2.2	324	338
1WYU	C D	C	337	L	1.3	324	338
1WYU	C D	C	339	P	1.3	339	362
1WYU	C D	C	341	G	1.0	339	362
1WYU	C D	C	344	E	1.8	339	362
1WYU	C D	C	347	L	1.4	339	362
1WYU	C D	C	350	V	1.4	339	362
1WYU	C D	C	390	R	2.2	386	396
1WYU	C D	D	7	F	2.1	6	10
1WYU	C D	D	50	L	2.0	47	59
1WYU	C D	D	54	Y	2.4	47	59
1WYU	C D	D	57	L	2.5	47	59
1WYU	C D	D	104	G	170.3	103	121
1WYU	C D	D	115	Y	1.2	103	121
1WYU	C D	D	119	L	1.1	103	121
1WYU	C D	D	134	H	2.2	132	149
1WYU	C D	D	167	G	64.0	167	176
1WYU	C D	D	172	T	1.0	167	176
1WYU	C D	D	174	S	1.0	167	176
1WYU	C D	D	324	F	1.4	324	338
1WYU	C D	D	331	W	1.7	324	338
1WYU	C D	D	337	L	1.1	324	338
1WYU	C D	D	339	L	1.1	339	363
1WYU	C D	D	348	L	1.7	339	363
1WYU	C D	D	351	L	4.2	339	363
1WYU	C D	D	354	R	1.0	339	363
1WYU	C D	D	355	Y	2.3	339	363

1WYU	C D	D	395	L	1.1	387	397
1WYU	C D	D	424	K	2.7	424	439
1WYU	E B	B	362	E	1.2	339	363
1WYU	E F	E	14	M	2.1	8	18
1WYU	E F	E	17	R	1.1	8	18
1WYU	E F	E	23	L	1.4	23	27
1WYU	E F	E	26	L	2.0	23	27
1WYU	E F	E	50	V	1.1	47	61
1WYU	E F	E	53	E	1.3	47	61
1WYU	E F	E	57	L	1.6	47	61
1WYU	E F	E	81	V	1.0	80	86
1WYU	E F	E	85	L	3.5	80	86
1WYU	E F	E	89	G	13.9	89	93
1WYU	E F	E	91	F	2.3	89	93
1WYU	E F	E	105	G	140.4	104	121
1WYU	E F	E	108	Q	1.2	104	121
1WYU	E F	E	111	F	2.4	104	121
1WYU	E F	E	112	E	3.0	104	121
1WYU	E F	E	115	T	1.7	104	121
1WYU	E F	E	116	M	1.5	104	121
1WYU	E F	E	119	E	3.1	104	121
1WYU	E F	E	166	V	1.2	161	174
1WYU	E F	E	170	Y	1.9	161	174
1WYU	E F	E	309	Y	1.8	308	312
1WYU	E F	E	332	M	1.6	324	338
1WYU	E F	E	337	L	1.2	324	338
1WYU	E F	E	339	P	1.2	339	363
1WYU	E F	E	341	G	2.4	339	363
1WYU	E F	E	344	E	1.1	339	363
1WYU	E F	E	347	L	1.1	339	363
1WYU	E F	E	390	R	2.3	386	396
1WYU	E F	F	7	F	1.9	6	10
1WYU	E F	F	29	L	2.6	26	30
1WYU	E F	F	50	L	2.7	47	59
1WYU	E F	F	51	V	1.2	47	59
1WYU	E F	F	53	H	1.5	47	59
1WYU	E F	F	54	Y	3.0	47	59
1WYU	E F	F	57	L	1.5	47	59
1WYU	E F	F	58	S	1.0	47	59
1WYU	E F	F	104	G	194.3	103	121
1WYU	E F	F	115	Y	1.3	103	121
1WYU	E F	F	119	L	1.2	103	121
1WYU	E F	F	134	H	2.5	132	150
1WYU	E F	F	167	G	72.5	167	176
1WYU	E F	F	324	F	1.5	324	338
1WYU	E F	F	337	L	1.2	324	338
1WYU	E F	F	339	L	1.2	339	363
1WYU	E F	F	348	L	1.5	339	363
1WYU	E F	F	351	L	3.6	339	363
1WYU	E F	F	354	R	1.8	339	363
1WYU	E F	F	355	Y	3.0	339	363
1WYU	E F	F	392	K	1.0	387	397
1WYU	E F	F	424	K	2.7	424	438
1WYU	G F	G	9	E	1.4	8	18
1WYU	G F	G	10	E	1.9	8	18
1WYU	G H	G	14	M	1.9	8	18
1WYU	G H	G	23	L	1.3	23	27
1WYU	G H	G	26	L	2.4	23	27
1WYU	G H	G	50	V	2.0	47	61
1WYU	G H	G	57	L	1.6	47	61

1WYU	G H	G	85	L	2.1	80	87
1WYU	G H	G	89	G	11.4	89	93
1WYU	G H	G	91	F	2.3	89	93
1WYU	G H	G	105	G	149.3	104	122
1WYU	G H	G	108	Q	1.1	104	122
1WYU	G H	G	111	F	1.6	104	122
1WYU	G H	G	112	E	1.0	104	122
1WYU	G H	G	115	T	1.7	104	122
1WYU	G H	G	116	M	1.4	104	122
1WYU	G H	G	119	E	2.5	104	122
1WYU	G H	G	162	E	1.8	161	174
1WYU	G H	G	166	V	1.2	161	174
1WYU	G H	G	170	Y	2.0	161	174
1WYU	G H	G	309	Y	1.7	308	312
1WYU	G H	G	390	R	2.9	386	396
1WYU	G H	G	391	R	1.0	386	396
1WYU	G H	H	7	F	2.1	6	10
1WYU	G H	H	29	L	2.5	26	30
1WYU	G H	H	50	L	2.1	47	59
1WYU	G H	H	54	Y	4.0	47	59
1WYU	G H	H	57	L	1.6	47	59
1WYU	G H	H	58	S	1.3	47	59
1WYU	G H	H	82	L	1.2	81	90
1WYU	G H	H	89	L	1.2	81	90
1WYU	G H	H	103	Q	1.0	103	121
1WYU	G H	H	104	G	158.3	103	121
1WYU	G H	H	119	L	1.1	103	121
1WYU	G H	H	134	H	2.4	132	149
1WYU	G H	H	144	R	1.3	132	149
1WYU	G H	H	167	G	73.7	167	176
1WYU	G H	H	172	T	1.3	167	176
1WYU	G H	H	174	S	1.5	167	176
1WYU	G H	H	175	M	1.1	167	176
1WYU	G H	H	324	F	1.5	324	338
1WYU	G H	H	325	L	1.0	324	338
1WYU	G H	H	331	W	1.6	324	338
1WYU	G H	H	335	R	1.0	324	338
1WYU	G H	H	337	L	1.1	324	338
1WYU	G H	H	339	L	1.5	339	363
1WYU	G H	H	348	L	2.4	339	363
1WYU	G H	H	351	L	3.6	339	363
1WYU	G H	H	354	R	1.1	339	363
1WYU	G H	H	355	Y	2.7	339	363
1WYU	G H	H	424	K	2.8	424	439
1WYW	A B	B	54	R	3.4	45	56
1X11	A C	A	476	G	2.2	468	490
1X11	A C	A	479	F	2.0	468	490
1X11	A C	A	483	Y	1.9	468	490
1X11	A C	A	486	F	2.2	468	490
1X11	B D	B	479	F	2.2	468	490
1X11	B D	B	483	Y	2.2	468	490
1X11	B D	B	486	F	2.7	468	490
1X11	B D	D	9	Y	2.0	7	12
1X11	B D	D	11	F	1.5	7	12
1X2T	A B	B	27	E	1.0	23	32
1X2T	C D	C	27	E	1.0	23	32
1X3Z	A B	A	12	F	2.8	12	31
1X3Z	A B	A	15	I	1.2	12	31
1X3Z	A B	A	20	L	1.6	12	31
1X3Z	A B	A	23	Y	2.0	12	31

1X3Z	A B	A	317	E	1.4	306	326
1X3Z	A B	B	266	R	1.8	259	270
1X3Z	A B	B	269	V	1.9	259	270
1X3Z	A B	B	276	L	1.8	276	285
1X3Z	A B	B	280	L	1.1	276	285
1X3Z	A B	B	306	L	2.0	298	308
1X75	A D	D	99	W	1.2	87	100
1X75	B C	C	99	W	1.4	87	100
1X79	A B	A	264	F	3.0	259	268
1X79	A B	A	281	L	2.0	275	298
1X79	A B	B	559	K	1.2	553	640
1X79	A B	B	560	L	1.0	553	640
1X79	A B	B	563	M	1.7	553	640
1X79	A C	C	561	Q	1.0	554	634
1X79	A C	C	564	L	1.9	554	634
1X79	A C	C	565	R	1.0	554	634
1X86	A B	A	934	M	1.7	932	941
1X86	A B	A	939	K	1.9	932	941
1X86	A B	B	69	L	1.7	67	75
1X86	A B	B	72	L	1.2	67	75
1X86	C D	C	787	K	1.9	783	813
1X86	C D	C	934	M	1.9	929	950
1X86	E F	E	794	E	1.5	783	812
1X86	E F	E	892	P	2.2	890	904
1X86	G H	G	791	V	1.5	785	797
1X86	G H	G	794	E	2.3	785	797
1X86	G H	G	934	M	1.2	932	939
1X86	G H	G	979	K	1.5	972	993
1X86	G H	H	67	D	3.5	67	71
1X86	G H	H	69	L	2.6	67	71
1XB2	A B	A	193	E	2.6	193	206
1XB2	A B	A	194	L	1.7	193	206
1XB2	A B	A	198	E	2.4	193	206
1XB2	A B	B	60	K	1.4	57	71
1XB2	A B	B	67	R	3.6	57	71
1XB2	A B	B	74	F	3.4	74	84
1XB2	A B	B	78	K	1.4	74	84
1XB2	A B	B	139	D	2.9	139	144
1XB2	A B	B	140	F	3.4	139	144
1XB2	A B	B	275	G	4.4	263	276
1XCG	A B	A	737	E	1.2	730	767
1XCG	A B	A	741	E	2.6	730	767
1XCG	A B	A	879	M	1.6	877	895
1XCG	A B	A	888	L	1.1	877	895
1XCG	A B	B	69	L	3.7	69	75
1XCG	A B	B	72	L	2.1	69	75
1XCG	E F	E	741	E	1.0	730	767
1XCG	E F	E	872	R	1.3	871	876
1XCG	E F	E	879	M	1.6	877	895
1XCG	E F	E	880	Q	1.6	877	895
1XCG	E F	E	914	R	1.4	901	938
1XCG	E F	E	918	K	1.1	901	938
1XCG	E F	E	924	V	1.0	901	938
1XCG	E F	F	68	R	1.0	67	75
1XCG	E F	F	69	L	2.6	67	75
1XCG	E F	F	72	L	1.1	67	75
1XCQ	A B	A	129	E	1.1	128	132
1XCQ	A B	A	130	Q	4.7	128	132
1XCQ	C M	M	53	Y	1.6	49	58
1XCQ	G H	G	129	E	1.0	128	133

1XCQ	G H	G	130	Q	1.2	128	133
1XCQ	G O	O	53	Y	1.5	46	57
1XCT	A B	A	130	Q	1.1	128	133
1XCT	A L	L	49	E	1.0	43	60
1XCT	C M	M	53	Y	1.1	43	56
1XD2	A C	A	67	M	1.0	65	75
1XD2	A C	A	70	Q	1.2	65	75
1XD2	A C	A	71	Y	1.1	65	75
1XD2	A C	C	688	R	3.2	672	699
1XD2	A C	C	729	W	4.1	724	743
1XD2	A C	C	973	Q	1.6	958	974
1XD2	B C	B	21	I	1.3	16	25
1XD2	B C	B	69	D	1.3	68	75
1XD2	B C	B	73	R	2.5	68	75
1XD2	B C	B	102	R	2.9	87	104
1XD2	B C	C	814	K	1.1	814	818
1XD2	B C	C	825	I	2.1	819	841
1XD2	B C	C	930	F	1.0	930	942
1XD2	B C	C	931	G	33.7	930	942
1XD2	B C	C	935	T	1.1	930	942
1XD2	B C	C	1007	D	2.6	1002	1017
1XD3	A B	A	213	M	1.2	201	216
1XD3	C D	C	213	M	1.2	201	215
1XDK	A B	A	348	G	7.5	348	364
1XDK	A B	A	398	R	1.7	391	411
1XDK	A B	A	399	E	1.6	391	411
1XDK	A B	A	402	Y	2.0	391	411
1XDK	A B	A	406	E	1.9	391	411
1XDK	A B	A	422	K	1.2	419	425
1XDK	A B	A	424	L	1.3	419	425
1XDK	A B	A	428	P	3.5	426	446
1XDK	A B	A	440	H	1.1	426	446
1XDK	A B	B	349	L	1.1	346	360
1XDK	A B	B	367	F	1.2	366	372
1XDK	A B	B	368	P	1.8	366	372
1XDK	A B	B	369	K	1.4	366	372
1XDK	A B	B	371	L	7.0	366	372
1XDK	A F	A	443	F	2.3	426	446
1XDK	E B	E	443	F	2.2	426	446
1XDK	E F	E	348	G	5.9	348	364
1XDK	E F	E	361	K	1.0	348	364
1XDK	E F	E	422	K	1.9	419	425
1XDK	E F	E	424	L	1.7	419	425
1XDK	E F	E	440	H	1.1	426	446
1XDK	E F	F	342	D	1.0	338	345
1XDK	E F	F	368	P	2.6	366	372
1XDK	E F	F	369	K	1.4	366	372
1XDK	E F	F	371	L	1.5	366	372
1XEW	X Y	X	148	I	1.5	147	153
1XEW	X Y	X	152	I	1.6	147	153
1XEW	X Y	X	162	L	7.4	156	167
1XEW	X Y	X	163	I	1.9	156	167
1XEW	X Y	X	166	I	1.1	156	167
1XEW	X Y	Y	1081	F	1.1	1071	1089
1XEW	X Y	Y	1085	I	1.4	1071	1089
1XEW	X Y	Y	1086	Q	1.7	1071	1089
1XEW	X Y	Y	1167	I	1.1	1157	1172
1XFU	A O	A	525	K	1.4	522	536
1XFU	A O	A	533	L	1.2	522	536
1XFU	A O	A	665	K	1.3	660	672

1XFU	A O	A	717	K	1.8	715	737
1XFU	A O	A	763	L	1.0	743	765
1XFU	A O	O	18	L	2.8	15	19
1XFU	A O	O	83	E	1.1	81	93
1XFU	A O	O	84	E	1.4	81	93
1XFU	A O	O	91	V	1.2	81	93
1XFU	B P	B	501	L	1.1	501	508
1XFU	B P	B	525	K	1.4	522	536
1XFU	B P	B	533	L	1.4	522	536
1XFU	B P	B	665	K	1.1	660	672
1XFU	B P	B	717	K	1.8	715	737
1XFU	B P	B	763	L	1.0	743	765
1XFU	B P	P	18	L	2.9	15	19
1XFU	B P	P	83	E	1.1	81	93
1XFU	B P	P	84	E	1.4	81	93
1XFU	B P	P	91	V	1.2	81	93
1XFU	C Q	C	501	L	1.1	501	508
1XFU	C Q	C	525	K	1.4	522	536
1XFU	C Q	C	533	L	1.2	522	536
1XFU	C Q	C	649	I	2.0	648	652
1XFU	C Q	C	665	K	1.5	660	672
1XFU	C Q	C	717	K	2.2	715	737
1XFU	C Q	C	718	R	1.0	715	737
1XFU	C Q	C	763	L	1.0	743	765
1XFU	C Q	Q	18	L	3.0	15	19
1XFU	C Q	Q	83	E	1.1	81	93
1XFU	C Q	Q	84	E	1.4	81	93
1XFU	C Q	Q	91	V	1.1	81	93
1XFU	C Q	Q	138	Y	1.1	138	147
1XFU	C Q	Q	140	E	1.4	138	147
1XFU	D R	D	501	L	1.1	501	508
1XFU	D R	D	513	W	1.2	510	518
1XFU	D R	D	525	K	1.4	522	536
1XFU	D R	D	533	L	1.3	522	536
1XFU	D R	D	665	K	1.1	660	672
1XFU	D R	D	717	K	2.2	715	737
1XFU	D R	D	763	L	1.0	743	765
1XFU	D R	R	18	L	2.6	15	19
1XFU	D R	R	83	E	1.1	81	93
1XFU	D R	R	84	E	1.3	81	93
1XFU	D R	R	91	V	1.1	81	93
1XFU	D R	R	140	E	1.4	138	147
1XFU	E S	E	501	L	1.1	501	508
1XFU	E S	E	525	K	1.4	522	536
1XFU	E S	E	533	L	1.3	522	536
1XFU	E S	E	664	I	1.5	660	672
1XFU	E S	E	665	K	1.7	660	672
1XFU	E S	E	691	K	1.1	686	698
1XFU	E S	E	717	K	2.2	715	737
1XFU	E S	E	763	L	1.0	743	765
1XFU	E S	S	18	L	3.1	15	19
1XFU	E S	S	83	E	1.8	81	93
1XFU	E S	S	84	E	1.4	81	93
1XFU	E S	S	91	V	1.1	81	93
1XFU	E S	S	138	Y	1.2	138	147
1XFU	F T	F	501	L	1.5	501	508
1XFU	F T	F	523	L	1.2	522	536
1XFU	F T	F	525	K	3.3	522	536
1XFU	F T	F	526	Q	1.0	522	536
1XFU	F T	F	527	K	2.1	522	536

1XFU	F T	F	529	V	2.4	522	536
1XFU	F T	F	530	T	1.3	522	536
1XFU	F T	F	531	N	1.2	522	536
1XFU	F T	F	533	L	1.2	522	536
1XFU	F T	F	649	I	1.9	648	652
1XFU	F T	F	665	K	1.2	660	672
1XFU	F T	F	717	K	2.2	715	737
1XFU	F T	T	18	L	2.8	15	19
1XFU	F T	T	83	E	1.2	81	93
1XFU	F T	T	84	E	1.5	81	93
1XFU	F T	T	87	E	1.6	81	93
1XFU	F T	T	91	V	1.1	81	93
1XFU	F T	T	124	M	1.0	121	129
1XFU	F T	T	127	E	1.7	121	129
1XFU	F T	T	138	Y	1.2	138	147
1XFU	F T	T	145	M	2.2	138	147
1XFV	A O	A	525	K	1.3	522	536
1XFV	A O	A	533	L	1.2	522	536
1XFV	A O	A	534	I	3.1	522	536
1XFV	A O	A	664	I	1.3	660	672
1XFV	A O	A	665	K	1.5	660	672
1XFV	A O	O	18	L	2.8	13	19
1XFV	A O	O	89	F	3.0	81	93
1XFV	B P	B	525	K	1.2	522	536
1XFV	B P	B	533	L	1.2	522	536
1XFV	B P	B	534	I	2.2	522	536
1XFV	B P	B	664	I	1.2	660	672
1XFV	B P	B	665	K	1.3	660	672
1XFV	B P	P	18	L	2.8	9	19
1XFV	B P	P	84	E	1.2	81	93
1XFV	C Q	C	525	K	1.6	522	536
1XFV	C Q	C	533	L	4.4	522	536
1XFV	C Q	C	664	I	1.1	660	672
1XFV	C Q	C	665	K	1.5	660	672
1XFV	C Q	C	704	Y	1.2	699	705
1XFV	C Q	C	717	K	1.7	714	737
1XFV	C Q	C	721	S	1.3	714	737
1XFV	C Q	Q	18	L	2.8	13	19
1XFV	C Q	Q	105	L	1.7	102	112
1XFV	C Q	Q	109	M	1.6	102	112
1XFV	C Q	Q	126	R	1.3	121	129
1XFV	C Q	Q	127	E	1.7	121	129
1XFV	C Q	Q	143	Q	2.3	138	147
1XFV	D R	D	527	K	1.2	522	536
1XFV	D R	D	533	L	1.1	522	536
1XFV	D R	D	534	I	1.4	522	536
1XFV	D R	D	665	K	1.3	660	672
1XFV	D R	R	18	L	2.9	13	19
1XFV	D R	R	89	F	3.9	81	93
1XFV	E S	E	504	I	3.8	501	506
1XFV	E S	E	523	L	1.3	522	536
1XFV	E S	E	525	K	1.3	522	536
1XFV	E S	E	533	L	1.1	522	536
1XFV	E S	E	534	I	1.1	522	536
1XFV	E S	E	665	K	1.3	660	672
1XFV	E S	E	704	Y	1.0	699	705
1XFV	E S	E	721	S	1.1	714	737
1XFV	E S	S	18	L	2.9	13	19
1XFV	E S	S	84	E	1.5	81	93
1XFV	E S	S	126	R	1.2	121	129

1XFV	E S	S	127	E	1.6	121	129
1XFV	E S	S	143	Q	1.3	138	147
1XFV	F T	F	525	K	1.2	522	536
1XFV	F T	F	533	L	1.2	522	536
1XFV	F T	F	664	I	1.1	660	672
1XFV	F T	F	665	K	1.3	660	672
1XFV	F T	F	704	Y	1.4	699	705
1XFV	F T	F	717	K	1.8	714	737
1XFV	F T	T	18	L	2.8	13	19
1XFV	F T	T	143	Q	1.5	138	147
1XG2	A B	B	99	S	1.2	97	118
1XG2	A B	B	101	N	2.6	97	118
1XG2	A B	B	102	I	1.4	97	118
1XG2	A B	B	109	D	1.9	97	118
1XG2	A B	B	113	T	2.0	97	118
1XG2	A B	B	116	D	1.9	97	118
1XG2	A B	B	143	L	1.0	126	149
1XGP	A B	A	123	E	1.1	122	127
1XGP	A B	A	124	Q	1.8	122	127
1XGP	A C	C	93	N	1.0	89	100
1XGP	A C	C	96	K	1.6	89	100
1XGP	B C	C	97	K	1.2	89	100
1XIU	A E	A	254	V	1.3	238	259
1XIU	A E	A	268	L	2.0	268	291
1XIU	A E	A	271	Q	1.1	268	291
1XIU	A E	A	275	L	1.9	268	291
1XIU	A E	A	276	R	1.5	268	291
1XIU	A E	E	690	L	1.8	688	697
1XIU	A E	E	691	H	2.2	688	697
1XIU	A E	E	693	L	1.9	688	697
1XIU	A E	E	694	L	2.9	688	697
1XK4	A C	A	5	L	2.7	4	21
1XK4	A C	A	6	E	3.8	4	21
1XK4	A C	A	9	L	2.4	4	21
1XK4	A C	A	13	I	1.5	4	21
1XK4	A C	A	15	V	1.3	4	21
1XK4	A C	A	68	F	1.8	68	87
1XK4	A C	A	72	L	1.5	68	87
1XK4	A C	A	76	I	2.1	68	87
1XK4	A C	A	80	V	1.7	68	87
1XK4	A C	A	83	H	1.4	68	87
1XK4	A C	C	8	L	1.8	7	26
1XK4	A C	C	9	E	1.6	7	26
1XK4	A C	C	12	I	1.5	7	26
1XK4	A C	C	16	I	1.5	7	26
1XK4	A C	C	76	F	2.6	76	92
1XK4	A C	C	80	I	2.0	76	92
1XK4	A C	C	88	W	1.6	76	92
1XK4	A C	C	91	H	2.5	76	92
1XK4	B D	B	5	L	2.6	4	23
1XK4	B D	B	6	E	5.2	4	23
1XK4	B D	B	9	L	2.3	4	23
1XK4	B D	B	12	I	1.0	4	23
1XK4	B D	B	13	I	1.6	4	23
1XK4	B D	B	15	V	2.0	4	23
1XK4	B D	B	41	E	1.2	31	42
1XK4	B D	B	68	F	2.2	68	87
1XK4	B D	B	72	L	1.8	68	87
1XK4	B D	B	76	I	1.6	68	87
1XK4	B D	B	78	M	1.0	68	87

1XK4	B D	B	80	V	2.1	68	87
1XK4	B D	B	83	H	1.6	68	87
1XK4	B D	D	8	L	2.3	7	24
1XK4	B D	D	9	E	1.2	7	24
1XK4	B D	D	12	I	1.5	7	24
1XK4	B D	D	16	I	1.6	7	24
1XK4	B D	D	76	F	2.9	76	94
1XK4	B D	D	80	I	1.8	76	94
1XK4	B D	D	88	W	1.5	76	94
1XK4	B D	D	91	H	2.3	76	94
1XK4	E G	E	5	L	2.5	4	21
1XK4	E G	E	6	E	4.7	4	21
1XK4	E G	E	9	L	2.2	4	21
1XK4	E G	E	13	I	1.1	4	21
1XK4	E G	E	15	V	1.4	4	21
1XK4	E G	E	41	E	1.3	31	42
1XK4	E G	E	68	F	1.9	68	87
1XK4	E G	E	72	L	1.4	68	87
1XK4	E G	E	83	H	1.8	68	87
1XK4	E G	G	8	L	1.9	7	24
1XK4	E G	G	9	E	1.7	7	24
1XK4	E G	G	12	I	1.3	7	24
1XK4	E G	G	16	I	1.6	7	24
1XK4	E G	G	76	F	2.4	76	95
1XK4	E G	G	80	I	1.9	76	95
1XK4	E G	G	88	W	2.0	76	95
1XK4	E G	G	91	H	1.8	76	95
1XK4	F H	F	5	L	2.5	4	21
1XK4	F H	F	6	E	4.1	4	21
1XK4	F H	F	9	L	1.8	4	21
1XK4	F H	F	11	S	1.0	4	21
1XK4	F H	F	13	I	1.7	4	21
1XK4	F H	F	15	V	1.3	4	21
1XK4	F H	F	68	F	2.1	68	86
1XK4	F H	F	72	L	1.6	68	86
1XK4	F H	F	76	I	1.1	68	86
1XK4	F H	F	80	V	1.0	68	86
1XK4	F H	F	83	H	1.7	68	86
1XK4	F H	H	8	L	2.4	7	24
1XK4	F H	H	9	E	1.0	7	24
1XK4	F H	H	12	I	1.6	7	24
1XK4	F H	H	16	I	1.6	7	24
1XK4	F H	H	76	F	2.5	76	92
1XK4	F H	H	80	I	1.1	76	92
1XK4	F H	H	88	W	1.2	76	92
1XK4	F H	H	91	H	2.5	76	92
1XK4	F L	F	4	E	1.6	4	21
1XK4	F L	F	7	K	1.0	4	21
1XK4	F L	L	22	Y	1.2	7	26
1XK4	F L	L	25	K	1.3	7	26
1XK4	F L	L	39	E	1.0	34	45
1XK4	I K	I	5	L	2.6	4	21
1XK4	I K	I	6	E	4.3	4	21
1XK4	I K	I	9	L	2.3	4	21
1XK4	I K	I	12	I	1.0	4	21
1XK4	I K	I	13	I	2.1	4	21
1XK4	I K	I	15	V	1.2	4	21
1XK4	I K	I	41	E	1.0	31	42
1XK4	I K	I	68	F	2.4	68	87
1XK4	I K	I	72	L	1.4	68	87

1XK4	I K	I	80	V	1.2	68	87
1XK4	I K	I	83	H	1.6	68	87
1XK4	I K	K	8	L	1.9	7	24
1XK4	I K	K	9	E	1.6	7	24
1XK4	I K	K	12	I	1.4	7	24
1XK4	I K	K	16	I	1.7	7	24
1XK4	I K	K	76	F	2.0	76	95
1XK4	I K	K	80	I	2.0	76	95
1XK4	I K	K	88	W	1.6	76	95
1XK4	I K	K	91	H	2.3	76	95
1XK4	J H	J	4	E	2.5	4	21
1XK4	J K	K	65	D	1.0	56	67
1XK4	J L	J	5	L	2.6	4	21
1XK4	J L	J	6	E	4.7	4	21
1XK4	J L	J	9	L	2.3	4	21
1XK4	J L	J	12	I	1.2	4	21
1XK4	J L	J	13	I	1.9	4	21
1XK4	J L	J	15	V	1.8	4	21
1XK4	J L	J	41	E	1.1	31	42
1XK4	J L	J	68	F	2.6	68	87
1XK4	J L	J	72	L	1.6	68	87
1XK4	J L	J	76	I	1.7	68	87
1XK4	J L	J	80	V	1.9	68	87
1XK4	J L	J	83	H	3.0	68	87
1XK4	J L	L	7	Q	1.0	7	26
1XK4	J L	L	8	L	2.3	7	26
1XK4	J L	L	9	E	1.5	7	26
1XK4	J L	L	16	I	1.3	7	26
1XK4	J L	L	76	F	2.3	76	95
1XK4	J L	L	80	I	1.8	76	95
1XK4	J L	L	87	T	1.0	76	95
1XK4	J L	L	88	W	1.9	76	95
1XK4	J L	L	91	H	2.1	76	95
1XKM	A B	A	12	L	2.0	7	21
1XKM	A B	B	13	L	1.6	2	24
1XKM	A B	B	17	H	2.2	2	24
1XKM	A B	B	20	L	2.6	2	24
1XKM	A D	A	9	F	2.1	7	21
1XKM	A D	A	13	I	1.3	7	21
1XKM	A D	D	6	L	1.4	6	24
1XKM	C B	B	12	Y	1.3	2	24
1XKM	C B	C	9	F	2.0	7	20
1XKM	C D	C	12	L	2.0	7	20
1XKM	C D	C	15	T	1.2	7	20
1XKM	C D	D	13	L	1.2	6	24
1XKM	C D	D	17	H	1.8	6	24
1XKM	C D	D	20	L	2.0	6	24
1XKP	A B	A	49	I	1.8	49	56
1XKP	A B	B	110	F	1.4	103	121
1XKP	A C	C	73	L	1.2	62	75
1XKP	A C	C	119	E	1.5	115	124
1XKP	B C	B	63	M	1.1	59	64
1XKP	B C	C	66	R	1.6	62	75
1XKP	B C	C	69	M	2.9	62	75
1XKP	B C	C	70	Q	1.3	62	75
1XKP	B C	C	73	L	2.7	62	75
1XL3	A C	A	216	W	1.8	212	220
1XL3	A C	A	278	F	4.7	278	283
1XL3	A C	A	279	W	4.4	278	283
1XL3	A C	A	282	F	2.9	278	283

1XL3	A C	C	5	L	1.1	5	17
1XL3	A C	C	8	F	1.8	5	17
1XL3	A C	C	10	G	2.3	5	17
1XL3	A C	C	13	V	2.2	5	17
1XL3	A C	C	16	V	1.4	5	17
1XL3	A C	C	33	F	2.4	23	34
1XL3	A C	C	44	F	2.8	43	48
1XL3	B C	B	213	Y	2.1	212	220
1XL3	B D	B	278	F	4.4	278	283
1XL3	B D	B	279	W	4.9	278	283
1XL3	B D	B	282	F	3.3	278	283
1XL3	B D	D	5	L	1.0	5	17
1XL3	B D	D	8	F	1.8	5	17
1XL3	B D	D	9	M	2.0	5	17
1XL3	B D	D	10	G	1.1	5	17
1XL3	B D	D	13	V	2.1	5	17
1XL3	B D	D	44	F	1.6	43	48
1XL3	B D	D	51	M	1.0	51	55
1XLS	A E	A	394	E	1.3	386	408
1XLS	A E	A	397	Y	1.6	386	408
1XLS	A E	A	426	R	2.0	414	442
1XLS	A E	A	427	S	4.6	414	442
1XLS	A E	E	321	K	1.6	318	342
1XLS	A E	E	328	D	1.7	318	342
1XLS	A I	A	284	K	1.9	264	285
1XLS	A I	I	744	L	1.0	743	749
1XLS	A I	I	745	L	2.4	743	749
1XLS	A I	I	748	L	1.2	743	749
1XLS	B F	B	352	E	2.1	345	360
1XLS	B F	B	397	Y	1.0	386	408
1XLS	B F	B	426	R	1.5	414	442
1XLS	B F	B	427	S	5.3	414	442
1XLS	B F	B	430	L	1.2	414	442
1XLS	B F	F	292	D	2.3	288	308
1XLS	B F	F	321	K	1.0	318	342
1XLS	B F	F	328	D	1.0	318	342
1XLS	B J	B	284	K	1.8	264	286
1XLS	B J	J	745	L	1.4	743	749
1XLS	C G	C	348	R	1.0	345	360
1XLS	C G	C	397	Y	1.6	386	408
1XLS	C G	C	420	L	1.1	414	442
1XLS	C G	C	427	S	5.5	414	442
1XLS	C G	C	430	L	1.9	414	442
1XLS	C G	G	296	E	1.0	288	308
1XLS	C G	G	321	K	1.2	318	342
1XLS	C K	C	284	K	1.8	264	286
1XLS	C K	K	745	L	2.4	743	749
1XLS	D H	D	394	E	1.0	386	408
1XLS	D H	D	397	Y	1.3	386	408
1XLS	D H	D	426	R	12.9	414	442
1XLS	D H	H	321	K	1.6	318	342
1XLS	D H	H	328	D	1.3	318	342
1XLS	D H	H	330	R	1.5	318	342
1XLS	D L	D	284	K	1.3	264	286
1XLS	D L	L	745	L	1.2	743	749
1XLS	D L	L	748	L	1.1	743	749
1XLS	E M	E	187	K	1.6	164	188
1XLS	E M	E	351	P	2.0	351	357
1XLS	E M	E	355	E	1.1	351	357
1XLS	E M	E	356	I	1.4	351	357

1XLS	E M	M	743	A	2.0	743	751
1XLS	E M	M	744	L	1.4	743	751
1XLS	E M	M	745	L	2.9	743	751
1XLS	E M	M	749	L	1.9	743	751
1XLS	F N	F	187	K	1.7	164	188
1XLS	F N	N	745	L	1.0	743	751
1XLS	F N	N	749	L	1.6	743	751
1XLS	G O	G	187	K	1.8	164	188
1XLS	G O	O	749	L	1.5	743	751
1XLS	H P	H	187	K	1.6	164	188
1XLS	H P	H	201	I	2.0	197	207
1XLS	H P	H	204	L	2.3	197	207
1XLS	H P	H	351	P	1.7	351	357
1XLS	H P	H	355	E	1.1	351	357
1XLS	H P	H	356	I	1.4	351	357
1XLS	H P	P	743	A	1.7	743	751
1XLS	H P	P	744	L	1.4	743	751
1XLS	H P	P	745	L	2.9	743	751
1XLS	H P	P	746	R	2.0	743	751
1XLS	H P	P	749	L	1.4	743	751
1XLT	B C	C	355	H	1.2	355	363
1XLT	D F	F	357	N	1.0	355	363
1XLT	E I	I	302	F	1.7	297	305
1XLT	H C	C	302	F	3.8	297	306
1XM4	A B	A	295	L	1.8	292	297
1XM4	A B	A	305	N	1.2	302	317
1XM4	A B	A	335	R	1.7	328	344
1XM4	A B	A	339	I	1.0	328	344
1XM4	A B	B	305	N	1.3	302	316
1XM4	A B	B	312	F	1.4	302	316
1XM4	A B	B	335	R	2.2	328	345
1XM4	A B	B	339	I	1.0	328	345
1XME	A B	A	66	Y	1.5	65	89
1XME	A B	A	303	L	1.2	292	327
1XME	A B	A	307	V	2.6	292	327
1XME	A B	A	314	F	2.9	292	327
1XME	A B	A	315	T	2.0	292	327
1XME	A B	A	370	T	1.1	370	375
1XME	A B	A	373	Y	2.3	370	375
1XME	A B	B	8	H	1.7	5	39
1XME	A B	B	11	I	1.3	5	39
1XME	A B	B	26	L	1.9	5	39
1XME	A B	B	30	I	1.3	5	39
1XME	A C	A	314	F	2.2	292	327
1XME	A C	A	321	E	1.8	292	327
1XME	A C	A	357	I	1.5	344	367
1XME	A C	A	371	L	1.9	370	375
1XME	A C	A	374	V	1.5	370	375
1XME	A C	A	380	W	1.0	379	400
1XME	A C	C	7	G	72.9	6	33
1XME	A C	C	12	I	1.2	6	33
1XME	A C	C	15	L	1.2	6	33
1XME	A C	C	22	F	2.3	6	33
1XME	A C	C	26	V	1.4	6	33
1XME	A C	C	30	F	1.2	6	33
1XME	B C	B	18	W	2.0	5	39
1XME	B C	B	21	F	1.2	5	39
1XME	B C	B	25	M	1.0	5	39
1XME	B C	B	29	F	5.0	5	39
1XME	B C	B	32	L	3.3	5	39

1XME	B C	C	9	L	1.3	6	33
1XME	B C	C	12	I	1.1	6	33
1XME	B C	C	16	T	1.0	6	33
1XME	B C	C	20	L	1.2	6	33
1XME	B C	C	23	W	5.3	6	33
1XME	B C	C	27	Y	1.5	6	33
1XME	B C	C	30	F	2.5	6	33
1XME	B C	C	31	F	1.4	6	33
1XMN	A B	A	14	E	1.0	14	14
1XMN	A B	A	14	E	1.7	14	14
1XMN	A B	A	14	L	1.9	14	14
1XMN	C D	C	14	E	1.7	14	14
1XMN	C D	C	14	E	2.7	14	14
1XMN	C D	C	14	L	2.0	14	14
1XMN	E F	E	14	E	1.4	14	14
1XMN	E F	E	14	E	1.9	14	14
1XMN	E F	E	14	L	1.7	14	14
1XMN	E F	E	14	S	1.0	14	14
1XMN	G H	G	14	E	1.1	14	14
1XMN	G H	G	14	E	2.3	14	14
1XMN	G H	G	14	L	1.9	14	14
1XMQ	C N	C	9	G	93.4	7	11
1XMQ	C N	N	49	H	2.1	41	51
1XMQ	D E	D	53	D	1.1	53	69
1XMQ	G K	K	59	Y	1.8	58	75
1XMQ	J N	N	45	R	1.8	41	51
1XMQ	L Q	L	11	V	1.2	7	14
1XOF	A B	A	116	L	1.4	111	119
1XOU	A B	A	35	L	1.4	35	47
1XOU	A B	A	38	K	1.0	35	47
1XOU	A B	A	42	F	3.1	35	47
1XOU	A B	A	46	I	1.5	35	47
1XOU	A B	A	160	I	1.0	148	162
1XOU	A B	A	167	L	1.7	165	176
1XOU	A B	A	170	L	2.0	165	176
1XOU	A B	A	174	R	2.0	165	176
1XOU	A B	A	183	R	1.1	179	189
1XOU	A B	A	187	G	38.9	179	189
1XOU	A B	A	188	I	1.4	179	189
1XOU	A B	B	13	L	1.7	3	31
1XOU	A B	B	14	D	1.4	3	31
1XOU	A B	B	17	I	3.5	3	31
1XOU	A B	B	21	I	1.5	3	31
1XOU	A B	B	24	I	1.9	3	31
1XOU	A B	B	27	I	1.0	3	31
1XOU	A B	B	28	I	2.1	3	31
1XOU	A B	B	35	K	1.5	32	48
1XOU	A B	B	67	E	1.0	66	84
1XOU	A B	B	70	L	1.4	66	84
1XOU	A B	B	71	Y	1.1	66	84
1XOU	A B	B	75	L	1.5	66	84
1XOU	A B	B	77	K	1.7	66	84
1XOU	A B	B	81	L	1.7	66	84
1XPK	D C	D	116	P	1.2	113	127
1XPK	D C	D	120	L	1.8	113	127
1XPK	D C	D	215	E	1.0	198	221
1XPK	D C	C	90	V	1.5	88	96
1XPK	D C	C	116	P	1.2	112	127
1XPK	D C	C	120	L	1.8	112	127
1XPK	D C	C	215	E	1.1	198	221

1XQ5	A B	A	31	R	1.8	21	36
1XQ5	A B	A	104	H	1.3	96	114
1XQ5	A B	A	123	H	1.2	120	138
1XQ5	A B	B	33	I	44.9	20	35
1XQ5	A B	B	112	I	2.0	100	119
1XQ5	A D	A	96	P	1.0	96	114
1XQ5	A D	D	37	W	1.8	36	42
1XQ5	A D	D	41	Y	1.2	36	42
1XQ5	C B	C	96	P	1.1	96	114
1XQ5	C B	B	36	P	1.3	36	42
1XQ5	C B	B	37	W	2.8	36	42
1XQ5	C B	B	41	Y	1.7	36	42
1XQ5	C D	C	31	R	2.8	21	36
1XQ5	C D	C	104	H	1.5	96	114
1XQ5	C D	C	108	V	1.1	96	114
1XQ5	C D	C	123	H	2.0	120	140
1XQ5	C D	D	30	R	1.7	20	35
1XQ5	C D	D	33	I	1.2	20	35
1XQ5	C D	D	34	V	2.4	20	35
1XQ5	C D	D	112	I	2.3	100	119
1XQS	A C	A	134	M	1.3	134	143
1XQS	A C	A	249	K	1.1	244	261
1XQS	A C	A	252	F	1.4	244	261
1XQS	A C	A	336	E	2.8	335	347
1XQS	A C	C	244	E	1.4	230	249
1XQS	A C	C	247	R	1.0	230	249
1XQS	A C	C	248	K	3.2	230	249
1XQS	A C	C	269	R	5.5	257	274
1XQS	B D	B	129	D	1.4	110	131
1XQS	B D	B	252	F	2.0	244	260
1XQS	B D	B	336	E	1.3	335	347
1XQS	B D	D	247	R	1.2	230	249
1XQS	B D	D	248	K	1.5	230	249
1XQS	B D	D	262	R	1.0	257	274
1XQS	B D	D	269	R	1.9	257	274
1XRS	A B	A	382	I	1.0	382	399
1XS9	A D	D	298	K	1.7	297	309
1XTC	A C	C	207	G	28.1	197	228
1XTC	A C	C	210	F	1.6	197	228
1XTC	A C	C	214	Y	1.4	197	228
1XTC	A H	A	17	K	1.0	13	20
1XTC	C E	C	235	R	1.3	232	239
1XTC	C E	C	236	I	2.4	232	239
1XTC	C E	E	63	K	2.1	59	74
1XTC	C F	C	223	F	1.1	197	228
1XTC	C F	C	227	Q	3.1	197	228
1XTC	C F	F	77	L	1.7	74	79
1XTC	C G	C	223	F	1.0	197	228
1XTC	C G	C	226	Y	1.3	197	228
1XTC	C G	G	74	I	1.4	68	79
1XTC	C H	H	70	D	1.0	62	78
1XTG	A B	A	106	M	1.7	102	114
1XTG	A B	A	113	R	1.4	102	114
1XTG	A B	A	312	Y	1.0	310	321
1XTG	A B	A	337	K	1.0	335	349
1XTG	A B	A	344	M	1.2	335	349
1XTG	A B	A	348	I	1.0	335	349
1XTG	A B	A	357	F	3.6	351	359
1XTG	A B	B	153	V	1.6	148	167
1XTG	A B	B	156	I	1.0	148	167

1XTG	A B	B	160	L	2.9	148	167
1XTG	A B	B	163	M	1.7	148	167
1XV9	A B	A	390	E	1.3	387	408
1XV9	A B	A	430	L	1.4	422	443
1XV9	A B	B	241	L	1.2	236	253
1XV9	A B	B	244	H	1.3	236	253
1XV9	A B	B	282	D	1.6	278	298
1XV9	A B	B	286	E	2.3	278	298
1XV9	A B	B	311	K	1.6	308	330
1XV9	A B	B	314	G	2.3	308	330
1XV9	A B	B	328	Y	1.8	308	330
1XV9	B F	B	177	K	1.5	154	178
1XV9	B F	B	191	I	2.1	187	198
1XV9	B F	F	690	L	1.5	688	694
1XV9	C D	C	419	L	1.1	414	442
1XV9	C D	C	423	P	1.4	414	442
1XV9	C D	C	428	I	1.1	414	442
1XV9	C D	D	286	E	1.1	278	298
1XV9	C D	D	311	K	1.2	308	330
1XV9	C D	D	313	L	1.5	308	330
1XV9	C D	D	314	G	27.6	308	330
1XV9	C D	D	320	R	1.7	308	330
1XV9	C G	C	277	F	1.0	276	285
1XV9	C G	C	294	L	1.1	294	303
1XV9	C G	C	302	R	1.2	294	303
1XV9	C G	C	453	E	2.7	449	454
1XV9	C G	G	632	I	4.3	631	637
1XV9	C G	G	633	L	1.1	631	637
1XV9	D H	D	173	I	1.0	154	178
1XV9	D H	H	690	L	1.7	688	694
1XWD	A C	A	43	S	1.1	41	46
1XWJ	A B	A	11	I	1.3	6	26
1XWJ	A B	A	22	L	1.1	6	26
1XWJ	A B	A	25	M	1.6	6	26
1XWJ	A B	A	53	L	2.0	40	62
1XWJ	A B	A	125	F	1.3	101	145
1XWJ	A B	B	1950	L	1.6	1949	1968
1XWJ	A B	B	1951	I	1.3	1949	1968
1XXH	A B	A	39	R	2.0	28	44
1XXH	A B	A	179	L	1.0	178	192
1XXH	A E	A	299	R	2.3	295	313
1XXH	A E	A	303	Q	1.1	295	313
1XXH	A E	E	310	L	2.8	309	313
1XXH	A E	E	311	L	1.5	309	313
1XXH	A E	E	317	L	1.2	314	324
1XXH	D E	D	347	M	1.3	345	359
1XXH	D E	E	246	H	1.3	241	252
1XXH	D E	E	283	P	1.0	283	287
1XXH	F G	F	183	Q	1.5	178	188
1XXH	F G	F	187	R	2.4	178	188
1XXH	F G	G	294	M	1.1	278	296
1XXH	F J	F	299	R	1.8	295	313
1XXH	F J	F	302	V	1.1	295	313
1XXH	F J	F	305	L	1.8	295	313
1XXH	F J	F	310	L	1.3	295	313
1XXH	F J	J	310	L	2.2	308	324
1XXH	F J	J	311	L	1.0	308	324
1XXH	I J	I	345	R	1.2	345	359
1XXH	I J	I	350	E	1.2	345	359
1XXH	I J	I	354	L	1.2	345	359

1XXI	A B	A	191	L	1.1	178	192
1XXI	A B	B	23	H	1.1	22	34
1XXI	A B	B	31	G	8.3	22	34
1XXI	A B	B	294	M	1.0	278	298
1XXI	A B	B	329	Y	1.0	322	342
1XXI	A E	A	258	V	1.0	249	263
1XXI	A E	A	299	R	2.7	295	313
1XXI	A E	A	302	V	1.0	295	313
1XXI	A E	A	310	L	1.1	295	313
1XXI	A E	E	310	L	2.5	308	324
1XXI	A E	E	320	E	1.2	308	324
1XXI	D E	D	220	L	1.7	214	223
1XXI	D E	D	345	R	1.8	345	359
1XXI	D E	D	347	M	1.9	345	359
1XXI	D E	E	253	M	2.0	241	260
1XXI	D E	E	283	P	1.9	283	303
1XXI	D E	E	295	H	1.2	283	303
1XXI	F G	F	29	L	1.4	28	46
1XXI	F G	F	39	R	1.0	28	46
1XXI	F G	F	179	L	2.7	178	192
1XXI	F G	F	187	R	1.1	178	192
1XXI	F G	F	190	L	1.0	178	192
1XXI	F G	G	23	H	1.3	22	34
1XXI	F G	G	294	M	1.0	278	298
1XXI	F G	G	297	L	1.0	278	298
1XXI	F J	F	299	R	1.5	295	313
1XXI	F J	F	302	V	1.0	295	313
1XXI	F J	J	310	L	2.5	308	324
1XXI	F J	J	317	L	1.3	308	324
1XXI	I J	I	347	M	1.6	345	359
1XXI	I J	J	253	M	1.8	241	260
1XXI	I J	J	257	K	1.2	241	260
1XXI	I J	J	283	P	1.2	283	303
1XZP	A B	A	129	L	2.9	120	131
1XZP	A B	A	130	I	1.0	120	131
1XZP	A B	A	138	L	1.7	135	146
1XZP	A B	A	142	L	1.3	135	146
1XZP	A B	B	86	L	2.1	85	98
1XZP	A B	B	90	K	1.5	85	98
1Y14	A B	A	59	I	1.0	52	72
1Y14	A B	A	66	R	3.7	52	72
1Y14	A B	A	141	L	1.0	139	151
1Y14	A B	A	147	Y	3.4	139	151
1Y14	A B	A	190	E	1.0	188	195
1Y14	A B	A	194	L	1.6	188	195
1Y14	C D	C	59	I	1.0	52	74
1Y14	C D	C	66	R	4.9	52	74
1Y14	C D	C	147	Y	3.3	139	151
1Y14	C D	C	175	F	2.4	174	181
1Y14	C D	C	194	L	1.9	188	195
1Y3A	A E	A	211	W	2.7	208	215
1Y3A	A E	E	5	W	4.2	5	10
1Y3A	A E	E	8	F	3.3	5	10
1Y3A	A E	E	9	L	1.8	5	10
1Y3A	B F	B	208	R	1.5	208	215
1Y3A	B F	B	211	W	3.1	208	215
1Y3A	B F	B	249	L	1.3	242	255
1Y3A	B F	F	5	W	4.5	5	11
1Y3A	B F	F	6	Y	2.1	5	11
1Y3A	B F	F	8	F	3.0	5	11

1Y3A	B F	F	9	L	1.8	5	11
1Y3A	C G	C	211	W	3.2	208	215
1Y3A	C G	C	249	L	1.1	242	255
1Y3A	C G	G	5	W	4.2	5	10
1Y3A	C G	G	6	Y	1.5	5	10
1Y3A	C G	G	8	F	3.9	5	10
1Y3A	C G	G	9	L	1.5	5	10
1Y3A	D H	D	211	W	2.6	208	215
1Y3A	D H	D	249	L	1.2	242	255
1Y3A	D H	H	5	W	4.0	5	10
1Y3A	D H	H	6	Y	1.3	5	10
1Y3A	D H	H	8	F	4.0	5	10
1Y3A	D H	H	9	L	1.9	5	10
1Y56	A B	A	435	I	1.8	433	440
1Y56	A B	A	438	R	1.5	433	440
1Y56	A B	B	149	F	1.3	148	162
1Y56	A B	B	278	Y	1.8	278	292
1Y64	A B	B	1411	R	5.4	1410	1414
1Y64	A B	B	1463	E	1.4	1459	1465
1Y74	A D	A	19	L	1.8	19	37
1Y74	A D	A	22	D	5.2	19	37
1Y74	A D	A	33	L	7.2	19	37
1Y74	A D	A	43	K	1.9	42	53
1Y74	A D	A	55	F	1.1	54	73
1Y74	A D	A	59	I	1.6	54	73
1Y74	A D	D	106	L	2.3	101	112
1Y74	A D	D	122	H	1.0	113	130
1Y74	C B	B	105	E	1.0	101	110
1Y74	C B	B	122	H	1.1	113	128
1Y74	C B	C	19	L	1.3	19	37
1Y74	C B	C	29	L	26.9	19	37
1Y74	C B	C	43	K	1.1	41	53
1Y74	C B	C	55	F	1.5	54	73
1Y75	A B	A	116	K	2.2	115	119
1Y76	A D	A	22	K	1.3	5	27
1Y76	A D	A	51	L	1.4	45	64
1Y76	A D	D	111	L	1.8	104	118
1Y76	A D	D	128	H	1.0	119	138
1Y76	C B	B	89	L	1.5	86	98
1Y76	C B	B	111	L	1.5	104	118
1Y76	C B	B	128	H	1.1	119	138
1Y76	C B	C	35	L	3.7	30	44
1Y76	C B	C	38	F	11.8	30	44
1Y76	C B	C	42	L	2.2	30	44
1Y76	C B	C	47	F	1.3	45	64
1Y76	C B	C	50	I	1.2	45	64
1Y76	C B	C	51	L	1.0	45	64
1Y76	C D	C	61	K	1.1	45	64
1Y76	C D	D	135	M	1.1	119	138
1Y8H	A B	A	31	R	1.6	21	36
1Y8H	A B	A	122	H	2.3	119	137
1Y8H	A B	B	30	R	2.3	21	35
1Y8H	A B	B	34	V	1.0	21	35
1Y8H	A B	B	112	V	1.1	100	118
1Y8H	A D	A	95	P	1.2	95	113
1Y8H	C D	C	31	R	1.9	21	36
1Y8H	C D	C	111	V	1.0	95	113
1Y8H	C D	D	34	V	1.2	21	35
1Y8H	C D	D	112	V	1.0	100	118
1Y8H	C D	D	116	R	1.5	100	118

1Y8R	A B	A	20	D	1.0	20	24
1Y8R	A B	A	53	K	1.2	46	59
1Y8R	A B	A	57	L	1.4	46	59
1Y8R	A B	A	305	V	1.6	300	319
1Y8R	A B	A	308	G	1.2	300	319
1Y8R	A B	A	309	I	1.1	300	319
1Y8R	A B	A	312	Q	1.0	300	319
1Y8R	A B	B	31	E	1.7	27	40
1Y8R	A B	B	38	L	1.7	27	40
1Y8R	A B	B	374	F	1.1	373	381
1Y8R	A B	B	389	T	2.3	388	407
1Y8R	A B	B	393	V	1.4	388	407
1Y8R	A B	B	396	G	94.4	388	407
1Y8R	B C	B	122	R	1.5	119	133
1Y8R	D E	D	28	L	1.1	28	36
1Y8R	D E	D	50	E	1.5	46	59
1Y8R	D E	D	57	L	1.3	46	59
1Y8R	D E	D	301	P	2.4	300	320
1Y8R	D E	D	308	G	80.9	300	320
1Y8R	D E	D	309	I	1.3	300	320
1Y8R	D E	E	34	K	2.9	27	40
1Y8R	D E	E	38	L	1.5	27	40
1Y8R	D E	E	393	V	1.4	388	408
1Y8R	D E	E	396	G	11.9	388	408
1Y8R	D E	E	400	L	2.2	388	408
1Y8X	A B	A	32	L	1.1	29	40
1Y8X	A B	B	399	S	1.0	398	403
1Y8X	A B	B	400	I	2.0	398	403
1Y96	A B	A	10	L	1.9	9	16
1Y96	A B	B	62	L	2.9	51	74
1Y96	A B	B	63	R	1.2	51	74
1Y96	A B	B	65	R	2.2	51	74
1Y96	C D	D	62	L	2.6	51	74
1YA7	A H	A	110	E	1.1	109	123
1YA7	A H	H	66	Y	1.1	49	71
1YA7	A N	A	97	Q	1.0	82	103
1YA7	A N	N	65	L	1.7	49	71
1YA7	A R	A	22	F	1.3	22	34
1YA7	A R	A	25	E	1.5	22	34
1YA7	B H	B	93	R	1.0	82	104
1YA7	B H	B	97	Q	1.2	82	104
1YA7	B H	H	64	E	1.4	49	71
1YA7	B H	H	65	L	1.0	49	71
1YA7	B H	H	68	L	1.2	49	71
1YA7	B I	B	103	Y	2.0	82	104
1YA7	B S	B	22	F	1.5	22	34
1YA7	B S	B	25	E	1.3	22	34
1YA7	C I	C	93	R	1.0	82	104
1YA7	C I	I	64	E	1.3	49	71
1YA7	C J	C	103	Y	2.6	82	104
1YA7	C J	C	110	E	2.2	109	123
1YA7	C T	C	22	F	2.2	22	32
1YA7	C T	C	24	V	1.3	22	32
1YA7	C T	C	26	Y	1.2	22	32
1YA7	D J	D	93	R	1.1	82	104
1YA7	D J	D	97	Q	1.2	82	104
1YA7	D J	J	64	E	1.3	49	71
1YA7	D J	J	65	L	1.0	49	71
1YA7	D J	J	68	L	1.0	49	71
1YA7	D K	D	103	Y	2.3	82	104

1YA7	D K	D	110	E	2.0	109	123
1YA7	D K	K	66	Y	2.7	49	71
1YA7	D K	K	70	R	1.3	49	71
1YA7	D U	D	22	F	1.0	22	34
1YA7	E K	E	93	R	1.5	82	104
1YA7	E K	K	68	L	1.2	49	71
1YA7	E L	E	103	Y	3.2	82	104
1YA7	E L	L	66	Y	1.1	49	71
1YA7	E O	E	22	F	1.4	22	33
1YA7	F L	F	93	R	1.1	82	104
1YA7	F L	F	97	Q	1.5	82	104
1YA7	F L	L	64	E	1.4	49	71
1YA7	F L	L	65	L	1.0	49	71
1YA7	F M	F	103	Y	2.1	82	104
1YA7	F M	M	66	Y	1.5	49	71
1YA7	F M	M	70	R	1.2	49	71
1YA7	F P	F	22	F	3.4	22	33
1YA7	F P	F	25	E	1.9	22	33
1YA7	G M	G	93	R	1.0	82	104
1YA7	G M	G	100	K	1.4	82	104
1YA7	G M	M	68	L	1.1	49	71
1YA7	G N	G	103	Y	2.1	82	104
1YA7	G N	G	110	E	1.4	109	123
1YA7	G N	N	66	Y	3.1	49	71
1YA7	G N	N	70	R	1.6	49	71
1YA7	G Q	G	22	F	1.2	22	34
1YAG	A G	A	143	Y	1.7	137	145
1YAG	A G	A	345	I	2.7	338	349
1YAG	A G	A	351	T	1.2	350	354
1YAG	A G	G	75	G	11.5	71	88
1YAG	A G	G	79	I	2.2	71	88
1YAG	A G	G	80	F	1.6	71	88
1YAG	A G	G	82	V	1.0	71	88
1YBQ	A B	A	154	I	1.0	148	155
1YBQ	A B	B	121	R	1.0	113	127
1YCP	J K	J	14	E	1.3	14	14
1YCP	J K	J	14	L	1.2	14	14
1YCP	J K	J	14	Y	1.0	14	14
1YCP	J M	J	14	E	1.4	14	14
1YCP	J M	J	14	L	1.0	14	14
1YCP	J M	J	14	Y	1.3	14	14
1YCP	K M	K	129	L	2.0	126	130
1YCP	K M	M	237	W	1.2	235	241
1YCP	K M	M	238	I	1.2	235	241
1YCP	L H	L	8	E	1.5	7	11
1YCP	L H	L	14	L	1.9	14	14
1YCP	L H	L	14	Y	3.2	14	14
1YCR	A B	A	54	L	1.5	50	64
1YCR	A B	A	58	G	85.7	50	64
1YCR	A B	B	19	F	2.5	19	24
1YCR	A B	B	22	L	2.5	19	24
1YCR	A B	B	23	W	6.1	19	24
1YCS	A B	A	280	R	1.0	278	287
1YD8	U H	H	227	L	1.2	210	234
1YD8	U H	H	231	M	1.2	210	234
1YD8	V G	G	227	L	2.0	210	234
1YD8	V G	G	231	M	1.1	210	234
1YD8	V G	G	243	G	1.0	242	267
1YD8	V G	G	251	L	2.1	242	267
1YDI	A B	A	12	I	1.2	7	26

1YDI	A B	A	23	L	2.7	7	26
1YDI	A B	A	47	V	1.6	41	65
1YDI	A B	A	54	L	1.7	41	65
1YDI	A B	A	57	V	1.1	41	65
1YDI	A B	A	108	L	1.0	102	150
1YDI	A B	A	115	I	1.0	102	150
1YDI	A B	A	126	F	1.4	102	150
1YDI	A B	B	743	W	5.8	743	764
1YDI	A B	B	746	L	1.5	743	764
1YDI	A B	B	747	L	2.6	743	764
1YDI	A B	B	750	I	1.8	743	764
1YDI	A B	B	754	I	1.7	743	764
1YDI	A B	B	758	E	1.2	743	764
1YDI	A B	B	761	I	2.0	743	764
1YE9	A E	A	250	L	1.3	247	258
1YE9	A E	A	254	M	2.7	247	258
1YE9	A E	A	255	W	2.4	247	258
1YE9	A E	E	318	H	2.1	317	329
1YE9	A E	E	321	E	2.1	317	329
1YE9	A E	E	322	L	1.7	317	329
1YE9	A E	E	408	L	1.8	407	423
1YE9	A E	E	410	G	318.9	407	423
1YE9	A E	E	422	R	1.8	407	423
1YE9	A E	E	507	H	1.5	505	513
1YE9	A E	E	508	P	1.1	505	513
1YE9	A E	E	511	F	3.9	505	513
1YE9	A E	E	539	I	1.4	537	549
1YE9	A F	A	242	Y	3.2	237	245
1YE9	A G	A	108	F	2.2	108	119
1YE9	A G	A	111	R	1.0	108	119
1YE9	A H	H	319	R	1.5	317	329
1YE9	A H	H	323	W	3.1	317	329
1YE9	A H	H	409	Q	1.6	406	415
1YE9	A H	H	413	F	1.1	406	415
1YE9	A H	H	418	T	1.1	416	423
1YE9	B E	B	219	H	1.0	214	222
1YE9	B E	B	241	D	1.3	237	245
1YE9	B E	B	242	Y	1.6	237	245
1YE9	B F	B	237	D	1.3	237	245
1YE9	B F	B	240	W	4.7	237	245
1YE9	B F	B	248	E	1.1	247	258
1YE9	B F	B	250	L	1.6	247	258
1YE9	B F	B	251	H	2.6	247	258
1YE9	B F	B	254	M	2.5	247	258
1YE9	B F	B	255	W	2.2	247	258
1YE9	B F	B	257	M	3.4	247	258
1YE9	B F	F	318	H	2.8	317	329
1YE9	B F	F	322	L	1.5	317	329
1YE9	B F	F	385	E	1.6	382	388
1YE9	B F	F	408	L	1.4	406	423
1YE9	B F	F	410	G	329.8	406	423
1YE9	B F	F	422	R	1.7	406	423
1YE9	B F	F	508	P	1.0	505	514
1YE9	B F	F	511	F	3.9	505	514
1YE9	B F	F	522	H	1.1	517	533
1YE9	B F	F	526	G	5.0	517	533
1YE9	B F	F	527	F	5.3	517	533
1YE9	B F	F	531	L	1.2	517	533
1YE9	B F	F	539	I	1.6	537	549
1YE9	B F	F	543	V	1.2	537	549

1YE9	B G	G	323	W	2.9	317	329
1YE9	B G	G	382	F	1.3	382	388
1YE9	B G	G	409	Q	1.4	407	423
1YE9	B G	G	413	F	1.1	407	423
1YE9	B G	G	418	T	1.2	407	423
1YE9	B H	B	108	F	2.5	108	119
1YE9	B H	B	112	E	8.4	108	119
1YE9	B H	B	116	H	2.1	108	119
1YE9	B H	H	416	T	7.6	416	423
1YE9	B H	H	420	I	1.0	416	423
1YE9	C E	C	108	F	26.0	108	119
1YE9	C E	C	111	R	1.3	108	119
1YE9	C E	C	116	H	1.5	108	119
1YE9	C E	E	416	T	24.6	407	423
1YE9	C E	E	420	I	1.2	407	423
1YE9	C F	C	111	R	1.0	108	119
1YE9	C F	F	319	R	2.4	317	329
1YE9	C F	F	323	W	1.4	317	329
1YE9	C F	F	324	E	1.4	317	329
1YE9	C F	F	409	Q	1.6	406	423
1YE9	C F	F	418	T	1.2	406	423
1YE9	C G	C	240	W	4.8	237	245
1YE9	C G	C	250	L	1.3	247	258
1YE9	C G	C	251	H	2.0	247	258
1YE9	C G	C	254	M	2.2	247	258
1YE9	C G	C	255	W	1.1	247	258
1YE9	C G	C	257	M	1.9	247	258
1YE9	C G	G	318	H	2.1	317	329
1YE9	C G	G	322	L	1.5	317	329
1YE9	C G	G	383	F	1.0	382	388
1YE9	C G	G	385	E	1.3	382	388
1YE9	C G	G	407	L	1.9	407	423
1YE9	C G	G	408	L	2.0	407	423
1YE9	C G	G	410	G	356.2	407	423
1YE9	C G	G	508	P	1.4	505	514
1YE9	C G	G	511	F	4.1	505	514
1YE9	C G	G	526	G	1.8	517	533
1YE9	C G	G	527	F	4.3	517	533
1YE9	C G	G	531	L	1.1	517	533
1YE9	C H	C	219	H	1.2	214	222
1YE9	C H	C	241	D	1.8	237	245
1YE9	C H	C	242	Y	1.1	237	245
1YE9	D E	E	319	R	1.4	317	329
1YE9	D E	E	323	W	1.7	317	329
1YE9	D E	E	409	Q	3.3	407	423
1YE9	D E	E	417	D	2.2	407	423
1YE9	D F	D	108	F	2.3	108	119
1YE9	D F	D	116	H	1.8	108	119
1YE9	D F	F	409	Q	1.0	406	423
1YE9	D F	F	420	I	1.1	406	423
1YE9	D G	D	219	H	1.4	214	222
1YE9	D G	D	241	D	1.5	237	245
1YE9	D G	D	242	Y	1.0	237	245
1YE9	D H	D	240	W	4.7	237	245
1YE9	D H	D	250	L	1.4	247	258
1YE9	D H	D	254	M	2.3	247	258
1YE9	D H	D	255	W	2.5	247	258
1YE9	D H	D	257	M	1.1	247	258
1YE9	D H	H	318	H	2.7	317	329
1YE9	D H	H	319	R	3.4	317	329

1YE9	D H	H	322	L	1.4	317	329
1YE9	D H	H	385	E	2.1	382	388
1YE9	D H	H	408	L	1.5	406	415
1YE9	D H	H	410	G	248.1	406	415
1YE9	D H	H	422	R	1.6	416	423
1YE9	D H	H	508	P	1.0	504	514
1YE9	D H	H	511	F	4.0	504	514
1YE9	D H	H	526	G	1.9	517	533
1YE9	D H	H	527	F	3.1	517	533
1YE9	D H	H	539	I	1.5	537	549
1YE9	D H	H	543	V	1.3	537	549
1YE9	I M	I	237	D	1.7	237	245
1YE9	I M	I	240	W	3.7	237	245
1YE9	I M	I	251	H	1.1	247	258
1YE9	I M	I	254	M	2.5	247	258
1YE9	I M	I	255	W	2.1	247	258
1YE9	I M	I	257	M	3.8	247	258
1YE9	I M	M	322	L	1.4	317	329
1YE9	I M	M	383	F	1.6	382	388
1YE9	I M	M	385	E	2.4	382	388
1YE9	I M	M	387	E	1.2	382	388
1YE9	I M	M	410	G	249.9	406	423
1YE9	I M	M	422	R	2.0	406	423
1YE9	I M	M	508	P	1.0	505	514
1YE9	I M	M	511	F	2.9	505	514
1YE9	I M	M	523	I	1.0	517	533
1YE9	I M	M	526	G	2.4	517	533
1YE9	I M	M	527	F	2.7	517	533
1YE9	I M	M	531	L	1.1	517	533
1YE9	I M	M	539	I	1.3	537	549
1YE9	I M	M	543	V	1.2	537	549
1YE9	I N	I	219	H	1.1	214	222
1YE9	I N	I	241	D	1.6	237	245
1YE9	I N	I	242	Y	1.2	237	245
1YE9	I O	I	108	F	2.5	108	119
1YE9	I O	O	409	Q	1.0	406	424
1YE9	I O	O	416	T	1.4	406	424
1YE9	I P	P	319	R	1.2	317	329
1YE9	I P	P	323	W	2.9	317	329
1YE9	I P	P	382	F	1.5	382	389
1YE9	I P	P	409	Q	1.8	406	423
1YE9	I P	P	413	F	1.2	406	423
1YE9	I P	P	417	D	1.1	406	423
1YE9	J M	J	219	H	1.3	211	222
1YE9	J N	J	240	W	2.3	237	245
1YE9	J N	J	248	E	3.7	247	258
1YE9	J N	J	250	L	1.2	247	258
1YE9	J N	J	251	H	1.1	247	258
1YE9	J N	J	254	M	2.2	247	258
1YE9	J N	J	255	W	2.2	247	258
1YE9	J N	J	257	M	2.1	247	258
1YE9	J N	N	318	H	3.0	317	329
1YE9	J N	N	319	R	1.0	317	329
1YE9	J N	N	322	L	1.6	317	329
1YE9	J N	N	385	E	1.0	382	388
1YE9	J N	N	408	L	1.4	406	423
1YE9	J N	N	410	G	261.1	406	423
1YE9	J N	N	422	R	2.0	406	423
1YE9	J N	N	507	H	1.1	505	514
1YE9	J N	N	508	P	1.7	505	514

1YE9	J N	N	511	F	3.5	505	514
1YE9	J N	N	527	F	2.3	517	533
1YE9	J N	N	531	L	1.1	517	533
1YE9	J N	N	539	I	2.2	537	549
1YE9	J N	N	543	V	1.2	537	549
1YE9	J O	O	319	R	1.1	317	329
1YE9	J O	O	409	Q	1.6	406	424
1YE9	J O	O	413	F	1.6	406	424
1YE9	J P	J	108	F	2.3	108	119
1YE9	K M	K	108	F	2.5	108	119
1YE9	K M	K	111	R	1.3	108	119
1YE9	K M	K	113	K	1.4	108	119
1YE9	K N	K	109	I	2.5	108	119
1YE9	K N	N	323	W	3.2	317	329
1YE9	K N	N	382	F	1.9	382	388
1YE9	K O	K	237	D	1.0	237	245
1YE9	K O	K	239	F	1.5	237	245
1YE9	K O	K	240	W	4.2	237	245
1YE9	K O	K	243	V	1.6	237	245
1YE9	K O	K	250	L	1.5	247	258
1YE9	K O	K	251	H	1.6	247	258
1YE9	K O	K	253	V	1.9	247	258
1YE9	K O	K	254	M	2.4	247	258
1YE9	K O	K	255	W	2.1	247	258
1YE9	K O	K	257	M	1.4	247	258
1YE9	K O	O	317	F	1.0	317	329
1YE9	K O	O	318	H	3.5	317	329
1YE9	K O	O	322	L	1.5	317	329
1YE9	K O	O	407	L	1.7	406	424
1YE9	K O	O	408	L	1.0	406	424
1YE9	K O	O	410	G	161.3	406	424
1YE9	K O	O	505	Y	1.1	505	514
1YE9	K O	O	508	P	1.3	505	514
1YE9	K O	O	511	F	3.4	505	514
1YE9	K O	O	523	I	4.9	517	533
1YE9	K O	O	526	G	1.4	517	533
1YE9	K O	O	527	F	3.9	517	533
1YE9	K O	O	529	F	1.6	517	533
1YE9	K O	O	531	L	3.5	517	533
1YE9	K O	O	539	I	1.5	537	549
1YE9	K O	O	543	V	3.2	537	549
1YE9	K O	O	546	Q	1.5	537	549
1YE9	K P	K	241	D	1.5	237	245
1YE9	K P	K	242	Y	1.0	237	245
1YE9	L M	M	319	R	1.1	317	329
1YE9	L M	M	323	W	1.2	317	329
1YE9	L M	M	409	Q	1.5	406	423
1YE9	L N	L	108	F	59.5	108	119
1YE9	L N	L	111	R	58.7	108	119
1YE9	L N	L	112	E	57.9	108	119
1YE9	L N	L	115	T	1.1	108	119
1YE9	L N	N	416	T	57.6	406	423
1YE9	L N	N	420	I	1.3	406	423
1YE9	L O	L	219	H	1.1	214	222
1YE9	L O	L	241	D	1.8	237	245
1YE9	L P	L	240	W	5.1	237	245
1YE9	L P	L	251	H	1.7	247	258
1YE9	L P	L	254	M	2.5	247	258
1YE9	L P	L	257	M	6.0	247	258
1YE9	L P	P	318	H	4.2	317	329

1YE9	L P	P	319	R	1.7	317	329
1YE9	L P	P	321	E	1.1	317	329
1YE9	L P	P	322	L	2.6	317	329
1YE9	L P	P	383	F	1.4	382	389
1YE9	L P	P	385	E	1.2	382	389
1YE9	L P	P	407	L	2.9	406	423
1YE9	L P	P	408	L	1.9	406	423
1YE9	L P	P	410	G	201.4	406	423
1YE9	L P	P	415	Y	1.2	406	423
1YE9	L P	P	422	R	1.7	406	423
1YE9	L P	P	504	Y	1.8	504	514
1YE9	L P	P	507	H	1.4	504	514
1YE9	L P	P	508	P	1.4	504	514
1YE9	L P	P	511	F	3.3	504	514
1YE9	L P	P	523	I	1.6	517	533
1YE9	L P	P	526	G	1.1	517	533
1YE9	L P	P	527	F	2.3	517	533
1YE9	L P	P	539	I	1.3	537	549
1YE9	L P	P	543	V	1.4	537	549
1YED	A B	A	127	Q	1.2	125	130
1YED	L H	L	127	Q	1.0	125	130
1YEW	A B	A	191	W	1.3	185	207
1YEW	A B	A	195	W	2.2	185	207
1YEW	A B	A	196	F	1.3	185	207
1YEW	A B	A	199	G	20.8	185	207
1YEW	A B	A	202	W	3.4	185	207
1YEW	A B	A	203	I	3.6	185	207
1YEW	A B	A	206	W	1.3	185	207
1YEW	A B	A	211	I	1.2	211	220
1YEW	A B	A	212	F	3.4	211	220
1YEW	A B	A	215	R	1.8	211	220
1YEW	A B	A	219	V	1.2	211	220
1YEW	A B	A	240	L	1.0	232	252
1YEW	A B	A	243	T	1.3	232	252
1YEW	A B	A	247	V	2.4	232	252
1YEW	A B	B	22	D	2.7	11	44
1YEW	A B	B	23	W	1.0	11	44
1YEW	A B	B	80	W	1.8	78	84
1YEW	A B	B	83	Y	1.3	78	84
1YEW	A B	B	90	T	1.0	88	112
1YEW	A B	B	94	L	2.1	88	112
1YEW	A B	B	125	V	1.9	124	137
1YEW	A B	B	126	P	1.5	124	137
1YEW	A B	B	129	I	1.8	124	137
1YEW	A B	B	130	I	1.2	124	137
1YEW	A B	B	155	I	1.5	141	166
1YEW	A B	B	162	P	1.0	141	166
1YEW	A B	B	180	I	1.3	180	188
1YEW	A B	B	182	D	1.5	180	188
1YEW	A B	B	186	Y	2.7	180	188
1YEW	A C	A	213	I	1.6	211	220
1YEW	A C	A	214	P	1.0	211	220
1YEW	A C	A	217	L	1.1	211	220
1YEW	B C	B	11	H	2.0	11	44
1YEW	B C	B	17	V	1.0	11	44
1YEW	B C	B	21	I	1.2	11	44
1YEW	B C	B	28	V	1.4	11	44
1YEW	B C	B	31	F	1.9	11	44
1YEW	B C	B	35	G	79.0	11	44
1YEW	B C	B	99	G	2.1	88	112

1YEW	B C	B	111	W	2.4	88	112
1YEW	B C	C	73	G	3.4	50	74
1YEW	B C	C	143	W	1.2	132	163
1YEW	B C	C	145	I	1.1	132	163
1YEW	B C	C	146	Y	1.2	132	163
1YEW	B C	C	150	S	1.3	132	163
1YEW	B C	C	159	W	2.0	132	163
1YEW	B C	C	160	H	1.6	132	163
1YEW	B C	C	173	H	2.1	171	178
1YEW	B C	C	192	F	1.0	179	197
1YEW	E F	E	187	N	1.3	185	207
1YEW	E F	E	191	W	3.8	185	207
1YEW	E F	E	192	H	2.6	185	207
1YEW	E F	E	195	W	2.3	185	207
1YEW	E F	E	199	G	5.0	185	207
1YEW	E F	E	202	W	3.6	185	207
1YEW	E F	E	203	I	1.9	185	207
1YEW	E F	E	206	W	2.3	185	207
1YEW	E F	E	211	I	1.5	211	220
1YEW	E F	E	212	F	3.1	211	220
1YEW	E F	E	219	V	1.1	211	220
1YEW	E F	E	232	D	2.4	232	252
1YEW	E F	E	236	A	1.9	232	252
1YEW	E F	E	237	M	1.9	232	252
1YEW	E F	E	240	L	2.6	232	252
1YEW	E F	E	243	T	1.3	232	252
1YEW	E F	E	247	V	1.5	232	252
1YEW	E F	F	22	D	2.3	11	44
1YEW	E F	F	80	W	3.4	78	84
1YEW	E F	F	83	Y	3.6	78	84
1YEW	E F	F	90	T	1.8	88	112
1YEW	E F	F	97	L	1.5	88	112
1YEW	E F	F	126	P	1.7	124	137
1YEW	E F	F	129	I	2.5	124	137
1YEW	E F	F	130	I	1.1	124	137
1YEW	E F	F	133	T	2.4	124	137
1YEW	E F	F	136	M	1.5	124	137
1YEW	E F	F	180	I	2.7	180	188
1YEW	E F	F	182	D	2.1	180	188
1YEW	E F	F	183	I	1.8	180	188
1YEW	E F	F	186	Y	7.2	180	188
1YEW	E G	E	213	I	1.6	211	220
1YEW	E G	E	217	L	1.1	211	220
1YEW	F G	F	11	H	1.8	11	44
1YEW	F G	F	17	V	1.1	11	44
1YEW	F G	F	21	I	1.2	11	44
1YEW	F G	F	27	F	1.5	11	44
1YEW	F G	F	28	V	1.0	11	44
1YEW	F G	F	31	F	1.6	11	44
1YEW	F G	F	35	G	62.2	11	44
1YEW	F G	F	99	G	2.1	88	112
1YEW	F G	F	108	F	4.2	88	112
1YEW	F G	F	111	W	3.0	88	112
1YEW	F G	G	73	G	2.3	50	74
1YEW	F G	G	143	W	1.5	132	154
1YEW	F G	G	145	I	1.1	132	154
1YEW	F G	G	146	Y	1.2	132	154
1YEW	F G	G	159	W	2.5	155	163
1YEW	F G	G	160	H	1.5	155	163
1YEW	F G	G	192	F	1.0	179	197

1YEW	I J	I	187	N	1.2	185	207
1YEW	I J	I	191	W	1.8	185	207
1YEW	I J	I	192	H	1.3	185	207
1YEW	I J	I	195	W	2.1	185	207
1YEW	I J	I	199	G	17.9	185	207
1YEW	I J	I	202	W	3.1	185	207
1YEW	I J	I	203	I	2.7	185	207
1YEW	I J	I	206	W	1.8	185	207
1YEW	I J	I	211	I	1.4	211	220
1YEW	I J	I	212	F	3.2	211	220
1YEW	I J	I	215	R	1.8	211	220
1YEW	I J	I	219	V	1.0	211	220
1YEW	I J	I	247	V	1.4	232	252
1YEW	I J	J	22	D	2.1	11	44
1YEW	I J	J	80	W	1.0	78	84
1YEW	I J	J	83	Y	1.5	78	84
1YEW	I J	J	125	V	1.2	124	137
1YEW	I J	J	126	P	1.6	124	137
1YEW	I J	J	129	I	1.9	124	137
1YEW	I J	J	162	P	1.2	141	166
1YEW	I J	J	180	I	1.4	180	185
1YEW	I J	J	182	D	1.3	180	185
1YEW	I K	I	213	I	1.6	211	220
1YEW	I K	I	217	L	2.7	211	220
1YEW	J K	J	11	H	1.6	11	44
1YEW	J K	J	21	I	1.3	11	44
1YEW	J K	J	28	V	1.1	11	44
1YEW	J K	J	31	F	1.9	11	44
1YEW	J K	J	32	V	1.1	11	44
1YEW	J K	J	35	G	60.4	11	44
1YEW	J K	J	99	G	2.1	88	112
1YEW	J K	J	111	W	4.9	88	112
1YEW	J K	K	73	G	1.7	50	74
1YEW	J K	K	143	W	1.8	132	163
1YEW	J K	K	145	I	1.2	132	163
1YEW	J K	K	146	Y	1.2	132	163
1YEW	J K	K	150	S	1.1	132	163
1YEW	J K	K	153	T	3.5	132	163
1YEW	J K	K	155	Q	1.1	132	163
1YEW	J K	K	156	D	1.1	132	163
1YEW	J K	K	159	W	3.5	132	163
1YEW	J K	K	160	H	1.7	132	163
1YEW	J K	K	188	G	290.3	179	197
1YFN	A E	E	6	P	1.3	6	10
1YFN	A E	E	9	W	2.7	6	10
1YFN	A E	E	14	F	3.6	13	18
1YFN	B F	F	9	W	3.6	6	10
1YFN	C G	G	9	W	4.4	6	11
1YFN	D H	H	6	P	1.1	6	11
1YFN	D H	H	9	W	3.6	6	11
1YHN	A B	B	263	F	1.5	250	277
1YHU	A C	A	26	R	1.0	22	41
1YHU	A C	A	59	P	2.1	59	78
1YHU	A C	A	60	E	1.0	59	78
1YHU	A C	A	70	G	5.6	59	78
1YHU	A C	A	73	D	1.8	59	78
1YHU	A C	A	91	H	1.7	82	99
1YHU	A C	C	29	R	1.7	26	44
1YHU	A C	C	62	P	1.8	62	81
1YHU	A C	C	66	G	18.0	62	81

1YHU	A C	C	69	V	1.4	62	81
1YHU	A C	C	70	R	1.4	62	81
1YHU	A C	C	76	D	1.7	62	81
1YHU	A C	C	77	I	1.2	62	81
1YHU	A D	A	7	L	2.3	6	21
1YHU	B C	B	10	L	1.1	6	20
1YHU	B C	B	14	R	1.4	6	20
1YHU	B D	B	73	D	2.0	59	78
1YHU	B D	B	91	H	1.0	82	97
1YHU	B D	D	28	R	1.0	26	43
1YHU	C H	C	130	P	1.2	130	145
1YHU	E G	E	26	R	1.0	22	41
1YHU	E G	E	59	P	3.4	59	78
1YHU	E G	E	70	G	4.7	59	78
1YHU	E G	E	73	D	1.6	59	78
1YHU	E G	E	91	H	1.8	82	99
1YHU	E G	G	29	R	1.1	26	44
1YHU	E G	G	62	P	1.8	62	81
1YHU	E G	G	66	G	15.2	62	81
1YHU	E G	G	70	R	1.1	62	81
1YHU	E G	G	76	D	1.7	62	81
1YHU	E G	G	77	I	1.2	62	81
1YHU	E G	G	91	M	1.1	85	102
1YHU	E H	E	7	L	2.0	6	21
1YHU	F G	F	14	R	1.4	6	20
1YHU	F G	G	18	D	1.2	6	20
1YHU	F H	F	73	D	1.8	59	78
1YHU	F H	F	84	V	1.0	82	97
1YHU	G L	G	130	P	1.2	130	145
1YHU	G L	L	138	R	1.2	129	144
1YHU	I K	I	26	R	1.0	22	41
1YHU	I K	I	59	P	2.0	59	78
1YHU	I K	I	70	G	3.1	59	78
1YHU	I K	I	73	D	1.7	59	78
1YHU	I K	I	91	H	1.7	82	99
1YHU	I K	K	29	R	1.1	26	44
1YHU	I K	K	62	P	1.7	62	81
1YHU	I K	K	66	G	23.3	62	81
1YHU	I K	K	76	D	1.7	62	81
1YHU	I L	I	7	L	2.2	6	21
1YHU	J K	J	14	R	1.1	6	20
1YHU	J K	K	18	D	1.1	6	20
1YHU	J L	J	26	R	1.6	26	41
1YHU	J L	J	73	D	1.8	59	81
1YHU	J L	J	91	H	1.0	82	97
1YHU	J L	L	89	E	1.0	84	100
1YHU	K D	K	130	P	1.5	130	145
1YHU	K D	K	131	D	3.0	130	145
1YHU	K D	D	138	R	1.4	129	144
1YHU	M O	M	59	P	1.0	59	78
1YHU	M O	M	67	R	1.3	59	78
1YHU	M O	M	70	G	4.6	59	78
1YHU	M O	M	73	D	1.7	59	78
1YHU	M O	M	91	H	1.6	82	99
1YHU	M O	O	29	R	1.2	26	44
1YHU	M O	O	62	P	1.3	62	81
1YHU	M O	O	70	R	2.0	62	81
1YHU	M O	O	76	D	4.7	62	81
1YHU	M O	O	77	I	1.2	62	81
1YHU	M O	O	91	M	1.2	85	102

1YHU	M O	O	94	H	1.9	85	102
1YHU	M P	M	7	L	2.4	6	21
1YHU	N O	N	14	R	1.2	6	20
1YHU	N O	O	18	D	1.3	6	20
1YHU	N P	N	62	R	1.3	59	78
1YHU	N P	N	73	D	1.7	59	78
1YHU	N P	N	77	A	2.4	59	78
1YHU	N P	N	83	P	1.3	82	97
1YHU	N P	N	84	V	3.4	82	97
1YHU	N P	N	91	H	1.0	82	97
1YHU	N P	P	28	R	3.4	26	43
1YHU	N P	P	69	R	2.9	61	80
1YHU	N P	P	89	E	1.0	84	100
1YHU	O T	O	130	P	1.3	130	145
1YHU	O T	T	84	P	1.2	84	100
1YHU	O T	T	138	R	1.3	129	144
1YHU	Q S	Q	26	R	1.0	22	41
1YHU	Q S	Q	59	P	4.7	59	78
1YHU	Q S	Q	70	G	3.5	59	78
1YHU	Q S	Q	73	D	1.5	59	78
1YHU	Q S	Q	91	H	1.7	82	99
1YHU	Q S	S	29	R	1.0	26	44
1YHU	Q S	S	62	P	1.5	62	81
1YHU	Q S	S	69	V	3.2	62	81
1YHU	Q S	S	70	R	4.7	62	81
1YHU	Q S	S	76	D	3.3	62	81
1YHU	Q S	S	77	I	1.2	62	81
1YHU	Q S	S	91	M	1.5	85	102
1YHU	Q T	Q	7	L	2.1	6	21
1YHU	R S	R	10	L	1.0	6	20
1YHU	R S	R	14	R	1.1	6	20
1YHU	R T	R	73	D	1.6	59	78
1YHU	R T	R	91	H	1.0	82	97
1YHU	S X	X	138	R	1.1	129	144
1YHU	U W	U	26	R	1.0	22	41
1YHU	U W	U	59	P	2.8	59	78
1YHU	U W	U	60	E	1.0	59	78
1YHU	U W	U	67	R	1.3	59	78
1YHU	U W	U	70	G	1.7	59	78
1YHU	U W	U	73	D	1.5	59	78
1YHU	U W	U	91	H	1.6	82	99
1YHU	U W	W	29	R	1.1	26	44
1YHU	U W	W	69	V	2.1	62	81
1YHU	U W	W	70	R	3.2	62	81
1YHU	U W	W	76	D	1.7	62	81
1YHU	U W	W	77	I	1.1	62	81
1YHU	U W	W	91	M	1.2	85	102
1YHU	U W	W	94	H	1.0	85	102
1YHU	U X	U	7	L	1.5	6	21
1YHU	V W	V	14	R	1.0	6	20
1YHU	V W	W	18	D	1.0	6	20
1YHU	V X	V	73	D	1.7	59	81
1YHU	W P	W	130	P	1.3	130	145
1YHU	W P	P	138	R	1.6	129	144
1YJD	L H	L	124	Q	1.2	122	127
1YKE	A B	A	116	I	1.4	112	135
1YKE	A B	A	123	L	1.8	112	135
1YKE	A B	A	130	Y	2.5	112	135
1YKE	A B	A	144	Y	1.0	143	164
1YKE	A B	A	155	L	1.3	143	164

1YKE	A B	A	162	L	1.9	143	164
1YKE	A B	A	168	H	1.6	166	204
1YKE	A B	A	182	L	1.1	166	204
1YKE	A B	A	189	I	2.0	166	204
1YKE	A B	A	192	I	1.5	166	204
1YKE	A B	B	5	L	1.5	4	19
1YKE	A B	B	9	Q	1.5	4	19
1YKE	A B	B	23	L	1.3	22	28
1YKE	A B	B	77	I	2.1	53	80
1YKE	A B	B	97	L	1.6	87	128
1YKE	A B	B	101	L	1.0	87	128
1YKE	A B	B	104	V	1.1	87	128
1YKE	A B	B	108	K	1.3	87	128
1YKE	C D	C	112	Y	1.4	112	133
1YKE	C D	C	126	L	1.2	112	133
1YKE	C D	C	127	L	1.0	112	133
1YKE	C D	C	130	Y	1.9	112	133
1YKE	C D	C	144	Y	1.1	141	162
1YKE	C D	C	151	I	1.1	141	162
1YKE	C D	C	159	H	2.8	141	162
1YKE	C D	C	168	H	1.8	165	203
1YKE	C D	C	171	R	1.1	165	203
1YKE	C D	C	175	I	2.4	165	203
1YKE	C D	C	185	K	1.8	165	203
1YKE	C D	C	189	I	1.8	165	203
1YKE	C D	C	192	I	1.8	165	203
1YKE	C D	D	15	M	2.6	4	25
1YKE	C D	D	19	F	4.4	4	25
1YKE	C D	D	23	L	1.7	4	25
1YKE	C D	D	97	L	1.0	97	106
1YKE	C D	D	105	E	1.0	97	106
1YKE	C D	D	108	K	2.2	107	129
1YKK	A B	A	19	I	1.0	17	21
1YKK	A B	A	20	G	178.5	17	21
1YKK	C D	C	19	I	1.0	17	21
1YKK	C D	C	20	G	162.4	17	21
1YKK	E F	E	19	I	1.9	17	22
1YKK	E F	E	20	G	147.8	17	22
1YKK	E F	E	21	L	2.0	17	22
1YKK	G H	G	19	I	1.3	17	22
1YKK	G H	G	20	G	182.8	17	22
1YKK	I J	I	19	I	1.8	17	21
1YKK	I J	I	20	G	166.0	17	21
1YKK	K L	K	19	I	1.1	17	21
1YKK	K L	K	20	G	138.5	17	21
1YKK	K L	L	327	S	1.4	325	330
1YL3	J L	J	78	R	2.7	70	82
1YL4	H K	H	151	L	1.2	145	153
1YL4	I U	U	75	I	1.6	60	76
1YL4	J L	L	41	V	1.2	41	46
1YM0	A B	A	238	I	1.0	235	244
1YMM	A B	A	70	L	1.4	56	77
1YMM	A B	A	74	T	1.0	56	77
1YMM	A B	B	82	N	6.3	78	86
1YMM	A B	B	83	Y	6.5	78	86
1YMM	A C	A	58	G	198.5	56	77
1YMM	A C	A	69	N	1.0	56	77
1YMM	B C	B	60	Y	1.3	52	64
1YMM	B C	B	78	Y	2.3	78	86
1YMM	B C	B	81	H	1.6	78	86

1YMM	B C	B	85	V	1.5	78	86
1YMM	B D	B	84	G	5.0	78	86
1YNJ	A C	A	34	V	1.2	32	47
1YNJ	A C	A	42	R	1.2	32	47
1YNJ	A C	A	45	L	1.5	32	47
1YNJ	A C	A	46	S	1.1	32	47
1YNJ	B D	B	77	E	1.3	75	84
1YNJ	B D	B	80	L	1.5	75	84
1YNJ	B D	D	848	E	1.1	846	855
1YNJ	C D	C	877	P	1.0	873	879
1YNJ	C D	C	1034	E	2.0	1034	1043
1YNJ	C D	C	1038	W	3.3	1034	1043
1YNJ	C D	C	1047	H	1.6	1046	1055
1YNJ	C D	C	1067	Y	1.1	1060	1072
1YNJ	C D	C	1070	I	2.5	1060	1072
1YNJ	C D	C	1085	F	1.0	1083	1095
1YNJ	C D	C	1088	L	1.5	1083	1095
1YNJ	C D	D	17	K	1.3	15	23
1YNJ	C D	D	21	W	2.7	15	23
1YNJ	C D	D	607	L	1.6	603	608
1YNJ	C D	D	614	F	1.4	614	618
1YNJ	C D	D	655	P	4.4	654	664
1YNJ	C D	D	656	F	1.5	654	664
1YNJ	C D	D	754	F	1.3	753	763
1YNJ	C D	D	785	I	1.1	785	793
1YNJ	C D	D	939	F	2.1	925	946
1YNJ	C D	D	1023	M	1.3	1019	1026
1YNJ	C D	D	1034	Q	1.1	1032	1040
1YNJ	C D	D	1068	L	1.5	1067	1073
1YNJ	C D	D	1071	F	4.0	1067	1073
1YNJ	C D	D	1096	R	1.7	1093	1105
1YNJ	C D	D	1223	V	1.3	1221	1235
1YNJ	C J	C	1085	F	1.2	1083	1095
1YNJ	C K	K	31	L	1.1	17	32
1YNJ	D K	D	925	E	2.0	925	946
1YNJ	D K	K	61	V	5.8	60	69
1YNJ	D K	K	65	M	1.7	60	69
1YNJ	J K	J	1495	I	1.2	1490	1497
1YNJ	J K	K	18	R	1.2	17	32
1YNJ	J K	K	21	V	1.7	17	32
1YNJ	J K	K	26	R	5.6	17	32
1YNK	L H	L	124	Q	1.5	122	127
1YNT	A B	A	124	Q	1.4	122	126
1YNT	C E	E	852	R	1.6	850	855
1YOK	A B	A	357	V	1.0	341	362
1YOK	A B	A	361	R	1.7	341	362
1YOK	A B	A	375	M	1.6	371	381
1YOK	A B	A	534	E	2.8	531	537
1YOK	A B	B	745	L	2.9	743	751
1YOK	A B	B	748	L	2.7	743	751
1YOK	A B	B	749	L	2.7	743	751
1YOV	A B	A	14	D	1.1	14	18
1YOV	A B	A	51	L	1.7	49	53
1YOV	A B	A	52	P	1.4	49	53
1YOV	A B	A	67	G	140.8	67	72
1YOV	A B	A	71	G	162.8	67	72
1YOV	A B	A	339	Y	1.0	336	367
1YOV	A B	A	340	I	1.2	336	367
1YOV	A B	A	478	Y	1.2	476	486
1YOV	A B	A	481	E	1.3	476	486

1YOV	A B	A	484	R	3.6	476	486
1YOV	A B	A	496	F	1.2	491	511
1YOV	A B	A	499	G	93.1	491	511
1YOV	A B	A	502	A	1.2	491	511
1YOV	A B	A	504	E	1.2	491	511
1YOV	A B	A	506	I	1.2	491	511
1YOV	A B	B	18	N	3.1	18	23
1YOV	A B	B	19	H	2.2	18	23
1YOV	A B	B	85	V	1.1	85	89
1YOV	A B	B	114	R	1.3	103	115
1YOV	A B	B	279	R	2.1	278	286
1YOV	A B	B	282	Q	1.1	278	286
1YOV	A B	B	283	G	1.3	278	286
1YOV	A B	B	293	A	1.2	293	313
1YOV	A B	B	297	A	1.2	293	313
1YOV	A B	B	298	V	2.3	293	313
1YOV	C D	C	15	R	1.7	14	20
1YOV	C D	C	18	R	1.3	14	20
1YOV	C D	C	19	L	1.8	14	20
1YOV	C D	C	51	L	1.5	49	53
1YOV	C D	C	52	P	1.3	49	53
1YOV	C D	C	340	I	1.2	336	369
1YOV	C D	C	496	F	2.5	491	511
1YOV	C D	C	499	G	102.9	491	511
1YOV	C D	C	500	A	1.1	491	511
1YOV	C D	C	502	A	1.1	491	511
1YOV	C D	C	504	E	1.0	491	511
1YOV	C D	D	110	F	1.3	103	115
1YOV	C D	D	114	R	1.9	103	115
1YOV	C D	D	293	A	1.1	293	313
1YOV	C D	D	294	S	1.7	293	313
1YOV	C D	D	297	A	1.1	293	313
1YOV	C D	D	298	V	1.5	293	313
1YOV	C D	D	302	V	1.5	293	313
1YOV	C D	D	306	E	2.0	293	313
1YPZ	E F	F	141	E	2.5	139	146
1YQ3	A B	A	108	I	2.3	103	114
1YQ3	A B	A	111	E	3.3	103	114
1YQ3	A B	A	155	H	1.4	153	167
1YQ3	A B	A	163	G	74.8	153	167
1YQ3	A B	A	166	L	1.8	153	167
1YQ3	A B	A	518	D	2.8	517	542
1YQ3	A B	B	119	Y	3.4	116	125
1YQ3	A B	B	146	I	1.3	146	153
1YQ3	A B	B	149	R	2.6	146	153
1YQ3	B D	B	173	W	1.2	169	174
1YQ3	B D	B	239	K	1.5	231	245
1YQ3	B D	B	242	M	2.2	231	245
1YQ3	B D	D	10	W	2.7	5	30
1YQ3	B D	D	57	D	5.6	33	59
1YQ3	C D	C	54	S	1.1	34	63
1YQ3	C D	C	56	F	1.6	34	63
1YQ3	C D	C	61	L	2.0	34	63
1YQ3	C D	C	67	F	3.1	67	76
1YQ3	C D	C	71	V	1.2	67	76
1YQ3	C D	C	103	I	1.3	81	110
1YQ3	C D	C	106	L	1.8	81	110
1YQ3	C D	C	109	D	1.1	81	110
1YQ3	C D	D	14	R	1.0	5	30
1YQ3	C D	D	21	L	1.1	5	30

1YQ3	C D	D	79	T	1.9	62	90
1YQ3	C D	D	82	G	77.7	62	90
1YQ3	C D	D	85	Y	1.1	62	90
1YQ3	C D	D	86	F	2.5	62	90
1YR5	A B	A	14	E	2.1	6	20
1YR5	A B	A	19	F	1.8	6	20
1YR5	A B	A	51	M	1.5	45	55
1YR5	A B	A	71	M	1.0	65	75
1YR5	A B	A	120	E	1.2	118	129
1YR5	A B	A	145	M	1.6	138	147
1YR5	A B	B	304	K	2.2	304	319
1YR5	A B	B	307	Q	1.6	304	319
1YR5	A B	B	309	V	1.4	304	319
1YR5	A B	B	311	L	1.8	304	319
1YR5	A B	B	312	I	2.7	304	319
1YR5	A B	B	317	R	1.2	304	319
1YR5	A B	B	318	L	1.0	304	319
1YRT	A B	A	202	R	1.1	202	210
1YRT	A B	A	238	I	1.5	235	253
1YRT	A B	A	241	L	1.7	235	253
1YRT	A B	A	242	W	5.2	235	253
1YRT	A B	A	248	G	75.7	235	253
1YRT	A B	A	250	R	2.3	235	253
1YRT	A B	B	91	V	2.0	82	93
1YRT	A B	B	92	F	1.2	82	93
1YRT	A B	B	105	L	1.1	102	112
1YRT	A B	B	109	M	1.1	102	112
1YRT	A B	B	124	M	1.3	118	129
1YRT	A B	B	144	M	1.7	138	147
1YSH	C D	C	51	R	2.4	51	62
1YSL	A B	A	90	V	1.3	88	96
1YSL	A B	A	94	R	1.0	88	96
1YSL	A B	A	127	L	1.2	113	128
1YSL	A B	A	215	E	1.6	198	221
1YSL	A B	B	90	V	1.6	88	96
1YSL	A B	B	94	R	1.3	88	96
1YSL	A B	B	127	L	1.1	112	128
1YSL	A B	B	215	E	1.2	198	221
1YTZ	I C	I	14	R	1.7	5	47
1YTZ	I C	I	17	L	1.4	5	47
1YTZ	I C	I	18	K	2.5	5	47
1YTZ	I C	I	21	M	2.2	5	47
1YTZ	I C	I	24	L	1.7	5	47
1YTZ	I C	I	29	I	1.5	5	47
1YTZ	I C	I	122	L	1.6	118	127
1YTZ	I C	I	126	L	1.8	118	127
1YTZ	I C	C	90	K	1.0	74	106
1YTZ	I C	C	91	G	1.9	74	106
1YTZ	I C	C	94	E	1.7	74	106
1YTZ	I C	C	95	E	1.3	74	106
1YTZ	I C	C	103	I	1.3	74	106
1YTZ	I C	C	104	F	1.4	74	106
1YTZ	I C	C	121	L	1.3	114	124
1YTZ	I C	C	136	L	1.2	130	141
1YTZ	T C	T	240	R	2.5	199	244
1YTZ	T C	C	151	D	1.2	150	157
1YTZ	T I	T	185	L	1.8	163	188
1YTZ	T I	T	209	L	1.0	199	244
1YTZ	T I	T	212	W	1.5	199	244
1YTZ	T I	T	216	L	1.5	199	244

1YTZ	T I	T	220	K	1.9	199	244
1YTZ	T I	T	223	F	1.0	199	244
1YTZ	T I	T	233	E	1.4	199	244
1YTZ	T I	T	234	I	1.4	199	244
1YTZ	T I	T	237	L	2.2	199	244
1YTZ	T I	T	241	I	1.3	199	244
1YTZ	T I	I	68	H	2.1	56	96
1YTZ	T I	I	71	I	2.9	56	96
1YTZ	T I	I	77	E	1.4	56	96
1YTZ	T I	I	78	R	1.2	56	96
1YTZ	T I	I	79	Y	2.3	56	96
1YTZ	T I	I	85	L	1.6	56	96
1YTZ	T I	I	92	L	1.0	56	96
1YU6	A C	A	64	H	1.2	64	73
1YU6	A C	A	104	Y	2.1	104	117
1YU6	B D	B	64	H	1.0	64	73
1YU6	B D	B	104	Y	1.6	104	117
1YU6	B D	B	222	M	1.3	220	238
1YUC	A C	A	354	F	1.0	341	362
1YUC	A C	A	357	V	1.0	341	362
1YUC	A C	A	361	R	1.1	341	362
1YUC	A C	A	371	V	1.3	371	381
1YUC	A C	A	375	M	2.9	371	381
1YUC	A C	A	531	L	1.6	531	538
1YUC	A C	C	20	I	1.4	19	27
1YUC	A C	C	21	L	2.4	19	27
1YUC	A C	C	24	L	1.3	19	27
1YUC	A C	C	25	L	1.9	19	27
1YUC	B D	B	371	V	1.1	371	381
1YUC	B D	B	375	M	1.4	371	381
1YUC	B D	B	531	L	1.1	531	537
1YUC	B D	D	21	L	2.0	19	27
1YUC	B D	D	25	L	1.5	19	27
1YUH	A B	A	127	E	1.2	125	130
1YUH	L H	L	126	E	1.1	125	130
1YV0	I C	I	13	R	1.4	8	30
1YV0	I C	I	16	H	1.1	8	30
1YV0	I C	I	17	L	1.7	8	30
1YV0	I C	I	20	A	1.0	8	30
1YV0	I C	I	21	M	5.6	8	30
1YV0	I C	I	24	L	1.8	8	30
1YV0	I C	I	28	E	1.9	8	30
1YV0	I C	C	117	L	9.3	114	121
1YV0	I C	C	120	I	2.1	114	121
1YV0	T C	T	232	Y	2.0	225	240
1YV0	T I	T	209	L	1.0	208	216
1YV0	T I	T	210	W	2.1	208	216
1YV0	T I	T	220	K	1.0	217	224
1YV0	T I	T	227	I	1.2	225	240
1YV0	T I	T	230	K	1.0	225	240
1YV0	T I	I	68	H	1.5	66	84
1YV0	T I	I	78	R	1.3	66	84
1YV0	T I	I	82	E	1.2	66	84
1YV0	T I	I	98	K	1.2	96	104
1YV0	T I	I	99	L	1.8	96	104
1YV0	T I	I	103	R	1.1	96	104
1YY8	A B	A	124	Q	1.6	122	127
1YY8	C D	C	123	E	1.0	122	127
1YY8	C D	C	124	Q	1.5	122	127
1YYF	B C	C	80	R	1.2	78	84

1YYL	L H	L	123	E	1.0	122	126
1YYP	A B	B	1231	F	4.2	1229	1234
1Z00	A B	A	234	R	1.2	224	240
1Z00	A B	A	237	E	1.3	224	240
1Z00	A B	A	260	L	1.5	260	266
1Z00	A B	A	264	I	2.1	260	266
1Z00	A B	B	836	G	62.4	835	843
1Z00	A B	B	837	P	2.2	835	843
1Z00	A B	B	840	F	2.3	835	843
1Z00	A B	B	857	H	1.0	849	859
1Z00	A B	B	865	L	1.1	862	868
1Z00	A B	B	889	F	4.2	880	891
1Z00	A B	B	890	I	1.1	880	891
1Z0J	A B	A	70	L	1.4	68	76
1Z0J	A B	B	738	L	1.5	736	756
1Z0J	A B	B	742	Q	1.6	736	756
1Z0J	A B	B	749	Y	1.2	736	756
1Z0J	A B	B	761	E	1.8	759	780
1Z0J	A B	B	764	V	1.3	759	780
1Z0J	A B	B	765	L	1.2	759	780
1Z0K	A B	A	29	I	1.8	21	30
1Z0K	A B	A	73	V	1.0	71	79
1Z0K	A B	B	458	P	1.0	458	476
1Z0K	A B	B	462	Q	2.1	458	476
1Z0K	A B	B	469	F	1.5	458	476
1Z0K	A B	B	485	L	1.6	479	500
1Z0K	C B	B	483	R	1.0	479	500
1Z0K	C D	C	29	I	1.5	21	31
1Z0K	C D	C	73	V	1.3	71	79
1Z0K	C D	D	462	Q	2.2	458	476
1Z0K	C D	D	469	F	1.4	458	476
1Z0K	C D	D	484	T	1.4	479	501
1Z0K	C D	D	485	L	1.4	479	501
1Z2C	A B	A	68	R	4.0	67	71
1Z2C	A B	A	69	L	1.1	67	71
1Z2C	A B	A	72	L	1.1	72	76
1Z2C	A B	A	105	H	1.8	95	107
1Z2C	A B	A	106	F	1.4	95	107
1Z2C	A B	B	100	K	1.6	98	106
1Z2C	A B	B	104	L	1.0	98	106
1Z2C	A B	B	115	M	1.9	109	122
1Z2C	A B	B	161	V	2.2	150	165
1Z2C	C D	C	69	L	1.0	69	75
1Z2C	C D	C	72	L	2.0	69	75
1Z2C	C D	C	105	H	1.8	89	107
1Z2C	C D	D	90	M	1.9	86	95
1Z2C	C D	D	100	K	1.3	98	107
1Z2C	C D	D	118	Q	1.1	109	122
1Z2C	C D	D	165	N	1.3	150	166
1Z3G	M I	M	123	Q	1.2	121	126
1Z56	A C	A	209	R	1.4	209	214
1Z56	A C	A	211	M	1.3	209	214
1Z56	A C	A	212	M	10.2	209	214
1Z56	A C	C	866	F	1.0	859	868
1Z5S	A B	A	115	G	1.3	109	121
1Z5S	A C	A	134	Y	1.1	131	140
1Z5S	A C	A	135	T	1.5	131	140
1Z5S	A D	A	11	Q	1.7	5	19
1Z5S	A D	A	18	K	1.1	5	19
1Z5S	A D	D	2677	F	1.8	2677	2685

1Z5S	B D	B	46	K	1.1	44	54
1Z5X	U E	U	432	Y	3.8	421	443
1Z5X	U E	U	450	F	1.5	449	455
1Z5X	U E	U	454	L	1.2	449	455
1Z5X	U E	U	457	L	1.3	457	466
1Z5X	U E	E	347	E	1.4	343	363
1Z5X	U E	E	375	K	1.2	369	400
1Z5X	U E	E	377	L	1.2	369	400
1Z5X	U E	E	384	R	1.1	369	400
1Z5Y	D E	E	81	P	1.3	81	86
1Z6O	A M	A	49	L	1.1	37	62
1Z6O	A M	A	53	Y	3.3	37	62
1Z6O	A M	A	57	L	1.6	37	62
1Z6O	A M	A	80	S	1.1	70	97
1Z6O	A M	A	81	D	1.2	70	97
1Z6O	A M	A	84	W	5.7	70	97
1Z6O	A M	A	88	I	1.4	70	97
1Z6O	A M	A	91	I	1.1	70	97
1Z6O	A M	A	189	I	1.2	157	191
1Z6O	A M	A	197	L	1.1	197	212
1Z6O	A M	M	40	L	2.6	19	46
1Z6O	A M	M	61	F	2.1	54	81
1Z6O	A M	M	65	S	1.0	54	81
1Z6O	A M	M	68	R	3.9	54	81
1Z6O	A M	M	79	L	1.9	54	81
1Z6O	A O	A	199	L	1.7	197	212
1Z6O	A O	A	202	Y	1.9	197	212
1Z6O	A O	A	206	E	1.1	197	212
1Z6O	A O	O	158	R	3.4	139	173
1Z6O	A O	O	162	G	8.5	139	173
1Z6O	A O	O	166	T	1.1	139	173
1Z6O	A O	O	170	L	2.3	139	173
1Z6O	A O	O	185	K	1.3	175	187
1Z6O	A X	A	180	G	20.1	157	191
1Z6O	A X	A	188	F	2.5	157	191
1Z6O	A X	A	207	Y	1.8	197	212
1Z6O	A X	X	177	L	2.8	175	187
1Z6O	A X	X	180	F	3.0	175	187
1Z6O	B M	B	199	L	1.3	197	212
1Z6O	B M	B	202	Y	3.3	197	212
1Z6O	B M	B	206	E	1.1	197	212
1Z6O	B M	M	158	R	1.7	139	173
1Z6O	B M	M	162	G	4.4	139	173
1Z6O	B M	M	170	L	2.3	139	173
1Z6O	B M	M	185	K	1.1	175	187
1Z6O	B N	B	49	L	1.1	37	62
1Z6O	B N	B	53	Y	3.8	37	62
1Z6O	B N	B	57	L	1.6	37	62
1Z6O	B N	B	80	S	1.1	70	97
1Z6O	B N	B	81	D	1.2	70	97
1Z6O	B N	B	84	W	5.7	70	97
1Z6O	B N	B	88	I	1.4	70	97
1Z6O	B N	B	91	I	1.1	70	97
1Z6O	B N	B	189	I	1.2	157	191
1Z6O	B N	B	197	L	1.1	197	212
1Z6O	B N	N	36	S	1.2	19	46
1Z6O	B N	N	40	L	2.6	19	46
1Z6O	B N	N	61	F	2.1	54	81
1Z6O	B N	N	68	R	3.9	54	81
1Z6O	B N	N	79	L	1.9	54	81

1Z6O	B P	B	180	G	17.9	157	191
1Z6O	B P	B	188	F	2.6	157	191
1Z6O	B P	B	207	Y	1.9	197	212
1Z6O	B P	P	177	L	3.0	175	187
1Z6O	B P	P	180	F	3.2	175	187
1Z6O	C N	C	199	L	1.9	197	212
1Z6O	C N	C	202	Y	1.6	197	212
1Z6O	C N	N	158	R	2.9	139	173
1Z6O	C N	N	162	G	14.9	139	173
1Z6O	C N	N	170	L	2.0	139	173
1Z6O	C O	C	49	L	1.1	37	62
1Z6O	C O	C	53	Y	3.8	37	62
1Z6O	C O	C	57	L	1.6	37	62
1Z6O	C O	C	80	S	1.1	70	97
1Z6O	C O	C	81	D	1.2	70	97
1Z6O	C O	C	84	W	5.7	70	97
1Z6O	C O	C	88	I	1.4	70	97
1Z6O	C O	C	91	I	1.1	70	97
1Z6O	C O	C	189	I	1.2	157	191
1Z6O	C O	C	197	L	1.1	197	212
1Z6O	C O	O	36	S	1.2	19	46
1Z6O	C O	O	40	L	2.6	19	46
1Z6O	C O	O	61	F	2.1	54	81
1Z6O	C O	O	65	S	1.0	54	81
1Z6O	C O	O	68	R	3.9	54	81
1Z6O	C O	O	79	L	1.9	54	81
1Z6O	C U	C	180	G	9.1	157	191
1Z6O	C U	C	184	D	2.0	157	191
1Z6O	C U	C	188	F	2.6	157	191
1Z6O	C U	C	207	Y	2.0	197	212
1Z6O	C U	U	177	L	2.6	175	187
1Z6O	C U	U	180	F	3.3	175	187
1Z6O	D P	D	49	L	1.1	37	62
1Z6O	D P	D	53	Y	3.8	37	62
1Z6O	D P	D	57	L	1.6	37	62
1Z6O	D P	D	80	S	1.1	70	97
1Z6O	D P	D	81	D	1.1	70	97
1Z6O	D P	D	84	W	5.7	70	97
1Z6O	D P	D	88	I	1.4	70	97
1Z6O	D P	D	91	I	1.1	70	97
1Z6O	D P	D	189	I	1.2	157	191
1Z6O	D P	D	197	L	1.1	197	212
1Z6O	D P	P	36	S	1.2	19	46
1Z6O	D P	P	40	L	2.6	19	46
1Z6O	D P	P	61	F	2.1	54	81
1Z6O	D P	P	68	R	3.8	54	81
1Z6O	D P	P	79	L	1.9	54	81
1Z6O	D R	D	199	L	1.8	197	212
1Z6O	D R	D	202	Y	2.4	197	212
1Z6O	D R	D	206	E	1.0	197	212
1Z6O	D R	R	158	R	3.6	139	173
1Z6O	D R	R	162	G	8.1	139	173
1Z6O	D R	R	166	T	1.1	139	173
1Z6O	D R	R	170	L	2.2	139	173
1Z6O	D R	R	185	K	1.0	175	187
1Z6O	D W	D	180	G	12.7	157	191
1Z6O	D W	D	188	F	2.4	157	191
1Z6O	D W	D	207	Y	2.0	197	212
1Z6O	D W	W	177	L	2.8	175	187
1Z6O	D W	W	180	F	3.1	175	187

1Z6O	E M	E	180	G	15.8	157	191
1Z6O	E M	E	188	F	2.5	157	191
1Z6O	E M	E	204	F	1.0	197	212
1Z6O	E M	E	207	Y	1.8	197	212
1Z6O	E M	M	177	L	2.9	175	187
1Z6O	E M	M	180	F	3.0	175	187
1Z6O	E P	E	199	L	1.9	197	212
1Z6O	E P	E	202	Y	1.3	197	212
1Z6O	E P	P	158	R	3.2	139	173
1Z6O	E P	P	162	G	6.2	139	173
1Z6O	E P	P	170	L	1.6	139	173
1Z6O	E Q	E	49	L	1.1	37	62
1Z6O	E Q	E	53	Y	3.3	37	62
1Z6O	E Q	E	57	L	1.6	37	62
1Z6O	E Q	E	80	S	1.1	70	97
1Z6O	E Q	E	81	D	1.2	70	97
1Z6O	E Q	E	84	W	5.7	70	97
1Z6O	E Q	E	88	I	1.4	70	97
1Z6O	E Q	E	91	I	1.1	70	97
1Z6O	E Q	E	189	I	1.2	157	191
1Z6O	E Q	E	197	L	1.1	197	212
1Z6O	E Q	Q	40	L	2.6	19	46
1Z6O	E Q	Q	61	F	2.1	54	81
1Z6O	E Q	Q	65	S	1.0	54	81
1Z6O	E Q	Q	68	R	3.9	54	81
1Z6O	E Q	Q	79	L	1.9	54	81
1Z6O	F Q	F	199	L	1.9	197	212
1Z6O	F Q	F	202	Y	2.3	197	212
1Z6O	F Q	F	206	E	1.2	197	212
1Z6O	F Q	Q	158	R	1.9	139	173
1Z6O	F Q	Q	162	G	10.4	139	173
1Z6O	F Q	Q	170	L	2.1	139	173
1Z6O	F R	F	49	L	1.1	37	62
1Z6O	F R	F	53	Y	3.8	37	62
1Z6O	F R	F	57	L	1.6	37	62
1Z6O	F R	F	80	S	1.1	70	97
1Z6O	F R	F	81	D	1.2	70	97
1Z6O	F R	F	84	W	5.7	70	97
1Z6O	F R	F	88	I	1.4	70	97
1Z6O	F R	F	91	I	1.1	70	97
1Z6O	F R	F	189	I	1.2	157	191
1Z6O	F R	F	197	L	1.1	197	212
1Z6O	F R	R	36	S	1.2	19	46
1Z6O	F R	R	40	L	2.6	19	46
1Z6O	F R	R	61	F	2.1	54	81
1Z6O	F R	R	68	R	3.9	54	81
1Z6O	F R	R	79	L	1.9	54	81
1Z6O	F V	F	180	G	10.4	157	191
1Z6O	F V	F	184	D	1.1	157	191
1Z6O	F V	F	188	F	2.6	157	191
1Z6O	F V	F	207	Y	2.1	197	212
1Z6O	F V	V	177	L	2.5	175	187
1Z6O	F V	V	180	F	3.2	175	187
1Z6O	G R	G	180	G	16.6	157	191
1Z6O	G R	G	188	F	2.5	157	191
1Z6O	G R	G	207	Y	1.9	197	212
1Z6O	G R	R	177	L	2.9	175	187
1Z6O	G R	R	180	F	3.1	175	187
1Z6O	G S	G	49	L	1.1	37	62
1Z6O	G S	G	53	Y	3.8	37	62

1Z6O	G S	G	57	L	1.6	37	62
1Z6O	G S	G	80	S	1.1	70	97
1Z6O	G S	G	81	D	1.2	70	97
1Z6O	G S	G	84	W	5.7	70	97
1Z6O	G S	G	88	I	1.4	70	97
1Z6O	G S	G	91	I	1.1	70	97
1Z6O	G S	G	189	I	1.2	157	191
1Z6O	G S	G	197	L	1.1	197	212
1Z6O	G S	S	36	S	1.2	19	46
1Z6O	G S	S	40	L	2.6	19	46
1Z6O	G S	S	61	F	2.1	54	81
1Z6O	G S	S	68	R	3.9	54	81
1Z6O	G S	S	79	L	1.9	54	81
1Z6O	G W	G	199	L	1.6	197	212
1Z6O	G W	G	202	Y	1.9	197	212
1Z6O	G W	G	206	E	1.1	197	212
1Z6O	G W	W	158	R	3.4	139	173
1Z6O	G W	W	162	G	7.2	139	173
1Z6O	G W	W	166	T	1.1	139	173
1Z6O	G W	W	170	L	2.3	139	173
1Z6O	G W	W	185	K	1.1	175	187
1Z6O	H O	H	180	G	12.7	157	191
1Z6O	H O	H	184	D	1.1	157	191
1Z6O	H O	H	188	F	2.7	157	191
1Z6O	H O	H	207	Y	2.2	197	212
1Z6O	H O	O	177	L	2.8	175	187
1Z6O	H O	O	180	F	3.5	175	187
1Z6O	H T	H	49	L	1.1	37	62
1Z6O	H T	H	53	Y	3.8	37	62
1Z6O	H T	H	57	L	1.6	37	62
1Z6O	H T	H	80	S	1.1	70	97
1Z6O	H T	H	81	D	1.2	70	97
1Z6O	H T	H	84	W	5.7	70	97
1Z6O	H T	H	88	I	1.4	70	97
1Z6O	H T	H	91	I	1.1	70	97
1Z6O	H T	H	189	I	1.2	157	191
1Z6O	H T	H	197	L	1.1	197	212
1Z6O	H T	T	36	S	1.2	19	46
1Z6O	H T	T	40	L	2.6	19	46
1Z6O	H T	T	61	F	2.1	54	81
1Z6O	H T	T	68	R	3.9	54	81
1Z6O	H T	T	79	L	1.9	54	81
1Z6O	H X	H	199	L	1.8	197	212
1Z6O	H X	H	202	Y	2.3	197	212
1Z6O	H X	H	206	E	1.0	197	212
1Z6O	H X	X	158	R	3.6	139	173
1Z6O	H X	X	162	G	8.6	139	173
1Z6O	H X	X	166	T	1.0	139	173
1Z6O	H X	X	170	L	2.3	139	173
1Z6O	H X	X	185	K	1.2	175	187
1Z6O	I S	I	199	L	1.8	197	212
1Z6O	I S	I	202	Y	2.0	197	212
1Z6O	I S	I	206	E	1.0	197	212
1Z6O	I S	S	158	R	2.6	139	173
1Z6O	I S	S	162	G	13.4	139	173
1Z6O	I S	S	166	T	1.1	139	173
1Z6O	I S	S	170	L	2.1	139	173
1Z6O	I S	S	185	K	1.3	175	187
1Z6O	I T	I	180	G	9.3	157	191
1Z6O	I T	I	184	D	1.0	157	191

1Z6O	I T	I	188	F	2.7	157	191
1Z6O	I T	I	207	Y	2.4	197	212
1Z6O	I T	T	177	L	2.6	175	187
1Z6O	I T	T	180	F	3.2	175	187
1Z6O	I U	I	49	L	1.1	37	62
1Z6O	I U	I	53	Y	3.8	37	62
1Z6O	I U	I	57	L	1.6	37	62
1Z6O	I U	I	80	S	1.1	70	97
1Z6O	I U	I	81	D	1.2	70	97
1Z6O	I U	I	84	W	5.7	70	97
1Z6O	I U	I	88	I	1.4	70	97
1Z6O	I U	I	91	I	1.1	70	97
1Z6O	I U	I	189	I	1.2	157	191
1Z6O	I U	I	197	L	1.1	197	212
1Z6O	I U	U	36	S	1.2	19	46
1Z6O	I U	U	40	L	2.6	19	46
1Z6O	I U	U	61	F	2.1	54	81
1Z6O	I U	U	65	S	1.0	54	81
1Z6O	I U	U	68	R	3.9	54	81
1Z6O	I U	U	79	L	1.9	54	81
1Z6O	J S	J	180	G	13.2	157	191
1Z6O	J S	J	184	D	1.0	157	191
1Z6O	J S	J	188	F	2.3	157	191
1Z6O	J S	J	203	V	1.1	197	212
1Z6O	J S	J	207	Y	1.4	197	212
1Z6O	J S	S	177	L	2.6	175	187
1Z6O	J S	S	180	F	2.7	175	187
1Z6O	J T	J	199	L	1.6	197	212
1Z6O	J T	J	202	Y	3.5	197	212
1Z6O	J T	J	206	E	1.1	197	212
1Z6O	J T	T	158	R	3.4	139	173
1Z6O	J T	T	162	G	7.2	139	173
1Z6O	J T	T	166	T	1.1	139	173
1Z6O	J T	T	170	L	2.3	139	173
1Z6O	J T	T	185	K	1.4	175	187
1Z6O	J V	J	49	L	1.1	37	62
1Z6O	J V	J	53	Y	3.3	37	62
1Z6O	J V	J	57	L	1.6	37	62
1Z6O	J V	J	80	S	1.1	70	97
1Z6O	J V	J	81	D	1.2	70	97
1Z6O	J V	J	84	W	5.7	70	97
1Z6O	J V	J	88	I	1.4	70	97
1Z6O	J V	J	91	I	1.1	70	97
1Z6O	J V	J	189	I	1.2	157	191
1Z6O	J V	J	197	L	1.2	197	212
1Z6O	J V	V	40	L	2.6	19	46
1Z6O	J V	V	61	F	2.1	54	81
1Z6O	J V	V	68	R	3.8	54	81
1Z6O	J V	V	79	L	1.9	54	81
1Z6O	K N	K	180	G	17.5	157	191
1Z6O	K N	K	184	D	1.0	157	191
1Z6O	K N	K	188	F	2.3	157	191
1Z6O	K N	K	203	V	1.0	197	212
1Z6O	K N	K	207	Y	1.3	197	212
1Z6O	K N	N	177	L	2.8	175	187
1Z6O	K N	N	180	F	2.7	175	187
1Z6O	K U	K	199	L	1.6	197	212
1Z6O	K U	K	202	Y	2.6	197	212
1Z6O	K U	K	206	E	1.1	197	212
1Z6O	K U	U	158	R	3.4	139	173

1Z6O	K U	U	162	G	7.7	139	173
1Z6O	K U	U	166	T	1.2	139	173
1Z6O	K U	U	170	L	2.3	139	173
1Z6O	K U	U	185	K	1.3	175	187
1Z6O	K W	K	49	L	1.1	37	62
1Z6O	K W	K	53	Y	3.8	37	62
1Z6O	K W	K	57	L	1.6	37	62
1Z6O	K W	K	80	S	1.1	70	97
1Z6O	K W	K	81	D	1.2	70	97
1Z6O	K W	K	84	W	5.7	70	97
1Z6O	K W	K	88	I	1.4	70	97
1Z6O	K W	K	91	I	1.1	70	97
1Z6O	K W	K	189	I	1.2	157	191
1Z6O	K W	K	197	L	1.2	197	212
1Z6O	K W	W	36	S	1.2	19	46
1Z6O	K W	W	40	L	2.6	19	46
1Z6O	K W	W	61	F	2.1	54	81
1Z6O	K W	W	68	R	3.9	54	81
1Z6O	K W	W	79	L	1.9	54	81
1Z6O	L Q	L	180	G	10.8	157	191
1Z6O	L Q	L	188	F	2.7	157	191
1Z6O	L Q	L	207	Y	2.1	197	212
1Z6O	L Q	Q	177	L	2.9	175	187
1Z6O	L Q	Q	180	F	3.4	175	187
1Z6O	L V	L	199	L	1.6	197	212
1Z6O	L V	L	202	Y	3.1	197	212
1Z6O	L V	L	206	E	1.0	197	212
1Z6O	L V	V	158	R	3.5	139	173
1Z6O	L V	V	162	G	7.9	139	173
1Z6O	L V	V	166	T	1.1	139	173
1Z6O	L V	V	170	L	2.3	139	173
1Z6O	L V	V	185	K	1.0	175	187
1Z6O	L X	L	49	L	1.1	37	62
1Z6O	L X	L	53	Y	3.8	37	62
1Z6O	L X	L	57	L	1.6	37	62
1Z6O	L X	L	80	S	1.1	70	97
1Z6O	L X	L	81	D	1.2	70	97
1Z6O	L X	L	84	W	5.7	70	97
1Z6O	L X	L	88	I	1.4	70	97
1Z6O	L X	L	91	I	1.1	70	97
1Z6O	L X	L	189	I	1.2	157	191
1Z6O	L X	L	197	L	1.1	197	212
1Z6O	L X	X	36	S	1.2	19	46
1Z6O	L X	X	40	L	2.6	19	46
1Z6O	L X	X	61	F	2.1	54	81
1Z6O	L X	X	68	R	3.9	54	81
1Z6O	L X	X	79	L	1.9	54	81
1Z7M	A E	A	192	L	1.1	192	200
1Z7M	A E	E	186	S	1.4	185	190
1Z7M	B G	G	59	E	2.7	51	60
1Z7M	B G	G	185	K	1.1	185	190
1Z7M	B G	G	186	S	1.0	185	190
1Z7M	B G	G	189	K	2.3	185	190
1Z7M	D F	F	59	E	2.3	51	60
1Z7M	D F	F	189	K	1.8	185	190
1Z7Q	a b	a	60	D	1.9	58	79
1Z7Q	a b	b	101	Y	2.3	89	105
1Z7Q	A B	B	20	Q	1.2	19	25
1Z7Q	A B	B	23	Y	2.7	19	25
1Z7Q	A B	B	80	P	1.7	79	92

1Z7Q	A G	A	27	Q	1.7	26	35
1Z7Q	A G	A	30	Y	3.1	26	35
1Z7Q	A G	A	87	I	1.4	87	107
1Z7Q	A G	G	120	Q	1.3	108	122
1Z7Q	A H	A	106	Y	2.1	87	107
1Z7Q	A i	A	30	Y	1.4	26	35
1Z7Q	A i	i	1105	L	1.4	1105	1124
1Z7Q	A I	I	66	H	2.8	49	70
1Z7Q	B C	C	24	Y	3.6	21	30
1Z7Q	B i	B	79	G	1.1	79	92
1Z7Q	B I	I	65	L	1.5	49	70
1Z7Q	B J	B	108	K	1.4	107	123
1Z7Q	B J	J	73	Y	1.0	56	77
1Z7Q	C D	D	19	Q	2.9	18	30
1Z7Q	C D	D	22	Y	1.3	18	30
1Z7Q	C D	D	81	D	1.1	79	99
1Z7Q	C J	C	100	K	1.1	81	102
1Z7Q	C J	J	68	Y	1.8	56	77
1Z7Q	C J	J	72	L	1.0	56	77
1Z7Q	C J	J	75	L	1.3	56	77
1Z7Q	D E	E	23	Q	3.2	22	34
1Z7Q	D E	E	26	Y	3.6	22	34
1Z7Q	D K	D	90	R	1.0	79	99
1Z7Q	D K	K	66	L	1.3	50	72
1Z7Q	E f	E	25	E	1.6	22	34
1Z7Q	E F	F	21	Q	2.3	20	32
1Z7Q	E F	F	24	Y	3.9	20	32
1Z7Q	E F	F	79	P	1.7	78	95
1Z7Q	E L	E	97	V	1.3	82	104
1Z7Q	E L	E	101	L	1.3	82	104
1Z7Q	E L	L	64	R	2.1	49	71
1Z7Q	E L	L	65	L	1.7	49	71
1Z7Q	E L	L	68	L	1.2	49	71
1Z7Q	E M	E	99	H	2.4	82	104
1Z7Q	E M	E	103	Y	2.5	82	104
1Z7Q	E M	M	75	Y	1.8	58	79
1Z7Q	E M	M	91	R	1.4	86	100
1Z7Q	E M	M	95	H	1.3	86	100
1Z7Q	F g	F	20	F	3.3	20	32
1Z7Q	F g	F	23	E	2.5	20	32
1Z7Q	F G	F	110	H	1.7	105	119
1Z7Q	F G	G	22	Q	2.8	21	31
1Z7Q	F G	G	25	Y	4.0	21	31
1Z7Q	F G	G	85	R	1.7	81	102
1Z7Q	F G	G	86	H	2.5	81	102
1Z7Q	F M	F	89	R	1.5	78	95
1Z7Q	F M	M	74	W	1.0	58	79
1Z7Q	F M	M	77	F	1.8	58	79
1Z7Q	F N	F	99	F	1.1	96	100
1Z7Q	F N	N	74	N	1.0	57	76
1Z7Q	G g	G	81	I	1.0	81	102
1Z7Q	G h	G	21	F	1.6	21	31
1Z7Q	G H	H	66	Y	1.1	49	70
1Z7Q	H b	H	60	Q	1.2	49	70
1Z7Q	H b	H	194	E	1.5	192	196
1Z7Q	H b	b	185	Y	1.0	170	187
1Z7Q	H I	I	88	F	2.2	76	90
1Z7Q	H N	H	87	Y	1.6	75	89
1Z7Q	H N	N	61	Q	1.2	57	76
1Z7Q	I a	a	145	L	1.3	145	155

1Z7Q	I a	a	193	E	1.2	177	194
1Z7Q	I b	b	146	F	1.0	146	152
1Z7Q	I b	b	150	M	1.6	146	152
1Z7Q	I b	b	183	V	1.9	170	187
1Z7Q	I J	I	51	D	2.6	49	70
1Z7Q	I J	J	95	Y	1.0	83	97
1Z7Q	I J	J	161	D	1.9	159	176
1Z7Q	I J	J	164	E	1.6	159	176
1Z7Q	I J	J	167	S	1.4	159	176
1Z7Q	I J	J	168	Q	1.6	159	176
1Z7Q	J a	J	147	G	26.2	142	150
1Z7Q	J a	J	148	M	1.4	142	150
1Z7Q	J a	J	175	D	1.1	159	176
1Z7Q	J a	a	149	F	1.3	145	155
1Z7Q	J a	a	190	S	1.2	177	194
1Z7Q	J K	K	85	R	1.3	77	93
1Z7Q	J K	K	138	F	1.6	135	148
1Z7Q	J Z	Z	166	H	1.6	150	168
1Z7Q	J Z	Z	193	V	1.4	193	203
1Z7Q	K L	K	51	G	273.4	50	72
1Z7Q	K L	K	58	E	1.2	50	72
1Z7Q	K L	L	88	Y	1.6	76	90
1Z7Q	K Z	K	139	Y	1.4	135	148
1Z7Q	K Z	K	145	D	3.3	135	148
1Z7Q	K Z	Z	135	F	2.6	133	144
1Z7Q	K Z	Z	137	Y	1.2	133	144
1Z7Q	K Z	Z	167	R	2.9	150	168
1Z7Q	L M	L	51	D	4.0	49	71
1Z7Q	L M	L	53	Q	1.8	49	71
1Z7Q	L M	L	54	F	1.5	49	71
1Z7Q	L M	M	98	Y	5.3	86	100
1Z7Q	M N	M	60	D	2.1	58	79
1Z7Q	M N	N	101	Y	2.2	89	105
1Z7Q	O P	P	20	Q	1.2	19	25
1Z7Q	O P	P	23	Y	2.7	19	25
1Z7Q	O P	P	80	P	2.4	79	92
1Z7Q	O U	O	27	Q	1.5	26	35
1Z7Q	O U	O	30	Y	3.4	26	35
1Z7Q	O U	O	87	I	1.4	87	107
1Z7Q	O U	U	120	Q	1.2	108	122
1Z7Q	O V	O	106	Y	2.7	87	107
1Z7Q	O V	V	64	E	1.3	49	70
1Z7Q	O W	W	66	H	2.5	49	70
1Z7Q	P Q	Q	21	Q	1.1	21	30
1Z7Q	P Q	Q	24	Y	3.1	21	30
1Z7Q	P W	P	91	K	1.0	79	92
1Z7Q	P W	W	65	L	1.7	49	70
1Z7Q	Q k	Q	23	E	1.8	21	30
1Z7Q	Q R	R	19	Q	2.9	18	30
1Z7Q	Q R	R	22	Y	1.4	18	30
1Z7Q	Q R	R	81	D	1.1	79	99
1Z7Q	Q X	Q	100	K	1.0	81	102
1Z7Q	Q X	X	68	Y	1.6	56	77
1Z7Q	Q X	X	75	L	1.5	56	77
1Z7Q	R k	R	29	R	3.4	18	30
1Z7Q	R k	R	79	N	3.6	79	99
1Z7Q	R S	S	23	Q	3.2	22	34
1Z7Q	R S	S	26	Y	3.5	22	34
1Z7Q	R S	S	84	D	1.0	82	104
1Z7Q	R Y	R	90	R	1.0	79	99

1Z7Q	R Y	R	98	L	1.1	79	99
1Z7Q	R Y	Y	66	L	1.6	50	72
1Z7Q	R Z	R	107	E	1.0	106	120
1Z7Q	R Z	R	111	R	1.0	106	120
1Z7Q	R Z	Z	81	K	1.1	76	90
1Z7Q	S a	S	103	Y	1.9	82	104
1Z7Q	S a	a	75	Y	1.1	58	79
1Z7Q	S a	a	91	R	1.4	86	100
1Z7Q	S m	S	22	F	1.2	22	34
1Z7Q	S T	T	21	Q	2.3	20	32
1Z7Q	S T	T	24	Y	4.1	20	32
1Z7Q	S T	T	79	P	1.6	78	95
1Z7Q	S Z	S	97	V	1.0	82	104
1Z7Q	S Z	S	101	L	1.2	82	104
1Z7Q	S Z	Z	64	R	1.9	49	71
1Z7Q	S Z	Z	65	L	1.1	49	71
1Z7Q	T a	T	86	N	1.0	78	95
1Z7Q	T a	T	90	Q	1.2	78	95
1Z7Q	T a	a	74	W	1.1	58	79
1Z7Q	T a	a	77	F	1.4	58	79
1Z7Q	T b	T	99	F	1.0	96	100
1Z7Q	T b	b	95	Y	1.0	89	105
1Z7Q	T U	U	22	Q	2.9	21	31
1Z7Q	T U	U	25	Y	4.3	21	31
1Z7Q	U V	U	98	F	1.4	81	102
1Z7Q	V b	V	87	Y	2.1	75	89
1Z7Q	V b	b	59	D	1.6	57	76
1Z7Q	V b	b	61	Q	1.2	57	76
1Z7Q	V N	N	146	F	1.4	146	152
1Z7Q	V W	W	88	F	2.2	76	90
1Z7Q	W M	M	145	L	2.2	145	155
1Z7Q	W M	M	193	E	2.0	177	194
1Z7Q	W N	N	150	M	1.1	146	152
1Z7Q	W N	N	183	V	1.4	170	187
1Z7Q	W X	X	161	D	1.8	159	176
1Z7Q	W X	X	164	E	1.7	159	176
1Z7Q	W X	X	167	S	1.3	159	176
1Z7Q	W X	X	168	Q	1.6	159	176
1Z7Q	X L	L	166	H	1.6	150	168
1Z7Q	X L	L	198	W	1.7	193	203
1Z7Q	X M	X	147	G	71.6	142	150
1Z7Q	X M	X	148	M	1.0	142	150
1Z7Q	X M	X	168	Q	1.0	159	176
1Z7Q	X Y	Y	85	R	1.4	77	93
1Z7Q	X Y	Y	138	F	1.5	135	148
1Z7Q	Y L	Y	139	Y	1.9	135	148
1Z7Q	Y L	Y	145	D	2.6	135	148
1Z7Q	Y L	Y	146	H	1.6	135	148
1Z7Q	Y L	L	135	F	1.2	133	144
1Z7Q	Y L	L	137	Y	2.2	133	144
1Z7Q	Y L	L	138	G	1.7	133	144
1Z7Q	Y L	L	167	R	2.5	150	168
1Z7Q	Y Z	Y	51	G	244.5	50	72
1Z7Q	Y Z	Z	88	Y	1.8	76	90
1Z7Q	Z a	Z	51	D	2.8	49	71
1Z7Q	Z a	Z	53	Q	1.9	49	71
1Z7Q	Z a	Z	54	F	2.4	49	71
1Z7Q	Z a	Z	55	W	1.1	49	71
1Z7Q	Z a	Z	57	T	2.0	49	71
1Z7Q	Z a	a	98	Y	5.0	86	100

1Z7X	X W	X	32	R	2.2	25	33
1Z7X	Z Y	Z	11	Q	1.2	4	13
1Z7X	Z Y	Z	32	R	2.5	25	33
1Z7X	Z Y	Y	443	E	1.1	440	453
1Z8U	A B	A	21	L	1.1	5	24
1Z8U	A B	A	43	D	1.1	34	52
1Z8U	A B	A	47	F	3.1	34	52
1Z8U	A B	A	48	Y	1.0	34	52
1Z8U	A B	A	51	Y	1.6	34	52
1Z8U	A B	B	103	H	1.8	95	112
1Z8U	A B	B	119	P	1.1	119	130
1Z8U	A B	B	122	H	1.7	119	130
1Z8U	A B	B	127	K	1.0	119	130
1Z8U	C D	C	43	D	1.7	34	54
1Z8U	C D	C	47	F	2.8	34	54
1Z8U	C D	C	48	Y	1.0	34	54
1Z8U	C D	C	51	Y	2.5	34	54
1Z8U	C D	D	103	H	2.1	95	113
1Z8U	C D	D	119	P	1.8	119	131
1Z8Y	I J	I	18	M	1.0	16	20
1Z8Y	I J	J	19	G	5.3	17	33
1Z8Y	K L	K	18	M	1.0	16	20
1Z8Y	K L	L	19	G	5.3	17	33
1Z8Y	M N	M	18	M	1.0	16	20
1Z8Y	M N	N	19	G	5.3	17	33
1Z8Y	O P	O	18	M	1.0	16	20
1Z8Y	O P	P	19	G	5.3	17	33
1Z92	A B	A	65	P	1.4	63	72
1Z92	A B	A	68	E	1.1	63	72
1ZA3	B S	B	98	Y	1.7	98	100
1ZA3	B S	B	99	Y	1.3	98	100
1ZA3	B S	B	100	Y	1.9	98	100
1ZA3	H R	H	98	Y	1.9	98	100
1ZA3	H R	H	99	Y	1.1	98	100
1ZA3	H R	H	100	Y	1.1	98	100
1ZA3	L H	L	123	Q	1.3	121	127
1ZA6	C D	C	130	Q	1.0	128	134
1ZAN	L H	L	125	Q	1.3	123	129
1ZAV	A U	A	141	Y	2.2	137	177
1ZAV	A U	A	145	V	1.5	137	177
1ZAV	A U	A	148	V	1.3	137	177
1ZAV	A U	A	149	K	1.3	137	177
1ZAV	A U	A	152	I	1.5	137	177
1ZAV	A U	U	18	L	1.4	15	30
1ZAV	A U	U	22	V	1.4	15	30
1ZAV	A U	U	29	F	2.9	15	30
1ZAV	A V	A	93	V	1.6	92	106
1ZAV	A V	A	140	L	2.1	137	177
1ZAV	A V	A	144	L	1.7	137	177
1ZAV	A V	A	147	R	1.2	137	177
1ZAV	A V	A	151	P	1.1	137	177
1ZAV	A V	V	15	V	1.6	15	29
1ZAV	A V	V	18	L	1.9	15	29
1ZAV	A V	V	20	E	1.0	15	29
1ZAV	A V	V	22	V	1.4	15	29
1ZAV	A W	A	152	I	1.0	137	177
1ZAV	A W	A	159	L	1.3	137	177
1ZAV	A W	A	163	L	1.5	137	177
1ZAV	A W	W	18	L	1.7	15	30
1ZAV	A W	W	22	V	1.2	15	30

1ZAV	A W	W	29	F	1.1	15	30
1ZAV	A X	A	154	G	1.2	137	177
1ZAV	A X	A	155	L	1.5	137	177
1ZAV	A X	A	162	I	1.0	137	177
1ZAV	A X	X	10	I	1.8	3	12
1ZAV	A X	X	18	L	1.9	15	29
1ZAV	A X	X	22	V	1.2	15	29
1ZAV	A X	X	25	L	1.0	15	29
1ZAV	A Y	A	163	L	1.6	137	177
1ZAV	A Y	A	170	L	1.5	137	177
1ZAV	A Y	A	174	K	1.8	137	177
1ZAV	A Y	Y	18	L	1.5	15	29
1ZAV	A Z	A	166	L	1.3	137	177
1ZAV	A Z	A	169	V	1.5	137	177
1ZAV	A Z	Z	18	L	1.0	15	27
1ZAV	A Z	Z	22	V	1.4	15	27
1ZBB	a b	a	50	E	1.8	45	57
1ZBB	a b	a	51	I	1.6	45	57
1ZBB	a b	a	54	Y	1.6	45	57
1ZBB	a b	a	67	F	1.2	64	79
1ZBB	a b	a	70	L	1.8	64	79
1ZBB	a b	a	74	I	2.1	64	79
1ZBB	a b	a	78	F	1.0	64	79
1ZBB	a b	a	92	L	2.0	86	114
1ZBB	a b	a	99	Y	2.4	86	114
1ZBB	a b	a	100	L	2.0	86	114
1ZBB	a b	a	101	V	1.7	86	114
1ZBB	a b	a	104	F	3.4	86	114
1ZBB	a b	a	121	P	1.5	121	132
1ZBB	a b	a	124	I	1.0	121	132
1ZBB	a b	b	36	R	3.2	31	41
1ZBB	a b	b	37	L	2.3	31	41
1ZBB	a b	b	39	R	3.2	31	41
1ZBB	a b	b	40	R	4.5	31	41
1ZBB	a b	b	50	I	2.7	50	76
1ZBB	a b	b	58	L	1.3	50	76
1ZBB	a b	b	61	F	3.4	50	76
1ZBB	a b	b	62	L	2.3	50	76
1ZBB	a b	b	66	I	2.9	50	76
1ZBB	a b	b	70	V	2.0	50	76
1ZBB	a b	b	86	V	1.8	83	93
1ZBB	A B	A	50	E	1.7	45	57
1ZBB	A B	A	51	I	1.6	45	57
1ZBB	A B	A	54	Y	1.7	45	57
1ZBB	A B	A	67	F	1.1	64	79
1ZBB	A B	A	70	L	1.8	64	79
1ZBB	A B	A	74	I	1.4	64	79
1ZBB	A B	A	78	F	3.8	64	79
1ZBB	A B	A	92	L	2.0	86	114
1ZBB	A B	A	99	Y	2.4	86	114
1ZBB	A B	A	100	L	2.0	86	114
1ZBB	A B	A	101	V	1.7	86	114
1ZBB	A B	A	104	F	3.4	86	114
1ZBB	A B	A	121	P	1.6	121	132
1ZBB	A B	A	124	I	1.1	121	132
1ZBB	A B	B	36	R	3.2	31	41
1ZBB	A B	B	37	L	2.3	31	41
1ZBB	A B	B	39	R	3.2	31	41
1ZBB	A B	B	40	R	4.5	31	41
1ZBB	A B	B	50	I	2.7	50	76

1ZBB	A B	B	58	L	1.3	50	76
1ZBB	A B	B	61	F	3.4	50	76
1ZBB	A B	B	62	L	2.4	50	76
1ZBB	A B	B	66	I	2.9	50	76
1ZBB	A B	B	67	R	2.4	50	76
1ZBB	A B	B	70	V	1.7	50	76
1ZBB	A B	B	86	V	1.8	83	93
1ZBB	a g	a	48	L	1.6	45	57
1ZBB	a g	a	55	Q	1.1	45	57
1ZBB	a g	a	94	E	1.3	86	114
1ZBB	a g	a	105	E	1.2	86	114
1ZBB	a g	a	112	I	1.1	86	114
1ZBB	A G	A	48	L	1.6	45	57
1ZBB	A G	A	55	Q	1.1	45	57
1ZBB	A G	A	94	E	1.3	86	114
1ZBB	A G	A	105	E	1.6	86	114
1ZBB	A G	A	112	I	1.1	86	114
1ZBB	A G	G	81	R	1.0	80	89
1ZBB	b d	b	72	Y	2.5	50	76
1ZBB	b d	b	75	H	2.8	50	76
1ZBB	b d	b	88	Y	2.0	83	93
1ZBB	b d	b	92	R	1.4	83	93
1ZBB	b d	d	77	L	1.0	53	81
1ZBB	b d	d	80	Y	1.2	53	81
1ZBB	b d	d	93	T	1.0	88	99
1ZBB	b d	d	97	L	1.7	88	99
1ZBB	B D	B	72	Y	2.2	50	76
1ZBB	B D	B	75	H	2.8	50	76
1ZBB	B D	B	88	Y	1.9	83	93
1ZBB	B D	B	92	R	1.2	83	93
1ZBB	B D	D	80	Y	3.1	53	81
1ZBB	B D	D	97	L	1.4	88	99
1ZBB	c d	c	29	R	1.3	27	37
1ZBB	c d	c	49	V	1.8	45	73
1ZBB	c d	c	50	Y	5.0	45	73
1ZBB	c d	c	51	L	2.1	45	73
1ZBB	c d	c	54	V	1.6	45	73
1ZBB	c d	c	55	L	2.4	45	73
1ZBB	c d	c	57	Y	2.5	45	73
1ZBB	c d	c	58	L	1.7	45	73
1ZBB	c d	c	63	L	2.9	45	73
1ZBB	c d	c	67	G	178.9	45	73
1ZBB	c d	c	80	P	1.4	80	89
1ZBB	c d	c	96	L	1.6	91	97
1ZBB	c d	d	37	Y	2.3	35	46
1ZBB	c d	d	41	V	1.7	35	46
1ZBB	c d	d	42	L	1.1	35	46
1ZBB	c d	d	58	I	2.0	53	81
1ZBB	c d	d	63	V	1.2	53	81
1ZBB	c d	d	67	F	3.9	53	81
1ZBB	c d	d	70	I	1.0	53	81
1ZBB	c d	d	91	I	2.1	88	99
1ZBB	c d	d	103	L	2.5	102	119
1ZBB	c d	d	111	G	123.8	102	119
1ZBB	c d	d	115	V	1.2	102	119
1ZBB	c d	d	117	K	1.0	102	119
1ZBB	c d	d	118	Y	2.7	102	119
1ZBB	C D	C	20	R	1.0	17	21
1ZBB	C D	C	29	R	1.3	27	37
1ZBB	C D	C	49	V	1.8	45	73

1ZBB	C D	C	50	Y	5.0	45	73
1ZBB	C D	C	51	L	2.1	45	73
1ZBB	C D	C	54	V	1.6	45	73
1ZBB	C D	C	55	L	2.4	45	73
1ZBB	C D	C	57	Y	2.1	45	73
1ZBB	C D	C	58	L	1.7	45	73
1ZBB	C D	C	63	L	2.8	45	73
1ZBB	C D	C	67	G	178.5	45	73
1ZBB	C D	C	80	P	1.2	80	89
1ZBB	C D	C	96	L	1.6	91	97
1ZBB	C D	D	37	Y	2.3	35	46
1ZBB	C D	D	41	V	1.7	35	46
1ZBB	C D	D	42	L	1.1	35	46
1ZBB	C D	D	58	I	2.2	53	81
1ZBB	C D	D	63	V	1.2	53	81
1ZBB	C D	D	67	F	3.7	53	81
1ZBB	C D	D	70	I	1.0	53	81
1ZBB	C D	D	91	I	2.1	88	99
1ZBB	C D	D	103	L	2.5	102	119
1ZBB	C D	D	111	G	124.7	102	119
1ZBB	C D	D	115	V	1.2	102	119
1ZBB	C D	D	117	K	1.0	102	119
1ZBB	C D	D	118	Y	2.8	102	119
1ZBB	e c	e	48	L	1.5	45	57
1ZBB	e c	e	94	E	1.4	86	114
1ZBB	e c	e	112	I	1.1	86	114
1ZBB	e c	c	81	R	1.1	80	89
1ZBB	E C	E	48	L	1.5	45	57
1ZBB	E C	E	94	E	1.4	86	114
1ZBB	E C	E	112	I	1.1	86	114
1ZBB	e f	e	51	I	1.9	45	57
1ZBB	e f	e	67	F	1.1	64	79
1ZBB	e f	e	70	L	1.9	64	79
1ZBB	e f	e	73	E	1.8	64	79
1ZBB	e f	e	74	I	2.1	64	79
1ZBB	e f	e	78	F	3.8	64	79
1ZBB	e f	e	92	L	1.9	86	114
1ZBB	e f	e	97	E	1.2	86	114
1ZBB	e f	e	99	Y	2.8	86	114
1ZBB	e f	e	100	L	1.6	86	114
1ZBB	e f	e	101	V	1.7	86	114
1ZBB	e f	e	104	F	3.2	86	114
1ZBB	e f	e	121	P	1.3	121	132
1ZBB	e f	e	124	I	1.0	121	132
1ZBB	e f	f	28	G	6.7	25	29
1ZBB	e f	f	36	R	3.0	31	41
1ZBB	e f	f	37	L	2.5	31	41
1ZBB	e f	f	39	R	1.6	31	41
1ZBB	e f	f	40	R	4.5	31	41
1ZBB	e f	f	50	I	2.3	50	76
1ZBB	e f	f	61	F	3.6	50	76
1ZBB	e f	f	62	L	1.5	50	76
1ZBB	e f	f	66	I	3.0	50	76
1ZBB	e f	f	67	R	1.2	50	76
1ZBB	e f	f	70	V	2.2	50	76
1ZBB	e f	f	73	T	1.4	50	76
1ZBB	e f	f	74	E	1.6	50	76
1ZBB	e f	f	86	V	1.7	83	93
1ZBB	E F	E	51	I	2.0	45	57
1ZBB	E F	E	67	F	1.2	64	79

1ZBB	E F	E	70	L	1.9	64	79
1ZBB	E F	E	73	E	1.8	64	79
1ZBB	E F	E	74	I	2.1	64	79
1ZBB	E F	E	78	F	2.6	64	79
1ZBB	E F	E	92	L	1.9	86	114
1ZBB	E F	E	97	E	1.2	86	114
1ZBB	E F	E	99	Y	2.1	86	114
1ZBB	E F	E	100	L	1.8	86	114
1ZBB	E F	E	101	V	1.7	86	114
1ZBB	E F	E	104	F	3.2	86	114
1ZBB	E F	E	121	P	1.6	121	132
1ZBB	E F	E	124	I	1.3	121	132
1ZBB	E F	F	28	G	6.6	25	29
1ZBB	E F	F	36	R	3.0	31	41
1ZBB	E F	F	37	L	2.5	31	41
1ZBB	E F	F	39	R	1.8	31	41
1ZBB	E F	F	40	R	4.6	31	41
1ZBB	E F	F	50	I	2.3	50	76
1ZBB	E F	F	61	F	3.3	50	76
1ZBB	E F	F	62	L	1.4	50	76
1ZBB	E F	F	66	I	3.0	50	76
1ZBB	E F	F	70	V	1.0	50	76
1ZBB	E F	F	86	V	1.7	83	93
1ZBB	f d	d	65	D	1.1	53	81
1ZBB	F D	D	65	D	1.1	53	81
1ZBB	f h	f	75	H	1.3	50	76
1ZBB	f h	f	88	Y	2.6	83	93
1ZBB	f h	h	80	Y	3.4	53	81
1ZBB	F H	F	75	H	1.7	50	76
1ZBB	F H	F	88	Y	2.5	83	93
1ZBB	F H	F	92	R	1.1	83	93
1ZBB	F H	H	73	E	1.0	53	81
1ZBB	F H	H	80	Y	3.3	53	81
1ZBB	g h	g	17	R	1.1	17	21
1ZBB	g h	g	29	R	1.8	27	36
1ZBB	g h	g	49	V	1.8	45	73
1ZBB	g h	g	50	Y	4.7	45	73
1ZBB	g h	g	51	L	2.0	45	73
1ZBB	g h	g	54	V	1.6	45	73
1ZBB	g h	g	55	L	2.1	45	73
1ZBB	g h	g	57	Y	2.7	45	73
1ZBB	g h	g	58	L	1.7	45	73
1ZBB	g h	g	63	L	2.8	45	73
1ZBB	g h	g	67	G	167.8	45	73
1ZBB	g h	g	80	P	1.3	80	89
1ZBB	g h	g	83	L	1.5	80	89
1ZBB	g h	g	96	L	1.7	91	97
1ZBB	g h	h	37	Y	2.1	35	46
1ZBB	g h	h	41	V	1.6	35	46
1ZBB	g h	h	42	L	1.2	35	46
1ZBB	g h	h	58	I	2.1	53	81
1ZBB	g h	h	59	M	1.8	53	81
1ZBB	g h	h	62	F	1.6	53	81
1ZBB	g h	h	63	V	1.1	53	81
1ZBB	g h	h	67	F	3.1	53	81
1ZBB	g h	h	69	R	1.3	53	81
1ZBB	g h	h	70	I	1.2	53	81
1ZBB	g h	h	91	I	2.0	88	99
1ZBB	g h	h	106	H	1.1	102	120
1ZBB	g h	h	111	G	94.0	102	120

1ZBB	g h	h	115	V	1.1	102	120
1ZBB	g h	h	118	Y	3.8	102	120
1ZBB	G H	G	17	R	1.1	17	21
1ZBB	G H	G	29	R	1.8	27	36
1ZBB	G H	G	49	V	1.8	45	73
1ZBB	G H	G	50	Y	4.7	45	73
1ZBB	G H	G	51	L	2.0	45	73
1ZBB	G H	G	54	V	1.6	45	73
1ZBB	G H	G	55	L	2.1	45	73
1ZBB	G H	G	57	Y	2.7	45	73
1ZBB	G H	G	58	L	1.7	45	73
1ZBB	G H	G	63	L	2.8	45	73
1ZBB	G H	G	67	G	167.6	45	73
1ZBB	G H	G	80	P	1.3	80	89
1ZBB	G H	G	83	L	1.4	80	89
1ZBB	G H	G	96	L	1.6	91	97
1ZBB	G H	H	37	Y	2.2	35	46
1ZBB	G H	H	41	V	1.6	35	46
1ZBB	G H	H	42	L	1.2	35	46
1ZBB	G H	H	58	I	2.1	53	81
1ZBB	G H	H	59	M	2.0	53	81
1ZBB	G H	H	62	F	1.6	53	81
1ZBB	G H	H	63	V	1.1	53	81
1ZBB	G H	H	67	F	3.1	53	81
1ZBB	G H	H	69	R	1.3	53	81
1ZBB	G H	H	70	I	1.3	53	81
1ZBB	G H	H	91	I	2.0	88	99
1ZBB	G H	H	106	H	1.1	102	120
1ZBB	G H	H	111	G	94.0	102	120
1ZBB	G H	H	115	V	1.1	102	120
1ZBB	G H	H	118	Y	3.8	102	120
1ZBD	A B	B	54	I	1.7	50	60
1ZBD	A B	B	145	E	1.2	138	147
1ZC4	A D	A	78	I	1.4	76	86
1ZC4	A D	D	272	K	1.4	258	283
1ZC4	C B	C	78	I	2.0	76	85
1ZC4	C B	B	272	K	1.0	258	281
1ZC4	C B	B	276	S	1.2	258	281
1ZDT	A P	A	277	V	1.2	262	283
1ZDT	A P	A	295	M	1.3	291	301
1ZDT	A P	A	299	Q	1.2	291	301
1ZDT	A P	P	744	L	1.9	743	751
1ZDT	A P	P	745	L	2.8	743	751
1ZDT	A P	P	748	L	1.2	743	751
1ZDT	A P	P	749	L	2.2	743	751
1ZE3	C D	C	95	K	1.7	95	99
1ZE3	C D	C	98	L	1.0	95	99
1ZE3	C D	D	22	F	2.7	20	24
1ZE3	C D	D	23	E	1.1	20	24
1ZGL	A B	A	48	F	3.8	46	50
1ZGL	A B	A	76	R	1.7	59	78
1ZGL	A C	A	65	V	1.4	59	78
1ZGL	B C	B	60	Y	1.5	54	63
1ZGL	B C	B	61	W	1.6	54	63
1ZGL	B C	B	78	Y	1.7	74	86
1ZGL	B C	B	81	H	1.3	74	86
1ZGL	B P	B	60	Y	13.4	54	63
1ZGL	D E	D	70	L	2.1	58	78
1ZGL	D E	D	76	R	2.0	58	78
1ZGL	D E	E	57	D	1.5	55	62

1ZGL	D F	D	65	V	1.5	58	78
1ZGL	D Q	D	58	G	164.2	58	78
1ZGL	D R	D	58	G	186.3	58	78
1ZGL	E F	E	60	Y	1.6	55	62
1ZGL	E F	E	61	W	1.5	55	62
1ZGL	E F	E	78	Y	1.4	74	86
1ZGL	E S	E	72	R	1.0	66	73
1ZGL	E T	E	60	Y	1.0	55	62
1ZGL	G H	G	76	R	1.2	58	77
1ZGL	G I	G	65	V	1.0	58	77
1ZGL	G T	G	58	G	18.8	58	77
1ZGL	H I	H	60	Y	1.2	55	62
1ZGL	H I	H	61	W	1.6	55	62
1ZGL	H I	H	78	Y	1.2	74	86
1ZGL	H I	H	85	V	1.2	74	86
1ZGL	H S	H	81	H	3.4	74	86
1ZGL	J K	J	48	F	2.3	46	52
1ZGL	J K	J	51	F	1.3	46	52
1ZGL	J K	J	76	R	2.0	59	78
1ZGL	J K	K	57	D	1.4	55	62
1ZGL	J L	J	65	V	1.5	59	78
1ZGL	K L	K	60	Y	1.5	55	62
1ZGL	K L	K	78	Y	1.9	74	86
1ZGL	K L	K	85	V	1.7	74	86
1ZGL	K M	K	55	R	2.2	55	62
1ZHI	A B	A	120	N	1.0	116	127
1ZHI	A B	A	121	K	1.4	116	127
1ZL8	A B	A	5	L	1.6	4	20
1ZL8	A B	A	15	L	2.7	4	20
1ZL8	A B	A	29	K	2.6	27	38
1ZL8	A B	A	45	V	1.3	40	53
1ZL8	A B	B	116	L	98.7	107	122
1ZL8	A B	B	144	L	1.3	139	155
1ZLA	A B	A	450	E	1.3	445	455
1ZLA	A B	A	451	I	2.1	445	455
1ZLA	A B	A	467	F	1.3	464	477
1ZLA	A B	A	497	E	1.1	486	514
1ZLA	A B	A	499	Y	2.3	486	514
1ZLA	A B	A	500	L	2.2	486	514
1ZLA	A B	A	501	V	1.6	486	514
1ZLA	A B	A	504	F	3.2	486	514
1ZLA	A B	A	521	P	1.3	521	532
1ZLA	A B	A	524	I	1.3	521	532
1ZLA	A B	B	36	R	1.3	31	41
1ZLA	A B	B	37	L	2.7	31	41
1ZLA	A B	B	39	R	2.1	31	41
1ZLA	A B	B	40	R	3.8	31	41
1ZLA	A B	B	61	F	3.3	50	76
1ZLA	A B	B	62	L	2.1	50	76
1ZLA	A B	B	66	I	2.4	50	76
1ZLA	A B	B	70	V	1.2	50	76
1ZLA	A G	A	448	L	1.5	445	455
1ZLA	A G	A	494	E	1.3	486	514
1ZLA	A G	A	512	I	1.3	486	514
1ZLA	B D	B	72	Y	6.0	50	76
1ZLA	B D	B	75	H	4.2	50	76
1ZLA	B D	B	88	Y	1.2	83	94
1ZLA	B D	D	1273	E	1.1	1253	1281
1ZLA	B D	D	1277	L	4.4	1253	1281
1ZLA	B D	D	1280	Y	2.5	1253	1281

1ZLA	B D	D	1289	R	1.6	1288	1299
1ZLA	B D	D	1296	R	1.9	1288	1299
1ZLA	B D	D	1297	L	5.7	1288	1299
1ZLA	C D	C	846	G	17.4	845	873
1ZLA	C D	C	850	Y	2.2	845	873
1ZLA	C D	C	851	L	1.0	845	873
1ZLA	C D	C	854	V	1.2	845	873
1ZLA	C D	C	857	Y	2.5	845	873
1ZLA	C D	C	858	L	1.7	845	873
1ZLA	C D	C	863	L	2.2	845	873
1ZLA	C D	C	867	G	34.7	845	873
1ZLA	C D	C	880	P	1.3	880	889
1ZLA	C D	C	896	L	1.6	891	897
1ZLA	C D	D	1241	V	1.3	1235	1246
1ZLA	C D	D	1242	L	15.8	1235	1246
1ZLA	C D	D	1245	V	1.0	1235	1246
1ZLA	C D	D	1258	I	1.3	1253	1281
1ZLA	C D	D	1262	F	1.6	1253	1281
1ZLA	C D	D	1269	R	1.4	1253	1281
1ZLA	C D	D	1275	S	1.1	1253	1281
1ZLA	C D	D	1291	I	2.1	1288	1299
1ZLA	C D	D	1303	L	2.0	1302	1320
1ZLA	C D	D	1311	G	158.8	1302	1320
1ZLA	C D	D	1315	V	1.2	1302	1320
1ZLA	C D	D	1317	K	1.2	1302	1320
1ZLA	C D	D	1318	Y	2.0	1302	1320
1ZLA	E C	E	648	L	1.4	645	655
1ZLA	E C	E	712	I	1.1	686	714
1ZLA	E F	E	650	E	1.2	645	655
1ZLA	E F	E	651	I	1.9	645	655
1ZLA	E F	E	654	Y	1.3	645	655
1ZLA	E F	E	667	F	1.1	664	679
1ZLA	E F	E	670	L	1.1	664	679
1ZLA	E F	E	673	E	2.1	664	679
1ZLA	E F	E	674	I	2.3	664	679
1ZLA	E F	E	678	F	2.0	664	679
1ZLA	E F	E	692	L	1.5	686	714
1ZLA	E F	E	697	E	1.1	686	714
1ZLA	E F	E	699	Y	2.5	686	714
1ZLA	E F	E	700	L	1.9	686	714
1ZLA	E F	E	701	V	1.5	686	714
1ZLA	E F	E	704	F	2.9	686	714
1ZLA	E F	E	721	P	1.5	721	732
1ZLA	E F	E	724	I	1.5	721	732
1ZLA	E F	F	236	R	2.2	231	241
1ZLA	E F	F	237	L	1.9	231	241
1ZLA	E F	F	239	R	2.0	231	241
1ZLA	E F	F	240	R	3.8	231	241
1ZLA	E F	F	250	I	1.9	250	276
1ZLA	E F	F	258	L	1.0	250	276
1ZLA	E F	F	261	F	3.4	250	276
1ZLA	E F	F	262	L	1.5	250	276
1ZLA	E F	F	266	I	2.9	250	276
1ZLA	E F	F	286	V	1.5	283	293
1ZLA	F D	D	1265	D	1.1	1253	1281
1ZLA	F H	F	272	Y	1.4	250	276
1ZLA	F H	F	275	H	3.1	250	276
1ZLA	F H	H	1493	T	1.0	1489	1499
1ZLA	F H	H	1497	L	1.5	1489	1499
1ZLA	G H	G	1030	V	1.3	1027	1036

1ZLA	G H	G	1034	L	1.0	1027	1036
1ZLA	G H	G	1049	V	1.7	1045	1073
1ZLA	G H	G	1050	Y	3.3	1045	1073
1ZLA	G H	G	1051	L	1.3	1045	1073
1ZLA	G H	G	1054	V	1.6	1045	1073
1ZLA	G H	G	1055	L	1.5	1045	1073
1ZLA	G H	G	1063	L	2.5	1045	1073
1ZLA	G H	G	1067	G	118.6	1045	1073
1ZLA	G H	G	1080	P	1.1	1080	1089
1ZLA	G H	G	1096	L	1.4	1091	1097
1ZLA	G H	H	1441	V	1.5	1435	1446
1ZLA	G H	H	1442	L	1.2	1435	1446
1ZLA	G H	H	1459	M	2.0	1453	1481
1ZLA	G H	H	1463	V	1.1	1453	1481
1ZLA	G H	H	1465	D	1.0	1453	1481
1ZLA	G H	H	1467	F	2.7	1453	1481
1ZLA	G H	H	1469	R	1.4	1453	1481
1ZLA	G H	H	1470	I	1.0	1453	1481
1ZLA	G H	H	1491	I	2.0	1489	1499
1ZLA	G H	H	1511	G	58.4	1502	1520
1ZLA	G H	H	1515	V	1.2	1502	1520
1ZLA	G H	H	1518	Y	2.3	1502	1520
1ZLA	G K	G	1057	Y	1.1	1045	1073
1ZLA	G K	G	1061	E	1.0	1045	1073
1ZLA	H K	H	1444	Q	1.2	1435	1446
1ZLA	H K	H	1506	H	1.8	1502	1520
1ZLH	A B	B	4	V	1.1	2	6
1ZLI	A B	B	4	V	1.5	2	6
1ZM2	A B	A	702	G	108.1	702	720
1ZM2	A B	A	703	G	129.3	702	720
1ZM2	A B	A	706	I	1.2	702	720
1ZM2	A B	A	711	R	1.0	702	720
1ZM2	C D	C	669	W	3.3	660	673
1ZM2	C D	C	702	G	1.3	702	720
1ZM2	C D	C	703	G	69.2	702	720
1ZM2	E F	E	669	W	2.0	660	673
1ZM2	E F	E	702	G	27.5	702	720
1ZM2	E F	E	703	G	76.7	702	720
1ZNV	A B	A	35	D	1.3	32	46
1ZNV	A B	A	52	D	1.2	51	56
1ZNV	A B	A	55	Y	1.5	51	56
1ZNV	A B	B	520	R	3.2	515	523
1ZNV	A D	A	12	E	1.2	12	27
1ZNV	A D	D	522	K	1.4	515	523
1ZNV	C B	C	12	E	1.2	12	27
1ZNV	C B	B	522	K	2.0	515	523
1ZNV	C D	C	35	D	1.8	32	46
1ZNV	C D	C	52	D	1.3	51	56
1ZNV	C D	C	55	Y	3.6	51	56
1ZNV	C D	D	520	R	2.6	515	523
1ZOQ	A C	A	330	I	1.3	322	335
1ZOQ	A C	A	375	L	1.5	370	382
1ZOQ	A C	C	2085	Q	2.2	2080	2092
1ZOQ	A C	C	2089	I	2.0	2080	2092
1ZOQ	A C	C	2096	L	1.1	2094	2105
1ZOQ	A C	C	2100	F	2.3	2094	2105
1ZOQ	A D	D	2080	P	1.6	2080	2092
1ZOQ	B C	C	2080	P	1.6	2080	2092
1ZOQ	B D	B	329	L	1.3	322	334
1ZOQ	B D	B	330	I	1.2	322	334

1ZOQ	B D	B	375	L	2.4	370	382
1ZOQ	B D	B	378	M	1.3	370	382
1ZOQ	B D	D	2085	Q	1.2	2080	2092
1ZOQ	B D	D	2089	I	1.9	2080	2092
1ZOQ	B D	D	2090	L	1.1	2080	2092
1ZOQ	B D	D	2096	L	1.6	2094	2105
1ZOQ	B D	D	2100	F	2.4	2094	2105
1ZOY	A B	A	59	V	1.3	57	61
1ZOY	A B	A	112	E	3.0	94	115
1ZOY	A B	A	156	H	2.1	154	169
1ZOY	A B	A	164	G	63.1	154	169
1ZOY	A B	A	167	L	1.7	154	169
1ZOY	A B	A	348	F	1.4	339	350
1ZOY	A B	A	519	D	1.0	518	543
1ZOY	A B	B	149	R	2.7	146	153
1ZOY	A B	B	152	L	4.0	146	153
1ZOY	B C	B	172	W	3.5	169	174
1ZOY	B C	C	12	M	1.1	8	21
1ZOY	B C	C	19	N	1.2	8	21
1ZOY	B D	D	43	W	2.1	38	63
1ZOY	C D	C	57	S	1.2	37	66
1ZOY	C D	C	59	F	2.1	37	66
1ZOY	C D	C	70	F	3.7	70	79
1ZOY	C D	D	54	L	1.3	38	63
1ZOY	C D	D	112	T	1.8	95	122
1ZOY	C D	D	115	G	206.1	95	122
1ZOY	C D	D	116	L	1.0	95	122
1ZOY	C D	D	119	F	2.4	95	122
1ZQ1	A C	A	125	K	1.6	120	127
1ZQ1	A C	C	445	D	1.1	445	454
1ZQ1	B D	D	445	D	1.6	445	454
1ZQ1	B D	D	452	K	1.5	445	454
1ZRT	C D	C	247	Y	15.3	247	270
1ZRT	C D	C	254	F	8.5	247	270
1ZRT	C D	C	261	L	1.1	247	270
1ZRT	C D	D	228	G	30.2	221	250
1ZRT	C D	D	235	L	1.4	221	250
1ZRT	D E	D	238	L	1.7	221	250
1ZRT	D E	E	16	Y	1.2	12	38
1ZRT	P E	P	179	W	2.1	172	182
1ZRT	P Q	P	95	Y	24.9	93	118
1ZRT	P Q	P	247	Y	1.2	247	269
1ZRT	P Q	P	254	F	1.9	247	269
1ZRT	P Q	Q	228	G	42.5	221	250
1ZRT	P Q	Q	235	L	1.4	221	250
1ZRT	P R	P	93	M	6.0	93	118
1ZRT	Q R	Q	238	L	1.8	221	250
1ZRT	Q R	Q	248	R	1.5	221	250
1ZRT	Q R	R	16	Y	1.0	12	38
1ZSZ	B C	B	8	K	2.6	8	23
1ZSZ	B C	B	11	Y	1.8	8	23
1ZSZ	B C	B	19	W	3.6	8	23
1ZSZ	B C	B	22	D	1.0	8	23
1ZSZ	B C	C	8	K	2.4	8	23
1ZSZ	B C	C	11	Y	3.3	8	23
1ZSZ	B C	C	12	Y	1.2	8	23
1ZSZ	B C	C	15	G	13.7	8	23
1ZSZ	B C	C	19	W	3.1	8	23
1ZT2	A B	A	202	Y	1.0	193	204
1ZT2	A B	A	222	V	1.1	221	226

1ZT2	A B	B	142	F	2.7	142	149
1ZT2	A B	B	143	I	1.2	142	149
1ZT2	C D	D	146	L	2.2	142	149
1ZTX	H L	L	124	Q	1.3	122	127
1ZUN	A B	A	7	H	1.5	7	26
1ZUN	A B	A	11	L	2.9	7	26
1ZUN	A B	A	20	R	1.6	7	26
1ZUN	A B	A	44	H	1.2	44	50
1ZUN	A B	A	192	D	1.4	190	201
1ZUZ	A B	A	11	E	1.0	6	20
1ZUZ	A B	A	71	M	1.0	65	75
1ZUZ	A B	A	92	F	2.2	82	93
1ZUZ	A B	A	105	L	2.0	102	113
1ZUZ	A B	A	124	M	1.7	118	129
1ZUZ	A B	A	141	F	1.0	138	147
1ZUZ	A B	A	144	M	2.8	138	147
1ZUZ	A B	A	145	M	1.9	138	147
1ZUZ	A B	B	304	R	1.9	304	319
1ZUZ	A B	B	305	W	6.6	304	319
1ZUZ	A B	B	307	L	1.6	304	319
1ZUZ	A B	B	309	F	3.2	304	319
1ZUZ	A B	B	312	V	2.2	304	319
1ZUZ	A B	B	314	L	1.6	304	319
1ZUZ	A B	B	317	H	2.3	304	319
1ZUZ	A B	B	318	L	1.7	304	319
1ZV5	L A	L	35	E	2.7	25	36
1ZV5	L A	L	114	R	1.6	109	116
1ZV8	A B	A	18	E	1.2	2	49
1ZV8	A B	A	22	T	1.8	2	49
1ZV8	A B	A	29	K	1.3	2	49
1ZV8	A B	A	33	V	1.2	2	49
1ZV8	A B	B	15	E	1.7	13	28
1ZV8	A B	B	18	R	1.5	13	28
1ZV8	A B	B	19	L	1.5	13	28
1ZV8	A B	B	26	L	1.1	13	28
1ZV8	A F	A	7	N	3.0	2	49
1ZV8	A F	A	17	Q	2.0	2	49
1ZV8	A F	A	20	L	1.4	2	49
1ZV8	A F	A	31	Q	1.8	2	49
1ZV8	A F	A	42	N	1.0	2	49
1ZV8	A F	F	13	Q	1.5	13	29
1ZV8	A F	F	16	I	2.5	13	29
1ZV8	A F	F	19	L	1.5	13	29
1ZV8	A F	F	26	L	1.1	13	29
1ZV8	C B	C	13	I	1.1	3	47
1ZV8	C B	C	20	L	1.2	3	47
1ZV8	C B	C	31	Q	1.8	3	47
1ZV8	C B	C	35	N	1.4	3	47
1ZV8	C B	B	16	I	2.4	13	28
1ZV8	C B	B	19	L	1.3	13	28
1ZV8	C B	B	26	L	2.9	13	28
1ZV8	C D	C	29	K	1.5	3	47
1ZV8	C D	C	30	L	1.4	3	47
1ZV8	C D	C	33	V	1.1	3	47
1ZV8	C D	D	15	E	2.1	13	29
1ZV8	C D	D	18	R	1.3	13	29
1ZV8	E D	E	17	Q	1.9	2	49
1ZV8	E D	E	20	L	1.3	2	49
1ZV8	E D	E	31	Q	1.4	2	49
1ZV8	E D	D	16	I	2.2	13	29

1ZV8	E D	D	19	L	1.0	13	29
1ZV8	E F	E	29	K	1.6	2	49
1ZV8	E F	E	33	V	1.4	2	49
1ZV8	E F	F	15	E	2.2	13	29
1ZV8	E F	F	18	R	1.1	13	29
1ZV8	E F	F	19	L	1.1	13	29
1ZV8	E F	F	22	V	1.3	13	29
1ZV8	E F	F	26	L	1.1	13	29
1ZV8	G H	G	18	E	1.5	2	50
1ZV8	G H	G	29	K	1.4	2	50
1ZV8	G H	G	33	V	1.4	2	50
1ZV8	G H	H	15	E	2.0	13	29
1ZV8	G H	H	18	R	1.7	13	29
1ZV8	G H	H	19	L	1.3	13	29
1ZV8	G H	H	22	V	1.0	13	29
1ZV8	G H	H	26	L	1.4	13	29
1ZV8	G L	G	20	L	1.8	2	50
1ZV8	G L	G	31	Q	1.4	2	50
1ZV8	G L	G	35	N	1.0	2	50
1ZV8	G L	G	42	N	1.4	2	50
1ZV8	G L	L	16	I	2.2	13	28
1ZV8	G L	L	19	L	2.0	13	28
1ZV8	G L	L	26	L	2.0	13	28
1ZV8	I F	I	11	K	1.5	2	49
1ZV8	I F	F	21	E	1.0	13	29
1ZV8	I H	I	10	N	1.2	2	49
1ZV8	I H	I	13	I	1.2	2	49
1ZV8	I H	I	20	L	1.5	2	49
1ZV8	I H	I	45	V	1.1	2	49
1ZV8	I H	H	16	I	1.1	13	29
1ZV8	I H	H	19	L	1.2	13	29
1ZV8	I H	H	26	L	1.5	13	29
1ZV8	I J	I	11	K	1.6	2	49
1ZV8	I J	I	30	L	1.4	2	49
1ZV8	I J	J	19	L	1.1	13	28
1ZV8	I J	J	22	V	1.0	13	28
1ZV8	I J	J	26	L	1.4	13	28
1ZV8	K J	K	13	I	1.1	2	50
1ZV8	K J	K	17	Q	2.3	2	50
1ZV8	K J	K	20	L	1.5	2	50
1ZV8	K J	K	35	N	1.2	2	50
1ZV8	K J	K	42	N	1.1	2	50
1ZV8	K J	J	19	L	1.0	13	28
1ZV8	K J	J	26	L	1.5	13	28
1ZV8	K L	K	29	K	1.4	2	50
1ZV8	K L	K	30	L	1.2	2	50
1ZV8	K L	K	33	V	1.4	2	50
1ZV8	K L	K	36	Q	1.5	2	50
1ZV8	K L	K	44	L	1.5	2	50
1ZV8	K L	L	15	E	2.3	13	28
1ZV8	K L	L	18	R	1.0	13	28
1ZV8	K L	L	19	L	1.1	13	28
1ZVV	A W	A	84	D	1.1	73	89
1ZVV	A W	A	304	L	6.1	294	307
1ZVV	A W	W	47	I	1.1	47	54
1ZVV	A W	W	48	M	1.6	47	54
1ZVV	B P	B	295	Y	1.9	294	310
1ZVV	B P	P	47	I	2.4	47	54
1ZVV	B P	P	51	M	2.0	47	54
1ZVV	G J	G	88	M	1.0	76	89

1ZVV	G J	G	295	Y	1.7	294	310
1ZVV	G J	J	47	I	1.9	47	51
1ZVY	A B	B	112	R	2.2	109	114
1ZW3	A B	A	11	I	1.3	6	27
1ZW3	A B	A	22	L	2.1	6	27
1ZW3	A B	A	53	L	1.5	40	63
1ZW3	A B	A	125	F	1.8	101	146
1ZW3	A B	B	1633	L	1.6	1631	1649
1ZW3	A B	B	1640	V	1.6	1631	1649
1ZW3	A B	B	1647	L	3.2	1631	1649
1ZW3	A B	B	1648	I	2.2	1631	1649
1ZY3	A B	A	63	L	1.0	59	67
1ZY3	A B	A	81	V	1.5	75	88
1ZY3	A B	A	84	E	1.3	75	88
1ZY3	A B	A	85	L	2.0	75	88
1ZY3	A B	A	93	G	1.0	92	112
1ZY3	A B	B	209	L	1.7	203	218
1ZY3	A B	B	216	M	1.2	203	218
1ZY8	A K	K	160	K	1.1	160	173
1ZY8	A K	K	161	E	1.3	160	173
1ZY8	B K	B	444	D	1.6	442	448
1ZY8	C L	C	443	E	1.1	442	447
1ZY8	C L	C	444	D	1.3	442	447
1ZY8	D L	L	133	P	1.6	133	142
1ZY8	D L	L	136	R	1.4	133	142
1ZY8	E M	E	443	E	1.8	442	447
1ZY8	E M	E	444	D	1.7	442	447
1ZY8	E M	M	160	K	2.5	160	172
1ZY8	E M	M	161	E	1.9	160	172
1ZY8	F M	F	444	D	1.4	442	448
1ZY8	F M	M	136	R	1.7	134	142
1ZY8	G N	G	443	E	1.3	442	447
1ZY8	H N	N	133	P	1.3	133	141
1ZY8	I O	I	443	E	1.0	442	448
1ZY8	I O	I	444	D	1.0	442	448
1ZY8	J O	O	133	P	2.0	133	140
1ZY8	J O	O	136	R	3.3	133	140
1ZY8	J O	O	137	N	1.6	133	140
2A0L	A D	A	116	F	2.0	116	138
2A0L	B F	B	117	R	1.8	116	138
2A0L	B F	B	119	V	1.8	116	138
2A0L	B F	B	120	R	1.0	116	138
2A19	A B	B	489	F	5.3	488	499
2A19	A B	B	490	E	1.4	488	499
2A1D	A B	A	14	F	1.4	14	14
2A1D	A B	A	14	Y	4.3	14	14
2A1D	A B	B	129	L	1.4	126	130
2A1D	B D	D	35	E	1.0	27	46
2A1D	B D	D	38	F	1.9	27	46
2A1D	B D	D	70	D	1.3	53	87
2A1D	B D	D	74	L	1.2	53	87
2A1D	E F	E	14	E	1.4	14	14
2A1D	E F	E	14	F	1.4	14	14
2A1D	E F	E	14	Y	1.0	14	14
2A1D	F H	H	38	F	2.0	27	46
2A1D	F H	H	70	D	1.6	53	87
2A1D	F H	H	74	L	1.1	53	87
2A1D	F H	H	187	E	2.0	182	197
2A1J	A B	A	840	F	2.0	838	843
2A1J	A B	A	841	L	1.4	838	843

2A1J	A B	A	862	I	1.8	862	868
2A1J	A B	A	889	F	2.5	880	891
2A1J	A B	A	890	I	1.3	880	891
2A1J	A B	B	231	F	1.6	221	240
2A1J	A B	B	235	V	1.2	221	240
2A1J	A B	B	260	L	1.3	260	265
2A1J	A B	B	288	V	1.0	279	291
2A1J	A B	B	289	L	1.1	279	291
2A1T	C R	R	253	D	1.1	249	254
2A1T	D R	D	277	Y	2.2	255	279
2A1T	D R	R	284	I	1.4	284	289
2A1T	D S	D	18	E	1.5	18	38
2A1T	D S	D	22	E	1.4	18	38
2A1T	D S	D	23	F	2.6	18	38
2A1T	D S	D	26	T	1.1	18	38
2A1T	D S	D	59	L	1.3	50	60
2A1T	D S	S	77	T	1.1	70	82
2A1T	D S	S	195	L	2.7	195	204
2A1T	D S	S	198	I	2.2	195	204
2A1T	R S	R	90	E	2.4	90	104
2A1T	R S	R	114	A	17.1	114	128
2A1T	R S	R	121	P	1.4	114	128
2A1T	R S	R	122	R	3.3	114	128
2A1T	R S	S	102	L	1.0	101	115
2A1T	R S	S	133	Q	1.3	133	142
2A1T	R S	S	136	Q	1.9	133	142
2A1T	R S	S	137	M	1.6	133	142
2A1T	R S	S	140	G	2.9	133	142
2A1T	R S	S	245	L	1.1	243	248
2A1T	R S	S	246	V	1.6	243	248
2A3I	A B	A	795	L	1.4	795	805
2A3I	A B	A	799	I	1.0	795	805
2A3I	A B	A	962	E	1.8	958	973
2A3I	A B	B	1434	L	1.1	1434	1440
2A3I	A B	B	1438	L	1.7	1434	1440
2A3I	A B	B	1439	L	2.5	1434	1440
2A40	A B	B	49	G	79.1	46	56
2A40	A B	B	53	D	1.4	46	56
2A40	A C	A	143	Y	1.3	137	145
2A40	A C	A	345	I	1.0	338	349
2A40	A C	C	439	L	1.1	435	446
2A40	A C	C	440	L	1.1	435	446
2A40	A C	C	443	I	2.5	435	446
2A40	D E	E	49	G	88.1	46	56
2A40	D E	E	53	D	1.0	46	56
2A40	D F	D	143	Y	1.1	137	145
2A40	D F	F	439	L	1.2	435	446
2A40	D F	F	443	I	1.9	435	446
2A45	A B	A	14	E	1.6	14	14
2A45	A B	A	14	L	2.5	14	14
2A45	D E	D	14	E	1.1	14	14
2A45	G H	G	48	G	78.0	48	72
2A45	G H	G	52	K	1.8	48	72
2A45	G H	G	53	G	121.7	48	72
2A45	G H	G	55	I	1.5	48	72
2A45	G H	H	82	L	1.6	79	100
2A45	G I	G	58	V	1.9	48	72
2A45	G I	G	62	F	1.1	48	72
2A45	G I	I	29	L	1.1	22	45
2A45	H I	H	79	G	8.7	79	100

2A45	H I	H	90	E	1.5	79	100
2A45	J K	J	52	K	1.5	49	73
2A45	J K	J	53	G	119.0	49	73
2A45	J K	K	82	L	1.4	79	99
2A45	J K	K	100	L	1.0	100	105
2A45	J L	J	69	L	1.4	49	73
2A45	J L	L	40	L	1.3	22	41
2A45	K L	K	79	G	3.0	79	99
2A4J	A B	A	109	A	7.1	100	114
2A4J	A B	A	126	L	3.5	123	134
2A4J	A B	A	145	M	3.7	139	150
2A4J	A B	A	162	F	1.4	159	168
2A4J	A B	A	166	M	1.4	159	168
2A4J	A B	B	2	W	4.2	2	9
2A4J	A B	B	5	L	2.0	2	9
2A4J	A B	B	10	L	8.5	10	14
2A5D	A B	A	73	L	1.6	71	76
2A5D	A B	B	30	Y	5.2	25	33
2A5D	A B	B	31	F	2.2	25	33
2A5T	A B	A	184	Y	1.0	180	188
2A5T	A B	A	266	L	1.2	260	274
2A5T	A B	A	269	L	1.3	260	274
2A5T	A B	A	272	H	1.1	260	274
2A5T	A B	A	273	E	1.5	260	274
2A5T	A B	B	261	L	1.1	254	269
2A5T	A B	B	264	L	1.6	254	269
2A5Y	A B	A	146	F	2.1	146	153
2A5Y	A B	A	201	Y	1.3	195	208
2A5Y	A B	B	120	L	2.2	112	122
2A5Y	A B	B	202	D	1.4	199	204
2A5Y	A B	B	206	D	1.3	205	212
2A6Q	A E	A	53	E	1.0	51	66
2A6Q	A E	A	59	E	2.9	51	66
2A6Q	A E	A	62	Y	2.6	51	66
2A6Q	A E	A	63	L	2.0	51	66
2A6Q	A E	A	69	N	1.4	67	82
2A6Q	A E	A	72	R	2.9	67	82
2A6Q	A E	A	73	L	1.8	67	82
2A6Q	A E	A	80	L	3.4	67	82
2A6Q	A E	E	8	E	2.9	7	18
2A6Q	B E	B	58	E	1.1	51	61
2A6Q	C F	C	59	E	2.6	51	64
2A6Q	C F	C	60	T	1.5	51	64
2A6Q	C F	C	62	Y	1.8	51	64
2A6Q	C F	C	63	L	2.0	51	64
2A6Q	C F	C	69	N	1.9	67	82
2A6Q	C F	C	72	R	2.2	67	82
2A6Q	C F	C	73	L	1.6	67	82
2A6Q	C F	C	76	S	1.3	67	82
2A6Q	C F	C	77	I	1.9	67	82
2A6Q	C F	C	80	L	3.1	67	82
2A6Q	C F	F	8	E	2.0	7	18
2A6Q	C F	F	10	W	2.5	7	18
2A6Q	C F	F	13	Y	2.2	7	18
2A78	A B	A	79	R	3.7	76	86
2A78	A B	A	82	Y	1.4	76	86
2A78	A B	A	110	Q	1.2	98	116
2A78	A B	B	105	I	1.7	102	117
2A78	A B	B	112	D	1.5	102	117
2A79	A B	A	203	R	1.5	192	205

2A79	A B	A	235	K	1.2	222	236
2A79	A B	B	66	M	1.0	62	68
2A7U	A B	A	12	I	2.4	5	18
2A7U	A B	A	13	K	1.4	5	18
2A7U	A B	B	9	P	3.4	4	21
2A7U	A B	B	71	N	2.7	70	82
2A7U	A B	B	78	V	1.0	70	82
2A7U	A B	B	81	E	1.0	70	82
2A9M	L H	H	131	H	1.7	130	134
2AA1	A B	A	31	R	2.1	21	36
2AA1	A B	A	35	V	1.0	21	36
2AA1	A B	A	104	H	1.9	96	114
2AA1	A B	A	123	H	3.9	120	138
2AA1	A B	B	30	R	3.6	22	35
2AA1	A B	B	33	V	1.0	22	35
2AA1	A B	B	34	V	1.8	22	35
2AA1	A B	B	112	I	1.4	100	119
2AA1	A B	B	127	Q	1.2	124	142
2AA1	A B	B	131	Q	1.7	124	142
2AA1	A D	A	41	I	2.3	37	43
2AA1	A D	A	42	Y	2.8	37	43
2AA1	A D	A	96	P	1.4	96	114
2AA1	A D	A	98	N	1.4	96	114
2AA1	A D	D	37	W	2.7	36	41
2AA1	A D	D	40	R	1.1	36	41
2AA1	C B	C	41	I	2.2	37	42
2AA1	C B	C	96	P	1.3	96	114
2AA1	C B	C	98	N	1.0	96	114
2AA1	C B	B	37	W	1.5	36	41
2AA1	C B	B	40	R	1.4	36	41
2AA1	C D	C	31	R	2.6	21	36
2AA1	C D	C	35	V	1.0	21	36
2AA1	C D	C	104	H	2.0	96	114
2AA1	C D	C	123	H	3.5	120	138
2AA1	C D	D	30	R	3.4	22	35
2AA1	C D	D	34	V	1.8	22	35
2AA1	C D	D	112	I	1.5	100	119
2AA1	C D	D	127	Q	1.1	124	142
2AA1	C D	D	131	Q	1.8	124	142
2AAB	L H	L	124	Q	1.5	122	127
2AAI	A B	A	183	Y	2.9	182	194
2AAI	A B	A	186	G	10.8	182	194
2AAI	A B	A	247	I	1.3	245	250
2ABZ	A C	C	41	P	1.0	41	47
2ABZ	A C	C	42	W	1.6	41	47
2ABZ	B E	E	42	W	2.1	41	47
2ACL	A B	A	356	K	1.0	343	360
2ACL	A B	A	394	E	1.9	386	408
2ACL	A B	A	397	Y	1.3	386	408
2ACL	A B	A	415	F	1.4	414	420
2ACL	A B	A	419	L	1.5	414	420
2ACL	A B	B	377	E	1.7	373	395
2ACL	A B	B	381	H	1.7	373	395
2ACL	A B	B	400	L	1.4	399	427
2ACL	A B	B	404	R	2.0	399	427
2ACL	A B	B	406	L	1.5	399	427
2ACL	A B	B	410	V	1.2	399	427
2ACL	A B	B	413	R	1.8	399	427
2ACL	A B	B	439	E	1.6	436	443
2ACL	A F	A	280	V	1.0	264	286

2ACL	A F	A	302	R	1.0	294	304
2ACL	A F	F	427	R	1.1	401	428
2ACL	C D	C	348	R	1.0	343	360
2ACL	C D	C	415	F	1.0	414	420
2ACL	C D	C	450	F	1.6	449	457
2ACL	C D	C	454	M	1.0	449	457
2ACL	C D	C	455	L	1.9	449	457
2ACL	C D	D	406	L	1.4	401	425
2ACL	C D	D	410	V	1.4	401	425
2ACL	C D	D	413	R	1.5	401	425
2ACL	C H	C	294	L	1.4	294	304
2ACL	C H	C	302	R	1.2	294	304
2ACL	E B	E	302	R	1.2	294	316
2ACL	E B	E	305	W	1.0	294	316
2ACL	E F	E	348	R	1.5	343	360
2ACL	E F	E	415	F	1.0	414	420
2ACL	E F	E	427	S	1.1	421	433
2ACL	E F	E	430	L	1.1	421	433
2ACL	E F	E	438	F	1.2	436	440
2ACL	E F	E	450	F	1.3	449	456
2ACL	E F	E	451	L	1.8	449	456
2ACL	E F	E	452	M	1.6	449	456
2ACL	E F	E	455	L	2.6	449	456
2ACL	E F	F	281	R	1.4	281	290
2ACL	E F	F	410	V	1.3	401	428
2ACL	E F	F	413	R	2.1	401	428
2ACL	E F	F	424	F	1.1	401	428
2ACL	E F	F	435	P	1.0	435	441
2ACL	G D	G	276	L	1.6	264	286
2ACL	G D	G	279	L	1.0	264	286
2ACL	G D	G	294	L	1.0	294	304
2ACL	G H	G	390	E	1.5	386	408
2ACL	G H	G	394	E	1.8	386	408
2ACL	G H	G	397	Y	1.1	386	408
2ACL	G H	G	423	P	3.2	421	433
2ACL	G H	G	426	R	3.5	421	433
2ACL	G H	G	438	F	1.3	436	442
2ACL	G H	G	451	L	1.0	450	455
2ACL	G H	H	285	I	1.5	281	290
2ACL	G H	H	288	L	1.7	281	290
2ACL	G H	H	400	L	2.4	400	425
2ACL	G H	H	404	R	2.1	400	425
2ACL	G H	H	406	L	1.0	400	425
2ACL	G H	H	424	F	1.8	400	425
2ACM	A B	A	1077	F	1.0	1064	1081
2ACM	A B	A	1080	I	2.9	1064	1081
2ACM	A B	B	1121	F	2.0	1114	1124
2ACZ	A B	A	47	V	1.2	45	49
2ACZ	A B	A	100	E	2.0	92	103
2ACZ	A B	A	101	H	1.0	92	103
2ACZ	A B	A	143	H	1.1	141	156
2ACZ	A B	B	140	R	2.7	137	144
2ACZ	B C	B	163	W	2.0	160	165
2ACZ	B C	C	103	F	1.9	103	129
2ACZ	B D	B	164	W	3.6	160	165
2ACZ	B D	D	12	G	186.1	12	38
2ACZ	B D	D	13	V	1.9	12	38
2ACZ	B D	D	16	F	1.0	12	38
2ACZ	B D	D	82	D	2.1	55	84
2ACZ	C D	C	38	F	3.4	22	54

2ACZ	C D	C	41	V	1.1	22	54
2ACZ	C D	C	42	G	4.6	22	54
2ACZ	C D	C	45	L	1.4	22	54
2ACZ	C D	C	58	F	2.4	55	65
2ACZ	C D	C	92	M	1.3	68	96
2ACZ	C D	D	30	I	1.0	12	38
2ACZ	C D	D	52	F	1.3	45	54
2ACZ	C D	D	76	M	1.3	55	84
2ACZ	C D	D	104	Y	2.5	87	114
2ADF	A H	A	1009	D	2.2	1007	1019
2ADF	A H	A	1012	G	2.1	1007	1019
2ADF	A H	A	1013	F	3.0	1007	1019
2ADF	A L	A	1009	D	1.7	1007	1019
2ADF	H L	L	122	E	1.0	121	127
2ADF	H L	L	123	Q	1.3	121	127
2ADG	A B	A	124	Q	1.5	122	127
2ADV	A C	A	39	F	2.0	35	50
2ADV	A C	A	40	Y	2.4	35	50
2ADV	A C	A	41	G	8.1	35	50
2ADV	A C	A	42	Y	2.4	35	50
2ADV	A C	A	46	Q	2.1	35	50
2ADV	A C	A	54	I	1.0	51	62
2ADV	A C	A	57	L	1.4	51	62
2ADV	A C	A	58	Y	1.7	51	62
2ADV	A C	A	74	E	1.2	74	83
2ADV	A C	A	78	V	1.1	74	83
2ADV	A C	A	79	W	1.3	74	83
2ADV	A C	A	92	W	4.0	85	95
2ADV	A C	A	100	F	3.8	98	118
2ADV	A C	A	107	F	3.9	98	118
2ADV	A C	A	145	M	1.6	134	147
2ADV	A C	A	156	T	2.2	153	157
2ADV	A C	C	150	L	1.5	149	158
2ADV	A C	C	153	Y	1.2	149	158
2ADV	A C	C	154	F	1.4	149	158
2ADV	A C	C	505	R	4.8	505	511
2ADV	A C	C	508	V	1.4	505	511
2ADV	B C	C	274	R	2.6	273	284
2ADV	B C	C	278	S	1.7	273	284
2ADV	B C	C	282	M	1.3	273	284
2ADV	B C	C	293	F	3.9	290	298
2AFF	A B	B	241	F	1.8	239	252
2AFF	A B	B	242	L	3.9	239	252
2AFF	A B	B	245	R	2.8	239	252
2AFF	A B	B	249	V	3.4	239	252
2AFH	A B	A	86	V	1.6	86	92
2AFH	A B	A	87	G	21.7	86	92
2AFH	A B	A	90	Q	1.4	86	92
2AFH	A B	A	91	Y	3.4	86	92
2AFH	A B	A	123	I	1.8	120	125
2AFH	A B	A	130	K	1.5	128	142
2AFH	A B	A	133	K	1.4	128	142
2AFH	A B	A	134	L	1.5	128	142
2AFH	A B	A	141	L	2.4	128	142
2AFH	A B	A	158	L	1.9	154	159
2AFH	A B	A	240	I	1.5	238	245
2AFH	A B	A	261	E	1.0	259	266
2AFH	A B	A	334	E	1.3	318	346
2AFH	A B	A	407	Y	1.3	406	417
2AFH	A B	A	429	F	3.7	425	434

2AFH	A B	A	430	I	1.4	425	434
2AFH	A B	A	458	I	1.0	453	468
2AFH	A B	B	20	Y	3.2	18	31
2AFH	A B	B	23	M	1.5	18	31
2AFH	A B	B	24	L	1.4	18	31
2AFH	A B	B	52	Y	3.1	50	58
2AFH	A B	B	94	G	261.7	93	108
2AFH	A B	B	98	Y	2.4	93	108
2AFH	A B	B	102	Y	1.6	93	108
2AFH	A B	B	157	V	1.6	153	158
2AFH	A B	B	428	W	1.8	427	437
2AFH	A B	B	447	Y	1.4	446	459
2AFH	A D	A	466	T	1.3	453	468
2AFH	A D	D	330	M	1.0	322	337
2AFH	A D	D	345	T	1.0	342	358
2AFH	A D	D	348	R	2.5	342	358
2AFH	A D	D	352	V	1.0	342	358
2AFH	A D	D	359	H	2.0	359	363
2AFH	A D	D	360	T	1.2	359	363
2AFH	A F	A	124	V	1.4	120	125
2AFH	B F	B	401	R	1.0	400	412
2AFH	C B	C	466	T	1.5	453	468
2AFH	C B	B	330	M	1.1	322	337
2AFH	C B	B	345	T	1.0	342	358
2AFH	C B	B	348	R	2.0	342	358
2AFH	C B	B	352	V	1.1	342	358
2AFH	C B	B	359	H	2.1	359	363
2AFH	C D	C	23	K	1.5	22	30
2AFH	C D	C	86	V	1.5	86	92
2AFH	C D	C	87	G	22.6	86	92
2AFH	C D	C	90	Q	1.3	86	92
2AFH	C D	C	91	Y	3.9	86	92
2AFH	C D	C	123	I	1.7	120	126
2AFH	C D	C	130	K	1.1	128	142
2AFH	C D	C	133	K	1.1	128	142
2AFH	C D	C	134	L	1.1	128	142
2AFH	C D	C	141	L	1.9	128	142
2AFH	C D	C	158	L	1.9	154	159
2AFH	C D	C	240	I	1.5	238	245
2AFH	C D	C	261	E	1.0	259	266
2AFH	C D	C	334	E	1.4	318	346
2AFH	C D	C	407	Y	1.3	406	417
2AFH	C D	C	425	I	1.0	425	434
2AFH	C D	C	429	F	3.7	425	434
2AFH	C D	C	430	I	1.4	425	434
2AFH	C D	D	20	Y	1.3	18	31
2AFH	C D	D	23	M	1.6	18	31
2AFH	C D	D	24	L	1.5	18	31
2AFH	C D	D	52	Y	2.5	50	58
2AFH	C D	D	94	G	245.1	93	108
2AFH	C D	D	98	Y	2.7	93	108
2AFH	C D	D	102	Y	2.1	93	108
2AFH	C D	D	133	D	1.5	128	142
2AFH	C D	D	137	N	1.0	128	142
2AFH	C D	D	157	V	2.0	153	158
2AFH	C D	D	428	W	1.8	427	434
2AFH	C D	D	447	Y	1.1	446	459
2AGH	A B	A	298	L	2.0	292	310
2AGH	A B	A	302	L	2.6	292	310
2AGH	A B	A	303	M	1.1	292	310

2AGH	A B	A	306	E	1.5	292	310
2AGH	A B	A	309	L	1.5	292	310
2AGH	A B	B	599	L	1.9	597	612
2AGH	A B	B	603	L	1.0	597	612
2AGH	A B	B	606	K	1.2	597	612
2AGH	A B	B	607	L	1.0	597	612
2AGH	A B	B	646	R	1.4	646	668
2AGH	A B	B	650	Y	2.1	646	668
2AGH	A B	B	653	L	1.2	646	668
2AGH	A B	B	657	I	1.4	646	668
2AGH	A B	B	662	K	1.4	646	668
2AGH	B C	B	631	Y	2.8	623	642
2AGH	B C	C	849	I	2.0	847	858
2AGH	B C	C	852	F	3.8	847	858
2AGH	B C	C	853	V	1.1	847	858
2AGJ	L H	L	125	Q	1.6	123	128
2AHM	A E	A	21	V	1.4	6	25
2AHM	A E	A	24	Q	1.7	6	25
2AHM	A E	A	54	F	1.6	50	69
2AHM	A E	A	58	V	1.7	50	69
2AHM	A E	A	61	L	2.1	50	69
2AHM	A E	A	65	L	1.4	50	69
2AHM	A E	E	89	T	1.4	82	104
2AHM	A E	E	92	M	1.0	82	104
2AHM	A E	E	96	L	2.8	82	104
2AHM	A E	E	97	F	1.6	82	104
2AHM	A E	E	100	L	1.5	82	104
2AHM	A E	E	103	L	2.1	82	104
2AHM	A E	E	108	L	1.9	106	117
2AHM	A E	E	111	I	1.5	106	117
2AHM	A H	H	88	V	1.2	37	104
2AHM	A H	H	95	M	2.1	37	104
2AHM	B F	B	17	V	1.0	7	25
2AHM	B F	B	21	V	1.6	7	25
2AHM	B F	B	54	F	2.0	50	69
2AHM	B F	B	58	V	1.5	50	69
2AHM	B F	B	65	L	1.7	50	69
2AHM	B F	F	96	L	1.5	84	104
2AHM	B F	F	100	L	1.5	84	104
2AHM	B F	F	103	L	1.8	84	104
2AHM	B F	F	108	L	2.2	106	117
2AHM	B G	G	95	M	1.4	37	104
2AHM	C F	F	88	V	1.0	84	104
2AHM	C F	F	95	M	1.4	84	104
2AHM	C G	C	17	V	1.4	6	25
2AHM	C G	C	21	V	1.6	6	25
2AHM	C G	C	54	F	2.1	50	67
2AHM	C G	C	58	V	1.6	50	67
2AHM	C G	C	61	L	2.7	50	67
2AHM	C G	C	62	S	1.3	50	67
2AHM	C G	C	65	L	1.3	50	67
2AHM	C G	C	76	L	1.2	73	77
2AHM	C G	G	93	Q	1.1	37	104
2AHM	C G	G	96	L	2.8	37	104
2AHM	C G	G	97	F	5.9	37	104
2AHM	C G	G	99	M	1.0	37	104
2AHM	C G	G	100	L	1.0	37	104
2AHM	C G	G	103	L	2.3	37	104
2AHM	C G	G	108	L	2.2	106	117
2AHM	C G	G	111	I	1.2	106	117

2AHM	C G	G	116	R	2.7	106	117
2AHM	D E	E	95	M	1.4	82	104
2AHM	D G	D	33	L	1.6	31	46
2AHM	D H	D	17	V	1.0	6	25
2AHM	D H	D	21	V	1.4	6	25
2AHM	D H	D	54	F	1.8	50	67
2AHM	D H	D	58	V	1.6	50	67
2AHM	D H	H	96	L	2.9	37	104
2AHM	D H	H	100	L	2.4	37	104
2AHM	D H	H	103	L	2.0	37	104
2AHM	D H	H	108	L	2.1	106	117
2AI0	L H	L	129	Q	1.3	127	132
2AI0	N J	N	129	Q	1.5	127	132
2AI0	O K	O	129	Q	1.1	127	131
2AJ3	C D	C	124	Q	1.6	122	128
2AJ3	E F	E	124	Q	1.5	122	128
2AJF	B F	B	31	K	1.1	21	53
2AJQ	A B	B	33	G	196.8	33	38
2AJQ	A B	B	34	P	2.1	33	38
2AJQ	F I	I	33	G	105.9	33	38
2AJQ	F I	I	34	P	2.1	33	38
2AJZ	A B	A	124	Q	1.5	122	126
2AJZ	L H	L	124	Q	1.2	122	126
2AK4	A C	A	66	I	2.4	57	85
2AK4	A C	A	74	Y	2.0	57	85
2AK4	A C	A	147	W	7.1	138	150
2AK4	A C	A	156	R	1.6	152	162
2AK4	A C	A	167	W	1.4	163	175
2AK4	D E	E	135	E	1.6	135	141
2AK4	D E	E	137	E	1.2	135	141
2AK4	D E	E	140	H	2.4	135	141
2AK4	F H	F	66	I	2.4	57	85
2AK4	F H	F	74	Y	1.8	57	85
2AK4	F H	F	147	W	7.2	138	150
2AK4	F H	F	156	R	1.8	152	162
2AK4	F H	F	167	W	1.5	163	175
2AK4	F J	F	72	Q	1.0	57	85
2AK4	F R	F	79	R	1.3	57	85
2AK4	I J	J	137	E	1.2	135	141
2AK4	I J	J	140	H	2.6	135	141
2AK4	K B	K	79	R	1.6	57	85
2AK4	K M	K	66	I	2.5	57	85
2AK4	K M	K	74	Y	1.7	57	85
2AK4	K M	K	147	W	3.2	138	150
2AK4	K M	K	167	W	1.3	163	175
2AK4	K N	K	154	E	1.8	152	162
2AK4	N P	P	137	E	1.2	135	141
2AK4	N P	P	140	H	1.9	135	141
2AK4	Q S	Q	66	I	2.4	57	85
2AK4	Q S	Q	74	Y	2.0	57	85
2AK4	Q S	Q	147	W	6.0	138	150
2AK4	Q T	Q	159	Y	1.6	152	162
2AK4	T U	U	137	E	1.3	135	141
2AK4	T U	U	140	H	1.6	135	141
2AKA	A B	A	762	I	1.0	750	765
2AKW	A B	A	107	E	1.5	102	117
2AKW	A B	A	232	H	2.1	230	245
2AKW	A B	A	235	G	117.6	230	245
2AKW	A B	B	344	R	2.0	340	350
2AKW	A B	B	410	Y	1.1	408	416

2AKW	A B	B	414	L	1.0	408	416
2AKW	A B	B	458	D	1.5	456	468
2AKW	A B	B	492	Y	2.4	490	506
2AL2	A B	A	184	R	1.5	179	201
2AL2	A B	A	188	E	2.4	179	201
2AL2	A B	A	191	H	1.3	179	201
2AL2	A B	A	404	E	2.2	404	420
2AL2	A B	A	406	L	1.2	404	420
2AL2	A B	A	410	N	2.5	404	420
2AL2	A B	A	413	L	1.0	404	420
2AL2	A B	A	414	R	1.1	404	420
2AL2	A B	A	417	E	1.5	404	420
2AL2	A B	B	184	R	1.0	179	201
2AL2	A B	B	188	E	1.3	179	201
2AL2	A B	B	191	H	1.6	179	201
2AL2	A B	B	404	E	2.8	404	420
2AL2	A B	B	406	L	1.2	404	420
2AL2	A B	B	410	N	2.2	404	420
2AL2	A B	B	414	R	3.0	404	420
2AL2	A B	B	417	E	1.8	404	420
2AP2	C Q	Q	2	V	1.0	2	13
2APO	A B	A	64	W	2.5	58	69
2APO	A B	A	217	D	1.5	215	228
2APO	A B	A	220	D	3.5	215	228
2APO	A B	A	224	F	1.3	215	228
2APO	A B	B	443	G	2.7	443	447
2APO	A B	B	446	R	2.6	443	447
2APO	A B	B	450	K	2.6	450	455
2AQ1	A B	B	23	N	1.3	21	29
2AQ1	A B	B	26	Y	1.2	21	29
2AQ1	A B	B	208	Q	1.4	208	215
2AQ1	C D	D	23	N	1.7	21	29
2AQ1	C D	D	208	Q	1.4	208	215
2AQ1	E F	F	23	N	1.9	21	29
2AQ1	E F	F	26	Y	1.2	21	29
2AQ1	G H	H	23	N	1.1	21	29
2AQ1	G H	H	26	Y	1.1	21	29
2AQ1	G H	H	208	Q	1.2	208	215
2ARJ	L H	L	124	Q	1.0	122	127
2ARP	A F	F	192	R	3.6	188	199
2ASQ	A B	A	46	K	1.2	44	56
2AST	A B	A	1101	F	2.7	1097	1111
2AST	A B	A	1104	I	1.5	1097	1111
2AST	A B	A	1127	I	1.3	1113	1128
2AST	A B	A	1135	I	1.4	1132	1136
2AST	A B	A	1153	V	1.0	1148	1157
2AST	A B	B	2108	I	2.0	2102	2111
2AST	A B	B	2127	W	1.5	2125	2132
2AST	A B	B	2128	Y	1.0	2125	2132
2AST	A B	B	2151	V	1.0	2149	2158
2AST	A B	B	2155	L	1.0	2149	2158
2AST	B C	C	3040	E	2.1	3040	3047
2AST	B C	C	3041	S	1.4	3040	3047
2AST	B C	C	3042	E	6.5	3040	3047
2AST	B C	C	3044	R	1.7	3040	3047
2AST	B C	C	3045	N	1.2	3040	3047
2AUH	A B	A	1039	R	1.1	1038	1053
2AUH	A B	A	1042	I	1.0	1038	1053
2AUH	A B	A	1219	L	1.0	1215	1225
2AUH	A B	B	403	G	17.2	392	408

2AUH	A B	B	406	W	1.3	392	408
2AUS	A B	A	65	W	1.9	59	70
2AUS	A B	A	218	H	2.3	217	230
2AUS	A B	A	226	F	3.1	217	230
2AUS	A B	A	229	E	1.5	217	230
2AUS	A B	A	235	Y	1.3	233	240
2AUS	A B	B	45	R	2.3	42	53
2AUS	A B	B	46	R	1.0	42	53
2AUS	A B	B	50	R	1.8	42	53
2AUS	C D	C	65	W	1.6	59	70
2AUS	C D	C	218	H	2.3	217	230
2AUS	C D	C	222	D	2.9	217	230
2AUS	C D	C	226	F	1.6	217	230
2AUS	C D	C	229	E	1.8	217	230
2AUS	C D	C	235	Y	1.4	233	240
2AUS	C D	D	42	G	2.7	42	54
2AUS	C D	D	49	K	1.0	42	54
2AUS	C D	D	53	L	1.2	42	54
2AVU	B E	B	34	F	2.8	29	37
2AVU	B E	B	87	L	2.1	85	106
2AVU	B E	B	90	I	1.8	85	106
2AVU	B E	B	93	G	6.8	85	106
2AVU	B E	B	94	I	2.6	85	106
2AVU	B E	B	98	T	1.2	85	106
2AVU	B E	E	71	V	2.1	67	86
2AVU	B E	E	82	F	3.4	67	86
2AVU	B E	E	97	K	1.4	91	106
2AVU	B E	E	101	L	1.3	91	106
2AVU	D F	D	34	F	2.5	29	37
2AVU	D F	D	87	L	1.5	85	105
2AVU	D F	D	90	I	1.4	85	105
2AVU	D F	D	91	H	1.1	85	105
2AVU	D F	D	93	G	3.3	85	105
2AVU	D F	D	94	I	2.4	85	105
2AVU	D F	D	101	L	1.1	85	105
2AVU	D F	F	71	V	1.0	68	87
2AVU	D F	F	82	F	3.8	68	87
2AVU	D F	F	101	L	1.2	90	106
2AXT	A B	A	253	G	7.5	249	260
2AXT	a c	a	5145	V	1.1	5143	5147
2AXT	a c	a	5284	W	1.3	5268	5293
2AXT	a c	a	5288	L	2.2	5268	5293
2AXT	a c	a	5292	T	1.1	5268	5293
2AXT	a c	c	5313	Q	1.3	5306	5323
2AXT	a c	c	5317	F	1.7	5306	5323
2AXT	a c	c	5435	F	1.9	5422	5449
2AXT	a c	c	5446	G	16.1	5422	5449
2AXT	A C	A	145	V	1.1	143	147
2AXT	A C	A	284	W	1.3	268	293
2AXT	A C	A	288	L	2.2	268	293
2AXT	A C	A	292	T	1.3	268	293
2AXT	A C	C	291	W	2.8	268	293
2AXT	A C	C	313	Q	1.8	306	323
2AXT	A C	C	317	F	1.8	306	323
2AXT	A C	C	435	F	2.0	422	449
2AXT	A C	C	446	G	29.3	422	449
2AXT	a d	a	5133	L	1.6	5131	5137
2AXT	a d	a	5143	I	1.5	5143	5147
2AXT	a d	a	5178	G	7.9	5176	5190
2AXT	a d	a	5180	F	1.4	5176	5190

2AXT	a d	a	5181	N	1.1	5176	5190
2AXT	a d	a	5205	V	1.1	5196	5221
2AXT	a d	a	5208	G	2.9	5196	5221
2AXT	a d	a	5212	C	17.4	5196	5221
2AXT	a d	a	5216	G	76.4	5196	5221
2AXT	a d	a	5254	Y	1.9	5249	5260
2AXT	a d	a	5258	L	2.0	5249	5260
2AXT	a d	a	5317	W	4.5	5317	5332
2AXT	a d	a	5327	G	169.4	5317	5332
2AXT	a d	a	5331	M	1.7	5317	5332
2AXT	a d	d	5132	I	1.2	5109	5136
2AXT	a d	d	5142	N	1.3	5142	5146
2AXT	a d	d	5180	R	1.5	5178	5190
2AXT	a d	d	5198	M	1.3	5195	5211
2AXT	a d	d	5214	H	1.9	5212	5220
2AXT	a d	d	5215	G	35.9	5212	5220
2AXT	a d	d	5251	R	2.0	5246	5255
2AXT	a d	d	5252	F	2.9	5246	5255
2AXT	a d	d	5265	R	2.7	5264	5289
2AXT	a d	d	5301	Q	1.6	5299	5308
2AXT	a d	d	5314	F	2.7	5314	5334
2AXT	a d	d	5321	L	1.2	5314	5334
2AXT	a d	d	5324	G	64.9	5314	5334
2AXT	a d	d	5328	W	2.0	5314	5334
2AXT	a i	a	5036	I	1.1	5032	5054
2AXT	a i	i	5015	F	1.1	5002	5025
2AXT	a i	i	5019	F	1.3	5002	5025
2AXT	a i	i	5022	G	476.6	5002	5025
2AXT	A I	A	18	C	1.1	13	22
2AXT	A I	A	19	N	3.9	13	22
2AXT	A I	A	36	I	1.1	32	54
2AXT	A I	A	135	Y	4.6	131	137
2AXT	A I	I	9	Y	1.0	2	25
2AXT	A I	I	19	F	1.9	2	25
2AXT	A I	I	22	G	519.2	2	25
2AXT	a v	a	5326	L	1.4	5317	5332
2AXT	b d	b	5257	W	4.9	5236	5258
2AXT	b d	b	5273	Y	1.3	5272	5277
2AXT	b d	b	5453	F	1.3	5447	5462
2AXT	b d	b	5464	F	1.2	5463	5474
2AXT	b d	d	5188	F	3.0	5178	5190
2AXT	b d	d	5326	R	1.3	5314	5334
2AXT	B D	B	257	W	5.3	236	258
2AXT	B D	B	453	F	1.4	447	462
2AXT	B D	B	460	L	1.3	447	462
2AXT	B D	B	463	F	1.1	463	474
2AXT	B D	B	464	F	1.2	463	474
2AXT	B D	B	467	I	1.0	463	474
2AXT	B D	D	188	F	2.9	178	190
2AXT	B D	D	280	W	1.7	264	289
2AXT	B D	D	284	I	1.0	264	289
2AXT	B D	D	288	G	1.3	264	289
2AXT	B D	D	326	R	1.0	314	334
2AXT	b h	b	5223	Q	1.2	5223	5229
2AXT	b h	b	5274	Q	3.1	5272	5277
2AXT	b h	h	5041	F	1.3	5028	5047
2AXT	B H	B	137	K	1.1	135	160
2AXT	B H	B	223	Q	1.2	223	229
2AXT	B H	B	274	Q	2.7	272	277
2AXT	B H	H	31	M	1.2	28	47

2AXT	B H	H	41	F	1.3	28	47
2AXT	b m	m	5025	L	1.1	5007	5031
2AXT	b T	b	5108	F	1.0	5093	5117
2AXT	b T	T	18	F	1.3	2	22
2AXT	B t	t	5018	F	1.2	5002	5022
2AXT	b u	u	5044	D	2.3	5042	5047
2AXT	B U	U	44	D	2.8	42	47
2AXT	c k	c	5059	L	1.1	5058	5075
2AXT	c k	c	5070	F	1.2	5058	5075
2AXT	c k	c	5112	F	2.0	5108	5121
2AXT	c k	k	5026	P	2.0	5019	5043
2AXT	C K	C	59	L	1.2	58	75
2AXT	C K	C	70	F	1.2	58	75
2AXT	C K	C	112	F	2.1	108	121
2AXT	C K	K	26	P	1.1	19	43
2AXT	c o	c	5377	L	1.1	5377	5382
2AXT	C O	C	377	L	1.2	377	382
2AXT	C V	V	129	K	1.0	128	133
2AXT	c z	z	5027	Y	2.5	5002	5029
2AXT	d e	d	5054	F	2.4	5042	5055
2AXT	d e	d	5103	R	1.6	5101	5107
2AXT	d e	e	5037	F	1.3	5025	5041
2AXT	d e	e	5044	Y	1.3	5042	5047
2AXT	d e	e	5073	K	1.0	5072	5083
2AXT	D E	D	54	F	2.4	36	55
2AXT	D E	D	103	R	1.5	101	107
2AXT	D E	E	37	F	1.3	25	41
2AXT	D E	E	44	Y	1.4	42	47
2AXT	D E	E	73	K	1.2	72	83
2AXT	D E	E	76	V	1.9	72	83
2AXT	d f	d	5054	F	1.0	5042	5055
2AXT	d f	f	5033	F	1.0	5018	5041
2AXT	d f	f	5040	M	1.0	5018	5041
2AXT	D F	D	54	F	1.0	36	55
2AXT	D F	F	33	F	1.0	18	41
2AXT	D F	F	40	M	1.0	18	41
2AXT	d h	d	5015	F	1.0	5014	5023
2AXT	D H	D	15	F	1.0	14	23
2AXT	d l	d	5195	P	1.0	5195	5211
2AXT	d l	l	5030	L	1.2	5014	5034
2AXT	d l	l	5031	F	1.4	5014	5034
2AXT	D L	D	195	P	1.0	195	211
2AXT	D L	L	30	L	1.3	14	34
2AXT	D L	L	31	F	1.5	14	34
2AXT	d m	d	5303	I	1.2	5299	5308
2AXT	D M	D	301	Q	1.6	299	308
2AXT	D M	D	303	I	1.1	299	308
2AXT	d o	d	5320	L	1.2	5314	5334
2AXT	D O	D	320	L	1.2	314	334
2AXT	d v	d	5328	W	1.0	5314	5334
2AXT	D V	D	328	W	1.0	314	334
2AXT	e f	e	5030	L	1.7	5025	5041
2AXT	e f	e	5034	G	60.2	5025	5041
2AXT	e f	e	5035	W	3.1	5025	5041
2AXT	e f	f	5031	I	1.4	5018	5041
2AXT	e f	f	5032	F	2.1	5018	5041
2AXT	e f	f	5035	G	87.9	5018	5041
2AXT	E F	E	30	L	1.7	25	41
2AXT	E F	E	31	F	1.2	25	41
2AXT	E F	E	34	G	60.1	25	41

2AXT	E F	E	35	W	3.2	25	41
2AXT	E F	F	31	I	1.3	18	41
2AXT	E F	F	32	F	2.0	18	41
2AXT	E F	F	35	G	89.9	18	41
2AXT	f j	j	5028	F	1.7	5012	5033
2AXT	F J	J	28	F	1.4	12	33
2AXT	k z	z	5054	V	3.6	5034	5060
2AXT	l m	l	5017	L	1.5	5014	5034
2AXT	l m	l	5020	G	16.2	5014	5034
2AXT	l m	l	5024	I	1.2	5014	5034
2AXT	l m	m	5007	G	49.0	5007	5031
2AXT	l m	m	5014	F	2.0	5007	5031
2AXT	l m	m	5026	Y	1.6	5007	5031
2AXT	L M	L	17	L	1.5	14	34
2AXT	L M	L	20	G	352.3	14	34
2AXT	L M	L	24	I	1.2	14	34
2AXT	L M	M	7	G	55.0	7	31
2AXT	L M	M	14	F	2.0	7	31
2AXT	L M	M	26	Y	1.6	7	31
2AXT	l t	l	5018	Y	3.4	5014	5034
2AXT	l t	l	5025	L	1.7	5014	5034
2AXT	l t	l	5029	L	1.4	5014	5034
2AXT	l t	t	5006	Y	1.3	5002	5022
2AXT	l t	t	5009	I	2.2	5002	5022
2AXT	l t	t	5013	I	1.5	5002	5022
2AXT	l t	t	5016	L	1.6	5002	5022
2AXT	L T	L	18	Y	3.7	14	34
2AXT	L T	L	25	L	1.7	14	34
2AXT	L T	L	29	L	1.3	14	34
2AXT	L T	T	6	Y	1.2	2	22
2AXT	L T	T	9	I	2.2	2	22
2AXT	L T	T	13	I	1.5	2	22
2AXT	L T	T	16	L	1.7	2	22
2AYO	A B	A	204	I	2.2	199	214
2AYO	A B	A	208	R	1.2	199	214
2AZE	A B	A	219	K	2.4	199	246
2AZE	A B	A	223	L	1.9	199	246
2AZE	A B	A	236	L	1.3	199	246
2AZE	A B	A	237	V	1.8	199	246
2AZE	A B	A	240	N	1.2	199	246
2AZE	A B	A	299	V	1.2	296	304
2AZE	A B	A	333	Y	1.0	331	339
2AZE	A B	B	203	L	2.5	202	236
2AZE	A B	B	210	L	1.5	202	236
2AZE	A B	B	217	E	1.5	202	236
2AZE	A B	B	221	D	1.6	202	236
2AZE	A B	B	223	L	1.0	202	236
2AZE	A B	B	224	M	1.6	202	236
2AZE	A B	B	231	L	1.6	202	236
2AZE	A B	B	251	L	1.7	248	254
2AZE	A C	A	222	Q	1.0	199	246
2AZE	A C	C	845	F	3.1	841	852
2AZE	B C	C	851	M	1.2	841	852
2B4C	G C	G	371	I	1.7	369	373
2B4J	A C	C	360	K	1.4	347	363
2B4J	B D	D	360	K	1.1	347	363
2B59	A B	A	114	I	1.5	114	121
2B59	A B	B	144	M	1.2	144	153
2B59	A B	B	148	M	1.8	144	153
2B59	A B	B	151	H	1.0	144	153

2B59	A B	B	152	K	2.2	144	153
2B5I	A B	A	12	L	1.0	7	29
2B5I	A B	A	13	Q	1.3	7	29
2B5I	A B	A	15	E	1.3	7	29
2B5I	A B	A	16	H	3.0	7	29
2B5I	A B	A	19	L	2.4	7	29
2B5I	A B	A	20	D	1.8	7	29
2B5I	A B	A	84	D	1.7	82	98
2B5I	A B	A	88	N	1.2	82	98
2B5I	A B	A	95	E	1.7	82	98
2B5I	A C	A	126	Q	2.0	114	133
2B5I	A C	A	130	S	5.8	114	133
2B5I	A D	A	38	R	1.9	35	42
2B5I	A D	A	65	P	2.1	63	72
2B5L	A C	C	24	V	2.1	23	33
2B5L	A C	C	27	F	2.6	23	33
2B5L	A C	C	127	Y	1.7	127	139
2B5L	B D	D	24	V	1.0	24	34
2B5L	B D	D	27	F	2.2	24	34
2B5L	B D	D	127	Y	1.6	127	138
2B5T	A B	A	1	F	1.8	1	1
2B5T	A B	A	14	E	1.9	14	14
2B5T	A B	A	14	E	1.6	14	14
2B5T	A B	A	14	L	1.1	14	14
2B5T	A B	B	242	I	1.3	235	244
2B5T	A I	A	1	R	1.1	1	1
2B5T	C D	C	14	E	1.3	14	14
2B5T	C D	C	14	E	1.0	14	14
2B5T	C D	C	14	L	1.3	14	14
2B7Y	C D	D	194	L	1.5	194	198
2B87	A B	A	10	G	500.0	4	18
2B87	A B	A	11	W	1.2	4	18
2B87	A B	A	14	W	3.5	4	18
2B87	A B	A	17	F	2.3	4	18
2B87	A B	A	34	L	1.2	24	37
2B87	A B	A	35	R	2.6	24	37
2B87	A B	B	9	R	1.5	6	19
2B87	A B	B	10	V	1.3	6	19
2B87	A B	B	14	G	185.7	6	19
2B87	A B	B	24	S	1.5	24	37
2B8K	A B	A	370	I	1.1	368	374
2B8K	A B	A	497	T	1.4	495	506
2B8K	A B	A	658	L	1.3	639	660
2B8K	A B	A	746	M	1.2	742	750
2B8K	A B	A	761	M	1.3	755	764
2B8K	A B	A	810	P	1.5	810	828
2B8K	A B	A	813	F	2.1	810	828
2B8K	A B	A	814	F	2.6	810	828
2B8K	A B	A	820	G	5.5	810	828
2B8K	A B	A	824	L	1.0	810	828
2B8K	A B	A	825	I	1.4	810	828
2B8K	A B	A	1410	F	1.1	1406	1411
2B8K	A B	B	1023	V	3.7	1023	1035
2B8K	A B	B	1134	E	5.1	1132	1142
2B8K	A B	B	1141	H	1.1	1132	1142
2B8K	A B	B	1146	F	1.8	1144	1152
2B8K	A B	B	1147	L	4.5	1144	1152
2B8K	A B	B	1148	K	1.4	1144	1152
2B8K	A B	B	1150	R	2.5	1144	1152
2B8K	A B	B	1203	L	1.8	1198	1210

2B8K	A B	B	1207	L	1.0	1198	1210
2B8K	A B	B	1208	M	1.3	1198	1210
2B8K	A E	A	942	F	1.1	935	944
2B8K	A E	A	1017	L	7.5	1017	1026
2B8K	A E	E	183	P	2.2	183	189
2B8K	A E	E	184	V	1.6	183	189
2B8K	A F	A	504	L	1.8	495	506
2B8K	A F	F	88	Y	2.9	87	103
2B8K	A F	F	95	G	20.6	87	103
2B8K	A G	G	22	M	1.3	22	33
2B8K	B C	C	27	L	1.6	27	40
2B8K	B C	C	38	I	1.0	27	40
2B8K	B C	C	62	F	1.0	60	70
2B8K	B C	C	69	L	1.0	60	70
2B8K	B I	B	308	W	1.7	308	321
2B8K	B J	B	190	Y	2.4	186	191
2B8K	B J	J	33	G	80.1	33	40
2B8K	B J	J	59	K	1.3	56	62
2B8K	C J	J	57	I	1.0	56	62
2B8K	C J	J	61	L	1.9	56	62
2B8K	C L	C	68	G	9.4	60	70
2B8K	D G	D	179	Q	3.9	178	182
2B9I	A C	A	113	H	2.3	111	131
2B9M	C E	C	135	K	1.1	130	144
2B9M	D E	D	53	D	1.2	53	69
2B9S	A B	A	270	F	3.3	260	279
2B9S	A B	A	271	E	1.2	260	279
2B9S	A B	A	415	S	1.0	406	424
2B9S	A B	A	418	L	1.0	406	424
2B9S	A B	A	422	F	3.6	406	424
2B9S	A B	A	437	L	1.4	433	452
2B9S	A B	A	440	F	1.9	433	452
2B9S	A B	A	445	T	1.5	433	452
2B9S	A B	A	447	V	1.5	433	452
2B9S	A B	A	448	A	1.2	433	452
2B9S	A B	A	449	I	1.6	433	452
2B9S	A B	B	215	L	1.4	215	223
2B9S	A B	B	218	S	1.4	215	223
2B9S	A B	B	221	N	1.0	215	223
2B9S	A B	B	222	Y	1.4	215	223
2B9S	A B	B	226	R	2.1	225	234
2B9S	A B	B	227	I	1.6	225	234
2B9S	A B	B	228	I	1.0	225	234
2B9S	A B	B	231	W	3.4	225	234
2B9S	A B	B	250	K	1.2	245	251
2BA0	A D	A	149	R	1.4	147	152
2BA0	A D	D	149	V	1.1	136	151
2BA0	A D	D	230	Y	1.0	212	241
2BA0	A D	D	234	R	2.7	212	241
2BA0	A D	D	238	L	1.1	212	241
2BA0	A D	D	247	E	1.7	242	252
2BA0	A D	D	248	M	1.3	242	252
2BA0	A D	D	251	I	1.7	242	252
2BA0	B E	B	149	R	1.1	147	151
2BA0	B E	E	234	R	1.9	212	241
2BA0	B E	E	238	L	1.0	212	241
2BA0	B E	E	247	E	1.7	242	252
2BA0	B E	E	248	M	1.3	242	252
2BA0	B E	E	251	I	1.9	242	252
2BA0	B G	B	187	S	1.6	183	199

2BA0	B G	B	194	Y	2.5	183	199
2BA0	B G	B	216	R	2.2	205	220
2BA0	B G	G	9	I	1.5	7	20
2BA0	B G	G	16	S	1.9	7	20
2BA0	C F	F	149	V	1.1	136	151
2BA0	C F	F	234	R	2.1	212	241
2BA0	C F	F	238	L	1.1	212	241
2BA0	C F	F	251	I	1.6	242	252
2BA0	C H	H	6	L	1.3	4	20
2BA0	C H	H	9	I	1.6	4	20
2BA0	C H	H	17	K	1.1	4	20
2BA0	D G	D	215	V	1.3	212	241
2BA0	D G	D	223	K	1.1	212	241
2BA0	D G	G	235	E	1.4	235	256
2BA0	D G	G	242	L	1.3	235	256
2BA0	E H	E	97	R	1.1	96	111
2BA0	E H	E	103	K	1.9	96	111
2BA0	E H	E	223	K	1.3	212	241
2BA0	E H	H	100	E	1.3	100	116
2BA0	E H	H	103	I	1.7	100	116
2BA0	E H	H	104	E	2.2	100	116
2BA0	E H	H	235	E	1.6	235	256
2BA0	E H	H	242	L	1.4	235	256
2BA0	F I	F	103	K	2.7	96	111
2BA0	F I	F	215	V	1.2	212	241
2BA0	F I	I	100	E	1.4	100	116
2BA0	F I	I	103	I	1.2	100	116
2BA0	F I	I	104	E	1.8	100	116
2BA0	F I	I	111	R	1.0	100	116
2BA0	F I	I	235	E	1.1	235	255
2BA0	F I	I	242	L	2.1	235	255
2BA1	A D	D	230	Y	1.8	212	246
2BA1	A I	I	5	I	1.4	2	20
2BA1	A I	I	9	I	1.0	2	20
2BA1	B E	E	241	Y	1.4	212	246
2BA1	B G	G	5	I	1.3	2	20
2BA1	B G	G	8	D	1.0	2	20
2BA1	B G	G	9	I	1.1	2	20
2BA1	B G	G	13	Y	1.0	2	20
2BA1	C H	H	5	I	1.6	2	20
2BA1	C H	H	11	R	1.2	2	20
2BA1	D G	D	97	R	1.8	96	111
2BA1	D G	D	100	E	2.4	96	111
2BA1	D G	D	103	K	2.8	96	111
2BA1	D G	D	104	V	1.4	96	111
2BA1	D G	D	212	R	1.7	212	246
2BA1	D G	D	215	V	9.5	212	246
2BA1	D G	D	216	K	1.2	212	246
2BA1	D G	G	100	E	1.6	99	117
2BA1	D G	G	103	I	1.7	99	117
2BA1	D G	G	104	E	1.1	99	117
2BA1	D G	G	107	R	2.0	99	117
2BA1	D G	G	111	R	1.4	99	117
2BA1	D G	G	116	S	1.0	99	117
2BA1	D G	G	242	L	1.8	235	255
2BA1	E H	E	100	E	1.5	96	113
2BA1	E H	E	103	K	1.7	96	113
2BA1	E H	E	212	R	1.1	212	246
2BA1	E H	E	215	V	1.4	212	246
2BA1	E H	E	216	K	1.4	212	246

2BA1	E H	H	103	I	1.8	99	116
2BA1	E H	H	104	E	1.8	99	116
2BA1	E H	H	111	R	1.2	99	116
2BA1	E H	H	242	L	2.3	235	254
2BA1	F I	F	100	E	2.3	96	113
2BA1	F I	F	103	K	2.6	96	113
2BA1	F I	F	212	R	3.0	212	246
2BA1	F I	F	215	V	1.4	212	246
2BA1	F I	F	216	K	1.1	212	246
2BA1	F I	F	223	K	1.2	212	246
2BA1	F I	I	103	I	1.2	99	117
2BA1	F I	I	107	R	1.1	99	117
2BA1	F I	I	111	R	2.0	99	117
2BA1	F I	I	235	E	1.5	235	258
2BA1	F I	I	242	L	1.6	235	258
2BAP	B D	B	259	I	1.4	244	260
2BAP	B D	D	1185	L	1.1	1183	1188
2BBA	A P	P	259	P	2.2	259	264
2BBA	A P	P	260	I	8.4	259	264
2BBA	A P	P	262	R	1.1	259	264
2BBM	A B	A	36	M	1.1	29	38
2BBM	A B	A	71	M	1.1	65	74
2BBM	A B	A	92	F	1.6	82	93
2BBM	A B	A	105	L	1.1	102	113
2BBM	A B	A	125	I	1.0	118	129
2BBM	A B	A	127	E	1.2	118	129
2BBM	A B	A	144	M	1.5	138	146
2BBM	A B	A	145	M	1.8	138	146
2BBM	A B	B	6	K	2.0	5	21
2BBM	A B	B	8	F	2.3	5	21
2BBM	A B	B	9	I	1.2	5	21
2BBM	A B	B	11	V	1.1	5	21
2BBM	A B	B	16	R	1.1	5	21
2BBM	A B	B	17	F	1.9	5	21
2BBU	A B	A	24	G	1.6	24	35
2BBV	A D	D	367	W	2.8	366	377
2BBV	A D	D	370	V	1.4	366	377
2BBV	A D	D	373	I	1.4	366	377
2BBV	A D	D	374	I	1.2	366	377
2BBV	B E	B	350	V	1.4	341	354
2BBV	B E	E	367	W	3.5	366	377
2BBV	B E	E	370	V	1.4	366	377
2BBV	B E	E	373	I	1.5	366	377
2BBV	B E	E	374	I	3.2	366	377
2BBV	C F	C	350	V	1.3	341	353
2BBV	C F	F	367	W	3.2	366	379
2BBV	C F	F	370	V	1.3	366	379
2BBV	C F	F	373	I	2.1	366	379
2BBV	C F	F	374	I	1.2	366	379
2BBV	C F	F	378	L	1.2	366	379
2BC4	A B	A	74	F	2.1	69	86
2BC4	A B	A	75	D	1.6	69	86
2BC4	A B	A	78	F	2.5	69	86
2BC4	A B	A	83	I	1.8	69	86
2BC4	A B	B	58	L	1.1	52	64
2BC4	A B	B	62	L	1.4	52	64
2BC4	A B	B	71	R	1.7	66	74
2BC4	A B	B	82	H	1.5	75	93
2BC4	A B	B	86	F	1.8	75	93
2BC4	A B	B	87	W	2.1	75	93

2BC4	A B	B	90	L	2.1	75	93
2BC4	C D	C	62	W	2.2	60	65
2BC4	C D	C	74	F	2.0	67	86
2BC4	C D	C	75	D	2.4	67	86
2BC4	C D	C	78	F	3.4	67	86
2BC4	C D	C	81	W	1.9	67	86
2BC4	C D	C	82	M	1.4	67	86
2BC4	C D	C	83	I	1.2	67	86
2BC4	C D	D	54	L	1.5	52	65
2BC4	C D	D	58	L	1.1	52	65
2BC4	C D	D	61	H	1.8	52	65
2BC4	C D	D	62	L	1.0	52	65
2BC4	C D	D	71	R	2.5	66	74
2BC4	C D	D	86	F	1.7	75	93
2BC4	C D	D	87	W	2.1	75	93
2BC4	C D	D	90	L	2.1	75	93
2BCJ	A Q	A	106	R	1.3	98	119
2BCJ	A Q	A	109	F	1.9	98	119
2BCJ	A Q	A	114	M	1.4	98	119
2BCJ	A Q	A	115	K	1.3	98	119
2BCJ	A Q	A	118	L	2.8	98	119
2BCJ	A Q	Q	213	R	1.0	210	218
2BCJ	A Q	Q	216	W	1.0	210	218
2BCJ	A Q	Q	217	I	1.7	210	218
2BCJ	B G	B	3	E	1.0	3	12
2BCJ	B G	B	4	L	2.7	3	12
2BCJ	B G	B	7	L	1.7	3	12
2BCJ	B G	B	14	L	2.3	13	26
2BCJ	B G	B	22	R	1.2	13	26
2BCJ	B G	G	9	I	1.8	5	24
2BCJ	B G	G	16	V	2.9	5	24
2BCJ	B G	G	19	L	1.3	5	24
2BCJ	B G	G	22	E	1.3	5	24
2BCJ	B G	G	37	L	1.6	30	44
2BCJ	B G	G	40	Y	2.5	30	44
2BCX	A B	A	14	E	1.3	6	18
2BCX	A B	A	32	L	1.3	29	39
2BCX	A B	A	51	M	1.2	45	56
2BCX	A B	A	71	M	2.0	65	77
2BCX	A B	A	92	F	1.2	84	93
2BCX	A B	A	124	M	1.5	118	129
2BCX	A B	B	3623	L	2.3	3617	3639
2BCX	A B	B	3626	K	1.0	3617	3639
2BCX	A B	B	3628	R	2.7	3617	3639
2BCX	A B	B	3629	R	1.6	3617	3639
2BCX	A B	B	3632	V	1.5	3617	3639
2BCX	A B	B	3633	V	1.8	3617	3639
2BCX	A B	B	3636	F	4.2	3617	3639
2BDN	A L	A	69	K	8.4	58	70
2BE6	A D	A	11	E	1.4	6	20
2BE6	A D	A	12	F	1.4	6	20
2BE6	A D	A	19	F	2.1	6	20
2BE6	A D	A	92	F	2.8	82	93
2BE6	A D	A	120	E	1.0	118	129
2BE6	A D	A	123	E	1.6	118	129
2BE6	A D	A	145	M	1.9	138	146
2BE6	A D	D	1614	T	1.3	1613	1637
2BE6	A D	D	1618	F	4.7	1613	1637
2BE6	A D	D	1622	F	2.2	1613	1637
2BE6	A D	D	1628	F	2.6	1613	1637

2BE6	A D	D	1631	F	2.0	1613	1637
2BE6	A D	D	1635	K	2.0	1613	1637
2BE6	B E	B	19	F	1.8	6	20
2BE6	B E	B	55	V	1.4	45	56
2BE6	B E	B	68	F	1.5	65	78
2BE6	B E	B	71	M	1.0	65	78
2BE6	B E	B	72	M	1.2	65	78
2BE6	B E	B	75	K	1.1	65	78
2BE6	B E	E	1614	T	1.3	1613	1625
2BE6	B E	E	1617	K	1.5	1613	1625
2BE6	B E	E	1618	F	4.5	1613	1625
2BE6	B E	E	1619	Y	1.6	1613	1625
2BE6	B E	E	1622	F	2.6	1613	1625
2BE6	B E	E	1623	L	1.0	1613	1625
2BE6	B E	E	1624	I	2.4	1613	1625
2BE6	C F	C	11	E	2.4	6	20
2BE6	C F	C	14	E	1.4	6	20
2BE6	C F	C	19	F	2.6	6	20
2BE6	C F	C	68	F	1.1	65	75
2BE6	C F	C	83	E	1.0	82	93
2BE6	C F	C	84	E	1.0	82	93
2BE6	C F	C	87	E	1.4	82	93
2BE6	C F	C	92	F	2.3	82	93
2BE6	C F	C	120	E	2.4	118	129
2BE6	C F	C	123	E	1.6	118	129
2BE6	C F	C	124	M	1.4	118	129
2BE6	C F	F	1618	F	5.0	1618	1636
2BE6	C F	F	1622	F	2.2	1618	1636
2BE6	C F	F	1623	L	1.6	1618	1636
2BE6	C F	F	1624	I	3.0	1618	1636
2BE6	C F	F	1626	E	1.5	1618	1636
2BE6	C F	F	1627	Y	3.1	1618	1636
2BE6	C F	F	1628	F	4.2	1618	1636
2BE6	C F	F	1629	R	3.3	1618	1636
2BE6	C F	F	1631	F	4.7	1618	1636
2BE6	C F	F	1633	K	1.1	1618	1636
2BE6	C F	F	1634	R	1.7	1618	1636
2BE6	C F	F	1635	K	2.0	1618	1636
2BE7	A D	A	115	L	1.5	112	118
2BE7	B E	B	115	L	1.0	112	118
2BE7	C F	C	115	L	1.2	112	118
2BE9	A B	A	109	R	1.0	107	115
2BE9	A B	A	110	F	3.4	107	115
2BEC	A B	A	34	R	1.9	25	39
2BEC	A B	A	66	I	1.4	63	70
2BEC	A B	A	122	L	2.6	112	124
2BEC	A B	B	531	L	1.9	518	539
2BEC	A B	B	533	G	30.5	518	539
2BEC	A B	B	534	I	1.5	518	539
2BEC	A B	B	537	I	1.2	518	539
2BEQ	A D	A	929	K	1.2	915	949
2BEQ	A D	A	930	L	1.2	915	949
2BEQ	A D	A	933	V	1.4	915	949
2BEQ	A D	D	1164	E	2.1	1162	1174
2BEQ	A D	D	1171	V	1.7	1162	1174
2BEQ	A F	A	920	L	1.3	915	949
2BEQ	A F	A	942	N	1.2	915	949
2BEQ	A F	A	945	V	1.2	915	949
2BEQ	A F	F	1165	I	1.8	1162	1174
2BEQ	A F	F	1168	L	1.2	1162	1174

2BEQ	B D	B	917	Q	1.0	915	949
2BEQ	B D	B	920	L	2.1	915	949
2BEQ	B D	B	942	N	1.2	915	949
2BEQ	B D	B	945	V	1.3	915	949
2BEQ	B E	B	918	E	1.2	915	949
2BEQ	B E	B	922	T	1.0	915	949
2BEQ	B E	B	929	K	1.7	915	949
2BEQ	B E	B	930	L	1.3	915	949
2BEQ	B E	B	933	V	1.1	915	949
2BEQ	B E	B	937	N	1.4	915	949
2BEQ	B E	B	944	L	3.0	915	949
2BEQ	B E	E	1164	E	2.3	1162	1174
2BEQ	B E	E	1167	R	1.3	1162	1174
2BEQ	B E	E	1168	L	1.2	1162	1174
2BEQ	B E	E	1171	V	1.1	1162	1174
2BEQ	C E	C	920	L	1.4	915	949
2BEQ	C E	C	935	N	1.3	915	949
2BEQ	C E	C	942	N	1.5	915	949
2BEQ	C E	C	945	V	1.5	915	949
2BEQ	C E	E	1165	I	1.1	1162	1174
2BEQ	C E	E	1168	L	1.3	1162	1174
2BEQ	C E	E	1175	L	1.1	1175	1179
2BEQ	C F	C	918	E	1.1	915	949
2BEQ	C F	C	929	K	1.6	915	949
2BEQ	C F	C	930	L	1.1	915	949
2BEQ	C F	C	933	V	1.1	915	949
2BEQ	C F	C	937	N	1.1	915	949
2BEQ	C F	F	1164	E	2.4	1162	1174
2BEQ	C F	F	1167	R	1.4	1162	1174
2BEQ	C F	F	1168	L	1.2	1162	1174
2BEX	A C	A	443	E	1.8	440	453
2BEX	A C	C	7	W	9.4	7	15
2BEX	A C	C	10	W	3.0	7	15
2BEX	A C	C	25	N	1.0	23	34
2BEX	B D	D	7	W	1.2	7	15
2BEX	B D	D	10	W	1.5	7	15
2BEX	B D	D	14	Q	1.6	7	15
2BEZ	C F	C	908	Q	1.4	899	972
2BEZ	C F	C	929	K	1.8	899	972
2BEZ	C F	C	930	L	1.4	899	972
2BEZ	C F	C	933	V	1.4	899	972
2BEZ	C F	C	937	N	1.0	899	972
2BEZ	C F	F	1164	E	2.3	1162	1175
2BEZ	C F	F	1167	R	1.2	1162	1175
2BFZ	A B	B	289	L	1.2	280	291
2BG9	A B	A	235	L	6.4	212	239
2BG9	A B	A	256	F	1.5	243	271
2BG9	A B	B	264	L	1.0	250	276
2BG9	A B	B	305	H	4.5	283	307
2BG9	A B	B	415	L	19.1	404	430
2BG9	D E	D	228	L	1.2	213	239
2BG9	D E	D	231	L	1.2	213	239
2BG9	D E	D	234	Y	4.5	213	239
2BG9	D E	D	238	D	1.8	213	239
2BG9	D E	E	266	F	1.7	250	272
2BG9	D E	E	304	L	1.3	283	307
2BG9	D E	E	415	C	11.3	414	441
2BGN	B E	E	84	Y	2.7	76	93
2BGN	B E	E	132	L	2.1	126	144
2BGN	B E	E	135	Q	2.4	126	144

2BGN	B E	E	136	G	1.7	126	144
2BGN	B E	E	139	E	2.3	126	144
2BGN	C G	G	80	K	1.1	77	93
2BGN	C G	G	84	Y	2.9	77	93
2BGN	C G	G	139	E	1.6	126	144
2BGN	C G	G	142	R	1.7	126	144
2BGN	D H	H	84	Y	3.0	76	93
2BH1	A X	X	21	F	2.3	19	25
2BH1	A X	X	51	L	1.7	48	59
2BH1	A X	X	53	E	1.7	48	59
2BH1	A X	X	56	R	1.2	48	59
2BH1	B Y	B	177	L	1.1	175	180
2BH1	B Y	Y	21	F	2.3	19	25
2BH1	B Y	Y	48	M	2.0	48	59
2BH1	B Y	Y	51	L	2.0	48	59
2BH1	B Y	Y	53	E	3.7	48	59
2BH1	B Y	Y	56	R	2.9	48	59
2BKI	A D	D	109	M	3.6	106	112
2BKR	A B	A	58	V	1.2	56	64
2BKR	A B	A	61	F	1.6	56	64
2BKR	A B	A	70	E	2.0	68	75
2BKR	A B	A	74	F	3.5	68	75
2BKY	A X	A	46	I	1.4	44	57
2BKY	A X	A	50	V	1.5	44	57
2BKY	A X	A	54	E	1.3	44	57
2BKY	A X	X	43	I	1.6	43	58
2BKY	A X	X	47	V	1.0	43	58
2BKY	B Y	B	46	I	1.4	44	61
2BKY	B Y	B	50	V	1.4	44	61
2BKY	B Y	Y	43	I	1.4	43	58
2BKY	B Y	Y	47	V	1.0	43	58
2BKY	B Y	Y	50	Y	1.0	43	58
2BL0	A B	A	783	I	1.0	779	823
2BL0	A B	A	784	V	1.1	779	823
2BL0	A B	A	785	K	1.0	779	823
2BL0	A B	A	786	V	1.1	779	823
2BL0	A B	A	787	V	1.9	779	823
2BL0	A B	A	788	Q	1.9	779	823
2BL0	A B	A	792	R	2.4	779	823
2BL0	A B	A	793	G	138.2	779	823
2BL0	A B	A	794	W	4.6	779	823
2BL0	A B	A	795	V	1.2	779	823
2BL0	A B	A	796	E	1.8	779	823
2BL0	A B	A	797	R	3.4	779	823
2BL0	A B	A	798	K	1.0	779	823
2BL0	A B	A	800	F	2.4	779	823
2BL0	A B	B	9	E	1.8	4	15
2BL0	A B	B	13	I	2.3	4	15
2BL0	A B	B	32	R	1.7	27	34
2BL0	A B	B	78	M	1.0	75	85
2BL0	A B	B	113	E	1.3	111	120
2BL0	A B	B	117	L	1.7	111	120
2BL0	A B	B	134	F	1.8	131	141
2BL0	A B	B	137	M	1.3	131	141
2BL0	A B	B	138	L	2.1	131	141
2BL0	A C	A	811	R	1.0	779	823
2BL0	A C	A	812	I	1.8	779	823
2BL0	A C	A	813	I	3.7	779	823
2BL0	A C	A	816	N	1.1	779	823
2BL0	A C	A	817	I	2.6	779	823

2BL0	A C	A	818	R	1.2	779	823
2BL0	A C	A	820	Y	1.3	779	823
2BL0	A C	A	821	L	1.3	779	823
2BL0	A C	A	828	W	5.0	827	838
2BL0	A C	A	829	W	1.3	827	838
2BL0	A C	A	831	L	3.2	827	838
2BL0	A C	A	832	F	2.5	827	838
2BL0	A C	C	26	L	1.3	15	27
2BL0	A C	C	40	L	1.1	37	47
2BL0	A C	C	59	M	2.0	53	64
2BL0	A C	C	62	E	1.1	53	64
2BL0	A C	C	79	M	1.5	73	84
2BL0	A C	C	80	M	1.7	73	84
2BL0	A C	C	83	R	1.0	73	84
2BL0	A C	C	93	L	1.1	90	100
2BL0	A C	C	97	F	1.5	90	100
2BL0	A C	C	117	L	1.9	110	120
2BL0	A C	C	148	F	2.7	146	153
2BL0	A C	C	152	M	1.1	146	153
2BMO	A B	A	262	D	1.2	261	282
2BMO	A B	A	344	D	2.2	336	350
2BMO	A B	A	348	R	2.5	336	350
2BMO	A B	A	355	F	1.6	355	373
2BMO	A B	A	362	E	1.5	355	373
2BMO	A B	B	94	Q	1.6	92	104
2BMO	A B	B	97	V	1.3	92	104
2BMO	A B	B	98	R	2.5	92	104
2BMO	A B	B	101	H	1.7	92	104
2BNQ	A D	A	65	R	1.2	57	85
2BNQ	A E	A	65	R	1.7	57	85
2BNQ	A E	A	72	Q	3.3	57	85
2BNQ	A E	A	73	T	1.6	57	85
2BNQ	D E	E	132	E	1.6	130	137
2BO9	C D	C	73	W	1.4	73	89
2BO9	C D	D	8	Y	2.1	8	25
2BOV	A B	A	140	E	1.1	139	149
2BOV	A B	A	147	E	1.7	139	149
2BOV	A B	B	1056	K	1.0	1052	1067
2BOV	A B	B	1081	K	1.4	1070	1082
2BP7	A D	A	214	G	10.7	213	218
2BP7	A D	A	404	Q	1.3	399	407
2BP7	A D	D	322	Y	1.1	319	323
2BP7	A F	F	236	Q	1.4	232	243
2BP7	C B	C	404	Q	1.6	399	407
2BR2	E F	E	108	I	2.2	106	122
2BR2	E F	E	109	E	2.8	106	122
2BR2	E F	E	112	R	3.9	106	122
2BR2	E F	E	116	R	1.7	106	122
2BR2	E F	E	120	D	2.3	106	122
2BR2	E F	E	248	L	2.3	248	273
2BR2	E F	E	250	D	1.4	248	273
2BR2	E F	E	251	I	2.4	248	273
2BR2	E F	F	98	R	1.2	98	115
2BR2	E F	F	99	R	2.1	98	115
2BR2	E F	F	101	I	1.2	98	115
2BR2	E F	F	102	E	4.3	98	115
2BR2	E F	F	104	S	1.7	98	115
2BR2	E F	F	105	K	2.1	98	115
2BR2	E F	F	106	V	1.0	98	115
2BR2	E F	F	109	E	1.4	98	115

2BR2	E F	F	214	F	2.5	211	239
2BR2	E F	F	218	F	1.2	211	239
2BR2	M N	M	108	I	2.1	106	122
2BR2	M N	M	109	E	1.7	106	122
2BR2	M N	M	248	L	1.8	248	273
2BR2	M N	M	251	I	2.4	248	273
2BR2	M N	N	101	I	1.1	98	115
2BR2	M N	N	102	E	1.0	98	115
2BR2	M N	N	105	K	1.6	98	115
2BR2	M N	N	109	E	1.2	98	115
2BR2	M N	N	211	P	1.0	211	239
2BR2	M N	N	214	F	2.5	211	239
2BR2	M N	N	218	F	1.0	211	239
2BR2	M X	M	14	I	1.2	13	25
2BR2	M X	X	233	R	1.4	211	239
2BR2	O P	O	108	I	1.5	106	122
2BR2	O P	O	109	E	2.2	106	122
2BR2	O P	O	112	R	1.7	106	122
2BR2	O P	O	113	V	1.3	106	122
2BR2	O P	O	116	R	3.0	106	122
2BR2	O P	O	120	D	1.1	106	122
2BR2	O P	O	248	L	1.5	248	273
2BR2	O P	O	250	D	1.6	248	273
2BR2	O P	O	251	I	2.1	248	273
2BR2	O P	P	102	E	2.7	98	115
2BR2	O P	P	105	K	1.6	98	115
2BR2	O P	P	106	V	1.2	98	115
2BR2	O P	P	112	E	4.3	98	115
2BR2	O P	P	214	F	2.0	211	238
2BR2	Q B	Q	14	I	1.2	13	25
2BR2	Q B	B	233	R	1.3	211	238
2BR2	Q R	Q	108	I	1.8	106	122
2BR2	Q R	Q	109	E	1.9	106	122
2BR2	Q R	Q	112	R	4.1	106	122
2BR2	Q R	Q	116	R	2.1	106	122
2BR2	Q R	Q	248	L	2.3	248	273
2BR2	Q R	Q	251	I	2.4	248	273
2BR2	Q R	R	102	E	3.2	98	115
2BR2	Q R	R	104	S	1.7	98	115
2BR2	Q R	R	105	K	1.7	98	115
2BR2	Q R	R	109	E	1.4	98	115
2BR2	Q R	R	214	F	2.2	211	238
2BR2	Q R	R	218	F	1.1	211	238
2BR2	S H	S	14	I	1.1	13	25
2BR2	S T	S	108	I	1.9	106	122
2BR2	S T	S	248	L	2.1	248	273
2BR2	S T	S	251	I	2.5	248	273
2BR2	S T	T	102	E	1.0	98	115
2BR2	S T	T	214	F	2.2	211	238
2BR2	S T	T	218	F	1.0	211	238
2BR2	U P	U	14	I	1.1	13	25
2BR2	U V	U	108	I	2.1	106	122
2BR2	U V	U	112	R	1.7	106	122
2BR2	U V	U	116	R	2.2	106	122
2BR2	U V	U	248	L	2.1	248	273
2BR2	U V	U	251	I	3.4	248	273
2BR2	U V	U	255	E	1.4	248	273
2BR2	U V	V	98	R	1.2	98	115
2BR2	U V	V	101	I	1.2	98	115
2BR2	U V	V	102	E	3.3	98	115

2BR2	U V	V	108	R	1.2	98	115
2BR2	U V	V	109	E	1.9	98	115
2BR2	U V	V	112	E	1.3	98	115
2BR2	U V	V	211	P	1.7	211	239
2BR2	U V	V	214	F	2.2	211	239
2BR2	U V	V	215	R	1.4	211	239
2BR2	U V	V	218	F	1.4	211	239
2BRR	H L	L	124	Q	1.8	122	127
2BRU	A C	C	80	N	1.5	79	87
2BRU	B C	B	1123	R	1.0	1122	1128
2BRU	B C	B	1178	L	3.6	1176	1188
2BRU	B C	B	1182	G	2.2	1176	1188
2BRU	B C	B	1185	N	2.4	1176	1188
2BRU	B C	B	1202	E	4.2	1198	1207
2BRU	B C	B	1203	Q	1.1	1198	1207
2BRU	B C	B	1206	S	2.6	1198	1207
2BS4	D E	D	98	R	1.9	83	103
2BS4	D E	D	158	H	2.0	156	171
2BS4	D E	D	351	Y	1.1	343	353
2BS4	D E	D	352	F	1.5	343	353
2BS4	D E	D	464	F	2.1	463	478
2BS4	D E	E	37	F	1.5	36	48
2BS4	D E	E	108	G	53.0	107	118
2BS4	D E	E	146	F	1.8	139	149
2BSK	A B	A	55	K	2.4	43	69
2BSK	A B	A	58	K	1.6	43	69
2BSK	A B	A	62	R	2.9	43	69
2BSK	A B	A	63	I	1.2	43	69
2BSK	A B	A	66	R	1.1	43	69
2BSK	A B	A	67	F	1.0	43	69
2BSK	A B	B	47	E	1.4	45	64
2BSK	A B	B	51	L	1.3	45	64
2BSK	A B	B	52	D	1.6	45	64
2BSK	A B	B	55	V	1.4	45	64
2BSK	A B	B	59	L	1.5	45	64
2BSK	A D	A	21	Y	2.7	14	33
2BSK	A D	A	29	F	3.4	14	33
2BSK	A D	D	52	D	1.1	45	64
2BSK	A D	D	57	K	2.9	45	64
2BSK	A D	D	58	Y	1.7	45	64
2BSK	A D	D	69	L	4.5	67	72
2BSK	C D	C	31	D	1.0	15	33
2BSK	C D	C	51	H	1.8	43	67
2BSK	C D	C	55	K	1.1	43	67
2BSK	C D	C	58	K	3.1	43	67
2BSK	C D	C	62	R	2.9	43	67
2BSK	C D	C	66	R	1.6	43	67
2BSK	C D	D	30	H	1.7	27	34
2BSK	C F	C	21	Y	1.3	15	33
2BSK	C F	C	29	F	3.0	15	33
2BSK	C F	F	13	L	1.0	11	16
2BSK	C F	F	33	C	4.6	27	34
2BSK	C F	F	61	I	1.4	45	64
2BSK	C F	F	69	L	1.4	67	71
2BSK	E B	E	29	F	3.5	16	33
2BSK	E B	E	50	E	1.7	43	69
2BSK	E B	E	53	L	1.1	43	69
2BSK	E B	B	32	K	1.4	27	33
2BSK	E B	B	58	Y	1.5	45	64
2BSK	E B	B	61	I	1.8	45	64

2BSK	E B	B	68	K	1.3	67	72
2BSK	E F	E	55	K	1.4	43	69
2BSK	E F	E	59	M	1.6	43	69
2BSK	E F	E	62	R	2.1	43	69
2BSK	E F	E	66	R	1.0	43	69
2BSK	E F	E	67	F	1.4	43	69
2BSK	E F	F	30	H	1.4	27	34
2BSK	E F	F	52	D	1.9	45	64
2BSK	E F	F	55	V	1.4	45	64
2BSK	E F	F	59	L	1.5	45	64
2BTO	A T	A	402	W	2.6	400	405
2BTQ	A B	A	258	E	1.2	256	264
2BTQ	A B	A	434	G	193.7	434	440
2BTQ	A B	B	109	E	1.3	108	113
2BTQ	A B	B	396	H	2.1	395	400
2BTQ	A B	B	397	W	2.9	395	400
2BTV	A C	A	547	D	1.4	546	559
2BTV	A C	C	41	N	1.4	27	45
2BTV	A F	A	622	R	1.5	620	624
2BTV	A F	F	35	I	2.4	27	43
2BTV	A F	F	39	R	1.0	27	43
2BTV	B G	G	34	G	3.9	27	45
2BTV	B G	G	42	G	1.7	27	45
2BTV	B H	B	211	E	1.2	211	227
2BTV	B H	H	34	G	1.2	27	45
2BTW	A B	A	55	F	2.0	52	58
2BTW	A B	B	55	F	2.1	52	58
2BV8	A B	A	5	I	1.7	4	15
2BV8	A B	A	6	T	1.1	4	15
2BV8	A B	A	9	I	2.2	4	15
2BV8	A B	A	13	D	1.7	4	15
2BV8	A B	A	24	L	1.3	21	47
2BV8	A B	A	31	Y	2.0	21	47
2BV8	A B	A	38	L	1.3	21	47
2BV8	A B	A	93	R	3.0	78	101
2BV8	A B	A	97	Y	3.1	78	101
2BV8	A B	A	100	V	1.6	78	101
2BV8	A B	A	110	Y	1.0	104	113
2BV8	A B	B	13	D	1.4	4	15
2BV8	A B	B	24	L	1.7	21	33
2BV8	A B	B	34	G	48.1	34	47
2BV8	A B	B	38	L	2.2	34	47
2BV8	A B	B	91	R	2.2	76	100
2BV8	A B	B	95	Y	3.7	76	100
2BV8	A B	B	98	I	1.2	76	100
2BV8	A F	A	93	R	1.0	78	101
2BV8	A F	A	109	E	1.1	104	113
2BV8	A F	A	110	Y	1.1	104	113
2BV8	A F	A	118	I	1.0	115	122
2BV8	A F	F	76	N	1.1	76	100
2BV8	A F	F	77	R	1.2	76	100
2BV8	A F	F	83	L	1.1	76	100
2BV8	E D	E	110	Y	1.2	105	113
2BV8	E D	E	117	E	1.2	115	122
2BV8	E D	E	118	I	1.6	115	122
2BV8	E D	D	77	R	1.2	76	100
2BV8	E D	D	79	M	1.2	76	100
2BV8	K P	K	118	I	1.8	115	122
2BV8	K P	P	76	N	1.6	76	100
2BV8	K P	P	77	R	1.0	76	100

2BV8	K P	P	83	L	1.2	76	100
2BV8	M L	M	93	R	1.0	78	101
2BV8	M L	M	118	I	1.9	115	122
2BV8	M L	L	76	N	1.0	76	100
2BV8	M L	L	79	M	1.8	76	100
2BV8	M L	L	83	L	1.6	76	100
2BV8	O N	O	109	E	1.1	104	113
2BV8	O N	O	110	Y	1.1	104	113
2BV8	O N	O	118	I	1.3	115	122
2BV8	O N	N	76	N	1.5	76	100
2BV8	O N	N	77	R	1.1	76	100
2BV8	O N	N	79	M	2.0	76	100
2BV8	O N	N	83	L	1.4	76	100
2BV8	O P	O	5	I	1.6	4	15
2BV8	O P	O	6	T	1.5	4	15
2BV8	O P	O	9	I	2.3	4	15
2BV8	O P	O	24	L	1.0	21	47
2BV8	O P	O	38	L	1.3	21	47
2BV8	O P	O	93	R	4.5	78	101
2BV8	O P	O	97	Y	3.8	78	101
2BV8	O P	O	100	V	1.6	78	101
2BV8	O P	P	9	V	1.4	4	15
2BV8	O P	P	24	L	1.8	21	33
2BV8	O P	P	31	I	1.9	21	33
2BV8	O P	P	34	G	69.0	34	47
2BV8	O P	P	38	L	1.8	34	47
2BV8	O P	P	91	R	1.7	76	100
2BV8	O P	P	95	Y	2.8	76	100
2BV8	O P	P	98	I	1.1	76	100
2BWE	K T	K	349	R	1.0	347	357
2BWE	L S	L	365	L	1.1	361	369
2BYK	B C	B	43	V	1.5	31	59
2BYK	B C	B	47	F	1.0	31	59
2BYK	B C	C	43	L	1.2	40	66
2BYK	D A	D	47	F	1.3	31	59
2BYK	D C	D	37	I	1.9	31	59
2BYK	D C	D	44	F	3.5	31	59
2BYK	D C	D	69	I	1.2	66	76
2BYK	D C	D	81	F	3.6	79	97
2BYK	D C	D	85	L	2.1	79	97
2BYK	D C	D	89	L	1.1	79	97
2BYK	D C	D	92	Y	3.3	79	97
2BYK	D C	C	41	E	7.2	40	66
2BYK	D C	C	42	V	1.3	40	66
2BYK	D C	C	44	F	3.7	40	66
2BYK	D C	C	45	L	1.7	40	66
2BYK	D C	C	46	M	1.5	40	66
2BYK	D C	C	52	L	1.3	40	66
2BYK	D C	C	53	F	3.9	40	66
2BYK	D C	C	54	V	1.5	40	66
2BYK	D C	C	62	Y	2.1	40	66
2BYK	D C	C	79	L	1.1	76	86
2BYP	A G	G	410	W	2.0	406	411
2BYP	B G	G	407	R	4.0	406	411
2BYP	B H	H	410	W	1.7	406	411
2BYP	C H	H	407	R	18.3	406	411
2BYP	C I	I	410	W	1.5	406	411
2BYP	D I	I	407	R	4.1	406	411
2BYP	D J	J	410	W	1.2	406	411
2BZW	A B	A	97	F	2.2	83	101

2BZW	A B	A	126	V	1.3	119	131
2BZW	A B	A	129	E	1.4	119	131
2BZW	A B	A	130	L	1.4	119	131
2BZW	A B	A	138	G	53.9	137	157
2BZW	A B	A	194	L	1.3	188	195
2BZW	A B	B	105	Y	2.8	100	119
2BZW	A B	B	106	G	80.2	100	119
2BZW	A B	B	109	L	2.5	100	119
2BZW	A B	B	114	D	2.0	100	119
2BZW	A B	B	116	F	3.7	100	119
2BZW	A B	B	117	E	1.2	100	119
2C0L	A B	A	561	N	2.5	556	569
2C0L	A B	A	564	I	1.1	556	569
2C0L	A B	A	609	L	1.5	601	615
2C0L	A B	A	620	Y	2.4	617	625
2C0L	A B	B	31	L	2.6	28	39
2C0L	A B	B	35	E	1.0	28	39
2C1M	A B	A	273	W	3.7	265	279
2C1M	A B	A	353	K	2.4	349	363
2C1M	A B	A	357	W	2.7	349	363
2C1M	A B	A	361	N	1.6	349	363
2C1M	A B	A	391	F	3.1	391	407
2C1M	A B	A	392	K	2.0	391	407
2C1M	A B	A	396	E	1.0	391	407
2C1M	A B	A	465	E	1.3	457	467
2C1M	A B	A	474	E	2.2	469	476
2C1M	A B	A	485	Y	3.6	482	493
2C2V	B C	C	42	F	1.8	40	53
2C2V	B C	C	45	L	13.1	40	53
2C2V	B C	C	48	L	1.5	40	53
2C2V	E F	F	42	F	3.0	40	54
2C2V	H I	I	49	E	1.2	40	54
2C2V	S B	B	10	R	1.3	10	22
2C2V	V K	K	10	R	1.3	10	22
2C35	A B	A	37	V	1.3	34	50
2C35	A B	A	44	R	1.1	34	50
2C35	A B	A	60	V	1.7	59	71
2C35	A B	A	67	Y	3.2	59	71
2C35	A D	A	132	D	1.8	124	138
2C35	C D	C	37	V	1.3	34	50
2C35	C D	C	60	V	1.5	59	71
2C35	C D	C	67	Y	3.4	59	71
2C35	E F	E	37	V	1.2	34	50
2C35	E F	E	44	R	1.0	34	50
2C35	E F	E	67	Y	1.7	59	71
2C35	E F	E	95	F	1.4	94	104
2C35	G H	G	37	V	1.2	34	50
2C35	G H	G	67	Y	1.7	59	71
2C35	G H	G	95	F	1.6	94	104
2C4F	H L	H	128	F	1.4	126	129
2C4F	T U	U	102	P	1.9	102	106
2C4F	T U	U	103	Y	1.4	102	106
2C4O	A D	A	8	K	1.3	8	15
2C4O	A D	D	111	C	13.7	99	112
2C52	A B	A	11	L	1.4	9	20
2C52	A B	A	15	L	2.5	9	20
2C52	A B	A	39	Q	1.0	38	50
2C52	A B	A	40	L	1.0	38	50
2C52	A B	A	44	F	1.3	38	50
2C52	A B	A	52	Y	4.8	51	56

2C52	A B	B	338	L	12.0	333	339
2C5I	T P	T	11	V	1.5	7	29
2C5I	T P	T	18	Q	1.3	7	29
2C5I	T P	T	21	R	2.8	7	29
2C5I	T P	T	25	Y	1.7	7	29
2C5I	T P	T	44	I	3.1	35	61
2C5I	T P	T	54	D	1.0	35	61
2C5I	T P	P	20	R	2.3	16	29
2C5I	T P	P	23	L	2.5	16	29
2C5I	T P	P	27	F	1.6	16	29
2C7J	A B	A	9	I	2.8	4	15
2C7J	A B	A	31	F	2.0	21	32
2C7J	A B	A	38	L	1.4	33	47
2C7J	A B	A	93	R	1.8	78	102
2C7J	A B	A	110	Y	1.2	104	113
2C7J	A B	B	24	I	1.1	21	33
2C7J	A B	B	38	L	1.3	34	47
2C7J	A B	B	91	R	1.7	76	100
2C7J	A B	B	95	Y	2.7	76	100
2C7J	A B	B	104	V	1.1	103	112
2C9W	A C	A	163	L	3.3	163	175
2C9W	A C	A	164	Q	1.7	163	175
2C9W	A C	A	166	L	1.0	163	175
2C9W	A C	A	171	I	1.5	163	175
2C9W	A C	A	187	L	1.5	185	194
2C9W	A C	C	76	Y	4.0	67	83
2C9W	A C	C	79	Y	1.1	67	83
2C9W	A C	C	101	L	2.2	100	110
2C9W	A C	C	103	L	1.0	100	110
2C9W	A C	C	104	L	3.1	100	110
2C9W	B C	B	34	I	1.8	24	35
2C9W	B C	C	68	H	3.6	67	83
2C9W	B C	C	82	R	1.1	67	83
2CCI	A B	A	49	I	1.1	46	58
2CCI	A B	A	53	S	1.2	46	58
2CCI	A B	B	182	I	2.1	179	193
2CCI	A B	B	185	Y	1.8	179	193
2CCI	A B	B	230	E	1.5	229	246
2CCI	A B	B	266	K	1.7	253	269
2CCI	A B	B	267	F	1.2	253	269
2CCI	A B	B	268	E	1.2	253	269
2CCI	A B	B	288	K	1.2	288	302
2CCI	B F	B	213	I	1.0	208	225
2CCI	B F	B	217	W	1.2	208	225
2CCI	B F	B	224	E	1.0	208	225
2CCI	B F	B	277	E	2.3	275	282
2CCI	B F	B	280	Y	2.4	275	282
2CCI	B F	B	281	I	1.0	275	282
2CCI	C D	C	53	S	1.0	46	57
2CCI	C D	C	278	K	1.9	277	281
2CCI	C D	D	178	Y	3.6	178	193
2CCI	C D	D	182	I	1.7	178	193
2CCI	C D	D	266	K	1.9	253	269
2CCI	C D	D	267	F	1.6	253	269
2CCI	C D	D	295	E	1.4	288	302
2CCI	D I	D	213	I	1.3	208	225
2CCI	D I	D	217	W	1.4	208	225
2CCL	A B	B	19	R	3.3	11	22
2CCL	C D	D	18	K	1.9	11	22
2CCL	C D	D	19	R	3.7	11	22

2CDE	C D	D	135	E	2.3	133	140
2CDE	E F	F	135	E	2.7	133	140
2CDF	A B	B	135	E	1.2	133	140
2CDG	A B	B	136	E	1.1	134	141
2CG5	A B	A	157	I	1.4	151	158
2CG5	A B	A	187	W	2.7	176	198
2CG9	A X	A	387	K	1.0	387	409
2CG9	A X	A	391	V	3.7	387	409
2CG9	B Y	B	387	K	1.0	387	409
2CG9	B Y	B	388	I	1.1	387	409
2CG9	B Y	B	390	K	1.1	387	409
2CJS	A C	A	137	E	2.1	135	154
2CJS	A C	A	141	W	2.4	135	154
2CJS	A C	A	145	L	1.7	135	154
2CJS	A C	C	138	R	2.7	135	141
2CJW	A B	A	234	G	3.6	228	244
2CKF	A B	A	210	W	2.4	205	212
2CKF	A B	A	344	R	2.3	336	350
2CKF	A B	A	348	R	3.3	336	350
2CKF	A B	A	361	G	7.2	355	371
2CKF	A B	B	77	E	1.9	75	86
2CKF	C D	C	344	R	2.6	336	350
2CKF	C D	C	348	R	3.3	336	350
2CKF	C D	C	361	G	7.9	355	371
2CKF	C D	C	362	E	1.5	355	371
2CKF	C D	D	77	E	1.3	75	86
2CKF	C D	D	81	R	1.9	75	86
2CKF	E F	E	210	W	1.6	205	212
2CKF	E F	E	344	R	1.4	336	350
2CKF	E F	E	348	R	4.6	336	350
2CKF	E F	E	359	D	5.0	355	360
2CKF	E F	E	361	G	4.6	361	371
2CKF	E F	E	362	E	2.9	361	371
2CKF	E F	F	76	E	1.1	75	86
2CKF	E F	F	77	E	2.5	75	86
2CKF	E F	F	81	R	2.0	75	86
2CKF	E F	F	84	R	1.9	75	86
2CLY	A B	A	110	M	1.0	80	118
2CLY	A B	A	125	F	2.3	121	182
2CLY	A B	A	129	R	1.5	121	182
2CLY	A B	A	132	I	1.6	121	182
2CLY	A B	A	134	M	1.5	121	182
2CLY	A B	A	136	L	1.2	121	182
2CLY	A B	A	138	V	1.1	121	182
2CLY	A B	A	139	T	1.7	121	182
2CLY	A B	A	140	Y	2.9	121	182
2CLY	A B	A	141	R	2.4	121	182
2CLY	A B	A	143	R	1.6	121	182
2CLY	A B	A	144	L	1.0	121	182
2CLY	A B	A	148	Y	3.1	121	182
2CLY	A B	A	155	L	2.6	121	182
2CLY	A B	A	156	D	1.4	121	182
2CLY	A B	B	15	F	1.3	12	17
2CLY	A B	B	41	L	1.8	24	44
2CLY	A B	B	56	Y	3.1	53	59
2CLY	A B	B	69	F	1.3	65	74
2CLY	A B	B	73	F	1.0	65	74
2CLY	A B	B	92	E	1.9	88	95
2CLY	A B	B	111	I	1.2	101	123
2CLY	A B	B	118	L	1.0	101	123

2CLY	A C	A	147	V	1.0	121	182
2CLY	A C	A	153	N	1.0	121	182
2CLY	A C	A	158	H	1.3	121	182
2CLY	A C	A	172	H	1.6	121	182
2CLY	A C	A	176	W	3.0	121	182
2CLY	A C	C	22	K	1.0	11	24
2CLY	A C	C	51	Y	2.4	34	52
2CLY	B C	B	33	W	2.8	24	44
2CLY	B C	B	69	F	2.3	65	74
2CLY	D E	D	123	Y	2.9	119	182
2CLY	D E	D	125	F	2.8	119	182
2CLY	D E	D	127	V	2.1	119	182
2CLY	D E	D	132	I	1.4	119	182
2CLY	D E	D	136	L	1.4	119	182
2CLY	D E	D	140	Y	1.3	119	182
2CLY	D E	D	141	R	1.8	119	182
2CLY	D E	D	143	R	1.7	119	182
2CLY	D E	D	145	H	1.5	119	182
2CLY	D E	D	148	Y	3.0	119	182
2CLY	D E	D	151	V	1.1	119	182
2CLY	D E	D	155	L	3.1	119	182
2CLY	D E	D	159	I	1.1	119	182
2CLY	D E	E	15	F	1.3	12	17
2CLY	D E	E	37	L	1.7	24	44
2CLY	D E	E	69	F	1.5	65	76
2CLY	D E	E	92	E	1.0	87	100
2CLY	D E	E	118	L	1.4	102	123
2CLY	D F	D	151	V	1.0	119	182
2CLY	D F	D	157	Y	2.0	119	182
2CLY	D F	D	158	H	1.6	119	182
2CLY	D F	D	164	M	1.3	119	182
2CLY	D F	F	19	Y	2.3	8	24
2CLY	D F	F	47	L	1.2	34	51
2CLY	E F	E	69	F	2.0	65	76
2CMR	H A	A	32	I	1.0	2	41
2CMR	H A	A	199	H	3.2	179	216
2CMR	H A	A	203	L	3.3	179	216
2CMR	H A	A	206	W	3.9	179	216
2CMR	H A	A	207	G	36.6	179	216
2CMR	L A	A	146	N	1.1	139	172
2CMY	A B	B	10	M	1.3	8	14
2CMY	A B	B	21	L	1.5	20	29
2CNW	A D	A	36	R	1.3	24	41
2CNW	A D	D	46	L	1.7	46	59
2CNW	A D	D	235	N	1.8	234	247
2CNW	B D	B	72	E	1.1	70	86
2CNW	B D	B	75	L	1.2	70	86
2CNW	B D	B	80	E	1.1	70	86
2CNW	B D	D	85	L	1.2	80	88
2CNW	B E	E	234	Q	1.6	234	247
2CNW	C F	C	8	R	1.8	7	15
2CNW	C F	C	36	R	1.5	24	41
2CNW	C F	C	144	Q	1.4	141	152
2CNW	C F	F	36	E	1.4	29	42
2CNW	C F	F	148	Q	1.4	145	156
2CNW	C F	F	151	E	1.8	145	156
2CNW	C F	F	152	W	1.9	145	156
2CZV	A C	A	26	W	1.2	17	27
2CZV	A C	A	131	L	1.0	131	136
2CZV	A C	A	187	V	1.4	178	188

2CZV	A C	C	79	Y	1.0	77	86
2CZV	A C	C	82	F	2.9	77	86
2CZV	A C	C	85	M	2.0	77	86
2CZV	A D	A	114	H	1.9	114	123
2CZV	A D	A	140	Y	1.4	139	159
2CZV	A D	A	151	K	2.1	139	159
2CZV	A D	D	43	L	1.5	31	47
2CZV	A D	D	48	E	1.0	48	55
2CZV	B C	B	114	H	2.2	114	123
2CZV	B C	B	140	Y	1.0	139	159
2CZV	B C	B	150	M	1.1	139	159
2CZV	B C	C	39	W	1.0	31	47
2CZV	B C	C	43	L	1.5	31	47
2CZV	B D	B	26	W	4.2	17	27
2CZV	B D	B	131	L	1.1	131	136
2CZV	B D	B	187	V	1.3	178	188
2CZV	B D	D	82	F	2.5	77	86
2CZV	B D	D	85	M	1.5	77	86
2CZY	A B	A	40	Y	1.4	34	48
2CZY	A B	A	41	L	1.1	34	48
2CZY	A B	A	58	F	2.1	52	68
2CZY	A B	A	62	M	1.9	52	68
2CZY	A B	A	65	F	1.2	52	68
2CZY	A B	B	49	L	1.9	44	55
2CZY	A B	B	52	V	1.2	44	55
2CZY	A B	B	54	L	1.2	44	55
2D03	L H	L	130	Q	1.3	128	134
2D07	A B	B	50	R	4.3	40	51
2D0O	A B	A	170	L	1.5	168	174
2D0O	A B	B	27	L	1.0	23	32
2D0O	A B	B	31	E	2.8	23	32
2D0O	A B	B	96	R	2.0	92	107
2D0O	C D	C	170	L	2.2	168	174
2D0O	C D	D	30	E	1.0	23	32
2D0O	C D	D	31	E	2.1	23	32
2D0O	C D	D	96	R	2.8	92	108
2D0O	C D	D	105	L	1.0	92	108
2D0V	A B	B	36	E	1.4	34	38
2D0V	A B	B	37	L	1.4	34	38
2D0V	A B	B	44	R	1.2	39	62
2D0V	A B	B	47	E	1.9	39	62
2D0V	A B	B	50	R	3.6	39	62
2D0V	A B	B	51	N	2.3	39	62
2D0V	A B	B	54	R	2.9	39	62
2D0V	A B	B	58	F	1.2	39	62
2D0V	D E	E	36	E	2.0	34	38
2D0V	D E	E	37	L	1.3	34	38
2D0V	D E	E	50	R	2.3	39	61
2D0V	D E	E	54	R	3.3	39	61
2D0V	D E	E	58	F	2.0	39	61
2D0V	I J	J	36	E	1.5	34	38
2D0V	I J	J	37	L	1.6	34	38
2D0V	I J	J	40	Q	1.1	39	62
2D0V	I J	J	47	E	2.3	39	62
2D0V	I J	J	50	R	2.3	39	62
2D0V	I J	J	51	N	2.2	39	62
2D0V	I J	J	58	F	1.7	39	62
2D10	A E	E	348	W	2.8	348	357
2D10	A E	E	351	K	1.7	348	357
2D10	A E	E	355	F	4.1	348	357

2D10	B F	F	348	W	5.8	348	357
2D10	B F	F	355	F	3.2	348	357
2D10	C G	G	348	W	3.0	348	358
2D10	C G	G	355	F	4.2	348	358
2D10	D H	H	348	W	7.3	348	358
2D10	D H	H	351	K	1.1	348	358
2D10	D H	H	355	F	4.5	348	358
2D1P	A B	A	84	R	2.3	79	85
2D1P	A B	A	112	L	1.3	112	122
2D1P	A B	A	120	L	1.9	112	122
2D1P	A C	A	23	F	3.4	15	30
2D1P	A C	C	79	Y	2.9	79	89
2D1P	A C	C	82	F	2.1	79	89
2D1P	A C	C	83	V	1.8	79	89
2D1P	A C	C	84	R	1.0	79	89
2D1P	A C	C	87	V	1.6	79	89
2D1P	A H	A	95	R	2.5	90	96
2D1P	A H	H	108	R	1.1	103	113
2D1P	A H	H	109	E	1.3	103	113
2D1P	B C	C	19	R	1.4	14	20
2D1P	D E	D	84	R	2.1	79	85
2D1P	D E	D	120	L	1.7	112	122
2D1P	D E	E	20	E	3.6	17	30
2D1P	D F	D	23	F	3.6	15	30
2D1P	D F	F	79	Y	2.8	79	89
2D1P	D F	F	82	F	2.3	79	89
2D1P	D F	F	83	V	2.1	79	89
2D1P	E F	E	85	E	1.0	80	86
2D1P	E F	E	107	R	1.1	103	111
2D1P	E F	F	19	R	1.4	14	20
2D1P	E I	E	45	F	2.1	42	48
2D1P	G H	G	84	R	2.4	79	85
2D1P	G H	G	120	L	2.1	112	122
2D1P	G I	G	23	F	3.5	15	30
2D1P	G I	G	26	A	1.4	15	30
2D1P	G I	G	27	L	1.3	15	30
2D1P	G I	I	79	Y	3.5	79	89
2D1P	G I	I	80	T	1.4	79	89
2D1P	G I	I	82	F	3.7	79	89
2D1P	G I	I	83	V	3.3	79	89
2D1P	G I	I	84	R	1.3	79	89
2D1P	G I	I	87	V	2.3	79	89
2D1P	H F	H	45	F	1.9	43	48
2D1P	H F	F	42	R	1.0	42	49
2D1P	H I	H	85	E	1.2	80	86
2D1P	H I	H	107	R	1.1	103	113
2D1P	H I	H	110	L	1.0	103	113
2D1P	H I	I	19	R	1.9	14	20
2D26	A B	A	54	P	1.1	54	58
2D26	A B	A	55	V	1.3	54	58
2D26	A B	A	263	L	3.0	260	265
2D2M	A C	A	5	L	2.1	4	21
2D2M	A C	A	8	I	1.8	4	21
2D2M	A C	A	9	L	1.8	4	21
2D2M	A D	A	64	L	1.0	57	72
2D2M	A D	A	65	R	1.0	57	72
2D2M	A D	A	68	G	28.2	57	72
2D2M	A D	A	86	D	1.9	80	94
2D2M	A D	A	89	H	3.4	80	94
2D2M	A D	A	93	Q	3.8	80	94

2D2M	A D	D	63	A	2.0	59	77
2D2M	A D	D	67	R	1.8	59	77
2D2M	A D	D	70	S	1.5	59	77
2D2M	A D	D	74	I	1.4	59	77
2D2M	A D	D	84	T	1.1	82	98
2D2M	A D	D	88	L	1.6	82	98
2D2M	B C	B	68	G	3.5	57	79
2D2M	B C	B	71	D	2.1	57	79
2D2M	B C	B	82	V	1.4	80	93
2D2M	B C	B	86	L	1.4	80	93
2D2M	B C	C	28	R	1.7	25	42
2D2M	B C	C	68	V	5.6	61	83
2D2M	B C	C	86	V	1.3	84	100
2D2M	B D	B	5	L	1.1	4	18
2D2M	B D	B	8	L	1.5	4	18
2D3G	A P	P	263	L	1.1	258	274
2D3G	A P	P	267	L	1.1	258	274
2D3G	B P	P	269	L	1.8	258	274
2D5R	A B	A	200	K	1.1	195	201
2D5R	A B	B	78	G	2.2	77	81
2D74	A B	A	160	Y	2.1	153	168
2D74	A B	B	8	Y	4.2	8	15
2D74	A B	B	91	Y	3.2	90	103
2D7C	A D	D	737	Y	1.4	723	745
2D7C	B C	C	737	Y	1.4	723	745
2D7D	A B	A	489	R	1.8	481	494
2D7D	A B	A	493	L	2.3	481	494
2D7D	A B	A	635	M	1.0	621	641
2D7D	A B	A	644	F	3.7	644	654
2D7D	A B	A	645	E	1.6	644	654
2D7D	A B	A	651	R	2.3	644	654
2D7D	A B	B	635	M	1.1	623	641
2D7D	A B	B	637	E	1.1	623	641
2D7D	A B	B	640	K	1.8	623	641
2D7D	A B	B	644	F	4.0	644	659
2D7D	A B	B	645	E	1.5	644	659
2D7D	A B	B	651	R	3.8	644	659
2D9Q	A B	A	16	K	1.4	11	34
2D9Q	A B	A	108	L	1.3	101	115
2DBU	A B	A	63	V	1.2	56	68
2DBU	A B	A	66	L	1.1	56	68
2DBU	A B	A	83	L	1.1	72	87
2DBU	A B	A	154	F	1.1	150	161
2DBU	A B	A	199	L	1.6	185	200
2DBU	A B	A	296	G	67.5	295	309
2DBU	A B	A	300	I	1.9	295	309
2DBU	A B	A	304	L	1.2	295	309
2DBU	A B	A	330	E	1.6	328	340
2DBU	A B	A	334	Y	1.2	328	340
2DBU	A B	B	488	I	2.2	487	493
2DBU	A B	B	492	L	1.7	487	493
2DBU	A B	B	499	I	2.7	496	501
2DBU	A D	D	531	P	1.1	531	541
2DBU	C B	B	531	P	1.2	531	541
2DBU	C D	C	63	V	1.3	56	69
2DBU	C D	C	66	L	1.1	56	69
2DBU	C D	C	67	K	1.0	56	69
2DBU	C D	C	83	L	1.1	72	87
2DBU	C D	C	154	F	1.0	150	161
2DBU	C D	C	190	D	2.3	185	201

2DBU	C D	C	199	L	1.8	185	201
2DBU	C D	C	296	G	68.0	296	309
2DBU	C D	C	334	Y	3.2	328	341
2DBU	C D	D	488	I	2.0	487	493
2DBU	C D	D	492	L	1.3	487	493
2DBU	C D	D	499	I	2.6	496	501
2DBU	C D	D	500	D	1.2	496	501
2DD4	A B	B	92	R	3.9	87	95
2DD4	A C	C	157	R	1.5	149	158
2DD4	A C	C	160	R	4.2	159	166
2DD4	A E	E	5	I	1.0	5	19
2DD4	A E	E	6	R	3.4	5	19
2DD4	A E	E	9	V	1.3	5	19
2DD4	A K	K	128	L	2.4	128	144
2DD4	A K	K	132	H	3.5	128	144
2DD4	B C	B	68	W	3.0	67	82
2DD4	B C	B	70	L	1.4	67	82
2DD4	B C	B	71	N	1.7	67	82
2DD4	B C	B	73	F	1.2	67	82
2DD4	B C	B	75	T	1.0	67	82
2DD4	B C	B	77	E	1.3	67	82
2DD4	B C	B	79	L	1.2	67	82
2DD4	B C	B	81	W	5.4	67	82
2DD4	B C	B	91	R	1.3	87	95
2DD4	B C	B	108	Y	1.6	108	123
2DD4	B C	B	109	Y	1.1	108	123
2DD4	B C	B	113	L	2.9	108	123
2DD4	B C	B	120	L	1.4	108	123
2DD4	B C	B	130	E	1.7	128	145
2DD4	B C	B	134	K	2.9	128	145
2DD4	B C	C	27	F	2.6	26	41
2DD4	B C	C	29	I	1.5	26	41
2DD4	B C	C	30	L	1.9	26	41
2DD4	B C	C	34	V	1.7	26	41
2DD4	B C	C	35	R	1.2	26	41
2DD4	B C	C	36	E	1.2	26	41
2DD4	B C	C	37	L	2.4	26	41
2DD4	B C	C	48	D	2.7	46	58
2DD4	B C	C	49	H	2.6	46	58
2DD4	B C	C	52	W	2.8	46	58
2DD4	B C	C	53	K	2.3	46	58
2DD4	B C	C	144	E	1.2	144	148
2DD4	B C	C	145	W	2.4	144	148
2DD4	B C	C	147	R	1.8	144	148
2DD4	B C	C	152	R	1.3	149	158
2DD4	B C	C	153	R	2.9	149	158
2DD4	B C	C	211	R	2.9	211	216
2DD4	B L	B	40	F	1.9	37	44
2DD4	B L	L	27	F	2.0	26	41
2DD4	D B	B	6	R	4.0	4	19
2DD4	D B	B	9	V	1.2	4	19
2DD4	D E	E	92	R	3.9	87	95
2DD4	D F	D	80	E	1.0	77	82
2DD4	D F	D	98	Q	1.4	98	102
2DD4	D F	F	157	R	1.3	149	158
2DD4	D F	F	160	R	4.4	159	166
2DD4	D H	H	128	L	2.3	128	145
2DD4	D H	H	132	H	3.4	128	145
2DD4	E F	E	68	W	3.3	67	82
2DD4	E F	E	73	F	1.3	67	82

2DD4	E F	E	77	E	1.3	67	82
2DD4	E F	E	79	L	1.3	67	82
2DD4	E F	E	81	W	2.2	67	82
2DD4	E F	E	91	R	1.4	87	95
2DD4	E F	E	103	Y	1.3	100	106
2DD4	E F	E	108	Y	1.8	108	123
2DD4	E F	E	109	Y	1.1	108	123
2DD4	E F	E	113	L	2.8	108	123
2DD4	E F	E	130	E	1.8	128	144
2DD4	E F	E	134	K	2.9	128	144
2DD4	E F	F	27	F	2.7	26	41
2DD4	E F	F	29	I	1.3	26	41
2DD4	E F	F	30	L	1.9	26	41
2DD4	E F	F	34	V	1.7	26	41
2DD4	E F	F	37	L	1.9	26	41
2DD4	E F	F	48	D	1.2	46	59
2DD4	E F	F	52	W	3.0	46	59
2DD4	E F	F	152	R	1.7	149	158
2DD4	E F	F	153	R	2.7	149	158
2DD4	E F	F	154	R	4.2	149	158
2DD4	E F	F	211	R	3.4	211	216
2DD4	E I	E	40	F	1.8	37	44
2DD4	E I	I	27	F	2.0	26	41
2DD4	G E	E	128	L	2.1	128	144
2DD4	G E	E	132	H	3.4	128	144
2DD4	G H	H	92	R	3.5	87	95
2DD4	G I	G	80	E	1.1	77	81
2DD4	G I	G	98	Q	1.5	98	102
2DD4	G I	I	97	V	1.0	96	100
2DD4	G I	I	157	R	1.2	149	158
2DD4	G I	I	160	R	4.3	159	166
2DD4	G K	K	6	R	3.9	4	19
2DD4	G K	K	9	V	1.2	4	19
2DD4	H F	H	40	F	1.6	37	44
2DD4	H F	F	27	F	2.0	26	41
2DD4	H F	F	149	P	1.1	149	158
2DD4	H I	H	67	I	1.0	67	82
2DD4	H I	H	68	W	1.6	67	82
2DD4	H I	H	70	L	1.1	67	82
2DD4	H I	H	71	N	1.1	67	82
2DD4	H I	H	73	F	1.0	67	82
2DD4	H I	H	77	E	1.4	67	82
2DD4	H I	H	79	L	1.2	67	82
2DD4	H I	H	81	W	5.1	67	82
2DD4	H I	H	91	R	1.3	87	95
2DD4	H I	H	108	Y	1.5	108	123
2DD4	H I	H	113	L	2.7	108	123
2DD4	H I	H	120	L	1.3	108	123
2DD4	H I	H	130	E	1.1	128	145
2DD4	H I	H	134	K	3.4	128	145
2DD4	H I	I	27	F	2.7	26	41
2DD4	H I	I	28	E	1.7	26	41
2DD4	H I	I	29	I	1.7	26	41
2DD4	H I	I	30	L	2.2	26	41
2DD4	H I	I	34	V	1.6	26	41
2DD4	H I	I	36	E	2.2	26	41
2DD4	H I	I	37	L	2.0	26	41
2DD4	H I	I	48	D	2.7	46	59
2DD4	H I	I	52	W	2.9	46	59
2DD4	H I	I	53	K	1.2	46	59

2DD4	H I	I	144	E	1.1	144	148
2DD4	H I	I	145	W	1.9	144	148
2DD4	H I	I	147	R	1.0	144	148
2DD4	H I	I	153	R	2.5	149	158
2DD4	H I	I	154	R	1.4	149	158
2DD4	H I	I	162	V	1.0	159	166
2DD4	H I	I	211	R	3.2	211	216
2DD4	H L	L	157	R	1.4	149	158
2DD4	J B	B	128	L	2.6	128	145
2DD4	J B	B	131	L	1.5	128	145
2DD4	J B	B	132	H	3.4	128	145
2DD4	J H	H	6	R	3.7	3	19
2DD4	J H	H	9	V	1.3	3	19
2DD4	J K	K	92	R	3.9	87	95
2DD4	J L	J	80	E	1.2	77	82
2DD4	J L	L	97	V	1.0	96	100
2DD4	J L	L	157	R	1.6	149	158
2DD4	J L	L	160	R	1.2	159	166
2DD4	K C	K	40	F	1.8	37	44
2DD4	K C	C	27	F	2.0	26	41
2DD4	K I	I	153	R	1.2	149	158
2DD4	K L	K	67	I	1.5	67	82
2DD4	K L	K	68	W	1.5	67	82
2DD4	K L	K	70	L	1.4	67	82
2DD4	K L	K	71	N	1.2	67	82
2DD4	K L	K	73	F	2.7	67	82
2DD4	K L	K	77	E	1.0	67	82
2DD4	K L	K	79	L	1.2	67	82
2DD4	K L	K	81	W	4.9	67	82
2DD4	K L	K	91	R	2.9	87	95
2DD4	K L	K	103	Y	1.4	100	106
2DD4	K L	K	108	Y	1.4	108	123
2DD4	K L	K	113	L	2.8	108	123
2DD4	K L	K	120	L	1.4	108	123
2DD4	K L	K	130	E	1.8	128	144
2DD4	K L	K	134	K	2.8	128	144
2DD4	K L	K	137	E	1.3	128	144
2DD4	K L	L	27	F	2.7	26	41
2DD4	K L	L	28	E	2.2	26	41
2DD4	K L	L	29	I	1.4	26	41
2DD4	K L	L	30	L	2.1	26	41
2DD4	K L	L	34	V	1.6	26	41
2DD4	K L	L	35	R	1.3	26	41
2DD4	K L	L	37	L	2.1	26	41
2DD4	K L	L	48	D	2.2	46	59
2DD4	K L	L	49	H	2.0	46	59
2DD4	K L	L	52	W	3.0	46	59
2DD4	K L	L	53	K	1.9	46	59
2DD4	K L	L	152	R	1.7	149	158
2DD4	K L	L	153	R	3.5	149	158
2DD4	K L	L	154	R	1.4	149	158
2DD4	K L	L	156	V	1.2	149	158
2DD4	K L	L	211	R	3.3	211	216
2DD8	H L	L	125	E	1.3	123	128
2DE5	A D	A	11	R	3.3	6	12
2DE5	B E	B	11	R	2.6	6	12
2DE5	C F	C	11	R	1.1	6	12
2DE5	C F	C	210	R	1.3	210	214
2DEN	A B	A	86	R	2.1	81	92
2DEN	A B	A	99	L	1.2	95	105

2DEN	A B	A	103	F	2.7	95	105
2DF4	A B	A	319	S	1.5	319	324
2DF4	A B	A	320	N	1.0	319	324
2DF4	A B	A	343	Y	2.7	339	351
2DF4	A B	A	347	R	2.0	339	351
2DF4	A B	A	366	L	1.1	353	367
2DF4	A C	A	308	S	1.2	305	318
2DF4	A C	A	311	V	1.5	305	318
2DF4	A C	A	344	K	1.1	339	351
2DF4	A C	A	360	F	3.7	353	367
2DF4	A C	A	364	F	1.5	353	367
2DF4	A C	A	374	Y	2.3	370	395
2DF4	A C	A	376	K	2.0	370	395
2DF4	A C	A	377	K	1.3	370	395
2DF4	A C	A	378	S	1.5	370	395
2DF4	A C	A	380	K	1.4	370	395
2DF4	A C	A	381	V	1.9	370	395
2DF4	A C	A	384	L	1.6	370	395
2DF4	A C	A	419	L	1.3	418	425
2DF4	A C	C	12	I	2.4	6	16
2DF4	A C	C	14	N	1.4	6	16
2DF4	A C	C	28	M	1.5	24	44
2DF4	A C	C	32	L	1.6	24	44
2DF4	A C	C	39	A	1.3	24	44
2DF4	B C	B	54	R	3.4	53	60
2DF4	B C	C	74	Q	1.6	74	80
2DFK	A B	A	57	E	2.2	47	83
2DFK	A B	A	148	H	1.4	148	159
2DFK	A B	A	184	G	1.2	182	206
2DFK	A B	A	187	L	1.5	182	206
2DFK	A B	B	67	L	2.0	67	73
2DFK	A B	B	70	L	2.0	67	73
2DFK	C B	C	132	L	1.0	128	134
2DFK	C B	C	368	R	1.2	357	381
2DFK	C B	B	123	P	2.1	123	132
2DFK	C D	C	57	E	3.0	47	83
2DFK	C D	C	149	L	1.2	135	161
2DFK	C D	C	184	G	3.9	182	194
2DFK	C D	C	187	L	1.2	182	194
2DFK	C D	C	191	Q	3.0	182	194
2DFK	C D	C	198	L	1.4	195	206
2DFK	C D	C	232	N	1.3	212	240
2DFK	C D	C	236	R	1.1	212	240
2DFK	C D	D	65	D	1.0	65	69
2DFK	C D	D	66	R	1.5	65	69
2DFK	C D	D	67	L	2.1	65	69
2DFS	A B	A	767	L	1.6	755	792
2DFS	A B	A	771	C	1.0	755	792
2DFS	A B	A	778	I	1.0	755	792
2DFS	A B	A	779	R	1.4	755	792
2DFS	A B	A	780	G	64.2	755	792
2DFS	A B	A	781	W	1.0	755	792
2DFS	A B	B	109	M	1.4	102	112
2DFS	A C	A	798	Q	1.0	793	875
2DFS	A C	A	802	R	2.1	793	875
2DFS	A C	A	803	G	68.2	793	875
2DFS	A C	A	804	H	1.1	793	875
2DFS	A C	A	807	R	2.8	793	875
2DFS	A C	C	45	E	1.8	45	51
2DFS	A C	C	123	E	1.4	118	125

2DFS	A D	A	827	R	2.3	793	875
2DFS	A D	A	831	V	1.2	793	875
2DFS	A D	A	832	R	2.6	793	875
2DFS	A D	A	835	Y	1.2	793	875
2DFS	A D	D	37	R	1.3	32	40
2DFS	A D	D	109	M	1.1	102	110
2DFS	A D	D	120	E	1.4	118	125
2DFS	A E	A	846	Q	1.6	793	875
2DFS	A E	A	849	L	2.0	793	875
2DFS	A E	A	850	R	2.1	793	875
2DFS	A E	A	851	G	12.5	793	875
2DFS	A E	A	852	Y	1.2	793	875
2DFS	A E	A	853	L	1.6	793	875
2DFS	A E	A	854	V	1.4	793	875
2DFS	A E	A	855	R	1.7	793	875
2DFS	A E	A	857	K	1.1	793	875
2DFS	A E	E	45	E	1.5	45	51
2DFS	A E	E	109	M	1.1	102	110
2DFS	A E	E	141	F	1.0	138	147
2DFS	A E	E	145	M	1.4	138	147
2DFS	A F	A	863	R	1.1	793	875
2DFS	A F	A	871	Q	2.1	793	875
2DFS	A F	F	34	T	1.3	32	37
2DFS	A F	F	45	E	1.4	45	54
2DFS	A F	F	109	M	1.0	102	110
2DFS	A G	A	890	I	2.2	878	906
2DFS	A G	A	894	Q	1.0	878	906
2DFS	A G	A	898	R	5.8	878	906
2DFS	A G	A	903	K	1.4	878	906
2DFS	A G	G	109	M	1.4	102	112
2DFS	A G	G	120	E	4.2	118	127
2DFS	M N	M	767	L	1.3	755	792
2DFS	M N	M	778	I	1.4	755	792
2DFS	M N	M	779	R	1.3	755	792
2DFS	M N	M	780	G	9.2	755	792
2DFS	M N	N	45	E	1.2	45	54
2DFS	M N	N	108	V	1.5	102	112
2DFS	M O	M	795	I	1.9	793	875
2DFS	M O	M	797	I	1.1	793	875
2DFS	M O	M	798	Q	2.2	793	875
2DFS	M O	M	800	Y	1.1	793	875
2DFS	M O	M	802	R	1.9	793	875
2DFS	M O	M	803	G	58.3	793	875
2DFS	M O	M	804	H	1.2	793	875
2DFS	M O	M	807	R	3.5	793	875
2DFS	M O	O	37	R	1.9	32	40
2DFS	M O	O	45	E	1.8	45	51
2DFS	M O	O	141	F	1.2	138	147
2DFS	M P	M	822	I	2.2	793	875
2DFS	M P	M	823	Q	4.0	793	875
2DFS	M P	M	825	F	1.3	793	875
2DFS	M P	M	827	R	3.0	793	875
2DFS	M P	M	831	V	1.3	793	875
2DFS	M P	M	832	R	2.8	793	875
2DFS	M P	M	835	Y	1.3	793	875
2DFS	M P	P	37	R	1.4	32	40
2DFS	M P	P	109	M	1.1	102	110
2DFS	M P	P	120	E	2.1	118	125
2DFS	M P	P	124	M	1.5	118	125
2DFS	M Q	M	844	A	3.4	793	875

2DFS	M Q	M	845	L	2.4	793	875
2DFS	M Q	M	847	A	3.4	793	875
2DFS	M Q	M	848	L	4.2	793	875
2DFS	M Q	M	849	L	4.6	793	875
2DFS	M Q	M	850	R	1.9	793	875
2DFS	M Q	M	851	G	12.3	793	875
2DFS	M Q	M	852	Y	8.5	793	875
2DFS	M Q	M	853	L	1.7	793	875
2DFS	M Q	M	854	V	1.4	793	875
2DFS	M Q	M	855	R	1.5	793	875
2DFS	M Q	M	857	K	1.1	793	875
2DFS	M Q	Q	37	R	1.9	32	40
2DFS	M Q	Q	109	M	4.4	102	111
2DFS	M Q	Q	120	E	1.5	118	125
2DFS	M Q	Q	121	V	3.4	118	125
2DFS	M Q	Q	123	E	1.1	118	125
2DFS	M Q	Q	124	M	4.1	118	125
2DFS	M Q	Q	141	F	2.0	138	147
2DFS	M Q	Q	144	M	1.9	138	147
2DFS	M Q	Q	145	M	5.7	138	147
2DFS	M R	M	863	R	1.5	793	875
2DFS	M R	M	871	Q	1.9	793	875
2DFS	M R	M	878	L	1.0	878	906
2DFS	M R	R	45	E	1.3	45	54
2DFS	M S	M	890	I	2.5	878	906
2DFS	M S	M	894	Q	1.1	878	906
2DFS	M S	M	897	Y	1.9	878	906
2DFS	M S	M	898	R	2.2	878	906
2DFS	M S	M	901	M	1.2	878	906
2DFS	M S	M	903	K	1.5	878	906
2DFS	M S	M	905	E	1.1	878	906
2DFS	M S	S	45	E	1.0	45	51
2DFS	M S	S	109	M	1.4	102	112
2DFX	E I	E	29	Q	1.5	24	33
2DFX	E I	I	94	D	1.1	80	97
2DOI	A B	B	317	R	3.6	306	326
2DOI	X C	C	310	L	3.1	307	326
2DOI	X C	C	314	K	1.9	307	326
2DOI	X C	C	318	H	1.1	307	326
2DOQ	A D	A	105	F	1.3	101	106
2DOQ	A D	A	118	L	1.0	115	125
2DOQ	A D	D	237	F	2.3	224	249
2DOQ	A D	D	240	W	3.8	224	249
2DOQ	A D	D	245	L	1.5	224	249
2DOQ	B D	B	32	F	1.2	19	33
2DOQ	B D	B	104	L	1.6	94	106
2DOQ	B D	B	105	F	2.5	94	106
2DOQ	B D	B	118	L	5.8	115	125
2DOQ	B D	B	121	V	1.1	115	125
2DOQ	B D	B	157	I	2.0	151	158
2DOQ	B D	D	258	F	3.2	252	292
2DOQ	B D	D	264	L	2.6	252	292
2DOQ	B D	D	268	F	2.2	252	292
2DOQ	B D	D	271	W	5.7	252	292
2DOQ	C D	C	47	V	1.2	42	48
2DOQ	C D	C	105	F	1.1	95	106
2DOQ	C D	D	278	F	2.0	252	292
2DOQ	C D	D	290	L	2.4	252	292
2DPP	A B	A	24	F	1.6	22	39
2DPP	A B	A	25	W	3.2	22	39

2DPP	A B	A	28	R	1.5	22	39
2DPP	A B	A	30	K	1.3	22	39
2DPP	A B	A	32	L	2.5	22	39
2DPP	A B	A	35	L	6.9	22	39
2DPP	A B	A	36	L	1.7	22	39
2DPP	A B	A	37	I	1.4	22	39
2DPP	A B	A	47	I	1.0	44	58
2DPP	A B	A	49	R	3.0	44	58
2DPP	A B	A	50	V	1.8	44	58
2DPP	A B	A	54	Y	3.6	44	58
2DPP	A B	A	142	R	1.7	137	146
2DPP	A B	A	144	V	1.4	137	146
2DPP	A B	A	145	K	2.1	137	146
2DPP	A B	A	153	E	1.9	147	154
2DPP	A B	B	31	W	1.9	30	45
2DPP	A B	B	33	R	1.0	30	45
2DPP	A B	B	36	F	3.8	30	45
2DPP	A B	B	37	G	60.8	30	45
2DPP	A B	B	38	L	2.3	30	45
2DPP	A B	B	41	G	3.5	30	45
2DPP	A B	B	65	V	1.1	64	68
2DPP	A B	B	66	D	2.2	64	68
2DPP	A B	B	67	Y	1.3	64	68
2DPP	A B	B	77	I	1.0	72	87
2DPP	A B	B	95	L	4.8	92	105
2DPP	A B	B	98	R	1.0	92	105
2DPP	A B	B	99	T	4.9	92	105
2DPP	A B	B	102	F	2.8	92	105
2DPP	A B	B	123	E	1.3	116	129
2DPP	A B	B	126	L	2.9	116	129
2DPP	A B	B	207	W	3.5	203	208
2DQF	B C	C	97	K	1.9	89	99
2DQF	E F	F	97	K	1.4	89	100
2DQT	L H	L	123	E	1.6	122	127
2DQT	L H	L	124	Q	2.1	122	127
2DRN	B C	B	23	L	1.8	11	26
2DS2	A B	A	9	F	3.0	5	11
2DS2	A B	A	21	F	3.2	16	28
2DS2	A B	A	22	I	2.5	16	28
2DS2	A B	A	23	H	1.2	16	28
2DS2	A B	A	25	R	1.9	16	28
2DS2	A B	B	7	L	1.6	6	17
2DS2	A B	B	26	L	1.6	22	37
2DS2	A B	B	33	V	1.7	22	37
2DS2	C D	C	9	F	3.0	3	12
2DS2	C D	C	19	Q	1.0	16	28
2DS2	C D	C	21	F	3.3	16	28
2DS2	C D	C	22	I	3.2	16	28
2DS2	C D	C	23	H	1.0	16	28
2DS2	C D	D	7	L	1.2	5	17
2DS2	C D	D	33	V	1.7	22	37
2DS2	C D	D	47	R	1.1	42	54
2DSQ	A C	A	69	L	5.6	68	74
2DSQ	A C	A	70	H	1.0	68	74
2DSQ	A C	A	73	M	1.4	68	74
2DSQ	A C	C	16	F	2.5	8	19
2DSQ	A C	C	54	L	1.6	54	60
2DSQ	B I	I	16	F	2.1	8	19
2DSQ	B I	I	54	L	1.4	54	60
2DSQ	C H	C	9	E	1.2	8	19

2DSQ	C H	C	10	L	2.3	8	19
2DSQ	C H	H	156	Y	2.6	150	162
2DSQ	I G	I	44	V	1.7	43	51
2DSQ	I G	I	48	C	1.4	43	51
2DSQ	I G	G	155	L	1.1	150	157
2DSQ	I G	G	159	V	1.1	158	164
2DSR	B I	B	69	L	2.7	68	74
2DSR	B I	B	72	L	1.2	68	74
2DSR	B I	B	73	M	1.6	68	74
2DSR	B I	I	9	E	1.4	8	19
2DSR	B I	I	16	F	3.3	8	19
2DSR	B I	I	54	L	1.7	54	60
2DSR	G I	G	157	L	1.2	152	167
2DSR	G I	G	161	L	1.5	152	167
2DSR	G I	G	175	L	1.0	172	178
2DSR	G I	I	9	E	1.1	8	19
2DSR	G I	I	44	V	1.5	43	49
2DSR	G I	I	48	C	1.1	43	49
2DT7	A B	A	81	F	2.3	80	97
2DT7	A B	A	84	F	2.8	80	97
2DT7	A B	A	87	R	1.0	80	97
2DT7	A B	A	95	H	1.4	80	97
2DT7	A B	B	169	L	1.9	161	178
2DT7	A B	B	173	F	2.8	161	178
2DT7	A B	B	181	F	2.7	179	189
2DVQ	B Q	B	155	Y	1.8	150	156
2DWZ	A B	B	338	R	2.1	338	351
2DWZ	A B	B	339	R	1.4	338	351
2DWZ	A B	B	342	R	3.7	338	351
2DWZ	A B	B	361	E	1.1	360	365
2DWZ	C D	C	115	S	1.3	109	116
2DWZ	C D	C	145	R	1.0	142	149
2DWZ	C D	D	338	R	1.3	338	349
2DWZ	C D	D	342	R	3.0	338	349
2DWZ	C D	D	361	E	1.9	360	365
2DWZ	C D	D	362	D	1.0	360	365
2DXB	A B	B	92	R	2.8	87	95
2DXB	A C	A	80	E	1.0	77	81
2DXB	A C	A	98	Q	1.5	98	102
2DXB	A C	C	97	V	1.0	96	100
2DXB	A C	C	157	R	1.5	149	158
2DXB	A C	C	160	R	1.2	159	166
2DXB	A E	E	6	R	3.5	5	19
2DXB	A E	E	9	V	1.2	5	19
2DXB	A K	K	128	L	1.5	128	145
2DXB	A K	K	132	H	3.2	128	145
2DXB	B C	B	67	I	1.0	67	82
2DXB	B C	B	68	W	1.8	67	82
2DXB	B C	B	70	L	1.1	67	82
2DXB	B C	B	73	F	1.4	67	82
2DXB	B C	B	77	E	1.3	67	82
2DXB	B C	B	79	L	1.1	67	82
2DXB	B C	B	81	W	3.8	67	82
2DXB	B C	B	91	R	1.3	87	95
2DXB	B C	B	108	Y	1.0	108	123
2DXB	B C	B	113	L	2.8	108	123
2DXB	B C	B	120	L	1.0	108	123
2DXB	B C	B	130	E	1.7	128	144
2DXB	B C	B	134	K	2.6	128	144
2DXB	B C	B	142	V	1.1	128	144

2DXB	B C	C	27	F	2.4	26	41
2DXB	B C	C	28	E	1.6	26	41
2DXB	B C	C	29	I	1.4	26	41
2DXB	B C	C	30	L	1.9	26	41
2DXB	B C	C	34	V	1.1	26	41
2DXB	B C	C	37	L	1.6	26	41
2DXB	B C	C	48	D	2.5	46	59
2DXB	B C	C	49	H	2.6	46	59
2DXB	B C	C	52	W	2.9	46	59
2DXB	B C	C	53	K	1.8	46	59
2DXB	B C	C	153	R	2.1	149	158
2DXB	B C	C	211	R	2.9	211	216
2DXB	B L	B	40	F	1.6	37	44
2DXB	B L	L	27	F	2.0	26	41
2DXB	D B	B	6	R	3.9	4	19
2DXB	D B	B	9	V	1.0	4	19
2DXB	D E	E	92	R	3.3	87	95
2DXB	D F	D	98	Q	1.5	98	102
2DXB	D F	F	97	V	1.0	96	100
2DXB	D F	F	157	R	1.4	149	158
2DXB	D F	F	160	R	3.9	159	166
2DXB	D H	H	128	L	1.9	128	145
2DXB	D H	H	132	H	3.3	128	145
2DXB	E F	E	68	W	2.7	67	82
2DXB	E F	E	73	F	1.5	67	82
2DXB	E F	E	77	E	1.2	67	82
2DXB	E F	E	79	L	1.1	67	82
2DXB	E F	E	81	W	5.4	67	82
2DXB	E F	E	91	R	1.2	87	95
2DXB	E F	E	110	G	1.2	108	123
2DXB	E F	E	113	L	2.3	108	123
2DXB	E F	E	120	L	1.4	108	123
2DXB	E F	E	130	E	1.8	128	145
2DXB	E F	E	134	K	3.1	128	145
2DXB	E F	E	141	R	1.0	128	145
2DXB	E F	F	27	F	2.5	26	41
2DXB	E F	F	28	E	1.0	26	41
2DXB	E F	F	29	I	1.7	26	41
2DXB	E F	F	30	L	1.8	26	41
2DXB	E F	F	34	V	1.4	26	41
2DXB	E F	F	36	E	2.0	26	41
2DXB	E F	F	37	L	2.0	26	41
2DXB	E F	F	48	D	2.4	46	58
2DXB	E F	F	49	H	2.0	46	58
2DXB	E F	F	52	W	2.8	46	58
2DXB	E F	F	53	K	1.5	46	58
2DXB	E F	F	153	R	2.0	149	158
2DXB	E F	F	154	R	2.3	149	158
2DXB	E F	F	211	R	3.5	211	216
2DXB	E I	E	40	F	1.3	37	44
2DXB	E I	I	27	F	2.1	26	41
2DXB	G E	E	128	L	1.7	128	145
2DXB	G E	E	132	H	3.1	128	145
2DXB	G H	H	92	R	2.9	87	95
2DXB	G I	G	80	E	1.0	77	82
2DXB	G I	I	97	V	1.0	96	100
2DXB	G I	I	157	R	1.5	149	158
2DXB	G I	I	160	R	4.3	159	166
2DXB	G K	K	6	R	3.7	4	19
2DXB	G K	K	9	V	1.2	4	19

2DXB	H F	H	40	F	2.0	37	44
2DXB	H F	F	27	F	2.1	26	41
2DXB	H I	H	67	I	1.0	67	82
2DXB	H I	H	68	W	4.1	67	82
2DXB	H I	H	70	L	1.3	67	82
2DXB	H I	H	71	N	1.7	67	82
2DXB	H I	H	73	F	1.1	67	82
2DXB	H I	H	75	T	1.8	67	82
2DXB	H I	H	77	E	1.2	67	82
2DXB	H I	H	79	L	1.2	67	82
2DXB	H I	H	81	W	4.1	67	82
2DXB	H I	H	91	R	1.2	87	95
2DXB	H I	H	108	Y	1.3	108	123
2DXB	H I	H	113	L	2.9	108	123
2DXB	H I	H	120	L	1.5	108	123
2DXB	H I	H	130	E	1.9	128	145
2DXB	H I	H	134	K	2.6	128	145
2DXB	H I	H	137	E	1.5	128	145
2DXB	H I	H	138	M	1.2	128	145
2DXB	H I	H	141	R	1.3	128	145
2DXB	H I	I	27	F	2.7	26	41
2DXB	H I	I	28	E	1.5	26	41
2DXB	H I	I	29	I	1.3	26	41
2DXB	H I	I	30	L	2.5	26	41
2DXB	H I	I	34	V	1.9	26	41
2DXB	H I	I	36	E	1.6	26	41
2DXB	H I	I	37	L	2.2	26	41
2DXB	H I	I	40	E	1.6	26	41
2DXB	H I	I	48	D	2.5	46	58
2DXB	H I	I	49	H	2.8	46	58
2DXB	H I	I	52	W	3.0	46	58
2DXB	H I	I	53	K	2.1	46	58
2DXB	H I	I	152	R	1.3	149	158
2DXB	H I	I	153	R	2.3	149	158
2DXB	H I	I	154	R	1.0	149	158
2DXB	H I	I	211	R	3.0	211	216
2DXB	J B	B	128	L	1.4	128	144
2DXB	J B	B	132	H	3.1	128	144
2DXB	J H	H	6	R	3.7	3	19
2DXB	J H	H	9	V	1.0	3	19
2DXB	J K	K	92	R	3.5	87	95
2DXB	J L	J	80	E	1.0	77	81
2DXB	J L	J	98	Q	1.3	98	102
2DXB	J L	L	97	V	1.0	96	100
2DXB	J L	L	157	R	1.3	149	158
2DXB	J L	L	160	R	3.9	159	166
2DXB	K C	K	40	F	1.7	37	44
2DXB	K C	C	27	F	1.8	26	41
2DXB	K L	K	68	W	3.0	67	82
2DXB	K L	K	70	L	1.3	67	82
2DXB	K L	K	71	N	1.4	67	82
2DXB	K L	K	73	F	1.2	67	82
2DXB	K L	K	75	T	1.1	67	82
2DXB	K L	K	77	E	1.3	67	82
2DXB	K L	K	79	L	1.2	67	82
2DXB	K L	K	81	W	4.3	67	82
2DXB	K L	K	91	R	1.1	87	95
2DXB	K L	K	110	G	2.5	108	123
2DXB	K L	K	113	L	2.6	108	123
2DXB	K L	K	120	L	1.4	108	123

2DXB	K L	K	130	E	1.7	128	145
2DXB	K L	K	134	K	3.3	128	145
2DXB	K L	L	27	F	2.5	26	41
2DXB	K L	L	29	I	1.5	26	41
2DXB	K L	L	30	L	1.9	26	41
2DXB	K L	L	34	V	1.4	26	41
2DXB	K L	L	36	E	1.8	26	41
2DXB	K L	L	37	L	2.2	26	41
2DXB	K L	L	48	D	1.5	46	58
2DXB	K L	L	49	H	2.6	46	58
2DXB	K L	L	52	W	3.0	46	58
2DXB	K L	L	53	K	1.9	46	58
2DXB	K L	L	153	R	2.2	149	158
2DXB	K L	L	154	R	1.4	149	158
2DXB	K L	L	211	R	3.0	211	216
2DXB	M N	N	92	R	3.8	87	95
2DXB	M O	M	80	E	1.3	77	82
2DXB	M O	M	98	Q	1.1	98	102
2DXB	M O	O	157	R	1.5	149	158
2DXB	M O	O	160	R	1.2	159	166
2DXB	M Q	Q	6	R	3.8	5	19
2DXB	M Q	Q	9	V	1.2	5	19
2DXB	M W	W	128	L	1.6	128	144
2DXB	M W	W	132	H	3.3	128	144
2DXB	M W	W	135	I	1.3	128	144
2DXB	N O	N	68	W	1.8	67	82
2DXB	N O	N	70	L	1.1	67	82
2DXB	N O	N	71	N	1.6	67	82
2DXB	N O	N	73	F	1.5	67	82
2DXB	N O	N	77	E	1.4	67	82
2DXB	N O	N	79	L	1.1	67	82
2DXB	N O	N	81	W	4.7	67	82
2DXB	N O	N	90	R	1.0	87	95
2DXB	N O	N	91	R	1.3	87	95
2DXB	N O	N	109	Y	1.2	108	123
2DXB	N O	N	110	G	2.8	108	123
2DXB	N O	N	113	L	2.9	108	123
2DXB	N O	N	120	L	1.5	108	123
2DXB	N O	N	130	E	1.7	128	145
2DXB	N O	N	134	K	2.9	128	145
2DXB	N O	N	142	V	1.2	128	145
2DXB	N O	O	27	F	2.6	26	41
2DXB	N O	O	29	I	1.6	26	41
2DXB	N O	O	30	L	1.9	26	41
2DXB	N O	O	34	V	1.7	26	41
2DXB	N O	O	36	E	1.6	26	41
2DXB	N O	O	37	L	2.2	26	41
2DXB	N O	O	48	D	2.6	46	59
2DXB	N O	O	49	H	1.6	46	59
2DXB	N O	O	52	W	2.7	46	59
2DXB	N O	O	53	K	1.9	46	59
2DXB	N O	O	144	E	1.0	144	148
2DXB	N O	O	145	W	1.9	144	148
2DXB	N O	O	147	R	1.0	144	148
2DXB	N O	O	152	R	1.1	149	158
2DXB	N O	O	153	R	2.6	149	158
2DXB	N O	O	154	R	1.3	149	158
2DXB	N O	O	156	V	1.1	149	158
2DXB	N O	O	211	R	2.1	211	216
2DXB	N X	N	40	F	1.7	37	44

2DXB	N X	X	27	F	2.0	26	41
2DXB	P N	N	6	R	4.0	4	19
2DXB	P N	N	9	V	1.3	4	19
2DXB	P Q	Q	92	R	2.5	87	95
2DXB	P R	P	80	E	1.2	77	82
2DXB	P R	P	98	Q	1.5	98	102
2DXB	P R	R	97	V	1.0	96	100
2DXB	P R	R	157	R	1.6	149	158
2DXB	P R	R	160	R	1.1	159	166
2DXB	P T	T	128	L	2.0	128	145
2DXB	P T	T	132	H	3.2	128	145
2DXB	Q R	Q	68	W	3.2	67	82
2DXB	Q R	Q	71	N	2.2	67	82
2DXB	Q R	Q	77	E	1.3	67	82
2DXB	Q R	Q	79	L	1.1	67	82
2DXB	Q R	Q	81	W	4.4	67	82
2DXB	Q R	Q	91	R	1.3	87	95
2DXB	Q R	Q	109	Y	1.2	108	123
2DXB	Q R	Q	110	G	1.7	108	123
2DXB	Q R	Q	113	L	2.8	108	123
2DXB	Q R	Q	120	L	1.4	108	123
2DXB	Q R	Q	134	K	1.3	128	144
2DXB	Q R	Q	137	E	1.0	128	144
2DXB	Q R	R	27	F	2.7	26	41
2DXB	Q R	R	29	I	1.3	26	41
2DXB	Q R	R	30	L	1.9	26	41
2DXB	Q R	R	32	M	1.0	26	41
2DXB	Q R	R	34	V	1.4	26	41
2DXB	Q R	R	36	E	1.5	26	41
2DXB	Q R	R	37	L	1.8	26	41
2DXB	Q R	R	48	D	2.3	46	58
2DXB	Q R	R	52	W	2.2	46	58
2DXB	Q R	R	151	Y	1.1	149	158
2DXB	Q R	R	153	R	2.4	149	158
2DXB	Q R	R	154	R	1.3	149	158
2DXB	Q R	R	211	R	2.8	211	216
2DXB	Q U	Q	40	F	1.4	37	44
2DXB	Q U	U	27	F	1.8	26	41
2DXB	S Q	Q	128	L	2.0	128	144
2DXB	S Q	Q	132	H	3.3	128	144
2DXB	S T	T	92	R	3.2	87	95
2DXB	S U	S	80	E	1.3	77	82
2DXB	S U	S	98	Q	1.1	98	102
2DXB	S U	U	157	R	1.3	149	158
2DXB	S U	U	160	R	4.3	159	166
2DXB	S W	W	6	R	3.8	4	19
2DXB	S W	W	9	V	1.1	4	19
2DXB	T R	T	40	F	1.8	37	44
2DXB	T R	R	27	F	2.0	26	41
2DXB	T U	T	68	W	1.9	67	82
2DXB	T U	T	71	N	1.4	67	82
2DXB	T U	T	73	F	1.1	67	82
2DXB	T U	T	75	T	1.0	67	82
2DXB	T U	T	77	E	1.5	67	82
2DXB	T U	T	79	L	1.1	67	82
2DXB	T U	T	81	W	4.9	67	82
2DXB	T U	T	91	R	1.1	87	95
2DXB	T U	T	108	Y	1.2	108	123
2DXB	T U	T	113	L	2.6	108	123
2DXB	T U	T	120	L	1.5	108	123

2DXB	T U	T	130	E	1.7	128	145
2DXB	T U	T	134	K	2.8	128	145
2DXB	T U	T	141	R	1.4	128	145
2DXB	T U	U	27	F	2.7	26	41
2DXB	T U	U	28	E	1.5	26	41
2DXB	T U	U	29	I	1.6	26	41
2DXB	T U	U	30	L	1.8	26	41
2DXB	T U	U	31	E	1.3	26	41
2DXB	T U	U	34	V	1.6	26	41
2DXB	T U	U	36	E	1.6	26	41
2DXB	T U	U	37	L	2.3	26	41
2DXB	T U	U	48	D	2.4	46	59
2DXB	T U	U	49	H	2.8	46	59
2DXB	T U	U	52	W	2.9	46	59
2DXB	T U	U	144	E	1.0	144	148
2DXB	T U	U	145	W	1.9	144	148
2DXB	T U	U	147	R	1.1	144	148
2DXB	T U	U	152	R	1.1	149	158
2DXB	T U	U	153	R	2.1	149	158
2DXB	T U	U	154	R	1.4	149	158
2DXB	T U	U	211	R	2.4	211	216
2DXB	V N	N	121	V	1.2	108	123
2DXB	V N	N	128	L	2.1	128	145
2DXB	V N	N	132	H	3.2	128	145
2DXB	V T	T	6	R	3.8	3	19
2DXB	V T	T	9	V	1.0	3	19
2DXB	V T	T	10	H	1.0	3	19
2DXB	V W	W	92	R	4.0	87	95
2DXB	V X	V	98	Q	1.5	98	102
2DXB	V X	X	97	V	1.0	96	100
2DXB	V X	X	157	R	1.5	149	158
2DXB	V X	X	160	R	4.2	159	166
2DXB	W O	W	40	F	2.0	37	44
2DXB	W O	O	27	F	2.2	26	41
2DXB	W O	O	149	P	1.1	149	158
2DXB	W X	W	68	W	3.0	67	82
2DXB	W X	W	70	L	1.4	67	82
2DXB	W X	W	71	N	1.4	67	82
2DXB	W X	W	73	F	1.5	67	82
2DXB	W X	W	75	T	1.1	67	82
2DXB	W X	W	77	E	1.1	67	82
2DXB	W X	W	79	L	1.1	67	82
2DXB	W X	W	81	W	4.2	67	82
2DXB	W X	W	91	R	1.2	87	95
2DXB	W X	W	113	L	2.9	108	123
2DXB	W X	W	120	L	1.0	108	123
2DXB	W X	W	130	E	1.8	128	144
2DXB	W X	W	134	K	2.7	128	144
2DXB	W X	X	27	F	2.6	26	41
2DXB	W X	X	28	E	1.5	26	41
2DXB	W X	X	29	I	1.3	26	41
2DXB	W X	X	30	L	2.0	26	41
2DXB	W X	X	34	V	1.7	26	41
2DXB	W X	X	37	L	2.2	26	41
2DXB	W X	X	48	D	2.6	46	59
2DXB	W X	X	49	H	2.5	46	59
2DXB	W X	X	52	W	2.9	46	59
2DXB	W X	X	53	K	2.0	46	59
2DXB	W X	X	56	V	1.0	46	59
2DXB	W X	X	151	Y	1.2	149	158

2DXB	W X	X	153	R	2.1	149	158
2DXB	W X	X	154	R	1.4	149	158
2DXB	W X	X	211	R	3.3	211	216
2DXB	W X	X	212	D	3.0	211	216
2DYM	A B	A	4	I	1.3	0	11
2DYM	A B	A	7	L	1.3	0	11
2DYM	A B	B	28	L	1.7	24	41
2DYM	A B	B	29	I	1.0	24	41
2DYM	A B	B	31	R	1.3	24	41
2DYM	A B	B	32	L	2.7	24	41
2DYM	A B	B	35	R	3.3	24	41
2DYM	A B	B	36	N	1.3	24	41
2DYM	A B	B	38	K	1.5	24	41
2DYM	C D	C	4	I	1.4	0	10
2DYM	C D	C	7	L	1.4	0	10
2DYM	C D	D	28	L	1.2	24	41
2DYM	C D	D	29	I	1.5	24	41
2DYM	C D	D	31	R	1.3	24	41
2DYM	C D	D	32	L	2.5	24	41
2DYM	E F	E	4	I	1.6	0	10
2DYM	E F	E	7	L	1.5	0	10
2DYM	E F	F	28	L	1.8	24	41
2DYM	E F	F	29	I	1.5	24	41
2DYM	E F	F	31	R	1.8	24	41
2DYM	E F	F	32	L	2.6	24	41
2DYM	E F	F	35	R	3.9	24	41
2DYM	E F	F	39	E	1.4	24	41
2DYM	G H	G	7	L	1.4	0	10
2DYM	G H	H	28	L	1.9	24	41
2DYM	G H	H	29	I	1.3	24	41
2DYM	G H	H	31	R	1.7	24	41
2DYM	G H	H	32	L	2.0	24	41
2DYM	G H	H	35	R	2.2	24	41
2DZN	A B	A	81	S	1.0	75	83
2DZN	A B	A	146	R	1.2	143	150
2DZN	A B	B	404	Q	1.2	404	413
2DZN	C D	C	42	W	1.3	39	46
2DZN	C D	C	45	S	1.7	39	46
2DZN	C D	C	180	H	1.7	177	184
2DZN	C D	D	369	D	1.1	368	373
2DZN	E F	E	81	S	1.0	75	83
2DZN	E F	E	116	G	9.1	110	117
2E 30	A B	A	142	M	1.3	142	146
2E 30	A B	A	175	E	1.0	172	183
2E 30	A B	A	185	V	1.2	185	189
2E 30	A B	B	522	I	5.5	518	538
2E 30	A B	B	523	H	1.0	518	538
2E 30	A B	B	533	G	158.7	518	538
2E 30	A B	B	535	E	1.2	518	538
2E 32	A B	A	62	V	1.5	56	65
2E 32	A B	A	70	E	1.3	68	76
2E 32	A B	A	83	K	1.7	80	87
2E 32	C D	C	58	L	1.2	56	66
2E 32	C D	C	62	V	1.7	56	66
2E 32	C D	C	65	E	1.8	56	66
2E 32	C D	C	70	E	1.2	68	76
2E 32	C D	C	83	K	1.7	80	87
2E 32	C D	D	98	G	4.4	97	104
2E 32	C D	D	101	F	1.7	97	104
2E 74	A B	A	21	V	2.9	14	22

2E 74	A B	A	46	I	1.2	35	56
2E 74	A B	A	66	Y	3.4	62	76
2E 74	A B	A	84	S	1.0	79	106
2E 74	A B	A	85	I	1.0	79	106
2E 74	A B	A	88	W	3.7	79	106
2E 74	A B	A	105	Y	2.0	79	106
2E 74	A B	A	122	V	1.4	115	137
2E 74	A B	A	132	G	75.8	115	137
2E 74	A B	A	142	Q	1.7	142	149
2E 74	A B	A	145	Y	1.5	142	149
2E 74	A B	A	146	W	14.2	142	149
2E 74	A B	B	51	I	1.8	33	58
2E 74	A B	B	54	L	1.3	33	58
2E 74	A B	B	95	L	1.1	94	103
2E 74	A B	B	112	P	1.5	104	115
2E 74	A B	B	133	F	3.2	127	148
2E 74	A D	D	37	P	2.4	13	43
2E 74	A D	D	41	Y	4.6	13	43
2E 74	A D	D	42	F	2.1	13	43
2E 74	A G	A	88	W	1.3	79	106
2E 74	A G	A	95	L	2.5	79	106
2E 74	A G	A	99	L	1.9	79	106
2E 74	A G	A	102	F	1.5	79	106
2E 74	A G	G	18	L	1.5	4	29
2E 74	A G	G	20	G	37.8	4	29
2E 74	A G	G	21	L	2.4	4	29
2E 74	B C	B	35	D	1.0	33	58
2E 74	B C	B	38	Y	3.2	33	58
2E 74	B C	B	42	V	1.5	33	58
2E 74	B C	B	45	M	1.0	33	58
2E 74	B C	B	52	V	1.3	33	58
2E 74	B C	C	258	M	1.9	252	288
2E 74	B C	C	261	F	1.3	252	288
2E 74	B C	C	272	L	1.7	252	288
2E 74	B C	C	276	K	1.8	252	288
2E 74	B G	B	141	I	1.0	127	148
2E 74	B G	G	10	V	1.4	4	29
2E 74	B G	G	18	L	1.1	4	29
2E 74	B G	G	22	F	1.6	4	29
2E 74	B H	B	42	V	1.0	33	58
2E 74	B H	B	57	L	1.6	33	58
2E 74	B H	H	7	G	3.0	3	26
2E 74	B H	H	8	W	2.5	3	26
2E 74	B H	H	11	L	1.6	3	26
2E 74	C D	C	261	F	1.9	252	288
2E 74	C D	C	272	L	1.0	252	288
2E 74	C D	D	30	V	1.3	13	43
2E 74	C E	C	266	M	1.2	252	288
2E 74	C E	C	270	L	1.9	252	288
2E 74	C E	E	15	F	2.6	2	28
2E 74	C H	C	255	V	1.5	252	288
2E 74	C H	C	259	I	1.0	252	288
2E 74	C H	C	262	I	1.1	252	288
2E 74	C H	H	3	I	1.0	3	26
2E 74	C H	H	7	G	2.8	3	26
2E 74	C H	H	17	W	1.0	3	26
2E 74	C H	H	25	G	254.1	3	26
2E 74	E H	E	7	F	1.4	2	28
2E 74	E H	E	11	F	1.6	2	28
2E 74	E H	H	5	V	1.0	3	26

2E 74	E H	H	6	L	4.4	3	26
2E 74	E H	H	9	V	1.8	3	26
2E 74	E H	H	17	W	1.9	3	26
2E 74	F G	G	8	G	52.4	4	29
2E 74	F G	G	12	G	27.2	4	29
2E 74	F H	F	19	G	3.2	3	31
2E 74	F H	F	23	G	40.1	3	31
2E 74	F H	F	26	L	1.1	3	31
2E 74	F H	H	15	F	1.1	3	26
2E1M	A C	A	23	L	2.1	19	29
2E1M	A C	A	26	E	1.9	19	29
2E1M	A C	A	40	K	2.1	39	51
2E1M	A C	A	42	R	1.0	39	51
2E1M	A C	A	43	Y	1.5	39	51
2E1M	A C	A	72	V	1.1	68	80
2E1M	A C	A	77	L	1.7	68	80
2E1M	A C	A	205	R	2.3	205	211
2E1M	A C	A	336	L	1.2	333	344
2E1M	A C	C	626	M	1.1	625	629
2E1M	A C	C	630	H	2.0	630	635
2E1M	A C	C	631	L	2.2	630	635
2E1M	A C	C	654	I	2.2	654	670
2E1M	A C	C	655	E	4.5	654	670
2E1M	A C	C	658	V	1.9	654	670
2E1M	A C	C	659	E	1.3	654	670
2E1M	A C	C	662	V	2.2	654	670
2E1M	A C	C	663	R	1.1	654	670
2E1M	A C	C	666	I	1.7	654	670
2E1M	B C	B	407	F	1.2	407	412
2E1M	B C	B	454	W	3.0	451	462
2E1M	B C	B	458	L	1.1	451	462
2E1M	B C	C	587	L	1.1	576	592
2E1M	B C	C	595	I	1.3	593	599
2E1M	B C	C	597	V	2.4	593	599
2E1M	B C	C	598	F	4.2	593	599
2E1M	B C	C	625	Q	1.3	625	629
2E2D	A C	A	222	H	1.1	216	228
2E2D	A C	A	226	H	2.5	216	228
2E2D	A C	C	1151	W	2.3	1150	1154
2E3K	C Q	C	428	Y	1.2	411	429
2E3X	A B	A	340	E	1.1	335	341
2E3X	B C	B	23	W	1.0	23	31
2E5L	C N	C	9	G	74.2	7	12
2E5L	C N	N	49	H	1.3	41	51
2E5L	D E	D	57	R	1.4	53	68
2E5L	D E	D	202	L	1.5	200	207
2E5L	D E	D	205	E	1.9	200	207
2E5L	D E	E	107	R	2.4	104	113
2E5L	E H	E	151	L	2.1	145	152
2E5L	F R	R	62	E	3.0	60	76
2E5L	G K	K	59	Y	2.8	58	75
2E5L	J N	N	44	L	1.7	41	51
2E5L	J N	N	45	R	1.1	41	51
2E5L	J N	N	49	H	1.2	41	51
2E5L	L Q	L	10	L	1.3	7	14
2E5L	L Q	L	11	V	1.0	7	14
2E7L	A E	E	155	Y	2.0	152	175
2E7L	B F	F	155	Y	2.0	152	172
2E9W	A C	C	78	K	1.1	72	91
2E9X	A C	A	10	I	2.5	4	16

2E9X	A C	A	14	H	1.3	4	16
2E9X	A C	A	71	R	3.3	58	94
2E9X	A C	A	74	R	1.9	58	94
2E9X	A C	A	81	Y	1.3	58	94
2E9X	A C	A	86	R	1.5	58	94
2E9X	A C	C	1022	L	2.3	1022	1028
2E9X	A C	C	1025	I	2.2	1022	1028
2E9X	A C	C	1026	L	2.5	1022	1028
2E9X	A C	C	1071	W	1.6	1070	1076
2E9X	A C	C	1075	G	36.7	1070	1076
2E9X	A D	A	33	L	1.8	26	50
2E9X	A D	A	36	M	1.3	26	50
2E9X	A D	A	40	Y	1.9	26	50
2E9X	A D	A	73	R	1.2	58	94
2E9X	A D	A	77	V	1.0	58	94
2E9X	A D	A	80	L	1.1	58	94
2E9X	A D	A	84	L	1.8	58	94
2E9X	A D	A	92	W	1.1	58	94
2E9X	A D	A	113	W	2.2	108	129
2E9X	A D	A	124	Y	2.1	108	129
2E9X	A D	D	55	M	1.3	48	61
2E9X	A D	D	87	Y	3.4	72	103
2E9X	A D	D	94	R	2.5	72	103
2E9X	A D	D	97	L	1.5	72	103
2E9X	A D	D	129	F	3.3	124	147
2E9X	A D	D	133	F	2.8	124	147
2E9X	A D	D	140	Y	3.1	124	147
2E9X	A D	D	141	L	1.2	124	147
2E9X	A F	A	102	L	1.0	100	105
2E9X	A F	A	104	F	2.2	100	105
2E9X	A F	F	130	V	1.0	110	138
2E9X	A F	F	137	R	1.0	110	138
2E9X	B C	B	121	W	1.9	110	138
2E9X	B C	B	129	R	2.2	110	138
2E9X	B C	B	151	M	1.6	150	171
2E9X	B C	B	155	T	1.0	150	171
2E9X	B C	B	156	S	2.4	150	171
2E9X	B C	B	159	F	6.8	150	171
2E9X	B C	B	162	Q	1.7	150	171
2E9X	B C	B	166	H	2.2	150	171
2E9X	B C	B	169	K	1.9	150	171
2E9X	B C	B	170	L	3.2	150	171
2E9X	B C	C	1117	Y	1.6	1116	1125
2E9X	B C	C	1139	L	1.1	1131	1145
2E9X	B C	C	1142	F	1.9	1131	1145
2E9X	B C	C	1143	I	1.0	1131	1145
2E9X	B C	C	1146	F	4.7	1146	1154
2E9X	B C	C	1150	M	3.6	1146	1154
2E9X	B C	C	1171	M	1.3	1170	1191
2E9X	B C	C	1175	L	3.6	1170	1191
2E9X	B C	C	1179	G	37.6	1170	1191
2E9X	B C	C	1181	K	1.2	1170	1191
2E9X	B C	C	1182	G	10.2	1170	1191
2E9X	B C	C	1185	D	1.3	1170	1191
2E9X	B C	C	1186	F	2.8	1170	1191
2E9X	B C	C	1189	W	4.0	1170	1191
2E9X	B D	B	5	E	1.8	3	11
2E9X	B D	B	8	F	2.9	3	11
2E9X	B D	B	9	L	1.0	3	11
2E9X	B D	B	47	W	1.6	46	55

2E9X	B D	B	52	L	1.0	46	55
2E9X	B D	B	153	I	1.2	150	171
2E9X	B D	B	164	L	1.0	150	171
2E9X	B D	D	31	E	1.8	23	40
2E9X	B D	D	34	W	2.0	23	40
2E9X	B D	D	35	M	1.0	23	40
2E9X	B D	D	38	K	1.5	23	40
2E9X	B D	D	39	F	1.2	23	40
2E9X	B D	D	73	L	2.1	72	103
2E9X	B D	D	77	I	2.0	72	103
2E9X	B D	D	84	R	3.7	72	103
2E9X	C D	D	98	M	4.3	72	103
2E9X	C D	D	102	K	3.4	72	103
2E9X	E F	F	8	F	1.0	3	11
2E9X	E G	E	10	I	2.6	4	16
2E9X	E G	E	64	F	2.4	58	95
2E9X	E G	E	67	C	1.0	58	95
2E9X	E G	E	74	R	2.7	58	95
2E9X	E G	E	81	Y	1.0	58	95
2E9X	E G	E	85	L	1.0	58	95
2E9X	E G	E	86	R	1.3	58	95
2E9X	E G	E	93	E	1.0	58	95
2E9X	E G	G	22	L	2.0	22	28
2E9X	E G	G	25	I	2.6	22	28
2E9X	E G	G	72	L	1.6	70	76
2E9X	E G	G	75	G	33.3	70	76
2E9X	E H	E	33	L	1.8	26	52
2E9X	E H	E	36	M	1.3	26	52
2E9X	E H	E	40	Y	1.9	26	52
2E9X	E H	E	73	R	1.0	58	95
2E9X	E H	E	80	L	1.1	58	95
2E9X	E H	E	84	L	1.4	58	95
2E9X	E H	E	92	W	1.2	58	95
2E9X	E H	E	113	W	2.3	108	127
2E9X	E H	E	117	Y	2.5	108	127
2E9X	E H	E	124	Y	2.7	108	127
2E9X	E H	H	55	M	1.0	48	64
2E9X	E H	H	87	Y	3.0	73	103
2E9X	E H	H	93	L	2.0	73	103
2E9X	E H	H	94	R	2.9	73	103
2E9X	E H	H	97	L	1.0	73	103
2E9X	E H	H	129	F	2.3	124	148
2E9X	E H	H	133	F	1.2	124	148
2E9X	E H	H	137	T	1.3	124	148
2E9X	E H	H	140	Y	2.6	124	148
2E9X	E H	H	144	V	1.0	124	148
2E9X	F G	F	97	K	1.2	92	102
2E9X	F G	F	121	W	2.2	110	138
2E9X	F G	F	129	R	1.1	110	138
2E9X	F G	F	151	M	1.5	150	172
2E9X	F G	F	155	T	1.0	150	172
2E9X	F G	F	159	F	4.9	150	172
2E9X	F G	F	166	H	2.5	150	172
2E9X	F G	F	167	M	1.0	150	172
2E9X	F G	F	170	L	2.8	150	172
2E9X	F G	G	117	Y	1.7	116	126
2E9X	F G	G	139	L	1.1	131	154
2E9X	F G	G	142	F	1.4	131	154
2E9X	F G	G	146	F	3.4	131	154
2E9X	F G	G	150	M	2.1	131	154

2E9X	F G	G	175	L	2.3	170	192
2E9X	F G	G	179	G	4.5	170	192
2E9X	F G	G	182	G	3.3	170	192
2E9X	F G	G	186	F	3.3	170	192
2E9X	F G	G	189	W	4.0	170	192
2E9X	F H	F	5	E	1.5	3	11
2E9X	F H	F	8	F	1.1	3	11
2E9X	F H	F	9	L	1.0	3	11
2E9X	F H	F	47	W	2.4	46	55
2E9X	F H	F	48	L	1.1	46	55
2E9X	F H	F	150	L	1.3	150	172
2E9X	F H	F	153	I	1.1	150	172
2E9X	F H	F	161	T	1.3	150	172
2E9X	F H	F	165	N	1.6	150	172
2E9X	F H	F	168	Y	1.6	150	172
2E9X	F H	H	23	P	1.3	23	40
2E9X	F H	H	34	W	2.5	23	40
2E9X	F H	H	73	L	1.6	73	103
2E9X	F H	H	74	K	1.5	73	103
2E9X	F H	H	77	I	2.4	73	103
2E9X	F H	H	78	H	1.0	73	103
2E9X	F H	H	81	E	1.1	73	103
2E9X	F H	H	84	R	2.8	73	103
2EC6	A B	A	811	L	1.5	801	812
2EC6	A B	A	815	Q	1.5	813	821
2EC6	A B	A	817	N	5.7	813	821
2EC6	A B	A	818	I	2.2	813	821
2EC6	A B	A	819	R	2.6	813	821
2EC6	A B	B	119	L	1.4	112	121
2EC6	A B	B	130	E	1.3	128	135
2EC6	A B	B	150	F	1.0	149	154
2EC6	A C	A	784	I	14.0	784	792
2EC6	A C	A	785	I	1.5	784	792
2EC6	A C	A	787	M	11.3	784	792
2EC6	A C	A	788	F	4.0	784	792
2EC6	A C	A	791	H	2.0	784	792
2EC6	A C	A	794	G	6.8	794	798
2EC6	A C	A	796	L	1.0	794	798
2EC6	A C	A	801	Y	1.7	801	812
2EC6	A C	C	39	R	1.5	37	41
2EC6	A C	C	47	N	12.3	47	52
2EC6	A C	C	87	Y	11.6	84	91
2EC6	A C	C	89	E	3.4	84	91
2EC6	A C	C	149	V	1.6	146	152
2EC6	A C	C	150	M	1.1	146	152
2EFC	A B	A	171	L	1.0	152	177
2EFC	A B	A	185	D	1.5	184	199
2EFC	A B	A	187	F	1.7	184	199
2EFC	A B	A	188	L	1.6	184	199
2EFC	A B	A	225	Y	4.7	222	239
2EFC	A B	A	228	T	1.0	222	239
2EFC	A B	A	236	F	2.3	222	239
2EFC	A B	B	23	K	1.5	23	32
2EFC	A B	B	75	L	1.9	75	80
2EFC	A B	B	79	Y	3.5	75	80
2EFC	A D	A	73	E	2.1	72	90
2EFC	A D	D	29	R	1.4	23	32
2EFC	C B	C	73	E	1.8	72	90
2EFC	C B	C	164	K	1.1	152	177
2EFC	C B	B	29	R	1.3	23	32

2EFC	C D	C	171	L	1.1	152	177
2EFC	C D	C	188	L	1.3	184	199
2EFC	C D	C	225	Y	4.7	222	239
2EFC	C D	C	236	F	2.0	222	239
2EFC	C D	D	23	K	1.3	23	32
2EFC	C D	D	75	L	1.8	73	80
2EFC	C D	D	79	Y	1.1	73	80
2EG4	A B	A	224	E	1.4	218	225
2EG4	A B	B	221	W	1.2	218	225
2EG4	A B	B	224	E	2.2	218	225
2EH8	L H	L	123	E	1.0	122	127
2EH8	L H	L	124	Q	1.2	122	127
2EHB	A D	A	64	L	1.3	57	65
2EHB	A D	A	74	F	1.3	73	83
2EHB	A D	A	119	Y	1.6	108	120
2EHB	A D	A	132	L	1.6	129	143
2EHB	A D	A	139	L	2.0	129	143
2EHB	A D	A	142	E	2.3	129	143
2EHB	A D	A	176	W	1.5	173	183
2EHB	A D	D	313	F	5.6	312	317
2EHB	A D	D	315	M	1.3	312	317
2EHB	A D	D	316	I	2.0	312	317
2EHO	A B	A	86	R	1.2	84	97
2EHO	A B	A	87	Y	3.1	84	97
2EHO	A B	A	93	L	1.1	84	97
2EHO	A B	A	129	F	2.2	124	133
2EHO	A B	A	137	T	1.1	136	148
2EHO	A B	A	140	Y	1.5	136	148
2EHO	A B	B	40	Y	1.4	38	42
2EHO	A B	B	80	L	1.1	58	92
2EHO	A B	B	84	L	1.0	58	92
2EHO	A B	B	113	W	2.3	113	124
2EHO	A B	B	117	Y	2.1	113	124
2EHO	A C	A	23	P	6.0	23	34
2EHO	A C	A	31	E	1.6	23	34
2EHO	A C	A	73	L	1.4	73	79
2EHO	A C	A	77	I	1.6	73	79
2EHO	A C	A	87	Y	1.4	84	97
2EHO	A C	C	8	F	1.3	3	11
2EHO	A C	C	47	W	2.1	46	55
2EHO	B D	B	10	I	3.0	9	15
2EHO	B D	B	14	H	2.1	9	15
2EHO	B D	B	74	R	1.0	58	92
2EHO	B D	B	78	A	8.6	58	92
2EHO	B D	B	82	D	1.1	58	92
2EHO	B D	D	22	L	1.7	22	26
2EHO	B D	D	75	G	7.4	70	77
2EHO	B D	D	76	L	1.0	70	77
2EHO	B H	B	104	F	1.3	101	105
2EHO	C D	C	97	K	1.4	95	103
2EHO	C D	C	129	R	1.7	124	138
2EHO	C D	C	159	F	2.6	156	166
2EHO	C D	D	175	L	1.4	173	184
2EHO	C D	D	179	G	7.0	173	184
2EHO	C D	D	182	G	1.2	173	184
2EHO	E F	E	87	Y	3.3	84	97
2EHO	E F	E	94	R	1.4	84	97
2EHO	E F	E	137	T	1.0	136	148
2EHO	E F	E	140	Y	2.5	136	148
2EHO	E F	E	141	L	1.1	136	148

2EHO	E F	F	40	Y	1.4	38	49
2EHO	E F	F	77	V	1.0	58	94
2EHO	E F	F	80	L	1.3	58	94
2EHO	E F	F	84	L	1.1	58	94
2EHO	E G	E	31	E	1.7	23	34
2EHO	E G	E	73	L	1.0	73	79
2EHO	E G	E	77	I	1.4	73	79
2EHO	E G	E	84	R	4.2	84	97
2EHO	E G	G	8	F	2.8	3	12
2EHO	E G	G	11	E	1.5	3	12
2EHO	E G	G	47	W	4.0	46	55
2EHO	E G	G	164	L	1.4	157	166
2EHO	F D	F	101	A	1.9	100	105
2EHO	F D	F	104	F	2.8	100	105
2EHO	F H	F	10	I	2.4	9	16
2EHO	F H	F	61	T	1.1	58	94
2EHO	F H	F	64	F	1.6	58	94
2EHO	F H	F	74	R	5.0	58	94
2EHO	F H	F	81	Y	1.2	58	94
2EHO	F H	F	85	L	1.0	58	94
2EHO	F H	F	86	R	1.3	58	94
2EHO	F H	H	72	L	1.6	70	77
2EHO	F H	H	75	G	3.5	70	77
2EHO	G H	G	97	K	1.3	95	99
2EHO	G H	G	159	F	1.4	157	166
2EHO	G H	G	162	Q	2.2	157	166
2EHO	G H	H	139	L	1.3	131	149
2EHO	G H	H	142	F	1.9	131	149
2EHO	G H	H	146	F	2.1	131	149
2EHO	G H	H	147	R	1.7	131	149
2EHO	G H	H	175	L	1.6	173	190
2EHO	G H	H	179	G	8.1	173	190
2EHO	G H	H	186	F	1.4	173	190
2EHO	G H	H	189	W	1.8	173	190
2EHO	I J	I	86	R	1.2	84	97
2EHO	I J	I	87	Y	2.1	84	97
2EHO	I J	I	93	L	1.1	84	97
2EHO	I J	I	132	E	1.4	124	133
2EHO	I J	I	136	N	1.3	136	148
2EHO	I J	I	140	Y	4.7	136	148
2EHO	I J	J	33	L	1.0	26	35
2EHO	I J	J	40	Y	1.8	38	52
2EHO	I J	J	77	V	1.0	58	92
2EHO	I J	J	84	L	1.7	58	92
2EHO	I J	J	116	N	1.5	113	124
2EHO	I J	J	120	S	1.0	113	124
2EHO	I K	I	78	H	1.1	72	79
2EHO	I K	I	84	R	2.8	84	97
2EHO	I K	I	87	Y	1.2	84	97
2EHO	I K	I	88	V	1.4	84	97
2EHO	I K	K	8	F	2.7	3	11
2EHO	I K	K	47	W	2.2	46	55
2EHO	I K	K	48	L	1.0	46	55
2EHO	I K	K	51	N	1.5	46	55
2EHO	I K	K	165	N	1.2	157	166
2EHO	J L	J	10	I	1.5	9	15
2EHO	J L	J	61	T	1.0	58	92
2EHO	J L	J	64	F	2.6	58	92
2EHO	J L	L	22	L	1.6	22	26
2EHO	J L	L	71	W	1.5	70	77

2EHO	J L	L	72	L	3.2	70	77
2EHO	J L	L	75	G	4.2	70	77
2EHO	J L	L	76	L	1.5	70	77
2EHO	K H	H	96	W	3.4	94	103
2EHO	K H	H	148	R	1.9	131	149
2EHO	K L	K	97	K	1.1	95	102
2EHO	K L	K	136	V	1.5	122	138
2EHO	K L	L	143	I	1.1	131	145
2EHO	K L	L	179	G	27.8	173	191
2EHO	K L	L	182	G	23.1	173	191
2EHO	K L	L	186	F	2.0	173	191
2EHO	K L	L	189	W	2.0	173	191
2EJF	A C	A	27	K	1.4	22	28
2EJF	B D	B	80	F	1.6	75	93
2EKE	A C	A	17	R	2.5	4	19
2EKE	B D	B	17	R	2.4	4	19
2EKV	A B	A	809	G	2.6	807	814
2EKV	A B	A	810	L	1.8	807	814
2EKV	A B	A	819	K	2.5	815	825
2EKV	A B	A	821	L	3.4	815	825
2EKV	A B	A	828	W	6.2	828	832
2EKV	A B	A	829	W	1.1	828	832
2EKV	A B	A	831	L	1.3	828	832
2EKV	A B	B	41	M	1.8	35	42
2EKV	A B	B	57	M	1.2	57	61
2EKV	A B	B	70	F	1.8	67	74
2EKV	A B	B	76	E	2.4	75	81
2EKV	A B	B	80	G	7.0	75	81
2EKV	A B	B	93	M	1.0	85	94
2EKV	A C	A	17	R	1.5	17	25
2EKV	A C	A	780	L	1.2	768	806
2EKV	A C	A	784	I	1.3	768	806
2EKV	A C	A	787	F	4.2	768	806
2EKV	A C	A	788	Q	7.0	768	806
2EKV	A C	A	790	H	1.5	768	806
2EKV	A C	A	791	I	10.5	768	806
2EKV	A C	A	792	R	9.1	768	806
2EKV	A C	A	793	G	37.5	768	806
2EKV	A C	A	794	Y	13.0	768	806
2EKV	A C	A	795	L	1.2	768	806
2EKV	A C	A	796	M	8.9	768	806
2EKV	A C	A	798	K	10.3	768	806
2EKV	A C	A	803	L	1.2	768	806
2EKV	A C	C	20	F	1.3	5	22
2EKV	A C	C	86	E	1.8	84	94
2EKV	A C	C	91	F	1.2	84	94
2EKV	A C	C	111	L	1.0	104	114
2EKV	A C	C	125	D	8.4	120	130
2EKV	A C	C	126	I	9.8	120	130
2EKV	A C	C	129	F	10.5	120	130
2EKV	A C	C	149	V	1.4	142	150
2EMT	B D	B	288	H	1.2	274	295
2EQ7	A C	C	133	P	1.2	133	142
2EQ7	B C	C	160	K	1.0	160	166
2EQ9	A C	A	431	E	2.5	419	432
2EQ9	A C	C	136	R	2.8	133	142
2EQ9	A C	C	140	R	1.1	133	142
2EQ9	B C	B	438	D	1.7	436	442
2EQ9	B C	B	441	L	1.4	436	442
2EQ9	B C	C	133	P	1.5	133	142

2EQ9	B C	C	137	K	1.1	133	142
2EQ9	D F	D	431	E	2.1	419	432
2EQ9	D F	F	136	R	2.2	133	142
2EQ9	D F	F	140	R	1.3	133	142
2EQ9	E F	E	438	D	1.1	436	442
2EQ9	E F	F	133	P	3.9	133	142
2EQ9	G I	I	137	K	1.1	133	142
2EQ9	G I	I	140	R	1.8	133	142
2EQ9	H I	H	438	D	1.2	436	441
2EQ9	J L	J	431	E	1.4	419	432
2EQ9	J L	L	136	R	2.3	133	143
2EQ9	J L	L	140	R	2.0	133	143
2EQ9	K L	K	438	D	1.9	436	441
2EQ9	K L	L	133	P	1.5	133	143
2EQB	A B	A	49	F	1.4	49	54
2EQB	A B	A	89	Y	1.4	83	93
2EQB	A B	B	102	E	2.4	84	137
2EQB	A B	B	103	D	1.3	84	137
2EQB	A B	B	109	F	3.2	84	137
2EQB	A C	A	49	F	2.2	49	54
2EQB	A C	A	53	I	1.6	49	54
2EQB	A C	A	85	I	1.3	83	93
2EQB	A C	C	104	L	1.3	91	136
2EQB	A C	C	108	L	1.4	91	136
2ERJ	A D	D	65	P	2.7	63	74
2ERJ	A D	D	72	L	1.2	63	74
2ERJ	B D	D	16	H	1.5	4	29
2ERJ	B D	D	19	L	1.1	4	29
2ERJ	B D	D	20	D	1.9	4	29
2ERJ	B D	D	84	D	1.1	82	98
2ERJ	B D	D	88	N	1.3	82	98
2ERJ	B D	D	95	E	1.1	82	98
2ERJ	C D	D	130	S	4.1	114	133
2ERJ	E H	H	35	K	1.5	35	41
2ERJ	E H	H	38	R	1.5	35	41
2ERJ	E H	H	65	P	1.4	63	71
2ERJ	F H	H	16	H	2.9	4	29
2ERJ	F H	H	19	L	1.0	4	29
2ERJ	F H	H	88	N	2.7	82	98
2ERJ	F H	H	91	V	1.7	82	98
2ERJ	F H	H	92	I	1.1	82	98
2ERJ	F H	H	95	E	1.2	82	98
2ES4	A D	A	63	E	1.4	61	77
2ES4	A D	A	66	L	2.8	61	77
2ES4	A D	A	312	N	1.4	303	317
2ES4	A D	A	313	R	2.7	303	317
2ES4	A D	A	316	L	1.4	303	317
2ES4	A D	D	87	E	1.7	83	91
2ES4	A D	D	158	M	1.0	155	174
2ES4	A D	D	188	Q	1.3	182	199
2ES4	A D	D	237	V	1.8	221	246
2ES4	A D	D	240	I	1.2	221	246
2ES4	A D	D	268	R	1.0	263	297
2ES4	A D	D	276	D	3.0	263	297
2ES4	A D	D	322	I	1.1	320	329
2ES4	A D	D	323	R	1.4	320	329
2ES4	A D	D	326	S	1.2	320	329
2ES4	B E	B	63	E	1.2	61	77
2ES4	B E	B	245	L	1.0	242	257
2ES4	B E	B	312	N	1.4	303	317

2ES4	B E	B	313	R	2.7	303	317
2ES4	B E	B	316	L	1.4	303	317
2ES4	B E	E	87	E	1.3	83	91
2ES4	B E	E	158	M	2.3	155	174
2ES4	B E	E	195	I	2.8	182	199
2ES4	B E	E	237	V	1.5	221	246
2ES4	B E	E	240	I	1.2	221	246
2ES4	B E	E	268	R	1.3	263	294
2ES4	B E	E	322	I	1.0	320	330
2ES4	B E	E	326	S	1.0	320	330
2ES4	B E	E	327	L	1.6	320	330
2ESV	A E	A	76	V	1.0	57	86
2ESV	A E	A	146	K	1.3	141	150
2ESV	D E	E	137	E	1.4	135	142
2ESV	D E	E	140	H	1.9	135	142
2EXW	C D	D	123	Q	1.1	121	125
2EY4	A C	A	189	H	1.5	183	194
2EY4	A C	A	192	L	1.5	183	194
2EY4	A E	A	68	W	2.4	62	73
2EY4	A E	A	221	H	2.4	220	233
2EY4	A E	A	225	D	3.0	220	233
2EY4	A E	A	229	F	2.4	220	233
2EY4	A E	A	238	Y	1.8	236	243
2EY4	A E	E	42	G	1.0	42	54
2EY4	A E	E	45	R	2.8	42	54
2EY4	A E	E	49	K	2.2	42	54
2EY4	A E	E	50	R	1.4	42	54
2EY4	A E	E	53	L	1.4	42	54
2EY4	B D	B	189	H	1.9	183	195
2EY4	B D	B	192	L	1.6	183	195
2EY4	B F	B	68	W	2.4	62	73
2EY4	B F	B	221	H	1.4	220	233
2EY4	B F	B	225	D	3.0	220	233
2EY4	B F	B	228	Y	1.0	220	233
2EY4	B F	B	229	F	2.3	220	233
2EY4	B F	B	232	E	1.3	220	233
2EY4	B F	F	42	G	3.1	42	54
2EY4	B F	F	45	R	1.3	42	54
2EY4	B F	F	50	R	1.2	42	54
2F2F	B C	B	42	E	1.5	41	53
2F2F	B C	B	47	I	1.7	41	53
2F2F	D F	D	74	P	1.7	72	76
2F2F	E F	E	42	E	1.5	41	53
2F2F	E F	E	47	I	1.7	41	53
2F2L	A X	A	398	L	2.5	393	411
2F2L	A X	X	387	F	3.0	374	393
2F2L	A X	X	392	W	1.9	374	393
2F43	A B	A	283	L	1.5	278	285
2F43	A B	A	284	L	1.1	278	285
2F43	A B	B	290	G	29.7	284	294
2F43	A B	B	380	D	1.0	365	387
2F43	A G	G	264	E	1.1	260	271
2F49	A C	A	116	Y	1.3	111	131
2F49	A C	A	119	Y	1.3	111	131
2F4O	A B	A	435	I	2.3	424	442
2F4O	A B	A	438	L	2.0	424	442
2F4O	A B	A	439	V	1.5	424	442
2F4O	A B	B	284	Q	1.2	283	294
2F4O	A B	B	288	M	1.4	283	294
2F54	A E	A	65	R	1.0	57	85

2F54	D E	E	134	H	1.7	129	136
2F54	F L	F	65	R	1.5	57	85
2F54	F L	F	72	Q	1.8	57	85
2F54	K L	L	134	H	2.0	129	136
2F5Z	A K	A	444	D	1.6	442	448
2F5Z	B K	K	160	K	1.2	160	169
2F5Z	C L	C	444	D	1.1	442	447
2F5Z	C L	L	136	R	1.2	135	141
2F5Z	D L	D	443	E	1.2	442	448
2F5Z	E M	E	437	E	2.0	425	438
2F5Z	E M	E	443	E	1.5	442	447
2F5Z	E M	E	444	D	1.5	442	447
2F5Z	E M	M	133	P	3.5	133	142
2F5Z	E M	M	136	R	1.8	133	142
2F5Z	F M	F	443	E	1.8	442	447
2F5Z	G N	G	444	D	2.2	442	448
2F5Z	G N	N	141	K	1.1	133	142
2F5Z	H N	H	443	E	1.2	442	447
2F5Z	H N	H	444	D	1.1	442	447
2F5Z	H N	N	160	K	1.2	160	166
2F5Z	I O	I	443	E	1.5	442	447
2F5Z	I O	O	136	R	1.2	135	140
2F5Z	J O	J	443	E	1.4	442	448
2F5Z	J O	O	160	K	1.7	160	166
2F66	A B	A	324	G	56.3	323	351
2F66	A B	A	349	L	1.1	323	351
2F66	A B	A	350	H	1.3	323	351
2F66	A B	A	356	L	2.7	356	381
2F66	A B	A	359	F	1.0	356	381
2F66	A B	A	368	R	1.1	356	381
2F66	A B	A	371	F	3.0	356	381
2F66	A B	A	375	W	2.3	356	381
2F66	A B	A	376	H	3.0	356	381
2F66	A B	B	37	I	1.3	31	59
2F66	A B	B	44	Y	1.3	31	59
2F66	A C	A	332	V	2.4	323	351
2F66	A C	A	340	D	6.5	323	351
2F66	A C	A	348	M	1.3	323	351
2F66	A C	A	366	L	1.1	356	381
2F66	A C	C	169	E	1.0	144	172
2F66	A C	C	184	F	1.0	178	203
2F66	A C	C	185	I	1.7	178	203
2F66	A C	C	188	Y	4.9	178	203
2F66	A C	C	189	L	1.7	178	203
2F66	A C	C	192	R	4.1	178	203
2F66	A C	C	196	H	2.4	178	203
2F66	A C	C	197	L	2.4	178	203
2F66	A C	C	200	E	2.3	178	203
2F66	A E	A	329	Y	1.4	323	351
2F66	A E	A	332	V	1.0	323	351
2F66	A E	A	336	Y	2.0	323	351
2F66	A E	E	112	I	2.1	108	117
2F66	A E	E	115	L	1.3	108	117
2F66	D B	D	332	V	1.4	323	351
2F66	D B	D	336	Y	2.5	323	351
2F66	D B	B	112	I	1.3	108	117
2F66	D B	B	115	L	1.2	108	117
2F66	D E	D	324	G	128.9	323	351
2F66	D E	D	356	L	1.0	356	382
2F66	D E	D	359	F	1.3	356	382

2F66	D E	D	368	R	1.1	356	382
2F66	D E	D	371	F	3.4	356	382
2F66	D E	D	372	L	1.1	356	382
2F66	D E	D	375	W	2.5	356	382
2F66	D E	D	376	H	4.7	356	382
2F66	D E	E	37	I	1.5	31	59
2F66	D E	E	44	Y	1.3	31	59
2F66	D E	E	52	H	1.0	31	59
2F66	D F	D	337	A	4.5	323	351
2F66	D F	D	340	D	3.0	323	351
2F66	D F	D	345	L	1.8	323	351
2F66	D F	D	347	R	1.6	323	351
2F66	D F	D	348	M	1.0	323	351
2F66	D F	F	169	E	2.3	146	171
2F66	D F	F	185	I	2.2	179	204
2F66	D F	F	188	Y	2.2	179	204
2F66	D F	F	189	L	1.1	179	204
2F66	D F	F	192	R	2.4	179	204
2F66	D F	F	196	H	2.0	179	204
2F8N	A B	A	454	Y	1.1	445	455
2F8N	A B	A	474	I	1.8	464	479
2F8N	A B	A	478	F	1.9	464	479
2F8N	A B	A	499	Y	1.9	486	514
2F8N	A B	A	500	L	1.0	486	514
2F8N	A B	A	501	V	1.3	486	514
2F8N	A B	A	504	F	2.9	486	514
2F8N	A B	A	521	P	1.7	521	532
2F8N	A B	A	524	I	1.2	521	532
2F8N	A B	B	36	R	2.4	31	41
2F8N	A B	B	37	L	2.6	31	41
2F8N	A B	B	40	R	1.2	31	41
2F8N	A B	B	50	I	1.6	48	76
2F8N	A B	B	61	F	3.0	48	76
2F8N	A B	B	66	I	2.6	48	76
2F8N	A B	B	70	V	1.2	48	76
2F8N	A G	A	448	L	1.1	445	455
2F8N	A G	A	512	I	1.5	486	514
2F8N	B D	B	84	M	1.0	83	92
2F8N	B D	D	1297	L	1.6	1288	1299
2F8N	B H	H	1461	S	2.4	1453	1481
2F8N	B H	H	1462	F	1.7	1453	1481
2F8N	B H	H	1465	D	1.2	1453	1481
2F8N	B H	H	1469	R	2.0	1453	1481
2F8N	D K	D	1241	V	1.1	1235	1246
2F8N	D K	D	1245	V	1.2	1235	1246
2F8N	D K	D	1258	I	1.3	1253	1281
2F8N	D K	D	1262	F	2.3	1253	1281
2F8N	D K	D	1263	V	1.1	1253	1281
2F8N	D K	D	1266	I	1.1	1253	1281
2F8N	D K	D	1267	F	3.8	1253	1281
2F8N	D K	D	1291	V	1.4	1288	1299
2F8N	D K	D	1306	H	1.2	1302	1319
2F8N	D K	D	1307	A	2.2	1302	1319
2F8N	D K	D	1311	G	176.7	1302	1319
2F8N	D K	D	1317	K	1.5	1302	1319
2F8N	D K	D	1318	Y	2.2	1302	1319
2F8N	D K	K	46	G	4.0	45	73
2F8N	D K	K	49	V	1.8	45	73
2F8N	D K	K	50	Y	3.8	45	73
2F8N	D K	K	51	L	1.9	45	73

2F8N	D K	K	54	V	1.5	45	73
2F8N	D K	K	55	L	2.3	45	73
2F8N	D K	K	80	P	1.4	80	89
2F8N	D K	K	92	E	1.4	91	97
2F8N	D K	K	96	L	2.0	91	97
2F8N	E F	E	650	E	1.6	645	657
2F8N	E F	E	651	I	2.0	645	657
2F8N	E F	E	654	Y	1.4	645	657
2F8N	E F	E	667	F	1.1	664	677
2F8N	E F	E	670	L	2.0	664	677
2F8N	E F	E	673	E	2.7	664	677
2F8N	E F	E	674	I	2.5	664	677
2F8N	E F	E	692	L	1.7	686	714
2F8N	E F	E	699	Y	2.0	686	714
2F8N	E F	E	700	L	1.9	686	714
2F8N	E F	E	701	V	1.6	686	714
2F8N	E F	E	704	F	3.0	686	714
2F8N	E F	E	721	P	1.7	721	732
2F8N	E F	E	724	I	1.0	721	732
2F8N	E F	F	236	R	1.5	231	241
2F8N	E F	F	237	L	2.8	231	241
2F8N	E F	F	239	R	1.5	231	241
2F8N	E F	F	240	R	4.2	231	241
2F8N	E F	F	250	I	2.8	250	276
2F8N	E F	F	261	F	3.0	250	276
2F8N	E F	F	262	L	2.2	250	276
2F8N	E F	F	266	I	3.2	250	276
2F8N	E F	F	270	V	2.0	250	276
2F8N	E F	F	286	V	1.7	283	293
2F8N	E K	E	648	L	1.9	645	657
2F8N	F D	D	1261	S	1.0	1253	1281
2F8N	F H	F	275	H	3.3	250	276
2F8N	F H	H	1489	R	3.2	1488	1499
2F8N	F H	H	1497	L	1.6	1488	1499
2F8N	H G	H	1441	V	1.6	1435	1445
2F8N	H G	H	1442	L	1.0	1435	1445
2F8N	H G	H	1458	I	2.3	1453	1481
2F8N	H G	H	1459	M	1.9	1453	1481
2F8N	H G	H	1462	F	2.5	1453	1481
2F8N	H G	H	1463	V	1.1	1453	1481
2F8N	H G	H	1467	F	3.9	1453	1481
2F8N	H G	H	1470	I	1.0	1453	1481
2F8N	H G	H	1491	I	2.9	1488	1499
2F8N	H G	H	1511	G	199.8	1501	1521
2F8N	H G	H	1515	V	1.2	1501	1521
2F8N	H G	H	1518	Y	2.6	1501	1521
2F8N	H G	G	1046	G	3.3	1045	1073
2F8N	H G	G	1049	V	1.7	1045	1073
2F8N	H G	G	1050	Y	2.9	1045	1073
2F8N	H G	G	1051	M	2.9	1045	1073
2F8N	H G	G	1054	V	1.5	1045	1073
2F8N	H G	G	1055	L	2.1	1045	1073
2F8N	H G	G	1057	Y	1.7	1045	1073
2F8N	H G	G	1063	L	1.6	1045	1073
2F8N	H G	G	1083	I	1.6	1080	1090
2F8X	C K	K	2072	E	1.7	2065	2073
2F8X	C M	M	34	H	2.1	17	70
2F8X	C M	M	38	E	2.4	17	70
2F8X	C M	M	49	L	1.5	17	70
2F8X	C M	M	52	E	1.1	17	70

2F8X	C M	M	53	R	1.1	17	70
2F8X	C M	M	55	H	1.3	17	70
2F8X	C M	M	56	T	1.4	17	70
2F8X	C M	M	59	L	3.6	17	70
2F8X	C M	M	60	H	3.1	17	70
2F93	A B	A	173	I	1.4	154	181
2F93	A B	A	191	T	1.2	190	222
2F93	A B	A	196	L	2.7	190	222
2F93	A B	A	200	L	1.0	190	222
2F93	A B	B	36	F	1.7	30	51
2F93	A B	B	43	E	1.2	30	51
2F93	A B	B	69	I	2.1	53	79
2F93	A B	B	73	I	2.2	53	79
2F93	A B	B	76	G	48.6	53	79
2F95	A B	A	170	L	1.0	154	181
2F95	A B	A	173	I	1.4	154	181
2F95	A B	A	191	T	1.0	190	222
2F95	A B	A	196	L	2.7	190	222
2F95	A B	A	199	Y	1.2	190	222
2F95	A B	B	36	F	1.6	28	51
2F95	A B	B	69	I	2.3	53	79
2F95	A B	B	73	I	2.0	53	79
2F95	A B	B	76	G	41.2	53	79
2F9D	A P	A	67	I	1.0	67	78
2F9D	A P	A	117	Y	1.7	103	118
2F9D	A P	P	388	W	1.2	380	395
2F9D	A P	P	392	I	1.4	380	395
2F9D	B Q	Q	388	W	1.2	380	396
2F9D	B Q	Q	395	R	1.2	380	396
2F9D	B Q	Q	403	E	1.6	401	406
2F9I	A B	A	163	K	1.1	163	168
2F9I	A B	A	166	E	1.8	163	168
2F9I	A B	A	174	I	1.1	170	183
2F9I	A B	A	178	L	1.2	170	183
2F9I	A B	A	179	I	1.8	170	183
2F9I	A B	A	199	G	4.3	199	204
2F9I	A B	A	202	L	1.3	199	204
2F9I	A B	A	251	I	1.1	248	254
2F9I	A B	A	303	F	2.3	295	308
2F9I	A B	A	307	R	3.9	295	308
2F9I	A B	B	139	S	1.0	139	155
2F9I	A B	B	143	E	3.5	139	155
2F9I	A B	B	150	D	1.6	139	155
2F9I	A B	B	174	I	2.5	174	193
2F9I	A B	B	175	I	1.3	174	193
2F9I	A B	B	177	L	2.4	174	193
2F9I	A B	B	178	M	1.4	174	193
2F9I	A B	B	179	Q	1.0	174	193
2F9I	A B	B	181	G	3.4	174	193
2F9I	A B	B	182	K	1.4	174	193
2F9I	A B	B	185	V	2.4	174	193
2F9I	A B	B	236	I	1.4	233	240
2F9I	A D	A	138	R	1.5	130	146
2F9I	A D	A	145	K	1.1	130	146
2F9I	A D	D	255	L	1.0	251	257
2F9I	A D	D	278	K	1.0	269	280
2F9I	A D	D	279	I	2.5	269	280
2F9I	C B	C	145	K	1.0	130	146
2F9I	C B	B	255	L	1.1	251	257
2F9I	C B	B	278	K	1.0	269	280

2F9I	C B	B	279	I	2.1	269	280
2F9I	C D	C	163	K	1.0	163	168
2F9I	C D	C	166	E	1.9	163	168
2F9I	C D	C	174	I	1.1	170	183
2F9I	C D	C	178	L	1.3	170	183
2F9I	C D	C	179	I	1.5	170	183
2F9I	C D	C	199	G	1.2	199	204
2F9I	C D	C	202	L	2.0	199	204
2F9I	C D	C	251	I	1.2	248	254
2F9I	C D	C	303	F	2.3	295	308
2F9I	C D	C	307	R	4.0	295	308
2F9I	C D	D	143	E	3.1	139	155
2F9I	C D	D	147	R	1.2	139	155
2F9I	C D	D	150	D	1.6	139	155
2F9I	C D	D	174	I	3.0	174	193
2F9I	C D	D	175	I	1.4	174	193
2F9I	C D	D	177	L	2.6	174	193
2F9I	C D	D	178	M	2.0	174	193
2F9I	C D	D	179	Q	1.0	174	193
2F9I	C D	D	181	G	4.3	174	193
2F9I	C D	D	185	V	2.2	174	193
2F9I	C D	D	236	I	1.4	233	241
2F9I	C D	D	240	I	1.0	233	241
2F9Y	A B	A	170	V	2.0	170	175
2F9Y	A B	A	173	E	1.6	170	175
2F9Y	A B	A	181	I	1.2	177	190
2F9Y	A B	A	185	L	1.1	177	190
2F9Y	A B	A	258	L	2.1	255	260
2F9Y	A B	A	310	Y	2.2	302	316
2F9Y	A B	A	313	L	1.6	302	316
2F9Y	A B	B	171	L	11.8	171	191
2F9Y	A B	B	174	L	1.6	171	191
2F9Y	A B	B	175	M	2.7	171	191
2F9Y	A B	B	182	A	1.1	171	191
2F9Y	A B	B	183	A	1.1	171	191
2F9Y	A B	B	184	L	1.0	171	191
2F9Y	A B	B	186	K	1.3	171	191
2F9Y	A B	B	189	E	1.4	171	191
2F9Y	A B	B	233	I	1.1	230	235
2FBJ	L H	L	123	Q	1.4	121	127
2FBW	A B	A	108	I	1.6	93	113
2FBW	A B	A	111	E	4.0	93	113
2FBW	A B	A	155	H	2.4	153	167
2FBW	A B	A	163	G	24.4	153	167
2FBW	A B	A	166	L	1.8	153	167
2FBW	A B	A	518	D	1.2	517	542
2FBW	A B	B	119	Y	3.5	116	125
2FBW	A B	B	146	I	1.3	146	153
2FBW	A B	B	149	R	2.8	146	153
2FBW	B C	B	172	W	3.6	169	174
2FBW	B C	B	223	R	1.2	220	225
2FBW	B C	C	12	F	2.8	5	18
2FBW	B C	C	16	N	1.6	5	18
2FBW	B C	C	108	W	1.1	81	110
2FBW	B C	C	116	L	1.6	116	139
2FBW	B D	B	173	W	1.6	169	174
2FBW	B D	D	10	W	2.4	5	30
2FBW	B D	D	53	Q	1.1	33	59
2FBW	B D	D	57	D	1.9	33	59
2FBW	C D	C	54	S	1.2	34	63

2FBW	C D	C	56	F	1.5	34	63
2FBW	C D	C	61	L	1.9	34	63
2FBW	C D	C	67	F	2.3	67	77
2FBW	C D	D	79	T	1.7	62	89
2FBW	C D	D	82	G	73.7	62	89
2FBW	C D	D	85	Y	1.4	62	89
2FBW	C D	D	86	F	2.5	62	89
2FBW	N O	N	108	I	1.6	93	113
2FBW	N O	N	111	E	4.2	93	113
2FBW	N O	N	155	H	1.4	153	166
2FBW	N O	N	163	G	15.0	153	166
2FBW	N O	N	518	D	1.3	517	542
2FBW	N O	O	119	Y	3.5	116	125
2FBW	N O	O	146	I	1.2	146	153
2FBW	N O	O	149	R	2.6	146	153
2FBW	O P	O	172	W	3.6	169	174
2FBW	O P	O	223	R	1.3	220	225
2FBW	O P	P	12	F	1.8	5	18
2FBW	O P	P	16	N	1.6	5	18
2FBW	O P	P	108	W	1.0	81	110
2FBW	O P	P	116	L	2.0	116	139
2FBW	O Q	O	173	W	1.6	169	174
2FBW	O Q	Q	10	W	2.4	5	30
2FBW	O Q	Q	53	Q	1.1	33	59
2FBW	O Q	Q	57	D	2.0	33	59
2FBW	P Q	P	54	S	1.2	34	63
2FBW	P Q	P	56	F	1.5	34	63
2FBW	P Q	P	61	L	2.0	34	63
2FBW	P Q	P	67	F	1.9	67	77
2FBW	P Q	Q	79	T	1.6	62	89
2FBW	P Q	Q	82	G	70.5	62	89
2FBW	P Q	Q	85	Y	1.4	62	89
2FBW	P Q	Q	86	F	2.3	62	89
2FCW	A B	A	256	K	1.4	237	277
2FCW	A B	A	266	I	1.3	237	277
2FCW	A B	A	270	K	3.0	237	277
2FCW	A B	A	282	R	1.0	280	320
2FCW	A B	A	285	R	1.0	280	320
2FD6	L H	L	123	Q	1.5	121	127
2FDB	M P	M	35	H	2.0	33	40
2FDB	M P	P	2160	E	1.1	2160	2164
2FDB	N R	N	1035	H	1.8	1033	1040
2FEP	A S	A	89	M	1.4	74	90
2FEP	A S	S	47	I	1.5	47	54
2FEP	A S	S	48	M	1.1	47	54
2FEW	A B	A	52	L	1.0	40	53
2FEW	A B	B	393	M	1.0	390	405
2FF6	G A	G	95	Q	1.8	95	112
2FF6	G A	G	99	G	22.5	95	112
2FF6	G A	G	103	I	1.7	95	112
2FF6	G A	G	104	F	2.3	95	112
2FF6	G A	G	106	V	1.5	95	112
2FF6	G A	A	143	Y	1.5	137	145
2FF6	G A	A	345	I	2.9	338	349
2FFD	A B	A	140	V	1.0	128	160
2FFD	A B	A	144	L	1.0	128	160
2FFD	A B	A	148	K	1.7	128	160
2FFD	A B	A	149	R	1.1	128	160
2FFD	A B	A	152	V	1.0	128	160
2FFD	A B	A	156	I	2.0	128	160

2FFD	A B	A	158	I	1.1	128	160
2FFD	A B	A	159	R	2.7	128	160
2FFD	A B	A	177	D	1.6	175	188
2FFD	A B	A	185	L	2.2	175	188
2FFD	A B	B	171	I	1.8	158	193
2FFD	A B	B	175	L	1.5	158	193
2FFD	A B	B	178	K	3.0	158	193
2FFD	A B	B	189	Q	1.4	158	193
2FFD	A B	B	192	Y	1.7	158	193
2FFD	A C	A	136	L	2.6	128	160
2FFD	A C	A	146	D	1.3	128	160
2FFD	A C	A	150	L	2.3	128	160
2FFD	A C	C	103	H	1.1	100	135
2FFD	A C	C	107	I	2.4	100	135
2FFD	A C	C	108	R	1.1	100	135
2FFD	A C	C	114	Y	1.0	100	135
2FFD	A C	C	125	K	1.2	100	135
2FFD	B C	B	165	L	1.3	158	193
2FFD	B C	B	172	L	1.8	158	193
2FFD	B C	B	179	I	2.3	158	193
2FFD	B C	B	183	E	1.1	158	193
2FFD	B C	B	186	V	1.4	158	193
2FFD	B C	B	190	M	1.3	158	193
2FFD	B C	C	110	L	1.7	100	135
2FFD	B C	C	120	K	1.6	100	135
2FFD	B C	C	124	L	2.1	100	135
2FFD	B C	C	131	L	3.1	100	135
2FFD	B C	C	210	Q	1.2	208	214
2FFD	D E	D	144	L	1.0	141	160
2FFD	D E	D	147	M	1.6	141	160
2FFD	D E	D	149	R	1.2	141	160
2FFD	D E	D	152	V	1.1	141	160
2FFD	D E	D	154	I	1.4	141	160
2FFD	D E	D	156	I	1.1	141	160
2FFD	D E	D	177	D	1.8	175	184
2FFD	D E	D	178	Y	1.2	175	184
2FFD	D E	E	168	L	1.0	166	193
2FFD	D E	E	174	N	1.0	166	193
2FFD	D E	E	175	L	1.2	166	193
2FFD	D E	E	178	K	2.5	166	193
2FFD	D E	E	182	L	1.3	166	193
2FFD	D E	E	192	Y	1.8	166	193
2FFD	D F	D	136	L	1.2	134	140
2FFD	D F	D	150	L	1.0	141	160
2FFD	D F	D	157	K	1.1	141	160
2FFD	D F	F	114	Y	1.4	111	116
2FFD	D F	F	128	V	1.6	117	134
2FFD	E F	E	172	L	1.9	166	193
2FFD	E F	E	179	I	1.9	166	193
2FFD	E F	E	186	V	1.0	166	193
2FFD	E F	E	190	M	1.2	166	193
2FFD	E F	F	124	L	2.4	117	134
2FFD	E F	F	127	K	1.5	117	134
2FFD	E F	F	131	L	2.2	117	134
2FFF	A B	B	339	L	1.6	338	359
2FGW	L H	L	124	Q	1.4	122	127
2FHH	A H	A	75	R	1.5	68	89
2FHH	A H	A	79	I	1.6	68	89
2FHH	A H	A	87	Y	2.5	68	89
2FHH	A H	H	364	E	1.7	349	371

2FHH	A H	H	367	E	2.0	349	371
2FHH	A H	H	368	K	1.3	349	371
2FHH	B C	B	75	R	2.1	68	89
2FHH	B C	B	76	R	1.2	68	89
2FHH	B C	B	79	I	1.9	68	89
2FHH	B C	B	87	Y	2.6	68	89
2FHH	B C	C	364	E	1.0	349	371
2FHH	B C	C	365	H	1.4	349	371
2FHH	B C	C	368	K	1.9	349	371
2FHH	B C	C	369	L	1.1	349	371
2FHH	D E	D	75	R	1.9	68	89
2FHH	D E	D	76	R	1.3	68	89
2FHH	D E	D	79	I	1.1	68	89
2FHH	D E	D	87	Y	2.7	68	89
2FHH	D E	E	357	R	1.0	349	371
2FHH	D E	E	364	E	2.4	349	371
2FHH	D E	E	365	H	1.4	349	371
2FHH	D E	E	367	E	1.9	349	371
2FHH	D E	E	368	K	1.2	349	371
2FHH	D E	E	369	L	1.2	349	371
2FHH	D R	D	85	R	1.0	68	89
2FHH	F G	F	75	R	1.9	68	89
2FHH	F G	F	76	R	1.1	68	89
2FHH	F G	F	79	I	1.9	68	89
2FHH	F G	F	87	Y	2.4	68	89
2FHH	F G	G	367	E	1.8	349	371
2FHH	F G	G	368	K	1.5	349	371
2FHH	F G	G	369	L	1.3	349	371
2FHH	F N	N	366	Y	1.8	349	371
2FHH	I C	C	378	G	1.8	376	389
2FHH	I J	I	75	R	2.3	68	89
2FHH	I J	I	79	I	1.3	68	89
2FHH	I J	I	83	D	1.5	68	89
2FHH	I J	I	87	Y	2.1	68	89
2FHH	I J	J	367	E	1.4	349	371
2FHH	I J	J	368	K	2.0	349	371
2FHH	K E	E	366	Y	1.0	349	371
2FHH	K L	K	75	R	1.3	68	89
2FHH	K L	K	76	R	1.4	68	89
2FHH	K L	K	79	I	1.4	68	89
2FHH	K L	K	83	D	1.3	68	89
2FHH	K L	K	87	Y	2.2	68	89
2FHH	K L	L	364	E	1.0	349	371
2FHH	K L	L	367	E	1.4	349	371
2FHH	K L	L	368	K	1.9	349	371
2FHH	K L	L	370	E	1.0	349	371
2FHH	M L	M	97	R	2.2	97	114
2FHH	M L	L	370	E	1.5	349	371
2FHH	M L	L	378	G	8.2	376	389
2FHH	M N	M	75	R	1.1	68	89
2FHH	M N	M	76	R	1.5	68	89
2FHH	M N	M	79	I	1.0	68	89
2FHH	M N	M	87	Y	2.6	68	89
2FHH	M N	N	357	R	1.2	349	371
2FHH	M N	N	368	K	2.3	349	371
2FHH	M N	N	369	L	1.0	349	371
2FHH	M N	N	370	E	1.1	349	371
2FHH	O P	O	75	R	1.7	68	89
2FHH	O P	O	76	R	1.8	68	89
2FHH	O P	O	79	I	2.0	68	89

2FHH	O P	O	87	Y	2.3	68	89
2FHH	O P	P	364	E	1.0	349	371
2FHH	O P	P	365	H	2.1	349	371
2FHH	O P	P	367	E	1.7	349	371
2FHH	O P	P	369	L	1.6	349	371
2FHH	O V	V	377	A	2.1	376	389
2FHH	O V	V	378	G	3.6	376	389
2FHH	Q R	Q	75	R	2.0	68	89
2FHH	Q R	Q	79	I	1.7	68	89
2FHH	Q R	Q	87	Y	2.0	68	89
2FHH	Q R	R	364	E	1.0	349	371
2FHH	Q R	R	367	E	2.5	349	371
2FHH	Q R	R	368	K	1.6	349	371
2FHH	Q R	R	369	L	1.0	349	371
2FHH	Q Z	Q	97	R	3.3	97	114
2FHH	Q Z	Z	366	Y	1.3	349	371
2FHH	Q Z	Z	378	G	5.0	376	389
2FHH	Q Z	Z	381	N	1.0	376	389
2FHH	S J	J	366	Y	1.5	349	371
2FHH	S J	J	378	G	1.6	376	389
2FHH	S T	S	75	R	1.9	68	89
2FHH	S T	S	76	R	2.0	68	89
2FHH	S T	S	79	I	1.9	68	89
2FHH	S T	S	87	Y	2.6	68	89
2FHH	S T	T	364	E	1.1	349	371
2FHH	S T	T	369	L	1.6	349	371
2FHH	U V	U	75	R	1.4	68	89
2FHH	U V	U	79	I	1.4	68	89
2FHH	U V	U	87	Y	2.3	68	89
2FHH	U V	V	364	E	1.0	349	371
2FHH	U V	V	367	E	1.1	349	371
2FHH	U V	V	368	K	1.3	349	371
2FHH	W G	G	378	G	2.1	376	389
2FHH	W X	W	75	R	1.8	68	89
2FHH	W X	W	79	I	1.3	68	89
2FHH	W X	W	87	Y	2.1	68	89
2FHH	W X	X	364	E	2.1	349	371
2FHH	W X	X	367	E	1.5	349	371
2FHH	Y X	X	370	E	2.0	349	371
2FHH	Y Z	Y	75	R	2.0	68	89
2FHH	Y Z	Y	76	R	1.6	68	89
2FHH	Y Z	Y	79	I	1.8	68	89
2FHH	Y Z	Y	87	Y	2.7	68	89
2FHH	Y Z	Z	364	E	1.1	349	371
2FHH	Y Z	Z	365	H	1.6	349	371
2FHH	Y Z	Z	368	K	3.2	349	371
2FHH	Y Z	Z	369	L	1.8	349	371
2FHJ	A D	D	188	D	1.5	176	192
2FHJ	B D	B	177	P	1.5	176	192
2FHJ	B D	D	177	P	1.5	176	192
2FHJ	C D	C	32	W	2.3	30	41
2FHJ	C D	C	39	E	1.8	30	41
2FHJ	C D	C	92	R	1.3	82	100
2FHJ	C D	C	126	F	1.5	120	128
2FHJ	C D	C	127	F	3.3	120	128
2FHJ	C D	C	180	L	2.1	176	192
2FHJ	C D	D	32	W	2.1	30	41
2FHJ	C D	D	39	E	1.4	30	41
2FHJ	C D	D	92	R	1.4	82	100
2FHJ	C D	D	94	G	1.5	82	100

2FHJ	C D	D	126	F	1.6	120	129
2FHJ	C D	D	127	F	3.1	120	129
2FHJ	C D	D	180	L	2.1	176	192
2FHO	A B	A	404	L	1.7	401	408
2FHO	A B	A	405	D	1.8	401	408
2FHO	A B	B	36	Y	3.0	32	40
2FHS	A C	A	204	R	1.6	201	214
2FHS	A C	C	42	E	1.7	39	52
2FHW	B A	B	14	F	1.2	12	23
2FHW	B A	B	18	V	2.0	12	23
2FHX	A B	A	90	L	1.6	89	106
2FHX	A B	A	150	K	1.3	139	151
2FHX	A B	A	150	F	3.1	139	151
2FHX	A B	B	94	T	1.9	89	106
2FHX	A B	B	150	K	1.4	139	151
2FHX	A B	B	150	F	3.4	139	151
2FHX	A B	B	160	I	2.1	154	164
2FHZ	A B	B	21	Q	1.3	16	25
2FIF	A B	B	54	D	1.9	36	71
2FIF	A B	B	65	E	1.0	36	71
2FIF	C D	D	54	D	2.5	36	70
2FIF	C D	D	62	Q	1.3	36	70
2FIF	C D	D	65	E	1.1	36	70
2FIF	E F	F	54	D	1.6	36	70
2FIF	E F	F	65	E	1.0	36	70
2FIF	E F	F	69	F	1.4	36	70
2FJ7	A B	A	54	Y	1.5	50	57
2FJ7	A B	A	66	P	3.1	65	77
2FJ7	A B	A	67	F	1.5	65	77
2FJ7	A B	A	70	L	1.5	65	77
2FJ7	A B	A	74	I	2.0	65	77
2FJ7	A B	A	97	E	1.5	86	114
2FJ7	A B	A	100	L	1.7	86	114
2FJ7	A B	A	101	V	1.5	86	114
2FJ7	A B	A	104	F	2.5	86	114
2FJ7	A B	A	124	I	1.4	121	132
2FJ7	A B	B	36	R	1.2	31	41
2FJ7	A B	B	37	L	3.4	31	41
2FJ7	A B	B	39	R	1.5	31	41
2FJ7	A B	B	40	R	1.0	31	41
2FJ7	A B	B	53	E	1.1	48	63
2FJ7	A B	B	58	L	1.6	48	63
2FJ7	A B	B	61	F	1.9	48	63
2FJ7	A B	B	66	I	2.8	64	76
2FJ7	A B	B	70	V	1.6	64	76
2FJ7	A B	B	86	V	1.3	83	93
2FJ7	A G	A	112	I	1.0	86	114
2FJ7	B D	B	71	T	1.8	64	76
2FJ7	B D	B	72	Y	2.4	64	76
2FJ7	B D	B	88	Y	2.0	83	93
2FJ7	B D	D	73	E	2.3	53	81
2FJ7	B D	D	80	Y	10.3	53	81
2FJ7	B D	D	93	T	1.8	88	99
2FJ7	C D	C	29	R	1.3	27	38
2FJ7	C D	C	49	V	1.7	45	73
2FJ7	C D	C	51	L	1.6	45	73
2FJ7	C D	C	55	L	5.5	45	73
2FJ7	C D	C	63	L	1.9	45	73
2FJ7	C D	C	67	G	45.8	45	73
2FJ7	C D	D	67	F	2.7	53	81

2FJ7	C D	D	75	S	11.3	53	81
2FJ7	C D	D	111	G	77.9	103	119
2FJ7	C D	D	118	Y	1.6	103	119
2FJ7	E F	E	51	I	1.6	46	56
2FJ7	E F	E	66	P	5.2	64	77
2FJ7	E F	E	67	F	1.5	64	77
2FJ7	E F	E	74	I	1.7	64	77
2FJ7	E F	E	121	P	1.5	121	131
2FJ7	E F	F	35	R	1.4	31	41
2FJ7	E F	F	37	L	1.8	31	41
2FJ7	E F	F	40	R	1.8	31	41
2FJ7	E F	F	61	F	2.6	57	72
2FJ7	E F	F	62	L	1.8	57	72
2FJ7	E F	F	66	I	2.5	57	72
2FJ7	E F	F	70	V	1.1	57	72
2FJ7	F D	D	65	D	1.3	53	81
2FJ7	F H	F	88	Y	1.6	83	93
2FJ7	F H	F	92	R	1.2	83	93
2FJ7	G H	G	46	G	1.4	45	73
2FJ7	G H	G	49	V	1.5	45	73
2FJ7	G H	G	50	Y	2.6	45	73
2FJ7	G H	G	57	Y	1.4	45	73
2FJ7	G H	G	62	I	3.1	45	73
2FJ7	G H	G	63	L	1.6	45	73
2FJ7	G H	G	67	G	8.0	45	73
2FJ7	G H	G	83	L	1.0	80	89
2FJ7	G H	H	62	F	2.2	59	79
2FJ7	G H	H	111	G	220.0	104	120
2FJF	E F	E	123	E	1.0	122	127
2FJF	E F	E	124	Q	1.2	122	127
2FJF	G I	G	124	Q	1.0	122	127
2FJF	M N	M	123	E	1.1	122	128
2FJF	O P	O	124	Q	1.6	122	127
2FJF	Q R	Q	123	E	1.1	122	128
2FJF	S T	S	124	Q	1.0	122	126
2FJF	W X	W	123	E	1.0	122	128
2FJF	W X	W	124	Q	1.7	122	128
2FJH	A B	A	124	Q	1.1	122	127
2FJH	V H	V	17	F	2.3	17	24
2FJH	V H	V	18	M	1.0	17	24
2FJH	V H	V	21	Y	1.7	17	24
2FJH	W A	W	19	D	1.4	17	24
2FJH	W A	W	23	R	1.3	17	24
2FJH	W B	W	18	M	1.1	17	24
2FJU	A B	A	70	L	2.2	65	71
2FK0	A B	B	93	T	1.0	75	126
2FK0	A B	B	100	V	1.3	75	126
2FK0	A B	B	111	H	1.3	75	126
2FK0	C D	D	55	I	1.1	38	60
2FK0	C D	D	59	M	1.6	38	60
2FK0	C D	D	89	L	1.1	75	126
2FK0	C D	D	92	W	1.9	75	126
2FK0	C D	D	93	T	1.2	75	126
2FK0	C D	D	100	V	1.1	75	126
2FK0	C D	D	101	L	1.0	75	126
2FK0	C D	D	105	E	1.4	75	126
2FK0	C D	D	108	L	1.5	75	126
2FK0	C D	D	111	H	1.2	75	126
2FK0	C F	C	107	E	1.9	105	112
2FK0	C F	C	110	H	1.5	105	112

2FK0	C F	F	76	R	2.1	75	126
2FK0	E B	E	107	E	1.6	105	112
2FK0	E B	E	110	H	1.7	105	112
2FK0	E B	B	76	R	1.6	75	126
2FK0	E D	D	50	N	1.4	38	60
2FK0	E F	F	55	I	1.7	38	60
2FK0	E F	F	56	I	1.0	38	60
2FK0	E F	F	59	M	1.3	38	60
2FK0	E F	F	89	L	1.0	75	126
2FK0	E F	F	92	W	1.3	75	126
2FK0	E F	F	93	T	1.1	75	126
2FK0	E F	F	100	V	1.3	75	126
2FK0	E F	F	101	L	4.0	75	126
2FK0	E F	F	111	H	1.4	75	126
2FK0	G H	H	52	V	1.1	38	60
2FK0	G H	H	56	I	1.0	38	60
2FK0	G H	H	89	L	1.0	75	126
2FK0	G H	H	100	V	1.8	75	126
2FK0	G H	H	111	H	1.6	75	126
2FK0	G H	H	112	D	1.3	75	126
2FK0	G J	G	107	E	2.2	105	112
2FK0	G J	G	110	H	2.0	105	112
2FK0	G J	J	75	R	1.2	75	126
2FK0	G J	J	76	R	1.7	75	126
2FK0	I J	J	55	I	1.3	38	60
2FK0	I J	J	59	M	1.5	38	60
2FK0	I J	J	100	V	1.3	75	126
2FK0	I J	J	101	L	1.0	75	126
2FK0	I J	J	108	L	1.6	75	126
2FK0	I J	J	111	H	1.3	75	126
2FK0	I J	J	112	D	1.1	75	126
2FK0	I L	I	107	E	1.2	105	114
2FK0	I L	I	110	H	1.0	105	114
2FK0	K H	K	107	E	1.7	105	112
2FK0	K H	K	110	H	1.6	105	112
2FK0	K H	H	76	R	2.2	75	126
2FK0	K J	J	50	N	1.2	38	60
2FK0	K L	L	52	V	2.4	38	60
2FK0	K L	L	56	I	1.0	38	60
2FK0	K L	L	59	M	1.3	38	60
2FK0	K L	L	92	W	1.2	75	126
2FK0	K L	L	93	T	1.1	75	126
2FK0	K L	L	100	V	1.4	75	126
2FK0	K L	L	111	H	1.8	75	126
2FK0	K L	L	122	V	1.0	75	126
2FK0	M N	N	56	I	1.2	39	60
2FK0	M N	N	104	N	2.8	75	126
2FK0	M N	N	108	L	1.2	75	126
2FK0	M N	N	111	H	1.4	75	126
2FK0	O P	P	89	L	1.3	75	108
2FK0	O P	P	93	T	1.3	75	108
2FK0	O P	P	100	V	2.4	75	108
2FK0	O P	P	104	N	2.8	75	108
2FK0	O P	P	105	E	1.8	75	108
2FK0	O P	P	111	H	1.7	109	126
2FK0	Q R	R	100	V	1.9	94	117
2FK0	Q R	R	111	H	2.0	94	117
2FKW	A B	A	12	P	1.2	12	37
2FKW	A B	B	11	L	1.3	5	36
2FKW	A B	B	12	H	2.5	5	36

2FKW	A D	D	11	L	1.0	5	36
2FKW	C D	D	11	L	1.5	5	36
2FKW	C D	D	12	H	2.6	5	36
2FKW	C F	F	11	L	1.0	5	36
2FKW	E F	E	12	P	1.2	12	37
2FKW	E F	F	11	L	1.3	5	36
2FKW	E F	F	12	H	2.0	5	36
2FKW	G H	G	12	P	1.2	12	36
2FKW	G H	H	11	L	1.2	5	36
2FKW	G H	H	12	H	2.7	5	36
2FKW	I J	I	12	P	1.3	12	37
2FKW	I J	I	40	W	1.6	39	47
2FKW	I J	J	11	L	1.3	5	36
2FKW	I J	J	12	H	2.8	5	36
2FKW	K J	K	44	Y	1.1	39	47
2FKW	K L	K	12	P	1.3	12	37
2FKW	K L	K	40	W	1.2	39	47
2FKW	K L	L	11	L	1.5	5	36
2FKW	K L	L	12	H	2.5	5	36
2FKW	M N	M	12	P	1.4	12	37
2FKW	M N	N	11	L	1.6	5	36
2FKW	M N	N	12	H	2.6	5	36
2FKW	O P	O	12	P	1.3	12	37
2FKW	O P	O	40	W	1.2	39	47
2FKW	O P	P	11	L	1.5	5	36
2FKW	O P	P	12	H	1.4	5	36
2FKW	O S	S	11	L	1.0	5	36
2FKW	R B	B	11	L	1.0	5	36
2FKW	R S	R	12	P	1.2	12	37
2FKW	R S	S	11	L	1.1	5	36
2FKW	R S	S	12	H	2.5	5	36
2FL5	A B	A	124	E	1.0	122	127
2FL5	E F	E	123	E	1.0	122	127
2FL5	L H	L	124	E	1.1	122	127
2FM8	A C	A	14	L	1.0	6	18
2FM8	A C	A	67	Q	2.6	62	69
2FM8	A C	A	123	Y	1.8	112	133
2FM8	A C	C	27	L	2.0	26	30
2FM8	B C	B	125	Y	1.4	112	133
2FM8	B C	B	128	V	1.4	112	133
2FM8	B C	C	54	F	3.0	54	70
2FM8	B C	C	58	I	1.3	54	70
2FMM	E C	E	68	R	1.0	60	73
2FMM	E D	E	21	R	2.4	13	39
2FMM	E D	E	25	L	1.7	13	39
2FMM	E D	E	62	R	1.1	60	73
2FNJ	A C	A	241	L	4.7	241	250
2FNJ	A C	A	245	C	1.4	241	250
2FNJ	A C	C	76	Y	4.1	67	83
2FNJ	A C	C	80	K	1.2	67	83
2FNJ	B C	B	34	I	1.5	24	35
2FNJ	B C	C	67	S	1.3	67	83
2FNJ	B C	C	68	H	3.4	67	83
2FNJ	B C	C	75	M	1.1	67	83
2FNJ	B C	C	82	R	1.5	67	83
2FO1	A D	D	63	F	1.9	62	67
2FO1	A D	D	71	R	2.3	68	84
2FO1	A D	D	81	Y	2.1	68	84
2FO1	A D	D	99	L	1.5	85	106
2FO1	A D	D	103	Y	1.9	85	106

2FO1	D E	D	63	F	1.0	62	67
2FO1	D E	D	69	L	3.1	68	84
2FO1	D E	D	70	H	1.2	68	84
2FO1	D E	E	1108	R	1.0	1107	1113
2FOI	A C	A	111	Y	1.9	111	122
2FOI	A C	A	114	G	82.5	111	122
2FOI	A C	A	115	I	1.0	111	122
2FOI	A C	A	119	L	1.0	111	122
2FOI	A C	A	268	H	1.4	268	272
2FOI	A C	C	368	F	2.6	368	380
2FOI	A C	C	369	I	1.0	368	380
2FOI	A C	C	391	I	2.3	388	399
2FOI	A C	C	392	G	33.7	388	399
2FOI	A D	A	300	G	3.0	281	303
2FOI	B C	B	300	G	3.2	281	303
2FOI	B C	B	301	R	1.3	281	303
2FOI	B C	C	379	Y	1.5	368	380
2FOI	B D	B	114	G	84.2	111	122
2FOI	B D	D	368	F	3.9	368	379
2FOI	B D	D	369	I	1.8	368	379
2FOI	B D	D	392	G	30.5	388	400
2FOI	B D	D	399	L	3.2	388	400
2FOT	A C	A	19	F	2.4	10	20
2FOT	A C	A	32	L	1.6	29	39
2FOT	A C	A	47	E	1.4	45	56
2FOT	A C	A	71	M	2.0	65	72
2FOT	A C	A	112	L	1.5	102	113
2FOT	A C	A	145	M	1.6	138	146
2FOT	A C	C	1191	P	1.7	1191	1211
2FOT	A C	C	1192	W	4.5	1191	1211
2FOT	A C	C	1196	R	2.1	1191	1211
2FOT	A C	C	1197	L	2.8	1191	1211
2FOT	A C	C	1199	V	2.3	1191	1211
2FOT	A C	C	1204	T	1.2	1191	1211
2FOT	A C	C	1205	F	4.4	1191	1211
2FOT	A C	C	1209	K	3.0	1191	1211
2FR4	A B	A	124	Q	1.7	122	127
2FR4	L H	L	124	Q	1.5	122	127
2FRV	A B	A	19	G	18.5	19	27
2FRV	A B	A	22	E	1.2	19	27
2FRV	A B	A	26	R	1.1	19	27
2FRV	A B	A	32	V	1.4	32	40
2FRV	A B	A	56	V	1.1	54	64
2FRV	A B	A	209	K	2.0	206	210
2FRV	A B	A	255	W	4.2	254	258
2FRV	A B	A	256	D	1.2	254	258
2FRV	A B	B	48	I	2.1	45	50
2FRV	A B	B	56	D	1.1	54	63
2FRV	A B	B	59	H	1.2	54	63
2FRV	A B	B	60	F	2.6	54	63
2FRV	A B	B	200	L	1.1	186	214
2FRV	A B	B	203	Q	1.3	186	214
2FRV	C D	C	19	G	18.7	19	27
2FRV	C D	C	22	E	1.2	19	27
2FRV	C D	C	26	R	1.1	19	27
2FRV	C D	C	32	V	1.4	32	40
2FRV	C D	C	56	V	1.1	54	64
2FRV	C D	C	209	K	2.0	206	210
2FRV	C D	C	255	W	4.2	254	258
2FRV	C D	C	256	D	1.2	254	258

2FRV	C D	D	48	I	2.1	45	50
2FRV	C D	D	56	D	1.1	54	63
2FRV	C D	D	59	H	1.2	54	63
2FRV	C D	D	60	F	2.7	54	63
2FRV	C D	D	200	L	1.1	186	214
2FRV	C D	D	203	Q	1.3	186	214
2FRV	E F	E	19	G	18.6	19	27
2FRV	E F	E	22	E	1.2	19	27
2FRV	E F	E	26	R	1.2	19	27
2FRV	E F	E	32	V	1.4	32	40
2FRV	E F	E	56	V	1.1	54	64
2FRV	E F	E	209	K	1.9	206	210
2FRV	E F	E	255	W	5.7	254	258
2FRV	E F	E	256	D	1.2	254	258
2FRV	E F	F	48	I	2.1	45	50
2FRV	E F	F	56	D	1.1	54	63
2FRV	E F	F	59	H	1.8	54	63
2FRV	E F	F	60	F	4.1	54	63
2FRV	E F	F	200	L	1.0	186	214
2FRV	E F	F	203	Q	1.3	186	214
2FRV	G H	G	19	G	18.6	19	27
2FRV	G H	G	22	E	1.3	19	27
2FRV	G H	G	26	R	1.1	19	27
2FRV	G H	G	32	V	1.4	32	40
2FRV	G H	G	56	V	1.1	54	64
2FRV	G H	G	209	K	1.9	206	210
2FRV	G H	G	255	W	4.2	254	258
2FRV	G H	G	256	D	1.2	254	258
2FRV	G H	H	48	I	2.1	45	50
2FRV	G H	H	56	D	1.1	54	63
2FRV	G H	H	59	H	1.2	54	63
2FRV	G H	H	60	F	2.6	54	63
2FRV	G H	H	200	L	1.1	186	214
2FRV	G H	H	203	Q	1.3	186	214
2FRV	G J	G	165	K	1.4	152	166
2FRV	G J	J	426	E	1.1	407	438
2FRV	I J	I	19	G	18.8	19	27
2FRV	I J	I	22	E	1.2	19	27
2FRV	I J	I	26	R	2.2	19	27
2FRV	I J	I	32	V	1.4	32	40
2FRV	I J	I	56	V	1.1	54	64
2FRV	I J	I	209	K	2.0	206	210
2FRV	I J	I	255	W	5.7	254	258
2FRV	I J	I	256	D	1.2	254	258
2FRV	I J	J	48	I	2.1	45	50
2FRV	I J	J	56	D	1.1	54	63
2FRV	I J	J	59	H	1.8	54	63
2FRV	I J	J	60	F	4.1	54	63
2FRV	I J	J	200	L	1.1	186	214
2FRV	I J	J	203	Q	1.3	186	214
2FRV	S L	S	19	G	18.5	19	27
2FRV	S L	S	22	E	1.2	19	27
2FRV	S L	S	26	R	1.1	19	27
2FRV	S L	S	32	V	1.4	32	40
2FRV	S L	S	56	V	1.1	54	64
2FRV	S L	S	209	K	2.0	206	210
2FRV	S L	S	255	W	5.7	254	258
2FRV	S L	S	256	D	1.2	254	258
2FRV	S L	L	48	I	2.1	45	50
2FRV	S L	L	56	D	1.1	54	63

2FRV	S L	L	59	H	1.9	54	63
2FRV	S L	L	60	F	6.0	54	63
2FRV	S L	L	200	L	1.1	186	214
2FRV	S L	L	203	Q	1.3	186	214
2FSE	A B	A	48	F	1.9	46	52
2FSE	A E	A	72	I	1.7	56	76
2FSE	B E	B	56	P	1.8	52	62
2FSE	B E	B	57	D	1.2	52	62
2FSE	B E	B	60	Y	1.3	52	62
2FSE	B E	B	61	W	4.2	52	62
2FSE	B E	B	78	Y	2.1	65	86
2FSE	B E	B	82	N	1.4	65	86
2FSE	C D	C	48	F	2.4	46	50
2FSE	C F	C	72	I	1.0	56	74
2FSE	D F	D	60	Y	2.2	55	64
2FSE	D F	D	61	W	3.0	55	64
2FSE	D F	D	67	L	1.3	65	77
2FSE	D F	D	78	Y	1.0	78	89
2FTK	A E	A	40	K	1.8	15	45
2FTK	A E	A	41	G	2.1	15	45
2FTK	A E	E	1214	G	3.0	1213	1221
2FTK	A E	E	1238	Q	1.0	1236	1247
2FTK	B F	B	230	H	1.3	215	245
2FTK	B F	B	240	K	1.1	215	245
2FTK	B F	B	241	G	11.8	215	245
2FTK	B F	F	1014	G	3.7	1013	1021
2FTK	B F	F	1037	L	1.4	1036	1047
2FTK	C G	G	1614	G	4.0	1613	1621
2FTK	D H	D	640	K	1.2	615	645
2FTK	D H	D	641	G	18.2	615	645
2FTK	D H	H	1414	G	4.1	1413	1421
2FU5	A D	D	37	F	3.3	36	42
2FU5	A D	D	38	I	2.1	36	42
2FU5	A D	D	41	I	1.2	36	42
2FU5	B C	C	37	F	2.5	37	42
2FU5	B C	C	38	I	2.5	37	42
2FU5	B C	C	41	I	1.2	37	42
2FUG	A B	A	139	R	1.8	139	155
2FUG	A B	A	191	S	1.2	185	193
2FUG	A B	B	17	K	1.0	8	18
2FUG	A B	B	28	M	1.9	27	38
2FUG	A B	B	62	G	4.9	57	67
2FUG	A B	B	66	F	2.8	57	67
2FUG	A B	B	86	L	2.1	86	90
2FUG	A B	B	89	K	1.1	86	90
2FUG	A C	A	362	G	4.4	357	375
2FUG	A C	A	373	K	1.0	357	375
2FUG	A C	A	390	L	1.0	381	396
2FUG	A C	A	393	L	1.1	381	396
2FUG	A C	C	106	G	26.6	98	114
2FUG	A C	C	107	M	5.1	98	114
2FUG	A C	C	113	L	1.7	98	114
2FUG	B C	B	66	F	1.4	57	67
2FUG	C D	D	324	V	1.2	324	333
2FUG	C D	D	326	Y	3.1	324	333
2FUG	C D	D	328	F	2.2	324	333
2FUG	C E	C	186	R	1.3	186	196
2FUG	D E	D	375	F	2.6	373	385
2FUG	D E	D	376	V	1.7	373	385
2FUG	D E	E	115	E	1.3	115	125

2FUG	D E	E	116	R	1.7	115	125
2FUG	D E	E	119	Y	2.0	115	125
2FUG	D E	E	120	D	1.0	115	125
2FUG	D F	D	68	K	1.2	66	71
2FUG	D F	F	49	E	1.6	45	50
2FUG	D G	D	162	W	1.6	151	164
2FUG	D G	D	327	H	2.0	324	333
2FUG	D G	D	331	Y	3.3	324	333
2FUG	D G	G	58	L	1.2	58	63
2FUG	D G	G	106	E	2.0	104	108
2FUG	E G	E	170	F	1.8	167	171
2FUG	F G	F	149	Y	2.4	144	156
2FUG	J K	J	139	R	1.9	139	155
2FUG	J K	J	181	I	2.5	180	184
2FUG	J K	K	28	M	1.2	23	38
2FUG	J K	K	62	G	2.6	57	67
2FUG	J K	K	66	F	2.2	57	67
2FUG	J K	K	86	L	2.0	86	90
2FUG	J K	K	89	K	1.5	86	90
2FUG	J K	K	94	E	1.6	93	105
2FUG	J L	J	358	P	9.4	357	375
2FUG	J L	J	362	G	11.7	357	375
2FUG	J L	J	366	F	8.6	357	375
2FUG	J L	J	390	L	6.1	381	396
2FUG	J L	L	106	G	40.7	98	114
2FUG	J L	L	107	M	5.8	98	114
2FUG	J L	L	110	F	1.9	98	114
2FUG	K L	K	66	F	1.4	57	67
2FUG	L M	M	326	Y	1.9	323	333
2FUG	L M	M	328	F	2.7	323	333
2FUG	L N	N	170	F	1.1	167	171
2FUG	M N	M	67	E	5.4	66	71
2FUG	M N	M	68	K	1.3	66	71
2FUG	M N	M	375	F	1.8	373	378
2FUG	M N	M	376	V	2.5	373	378
2FUG	M O	M	81	Y	1.6	75	83
2FUG	M O	O	144	P	1.1	144	156
2FUG	M P	M	81	Y	1.2	75	83
2FUG	M P	M	162	W	1.4	151	164
2FUG	M P	M	327	H	1.9	323	333
2FUG	M P	M	331	Y	2.9	323	333
2FUG	M P	P	58	L	1.0	58	63
2FUG	M P	P	106	E	1.9	104	108
2FUG	N P	N	170	F	1.7	167	171
2FUG	O P	O	149	Y	2.9	144	156
2FUG	S T	S	139	R	2.0	139	155
2FUG	S T	S	181	I	4.2	180	184
2FUG	S T	T	17	K	1.0	8	18
2FUG	S T	T	62	G	4.0	57	67
2FUG	S T	T	66	F	2.8	57	67
2FUG	S T	T	95	E	1.3	93	105
2FUG	S U	S	362	G	4.7	357	375
2FUG	S U	S	366	F	1.2	357	375
2FUG	S U	S	373	K	1.0	357	375
2FUG	S U	S	393	L	1.1	381	396
2FUG	S U	U	106	G	53.2	98	114
2FUG	S U	U	107	M	4.4	98	114
2FUG	S U	U	113	L	1.6	98	114
2FUG	T U	T	57	P	1.0	57	67
2FUG	T U	T	58	T	1.1	57	67

2FUG	T U	T	59	E	1.1	57	67
2FUG	U V	V	324	V	1.1	324	333
2FUG	U V	V	326	Y	2.5	324	333
2FUG	U V	V	328	F	2.6	324	333
2FUG	U V	V	329	K	1.2	324	333
2FUG	U V	V	332	T	1.4	324	333
2FUG	V W	V	67	E	57.6	66	71
2FUG	V W	V	375	F	1.3	373	385
2FUG	V W	W	120	D	1.2	115	125
2FUG	V X	V	81	Y	1.4	75	84
2FUG	V X	X	49	E	2.7	45	52
2FUG	V X	X	87	K	1.7	86	98
2FUG	V Y	V	162	W	1.5	151	164
2FUG	V Y	V	327	H	2.0	324	333
2FUG	V Y	V	331	Y	2.8	324	333
2FUG	V Y	Y	58	L	1.1	58	63
2FUG	V Y	Y	106	E	1.9	104	108
2FUG	W Y	W	170	F	1.3	167	171
2FUG	X Y	X	149	Y	2.9	144	156
2FUG	X Y	Y	149	E	1.2	144	150
2FUN	A B	B	2449	E	2.6	2439	2453
2FUN	C D	D	3449	E	2.1	3439	3453
2FV4	A B	A	140	L	1.0	134	146
2FV4	A B	A	211	V	1.0	206	221
2FV4	A B	A	214	R	1.5	206	221
2FV4	A B	A	217	L	1.2	206	221
2FV4	A B	B	161	K	1.7	158	168
2FV4	A B	B	201	F	2.4	200	212
2FV4	A B	B	205	K	1.0	200	212
2FX8	M I	M	124	Q	1.6	122	128
2FX8	N J	N	123	E	1.0	122	127
2FX8	N J	N	124	Q	1.3	122	127
2FYL	A B	A	24	K	1.4	23	35
2FYM	A B	A	119	K	1.3	107	125
2FYM	A B	A	407	Q	1.3	399	416
2FYM	C B	C	119	K	1.3	107	125
2FYM	C B	B	4	E	2.0	3	8
2FYM	D E	D	119	K	1.4	107	125
2FYM	D E	E	4	E	2.7	3	8
2FYM	F E	F	119	K	1.6	107	125
2FYM	F E	F	407	Q	1.3	399	416
2FYN	A B	A	85	R	2.0	73	87
2FYN	A B	A	95	Y	2.6	90	118
2FYN	A B	A	247	Y	2.6	247	270
2FYN	A B	A	250	I	1.1	247	270
2FYN	A B	A	254	F	2.3	247	270
2FYN	A B	A	268	G	8.6	247	270
2FYN	A B	A	269	F	3.2	247	270
2FYN	A B	A	379	W	1.0	361	382
2FYN	A B	A	428	F	1.7	424	430
2FYN	A B	B	226	R	2.1	223	250
2FYN	A B	B	230	G	2.9	223	250
2FYN	A B	B	237	L	1.3	223	250
2FYN	A C	C	34	L	1.2	17	39
2FYN	A F	A	157	W	1.4	153	169
2FYN	A F	A	164	G	3.9	153	169
2FYN	A F	A	179	W	2.0	172	182
2FYN	A F	F	38	M	1.6	17	39
2FYN	B C	B	240	L	1.1	223	250
2FYN	B C	B	243	L	1.2	223	250

2FYN	B C	C	15	L	1.7	12	16
2FYN	D C	D	157	W	1.4	153	169
2FYN	D C	D	164	G	3.6	153	169
2FYN	D C	D	179	W	2.1	172	182
2FYN	D C	C	38	M	1.7	17	39
2FYN	D E	D	91	F	1.6	90	118
2FYN	D E	D	95	Y	1.5	90	118
2FYN	D E	D	247	Y	3.3	247	270
2FYN	D E	D	248	F	1.1	247	270
2FYN	D E	D	250	I	1.2	247	270
2FYN	D E	D	254	F	1.8	247	270
2FYN	D E	D	261	L	1.3	247	270
2FYN	D E	D	268	G	6.9	247	270
2FYN	D E	D	269	F	3.0	247	270
2FYN	D E	E	121	L	1.2	118	123
2FYN	D E	E	226	R	2.3	223	250
2FYN	D E	E	230	G	1.4	223	250
2FYN	D E	E	237	L	1.2	223	250
2FYN	D F	F	34	L	1.2	17	39
2FYN	E F	E	240	L	1.3	223	250
2FYN	E F	F	15	L	1.9	12	16
2FYN	G H	G	77	F	1.0	73	87
2FYN	G H	G	85	R	2.2	73	87
2FYN	G H	G	91	F	1.7	90	118
2FYN	G H	G	247	Y	7.6	247	270
2FYN	G H	G	248	F	1.0	247	270
2FYN	G H	G	250	I	1.1	247	270
2FYN	G H	G	254	F	2.4	247	270
2FYN	G H	G	261	L	1.6	247	270
2FYN	G H	G	268	G	10.3	247	270
2FYN	G H	G	269	F	3.4	247	270
2FYN	G H	G	379	W	1.1	361	382
2FYN	G H	H	121	L	1.0	118	122
2FYN	G H	H	230	G	2.6	223	250
2FYN	G H	H	234	V	1.3	223	250
2FYN	G I	I	34	L	1.0	17	38
2FYN	G L	G	157	W	1.5	153	169
2FYN	G L	G	179	W	2.3	172	182
2FYN	G L	L	38	M	1.4	17	39
2FYN	H I	H	240	L	1.2	223	250
2FYN	H I	I	15	L	1.6	12	16
2FYN	J I	J	157	W	1.2	153	169
2FYN	J I	J	179	W	2.3	172	182
2FYN	J K	J	91	F	1.1	90	118
2FYN	J K	J	247	Y	1.7	247	270
2FYN	J K	J	248	F	1.1	247	270
2FYN	J K	J	250	I	1.2	247	270
2FYN	J K	J	254	F	2.2	247	270
2FYN	J K	J	261	L	1.4	247	270
2FYN	J K	J	268	G	8.9	247	270
2FYN	J K	J	269	F	2.3	247	270
2FYN	J K	J	379	W	1.1	361	382
2FYN	J K	J	428	F	2.1	424	430
2FYN	J K	K	226	R	1.7	223	250
2FYN	J K	K	230	G	1.3	223	250
2FYN	J K	K	237	L	2.9	223	250
2FYN	J L	L	34	L	1.2	17	39
2FYN	K L	K	240	L	1.2	223	250
2FYN	K L	K	243	L	1.0	223	250
2FYN	K L	L	15	L	1.8	12	16

2FYN	M N	M	77	F	1.0	73	87
2FYN	M N	M	85	R	1.9	73	87
2FYN	M N	M	91	F	1.1	90	118
2FYN	M N	M	247	Y	3.8	247	270
2FYN	M N	M	250	I	1.1	247	270
2FYN	M N	M	254	F	2.2	247	270
2FYN	M N	M	261	L	1.1	247	270
2FYN	M N	M	268	G	9.0	247	270
2FYN	M N	M	379	W	1.1	361	382
2FYN	M N	M	428	F	1.2	424	430
2FYN	M N	N	230	G	2.7	223	250
2FYN	M N	N	237	L	1.5	223	250
2FYN	M R	M	157	W	1.3	153	169
2FYN	M R	M	179	W	1.8	172	182
2FYN	M R	M	193	R	1.3	188	218
2FYN	M R	R	38	M	1.6	17	39
2FYN	N O	N	240	L	1.3	223	250
2FYN	N O	N	243	L	1.1	223	250
2FYN	N O	O	15	L	1.8	12	16
2FYN	P O	P	157	W	1.4	153	169
2FYN	P O	P	164	G	4.2	153	169
2FYN	P O	P	179	W	1.9	172	182
2FYN	P O	O	38	M	1.5	17	39
2FYN	P Q	P	77	F	1.0	73	87
2FYN	P Q	P	85	R	2.7	73	87
2FYN	P Q	P	91	F	6.4	90	118
2FYN	P Q	P	247	Y	2.5	247	270
2FYN	P Q	P	250	I	1.2	247	270
2FYN	P Q	P	254	F	1.5	247	270
2FYN	P Q	P	261	L	1.4	247	270
2FYN	P Q	P	268	G	9.8	247	270
2FYN	P Q	P	269	F	3.3	247	270
2FYN	P Q	Q	121	L	1.1	118	122
2FYN	P Q	Q	227	K	1.3	223	250
2FYN	P Q	Q	230	G	2.4	223	250
2FYN	P Q	Q	237	L	2.5	223	250
2FYN	P Q	Q	244	L	1.0	223	250
2FYN	P R	R	34	L	1.0	17	39
2FYN	Q R	Q	240	L	1.4	223	250
2FYN	Q R	Q	243	L	1.0	223	250
2FYN	Q R	R	15	L	1.9	12	16
2FYN	Q R	R	19	T	1.1	17	39
2FYZ	A B	B	449	I	1.4	449	477
2FYZ	A B	B	456	V	1.2	449	477
2FYZ	A B	B	466	Y	2.3	449	477
2FYZ	A B	B	470	S	1.0	449	477
2FYZ	A D	A	141	K	1.6	125	174
2FYZ	A D	A	144	I	2.0	125	174
2FYZ	A D	A	148	N	1.2	125	174
2FYZ	A D	D	453	L	1.4	449	476
2FYZ	A D	D	460	L	1.4	449	476
2FYZ	A D	D	467	I	1.5	449	476
2FYZ	A D	D	474	L	2.4	449	476
2FYZ	C D	C	153	E	1.9	124	172
2FYZ	C D	D	449	I	1.5	449	476
2FYZ	C D	D	456	V	1.7	449	476
2FYZ	C D	D	466	Y	2.6	449	476
2FYZ	C F	C	141	K	1.7	124	172
2FYZ	C F	C	148	N	1.1	124	172
2FYZ	C F	C	155	K	1.9	124	172

2FYZ	C F	C	166	Q	1.3	124	172
2FYZ	C F	F	460	L	2.0	445	476
2FYZ	C F	F	467	I	1.7	445	476
2FYZ	C F	F	474	L	1.7	445	476
2FYZ	E B	E	141	K	1.9	121	173
2FYZ	E B	E	148	N	1.7	121	173
2FYZ	E B	E	152	F	1.1	121	173
2FYZ	E B	E	155	K	1.7	121	173
2FYZ	E B	B	453	L	1.7	449	477
2FYZ	E B	B	460	L	2.2	449	477
2FYZ	E B	B	467	I	1.6	449	477
2FYZ	E B	B	474	L	1.9	449	477
2FYZ	E F	E	153	E	1.3	121	173
2FYZ	E F	E	160	R	1.5	121	173
2FYZ	E F	F	449	I	1.4	445	476
2FYZ	E F	F	466	Y	4.2	445	476
2FYZ	E F	F	473	Q	1.1	445	476
2G2R	L H	L	123	E	1.0	122	128
2G2S	A B	A	4	G	113.8	3	8
2G2S	A B	A	7	L	1.7	3	8
2G2S	A B	A	61	V	2.0	61	65
2G2S	A B	A	64	L	1.2	61	65
2G2S	A B	B	85	K	2.2	83	87
2G2U	A B	A	107	P	1.1	107	112
2G2U	A B	A	110	E	1.1	107	112
2G2U	A B	A	272	M	1.1	272	289
2G30	A P	A	834	R	1.1	834	844
2G30	A P	A	838	L	3.1	834	844
2G30	A P	A	841	W	3.1	834	844
2G30	A P	P	8	F	5.1	5	15
2G30	A P	P	11	L	1.5	5	15
2G38	A B	A	24	R	1.7	9	32
2G38	A B	A	36	T	1.2	33	38
2G38	A B	A	47	V	2.1	46	83
2G38	A B	A	48	S	1.3	46	83
2G38	A B	A	54	F	4.8	46	83
2G38	A B	A	55	L	1.8	46	83
2G38	A B	A	58	Y	3.4	46	83
2G38	A B	A	62	Y	3.0	46	83
2G38	A B	A	72	V	1.7	46	83
2G38	A B	A	73	L	1.2	46	83
2G38	A B	B	31	W	3.5	22	50
2G38	A B	B	37	E	2.0	22	50
2G38	A B	B	45	F	1.7	22	50
2G38	A B	B	71	F	2.0	69	103
2G38	A B	B	96	Y	1.6	69	103
2G38	A B	B	153	Y	3.0	129	164
2G38	A B	B	161	L	1.9	129	164
2G38	C D	C	17	E	1.6	10	37
2G38	C D	C	21	I	1.1	10	37
2G38	C D	C	47	V	2.5	46	83
2G38	C D	C	55	L	1.5	46	83
2G38	C D	C	62	Y	3.8	46	83
2G38	C D	C	72	V	2.4	46	83
2G38	C D	C	76	F	2.8	46	83
2G38	C D	C	80	L	1.9	46	83
2G38	C D	D	31	W	2.8	22	52
2G38	C D	D	45	F	1.5	22	52
2G38	C D	D	47	R	1.3	22	52
2G38	C D	D	71	F	2.0	59	103

2G38	C D	D	74	W	1.0	59	103
2G38	C D	D	92	I	1.0	59	103
2G38	C D	D	153	Y	2.2	129	164
2G3Q	A B	A	1378	L	1.0	1370	1380
2G4D	A B	A	455	K	1.3	454	460
2G4D	A B	A	456	D	2.1	454	460
2G4D	A B	A	468	D	3.2	468	484
2G4D	A B	A	469	E	1.2	468	484
2G4D	A B	A	472	N	6.4	468	484
2G4D	A B	A	496	F	3.7	496	505
2G4D	C D	C	468	D	1.8	468	482
2G4D	C D	C	472	N	1.3	468	482
2G4D	C D	C	496	F	2.5	496	504
2G5B	A B	A	123	Q	1.0	121	126
2G5B	C D	C	123	Q	1.0	121	126
2G5B	E F	E	123	Q	2.1	121	126
2G5B	G H	G	123	Q	1.9	121	126
2G60	L H	L	123	E	1.0	122	128
2G75	A B	B	125	E	1.3	123	127
2G75	C D	D	125	E	1.0	123	127
2G77	A B	A	336	Q	1.1	331	342
2G77	A B	A	481	F	1.6	476	486
2G77	A B	A	595	F	1.6	595	604
2G77	A B	A	603	Q	2.1	595	604
2G77	A B	B	94	R	2.5	93	97
2G77	A B	B	99	M	2.1	98	102
2G9H	A B	A	48	F	3.1	46	52
2G9H	A B	A	66	D	3.8	56	77
2G9H	A B	A	70	L	2.0	56	77
2G9H	A B	A	73	M	1.5	56	77
2G9H	A B	A	76	R	2.0	56	77
2G9H	A B	B	57	D	1.3	55	64
2G9H	A B	B	83	Y	1.0	65	86
2G9H	A C	A	58	G	53.7	56	77
2G9H	A C	A	62	N	1.5	56	77
2G9H	B C	B	60	Y	1.5	55	64
2G9H	B C	B	61	W	3.5	55	64
2G9H	B C	B	78	Y	1.8	65	86
2G9H	B C	B	82	N	1.3	65	86
2G9H	B C	B	85	V	1.9	65	86
2G9H	B D	B	77	T	1.0	65	86
2G9H	B D	B	81	H	2.3	65	86
2G9H	B D	B	84	G	199.4	65	86
2G9J	C B	C	280	D	1.1	253	281
2G9J	D B	B	4	I	2.4	2	32
2G9J	D B	B	7	K	1.1	2	32
2G9J	D B	B	11	L	1.4	2	32
2GAG	A B	A	497	R	3.1	492	502
2GAG	A B	A	508	H	3.5	506	514
2GAG	A B	A	512	Y	2.5	506	514
2GAG	A B	A	559	F	5.9	559	564
2GAG	A B	A	562	L	1.3	559	564
2GAG	A B	B	122	R	1.4	114	129
2GAG	A B	B	178	W	1.9	173	187
2GAG	A B	B	299	F	2.2	299	313
2GAG	A B	B	306	M	1.3	299	313
2GAG	A B	B	310	V	1.1	299	313
2GAG	A C	C	184	H	2.3	182	196
2GAG	A C	C	195	E	3.3	182	196
2GAG	A D	A	702	D	1.3	697	712

2GAG	A D	A	707	W	1.6	697	712
2GAG	A D	A	709	Q	1.3	697	712
2GAG	A D	D	36	D	1.4	36	44
2GAG	A D	D	39	W	4.0	36	44
2GAG	A D	D	43	L	1.0	36	44
2GAG	B D	B	300	H	1.9	299	313
2GAG	B D	B	389	F	1.0	386	392
2GAG	B D	B	390	E	1.6	386	392
2GAG	B D	D	41	R	1.0	36	44
2GBW	A B	A	218	Q	1.1	213	220
2GBW	A B	A	344	R	1.8	336	350
2GBW	A B	A	348	R	3.5	336	350
2GBW	A B	A	359	D	2.1	355	371
2GBW	A B	A	361	G	7.2	355	371
2GBW	A B	A	362	E	2.7	355	371
2GBW	A B	B	77	E	2.9	75	85
2GBW	A B	B	81	R	1.6	75	85
2GBW	A B	B	84	R	3.3	75	85
2GBW	C D	C	210	W	1.0	205	212
2GBW	C D	C	344	R	2.6	336	350
2GBW	C D	C	345	E	1.0	336	350
2GBW	C D	C	348	R	4.3	336	350
2GBW	C D	C	359	D	1.9	355	371
2GBW	C D	C	361	G	6.7	355	371
2GBW	C D	C	362	E	3.0	355	371
2GBW	C D	D	77	E	2.6	75	85
2GBW	C D	D	81	R	1.1	75	85
2GBW	C D	D	84	R	2.8	75	85
2GBW	E F	E	210	W	2.1	205	212
2GBW	E F	E	344	R	1.7	336	350
2GBW	E F	E	348	R	3.1	336	350
2GBW	E F	E	359	D	2.4	355	360
2GBW	E F	E	361	G	4.7	361	371
2GBW	E F	E	362	E	2.5	361	371
2GBW	E F	F	77	E	1.5	75	88
2GBW	E F	F	81	R	2.0	75	88
2GBW	E F	F	84	R	3.7	75	88
2GC4	A F	A	12	E	1.2	9	28
2GC4	A F	A	14	Q	1.6	9	28
2GC4	A F	A	15	G	14.2	9	28
2GC4	A F	A	18	A	1.1	9	28
2GC4	A F	A	26	L	1.3	9	28
2GC4	E B	E	15	G	8.9	9	28
2GC4	E B	E	26	L	1.7	9	28
2GC4	I N	I	15	G	12.3	9	28
2GC4	I N	I	26	L	1.8	9	28
2GC4	M J	M	15	G	12.1	9	28
2GC4	M J	M	26	L	1.3	9	28
2GCO	A B	A	176	R	1.4	167	180
2GCO	A B	B	176	R	1.0	167	180
2GD4	A B	B	127	W	5.4	126	133
2GD4	L H	H	127	W	4.8	126	133
2GEZ	A B	A	31	L	1.8	21	44
2GEZ	A B	A	35	L	2.1	21	44
2GEZ	A B	A	52	V	1.3	48	62
2GEZ	A B	A	56	V	1.8	48	62
2GEZ	A B	A	59	L	1.1	48	62
2GEZ	A B	A	60	E	1.7	48	62
2GEZ	A D	A	125	G	159.6	124	133
2GEZ	A D	D	247	E	1.7	246	252

2GEZ	A D	D	250	I	1.0	246	252
2GEZ	C B	C	125	G	144.4	124	134
2GEZ	C B	B	247	E	2.0	246	252
2GEZ	C D	C	24	R	1.1	21	44
2GEZ	C D	C	27	R	1.0	21	44
2GEZ	C D	C	31	L	3.1	21	44
2GEZ	C D	C	35	L	2.3	21	44
2GEZ	C D	C	52	V	2.1	48	61
2GEZ	C D	C	56	V	1.9	48	61
2GEZ	C D	C	60	E	1.3	48	61
2GEZ	E F	E	31	L	1.9	21	44
2GEZ	E F	E	35	L	1.8	21	44
2GEZ	E F	E	52	V	1.9	48	61
2GEZ	E F	E	56	V	1.9	48	61
2GEZ	E F	E	60	E	1.1	48	61
2GEZ	E H	E	125	G	117.4	124	133
2GEZ	E H	H	247	E	2.7	246	252
2GEZ	G F	G	125	G	122.8	124	134
2GEZ	G F	F	250	I	1.0	246	252
2GEZ	G H	G	31	L	1.9	23	44
2GEZ	G H	G	35	L	2.1	23	44
2GEZ	G H	G	52	V	3.0	48	62
2GEZ	G H	G	55	V	1.1	48	62
2GEZ	G H	G	56	V	2.1	48	62
2GEZ	G H	G	59	L	2.0	48	62
2GEZ	G H	G	60	E	1.4	48	62
2GFB	A B	A	123	E	1.6	122	127
2GFB	A B	A	124	Q	1.0	122	127
2GFB	C D	C	124	Q	1.5	122	127
2GFB	E B	E	185	E	1.0	183	187
2GFB	E F	E	124	Q	2.3	122	127
2GFB	G H	G	124	Q	1.1	122	128
2GFB	I J	I	124	Q	1.3	122	128
2GFB	K L	K	123	E	1.4	122	128
2GFB	K L	K	124	Q	1.2	122	128
2GFB	M N	M	124	Q	1.3	122	127
2GFB	O P	O	124	Q	1.2	122	128
2GGM	A C	A	112	L	1.3	99	114
2GGM	A C	A	113	F	2.9	99	114
2GGM	A C	A	126	L	1.3	123	133
2GGM	A C	A	132	E	1.0	123	133
2GGM	A C	C	848	W	5.4	848	863
2GGM	A C	C	851	L	2.1	848	863
2GGM	A C	C	854	G	6.7	848	863
2GGM	A C	C	855	L	2.9	848	863
2GGM	A C	C	856	L	1.8	848	863
2GGM	B C	C	857	I	1.0	848	863
2GGM	B D	B	112	L	1.3	99	114
2GGM	B D	B	113	F	2.9	99	114
2GGM	B D	B	126	L	1.0	123	133
2GGM	B D	B	129	V	1.0	123	133
2GGM	B D	D	848	W	5.6	848	858
2GGM	B D	D	851	L	1.8	848	858
2GGM	B D	D	854	G	11.9	848	858
2GGM	B D	D	855	L	3.1	848	858
2GGM	B D	D	856	L	2.1	848	858
2GGP	A B	A	24	K	1.3	18	29
2GGP	A B	A	59	K	1.2	53	64
2GGP	A B	A	62	K	1.2	53	64
2GGP	A B	B	19	T	1.0	14	25

2GGP	A B	B	57	E	1.2	52	61
2GH0	C A	A	183	G	30.5	173	186
2GH0	D B	B	167	M	1.1	161	172
2GH0	D B	B	180	K	1.3	173	186
2GH0	D B	B	183	G	2.7	173	186
2GHO	A C	A	34	V	1.1	32	45
2GHO	A C	A	42	R	1.6	32	45
2GHO	A C	A	80	L	1.0	76	85
2GHO	A C	C	932	E	2.5	911	933
2GHO	A C	C	938	K	1.1	938	950
2GHO	B D	B	84	E	1.4	75	85
2GHO	B D	D	557	E	1.3	555	564
2GHO	B D	D	597	E	1.0	586	598
2GHO	C D	C	1034	E	1.0	1034	1043
2GHO	C D	C	1035	M	5.5	1034	1043
2GHO	C D	C	1036	E	4.3	1034	1043
2GHO	C D	C	1039	A	5.4	1034	1043
2GHO	C D	C	1088	L	1.5	1085	1094
2GHO	C D	D	17	K	1.4	15	21
2GHO	C D	D	253	Y	4.9	249	254
2GHO	C D	D	312	L	14.2	312	317
2GHO	C D	D	315	I	4.7	312	317
2GHO	C D	D	316	L	6.4	312	317
2GHO	C D	D	323	F	1.3	323	327
2GHO	C D	D	648	F	1.1	643	651
2GHO	C D	D	776	V	1.0	776	780
2GHO	C D	D	777	L	5.9	776	780
2GID	A B	A	214	H	1.8	206	218
2GID	A B	B	152	V	1.2	149	167
2GID	A B	B	156	H	1.5	149	167
2GID	A D	A	208	F	1.6	206	218
2GID	A D	D	168	F	5.7	168	172
2GID	A D	D	171	H	1.8	168	172
2GID	G B	G	215	Y	1.5	206	217
2GID	G D	G	206	Q	1.3	206	217
2GID	G D	G	214	H	1.4	206	217
2GID	G D	D	152	V	1.2	149	164
2GID	G D	D	156	H	1.5	149	164
2GID	H J	H	207	R	1.2	206	216
2GID	H J	H	208	F	1.0	206	216
2GID	H J	J	95	Y	1.3	90	101
2GID	H J	J	166	F	2.3	149	167
2GID	H K	H	214	H	1.8	206	216
2GID	H K	K	152	V	1.2	149	165
2GID	H K	K	156	H	1.2	149	165
2GID	H K	K	164	E	2.1	149	165
2GID	P J	P	214	H	1.6	212	218
2GID	P J	J	149	H	1.3	149	167
2GID	P J	J	164	E	1.0	149	167
2GID	P K	P	199	V	1.0	199	203
2GID	P K	P	208	F	1.4	206	211
2GID	P K	K	95	Y	1.3	90	101
2GJ7	A F	A	248	K	1.1	247	252
2GJ7	A F	A	314	L	47.5	310	315
2GJ7	B E	B	310	H	2.4	310	315
2GJ7	B E	B	311	Q	4.9	310	315
2GJE	A D	A	208	F	1.8	206	217
2GJE	A D	D	90	H	4.5	90	101
2GJE	A D	D	168	F	4.4	168	173
2GJE	A D	D	171	H	1.4	168	173

2GJE	A D	D	172	Y	4.1	168	173
2GJX	A B	A	504	R	1.5	493	510
2GJX	A B	B	533	R	1.8	522	539
2GJX	A C	A	69	R	1.1	59	73
2GJX	D B	D	69	R	1.5	59	73
2GJX	E F	F	533	R	1.8	532	539
2GJX	H G	G	533	R	2.0	522	539
2GJZ	A B	A	124	Q	1.4	122	128
2GJZ	L H	L	124	Q	1.4	122	128
2GKV	E A	E	57	H	1.0	56	60
2GL7	A B	A	253	F	1.6	249	265
2GL7	A B	A	292	K	1.7	291	306
2GL7	A B	A	296	I	1.8	291	306
2GL7	A B	A	312	K	1.1	309	318
2GL7	A B	A	387	N	2.0	375	390
2GL7	A B	A	422	G	7.2	414	429
2GL7	A B	A	426	N	2.1	414	429
2GL7	A B	A	435	K	2.1	432	441
2GL7	A B	B	40	D	1.0	39	49
2GL7	A B	B	44	V	1.5	39	49
2GL7	A B	B	45	K	1.2	39	49
2GL7	A B	B	48	L	3.6	39	49
2GL7	A C	A	159	L	1.0	143	161
2GL7	A C	A	167	V	1.7	165	181
2GL7	A C	C	359	R	2.1	353	374
2GL7	A C	C	363	L	1.2	353	374
2GL7	A C	C	373	L	1.6	353	374
2GL7	D E	D	253	F	1.7	249	265
2GL7	D E	D	257	T	1.7	249	265
2GL7	D E	D	292	K	1.2	291	306
2GL7	D E	D	296	I	1.2	291	306
2GL7	D E	D	349	V	1.1	334	350
2GL7	D E	D	386	R	1.3	375	391
2GL7	D E	D	387	N	1.8	375	391
2GL7	D E	D	422	G	8.0	414	429
2GL7	D E	D	426	N	1.6	414	429
2GL7	D E	D	435	K	1.5	432	441
2GL7	D E	D	470	H	1.4	458	472
2GL7	D E	D	515	R	1.1	504	520
2GL7	D E	D	519	L	1.0	504	520
2GL7	D E	E	44	V	1.1	42	50
2GL7	D E	E	48	L	3.6	42	50
2GL7	D E	E	49	V	1.6	42	50
2GL7	D F	D	167	V	1.1	165	181
2GL7	D F	F	363	L	1.0	356	369
2GL7	D F	F	366	L	1.5	356	369
2GMI	A B	B	8	F	5.5	6	19
2GMI	A B	B	11	L	1.0	6	19
2GMI	A B	B	18	E	1.4	6	19
2GOL	A B	B	153	N	1.3	149	163
2GOO	A B	A	66	L	1.3	59	71
2GOO	A B	A	69	S	1.5	59	71
2GOO	A B	B	85	F	1.0	83	89
2GOO	D E	D	62	I	8.3	59	71
2GOO	D E	D	66	L	1.0	59	71
2GOX	A B	B	110	K	1.2	102	125
2GOX	A B	B	130	H	2.2	127	140
2GOX	A B	B	131	R	1.1	127	140
2GOX	A B	B	138	N	2.0	127	140
2GOX	A B	B	139	L	1.1	127	140

2GOX	A B	B	159	L	1.0	145	162
2GOX	C D	C	1042	R	1.0	1039	1059
2GOX	C D	D	130	H	2.1	127	140
2GOX	C D	D	131	R	1.9	127	140
2GOX	C D	D	138	N	2.8	127	140
2GOX	C D	D	148	K	1.2	145	162
2GPP	B D	B	280	I	2.8	261	285
2GPP	B D	B	281	G	1.6	261	285
2GPP	B D	B	284	K	1.4	261	285
2GPP	B D	B	294	L	1.6	294	304
2GPP	B D	B	298	M	2.7	294	304
2GPP	B D	B	301	L	1.4	294	304
2GPP	B D	B	449	L	1.3	448	455
2GPP	B D	B	452	E	1.6	448	455
2GPP	B D	D	381	L	1.6	379	386
2GPP	B D	D	383	L	2.6	379	386
2GPP	B D	D	384	L	1.1	379	386
2GPP	B D	D	385	K	1.1	379	386
2GPV	A G	A	305	W	1.6	305	317
2GPV	A G	G	1324	I	2.0	1321	1330
2GPV	A G	G	1328	L	2.2	1321	1330
2GPV	B H	B	305	W	1.0	305	317
2GPV	B H	H	1320	L	1.8	1320	1330
2GPV	B H	H	1324	I	2.0	1320	1330
2GPV	B H	H	1328	L	1.6	1320	1330
2GPV	C I	C	298	M	1.0	294	304
2GPV	C I	I	1320	L	1.5	1320	1330
2GPV	C I	I	1323	I	1.6	1320	1330
2GPV	C I	I	1324	I	1.9	1320	1330
2GPV	C I	I	1328	L	1.9	1320	1330
2GRN	A B	A	134	Y	2.3	131	140
2GRN	A B	B	562	F	2.3	553	565
2GS0	A B	B	54	F	1.5	47	56
2GSI	G H	G	123	E	1.2	122	126
2GSI	G H	G	124	Q	2.0	122	126
2GTL	A B	B	7	L	1.1	6	21
2GTL	A D	A	96	H	1.0	88	103
2GTL	A D	D	72	R	1.0	64	82
2GTL	A D	D	78	D	1.1	64	82
2GTL	A G	A	12	R	5.1	9	20
2GTL	A G	A	88	L	1.1	88	103
2GTL	A M	A	13	R	1.6	9	20
2GTL	B C	B	59	P	1.2	59	77
2GTL	B C	B	74	I	1.7	59	77
2GTL	B C	B	87	E	1.0	82	97
2GTL	B C	C	65	P	12.8	65	83
2GTL	B C	C	79	D	1.5	65	83
2GTL	B C	C	80	L	1.0	65	83
2GTL	B M	B	35	R	3.8	24	41
2GTL	B M	B	115	H	1.6	103	121
2GTL	C D	D	15	L	1.7	11	26
2GTL	C O	C	9	E	1.6	9	23
2GTL	E F	F	10	L	1.4	6	21
2GTL	E H	E	89	V	1.3	88	103
2GTL	E H	E	93	H	1.1	88	103
2GTL	E H	E	96	H	1.7	88	103
2GTL	E H	H	64	P	1.0	64	82
2GTL	E H	H	65	E	1.1	64	82
2GTL	E H	H	67	G	1.3	64	82
2GTL	E H	H	72	R	1.8	64	82

2GTL	E H	H	78	D	1.2	64	82
2GTL	E H	H	89	M	1.4	87	100
2GTL	E K	E	12	R	1.6	9	20
2GTL	E K	K	10	E	1.3	9	23
2GTL	E K	K	11	D	2.0	9	23
2GTL	E N	E	17	H	1.0	9	20
2GTL	F G	F	20	Y	1.0	6	21
2GTL	F G	F	59	P	2.5	59	77
2GTL	F G	F	74	I	1.3	59	77
2GTL	F G	G	79	D	1.8	65	83
2GTL	F G	G	80	L	1.3	65	83
2GTL	F N	F	115	H	2.3	103	121
2GTL	G H	G	34	G	4.6	28	47
2GTL	G H	H	15	L	1.2	11	26
2GTL	I C	C	11	D	1.6	9	23
2GTL	I C	C	14	I	1.0	9	23
2GTL	I J	J	7	L	1.1	6	21
2GTL	I J	J	10	L	1.5	6	21
2GTL	I L	L	78	D	1.5	64	82
2GTL	I L	L	89	M	2.1	87	100
2GTL	J K	J	87	E	1.1	82	97
2GTL	J K	K	65	P	1.2	65	83
2GTL	J K	K	79	D	1.8	65	83
2GTL	J K	K	80	L	1.1	65	83
2GTL	J O	J	35	R	4.4	24	41
2GTL	K L	L	15	L	1.5	11	26
2GTL	K N	K	9	E	1.1	9	23
2GTL	M N	M	24	L	2.9	12	30
2GTL	M N	M	27	K	1.2	12	30
2GTL	M N	M	53	R	1.1	44	58
2GTL	M N	M	57	L	1.5	44	58
2GTL	M N	N	28	I	2.4	18	41
2GTL	M O	M	18	N	19.5	12	30
2GTL	M O	M	28	L	1.6	12	30
2GTL	M O	M	54	I	1.0	44	58
2GTL	M O	O	57	L	1.8	41	58
2GTL	N O	N	31	L	2.9	18	41
2GTL	N O	N	34	K	1.3	18	41
2GTL	N O	N	35	L	1.6	18	41
2GTL	N O	N	50	I	1.0	43	59
2GTL	N O	N	57	I	1.7	43	59
2GTL	N O	O	32	E	2.8	20	38
2GTL	N O	O	35	L	1.5	20	38
2GTL	N O	O	36	D	1.0	20	38
2GTL	N O	O	51	R	1.7	41	58
2GTP	A D	D	140	F	1.7	140	152
2GTP	A D	D	168	L	1.3	159	179
2GTP	A D	D	172	D	1.3	159	179
2GTP	B C	B	207	E	1.1	205	214
2GTP	B C	B	213	H	1.3	205	214
2GTP	B C	C	140	F	1.6	140	152
2GTP	B C	C	168	L	1.3	159	179
2GTP	B C	C	172	D	1.3	159	179
2GUZ	A B	A	112	E	1.5	110	117
2GUZ	A B	A	149	F	1.2	148	165
2GUZ	A B	A	150	L	1.9	148	165
2GUZ	A B	A	154	I	2.1	148	165
2GUZ	A B	B	60	K	1.0	55	62
2GUZ	A B	B	83	L	1.3	73	87
2GUZ	A B	B	95	F	2.2	95	117

2GUZ	A B	B	96	Y	2.6	95	117
2GUZ	A B	B	97	L	2.1	95	117
2GUZ	A B	B	102	Y	2.3	95	117
2GUZ	A B	B	103	R	2.4	95	117
2GUZ	A F	F	85	E	1.0	73	87
2GUZ	A P	P	78	N	1.0	73	87
2GUZ	A P	P	79	R	1.2	73	87
2GUZ	A P	P	82	Y	1.1	73	87
2GUZ	C D	C	116	I	1.0	110	117
2GUZ	C D	C	149	F	1.5	148	165
2GUZ	C D	C	150	L	2.0	148	165
2GUZ	C D	C	154	I	1.8	148	165
2GUZ	C D	D	57	E	1.2	55	62
2GUZ	C D	D	61	I	1.0	55	62
2GUZ	C D	D	79	R	1.2	73	87
2GUZ	C D	D	83	L	1.2	73	87
2GUZ	C D	D	95	F	2.3	95	117
2GUZ	C D	D	96	Y	6.0	95	117
2GUZ	C D	D	97	L	2.5	95	117
2GUZ	C D	D	102	Y	2.1	95	117
2GUZ	C D	D	103	R	2.6	95	117
2GUZ	C J	J	84	F	1.1	73	87
2GUZ	C J	J	85	E	1.1	73	87
2GUZ	E F	E	136	I	1.1	126	140
2GUZ	E F	E	149	F	2.1	148	165
2GUZ	E F	E	150	L	2.2	148	165
2GUZ	E F	E	154	I	1.4	148	165
2GUZ	E F	F	57	E	1.6	55	62
2GUZ	E F	F	61	I	1.4	55	62
2GUZ	E F	F	79	R	2.0	73	87
2GUZ	E F	F	95	F	1.9	95	117
2GUZ	E F	F	96	Y	2.0	95	117
2GUZ	E F	F	97	L	2.4	95	117
2GUZ	E F	F	100	K	1.8	95	117
2GUZ	E F	F	102	Y	1.6	95	117
2GUZ	E F	F	103	R	2.6	95	117
2GUZ	E H	H	78	N	1.1	73	87
2GUZ	E H	H	79	R	1.1	73	87
2GUZ	E H	H	82	Y	1.4	73	87
2GUZ	G B	G	138	L	1.1	126	140
2GUZ	G B	B	107	R	2.3	95	117
2GUZ	G B	B	110	W	1.2	95	117
2GUZ	G F	F	78	N	1.4	73	87
2GUZ	G F	F	79	R	1.6	73	87
2GUZ	G F	F	82	Y	1.8	73	87
2GUZ	G H	G	149	F	2.2	148	165
2GUZ	G H	G	150	L	2.0	148	165
2GUZ	G H	G	154	I	1.7	148	165
2GUZ	G H	H	57	E	1.8	55	62
2GUZ	G H	H	61	I	1.2	55	62
2GUZ	G H	H	79	R	2.1	73	87
2GUZ	G H	H	82	Y	1.6	73	87
2GUZ	G H	H	95	F	2.0	95	117
2GUZ	G H	H	96	Y	2.3	95	117
2GUZ	G H	H	97	L	2.3	95	117
2GUZ	G H	H	102	Y	1.8	95	117
2GUZ	G H	H	103	R	3.3	95	117
2GUZ	I D	D	85	E	1.4	73	87
2GUZ	I J	I	116	I	1.0	110	117
2GUZ	I J	I	136	I	1.1	126	140

2GUZ	I J	I	149	F	2.3	148	165
2GUZ	I J	I	150	L	2.1	148	165
2GUZ	I J	I	154	I	1.5	148	165
2GUZ	I J	J	57	E	1.8	55	62
2GUZ	I J	J	61	I	1.1	55	62
2GUZ	I J	J	79	R	2.5	73	87
2GUZ	I J	J	95	F	1.9	95	117
2GUZ	I J	J	96	Y	3.1	95	117
2GUZ	I J	J	97	L	2.5	95	117
2GUZ	I J	J	102	Y	1.6	95	117
2GUZ	I J	J	103	R	2.6	95	117
2GUZ	I L	L	78	N	1.5	73	87
2GUZ	I L	L	79	R	1.2	73	87
2GUZ	I L	L	82	Y	1.1	73	87
2GUZ	K D	K	134	R	2.5	126	140
2GUZ	K D	D	107	R	1.3	95	117
2GUZ	K D	D	110	W	3.3	95	117
2GUZ	K J	J	78	N	1.1	73	87
2GUZ	K J	J	79	R	1.5	73	87
2GUZ	K J	J	82	Y	1.9	73	87
2GUZ	K L	K	136	I	1.0	126	140
2GUZ	K L	K	149	F	2.2	148	165
2GUZ	K L	K	150	L	2.3	148	165
2GUZ	K L	K	154	I	1.6	148	165
2GUZ	K L	L	57	E	1.7	55	62
2GUZ	K L	L	61	I	1.2	55	62
2GUZ	K L	L	79	R	2.2	73	87
2GUZ	K L	L	95	F	1.8	95	117
2GUZ	K L	L	96	Y	4.7	95	117
2GUZ	K L	L	97	L	2.3	95	117
2GUZ	K L	L	100	K	1.1	95	117
2GUZ	K L	L	102	Y	1.8	95	117
2GUZ	K L	L	103	R	2.2	95	117
2GUZ	O B	B	78	N	1.0	73	87
2GUZ	O B	B	82	Y	1.7	73	87
2GUZ	O F	O	134	R	1.5	126	140
2GUZ	O F	F	110	W	1.8	95	117
2GUZ	O P	O	112	E	1.2	110	117
2GUZ	O P	O	116	I	1.4	110	117
2GUZ	O P	O	148	P	18.1	148	165
2GUZ	O P	O	150	L	20.1	148	165
2GUZ	O P	O	153	K	18.7	148	165
2GUZ	O P	P	57	E	18.4	55	62
2GUZ	O P	P	60	K	6.8	55	62
2GUZ	O P	P	61	I	18.4	55	62
2GUZ	O P	P	79	R	19.6	73	87
2GUZ	O P	P	95	F	3.4	95	117
2GUZ	O P	P	96	Y	1.5	95	117
2GUZ	O P	P	97	L	2.3	95	117
2GUZ	O P	P	99	S	1.2	95	117
2GUZ	O P	P	102	Y	1.9	95	117
2GUZ	O P	P	103	R	3.4	95	117
2GV5	A C	A	104	L	1.0	94	106
2GV5	A C	A	105	F	2.3	94	106
2GV5	A C	A	118	L	1.5	115	125
2GV5	A C	A	157	I	1.1	151	158
2GV5	A C	C	644	L	1.4	643	692
2GV5	A C	C	647	I	1.2	643	692
2GV5	A C	C	648	L	1.6	643	692
2GV5	A C	C	651	Y	1.2	643	692

2GV5	A C	C	659	L	1.2	643	692
2GV5	A C	C	664	F	2.5	643	692
2GV5	A C	C	667	W	4.6	643	692
2GV5	B C	B	20	E	1.0	19	32
2GV5	B C	B	27	E	1.2	19	32
2GV5	B C	B	31	L	1.1	19	32
2GV5	B C	B	43	H	1.0	42	48
2GV5	B C	B	105	F	2.3	94	106
2GV5	B C	B	154	F	1.0	151	159
2GV5	B C	C	674	Y	1.5	643	692
2GV5	B C	C	678	C	1.2	643	692
2GV5	B C	C	685	K	1.4	643	692
2GV5	B C	C	688	Y	1.1	643	692
2GV5	B C	C	695	L	1.7	695	710
2GV5	B C	C	697	K	1.5	695	710
2GV5	B C	C	701	R	1.0	695	710
2GV5	B C	C	702	L	1.6	695	710
2GV5	D F	D	104	L	2.0	94	106
2GV5	D F	D	105	F	2.4	94	106
2GV5	D F	D	118	L	1.7	115	125
2GV5	D F	D	154	F	1.1	151	158
2GV5	D F	D	157	I	1.7	151	158
2GV5	D F	F	644	L	1.2	643	692
2GV5	D F	F	647	I	1.2	643	692
2GV5	D F	F	648	L	1.4	643	692
2GV5	D F	F	651	Y	1.1	643	692
2GV5	D F	F	659	L	1.2	643	692
2GV5	D F	F	664	F	3.0	643	692
2GV5	D F	F	667	W	5.5	643	692
2GV5	D F	F	668	R	1.3	643	692
2GV5	D F	F	670	R	1.4	643	692
2GV5	D F	F	671	F	1.2	643	692
2GV5	D F	F	674	Y	1.1	643	692
2GV5	E F	E	27	E	1.2	19	32
2GV5	E F	E	31	L	1.2	19	32
2GV5	E F	E	43	H	1.0	42	48
2GV5	E F	E	105	F	1.7	94	106
2GV5	E F	F	674	Y	2.1	643	692
2GV5	E F	F	678	C	2.4	643	692
2GV5	E F	F	685	K	1.1	643	692
2GV5	E F	F	695	L	1.4	695	710
2GV5	E F	F	697	K	1.6	695	710
2GV5	E F	F	698	F	2.0	695	710
2GV5	E F	F	701	R	3.4	695	710
2GV5	E F	F	702	L	1.5	695	710
2GV5	E F	F	704	E	2.3	695	710
2GW4	A B	A	54	Y	1.8	54	59
2GW4	A B	A	56	I	2.1	54	59
2GW4	C D	C	54	Y	1.5	54	59
2GW4	C D	C	56	I	1.7	54	59
2GW4	C D	D	80	K	1.4	78	82
2GWF	A B	A	241	D	1.8	241	249
2GWF	A B	A	244	K	1.0	241	249
2GWF	A B	B	262	L	1.7	262	268
2GWF	A B	B	265	R	1.8	262	268
2GWF	A F	A	212	D	1.1	207	213
2GWF	C D	D	262	L	2.2	262	268
2GWF	C D	D	266	Q	1.1	262	268
2GWF	C F	F	270	R	1.5	269	275
2GWF	E F	E	241	D	1.7	241	249

2GWF	E F	F	262	L	1.2	262	268
2GWF	E F	F	265	R	2.0	262	268
2GWF	E F	F	269	R	1.0	269	275
2GWW	A B	A	12	I	1.8	7	26
2GWW	A B	A	16	V	1.3	7	26
2GWW	A B	A	43	P	1.1	41	65
2GWW	A B	A	47	V	1.2	41	65
2GWW	A B	A	54	L	1.7	41	65
2GWW	A B	A	126	F	1.9	102	149
2GWW	A B	B	612	I	1.9	611	625
2GWW	A B	B	619	V	1.5	611	625
2GWW	A B	B	623	L	2.1	611	625
2GY9	C E	C	130	R	1.1	129	143
2GYA	C J	C	32	V	4.9	32	40
2GYA	M U	M	16	R	1.1	16	22
2GYK	A B	A	30	E	2.0	30	45
2GYK	A B	A	54	Y	2.9	50	55
2GYK	E F	E	30	E	3.0	30	45
2GYK	E F	E	33	L	1.0	30	45
2GYK	E F	E	34	V	1.4	30	45
2GYK	E F	E	54	Y	3.2	50	55
2GYK	E F	F	54	R	1.2	50	64
2GZD	A C	C	478	E	1.0	470	488
2GZD	A C	C	482	D	1.6	470	488
2GZD	A C	C	485	L	1.3	470	488
2GZD	A D	D	480	Y	1.3	471	488
2GZD	B C	C	480	Y	1.5	470	488
2GZD	B D	D	485	L	4.9	471	488
2H0D	A B	A	9	I	1.6	9	15
2H0D	A B	A	12	L	1.9	9	15
2H0D	A B	A	13	N	1.0	9	15
2H0D	A B	A	44	V	1.2	40	47
2H0D	A B	A	78	I	1.5	73	83
2H0D	A B	A	81	K	1.4	73	83
2H0D	A B	A	82	L	1.2	73	83
2H0D	A B	A	90	E	1.7	86	101
2H0D	A B	A	94	R	1.7	86	101
2H0D	A B	A	97	F	2.2	86	101
2H0D	A B	B	22	Y	3.1	21	25
2H0D	A B	B	23	E	1.1	21	25
2H0D	A B	B	109	L	2.1	104	114
2H0D	A B	B	113	I	1.4	104	114
2H1L	A M	A	612	Y	2.7	609	622
2H1L	A M	M	178	H	1.2	177	181
2H1L	B N	B	609	L	1.1	609	622
2H1L	B N	B	612	Y	2.4	609	622
2H1L	C O	C	597	V	1.7	593	607
2H1L	C O	C	600	K	2.2	593	607
2H1L	C O	C	604	D	1.6	593	607
2H1L	D P	D	581	W	1.2	572	583
2H1L	D P	D	604	D	1.2	600	607
2H1L	D P	D	609	L	1.3	609	622
2H1L	E Q	E	597	V	1.7	593	598
2H1L	E Q	E	604	D	1.2	599	605
2H1L	F R	F	604	D	1.3	593	607
2H1L	F R	R	177	P	1.2	177	181
2H1L	F R	R	178	H	1.8	177	181
2H1L	G S	G	604	D	1.6	592	607
2H1L	G S	G	612	Y	1.1	609	622
2H1L	H T	T	280	R	1.0	278	288

2H1L	I U	I	609	L	1.2	609	622
2H1L	J V	V	281	D	1.2	278	288
2H1L	K W	W	285	E	1.3	278	288
2H1O	A E	A	13	L	1.2	6	14
2H1O	A E	A	25	L	1.3	19	27
2H1O	A E	A	46	G	6.4	37	49
2H1O	A E	E	48	L	2.6	48	59
2H1O	A E	E	49	G	56.9	48	59
2H1O	A E	E	52	L	1.3	48	59
2H1O	A E	E	56	G	25.9	48	59
2H1O	A E	E	58	E	1.7	48	59
2H1O	B F	B	46	G	36.7	37	49
2H1O	B F	B	59	L	1.4	54	71
2H1O	B F	B	62	R	1.3	54	71
2H1O	B F	F	48	L	2.6	48	59
2H1O	B F	F	49	G	80.2	48	59
2H1O	B F	F	52	L	1.2	48	59
2H1O	B F	F	55	I	1.6	48	59
2H1O	B F	F	56	G	33.0	48	59
2H1O	C F	F	19	F	2.8	11	23
2H1O	C G	C	13	L	1.1	6	14
2H1O	C G	C	46	G	3.7	37	49
2H1O	C G	C	59	L	1.4	54	71
2H1O	C G	C	62	R	1.8	54	71
2H1O	C G	G	48	L	1.8	48	59
2H1O	C G	G	49	G	15.3	48	59
2H1O	C G	G	52	L	1.9	48	59
2H1O	C G	G	55	I	1.7	48	59
2H1O	C G	G	56	G	26.4	48	59
2H1O	D H	D	26	D	1.2	19	27
2H1O	D H	D	46	G	179.9	37	49
2H1O	D H	D	47	V	1.0	37	49
2H1O	D H	D	62	R	1.7	54	71
2H1O	D H	H	48	L	2.5	48	59
2H1O	D H	H	49	G	93.9	48	59
2H1O	D H	H	50	S	1.4	48	59
2H1O	D H	H	55	I	1.8	48	59
2H1O	D H	H	56	G	9.5	48	59
2H1P	L H	L	129	Q	1.5	127	132
2H4C	A B	A	2	F	2.5	2	10
2H4C	A B	B	49	D	1.8	40	50
2H4C	C D	C	2	F	2.2	2	12
2H4C	C D	D	3	F	1.0	3	12
2H4C	C D	D	49	D	1.0	40	54
2H4C	E F	E	2	F	3.4	2	12
2H4C	E F	E	6	A	4.8	2	12
2H4C	E F	E	7	E	4.9	2	12
2H4C	E F	E	9	I	5.1	2	12
2H4C	E F	F	2	L	2.3	2	13
2H4C	E F	F	4	Q	1.0	2	13
2H4C	G H	G	2	F	1.5	2	12
2H4C	G H	G	3	F	4.3	2	12
2H4C	G H	H	3	F	1.9	2	12
2H4C	G H	H	5	F	1.0	2	12
2H4M	A C	A	460	W	1.9	452	464
2H4M	A C	A	502	S	1.6	494	512
2H4M	A C	A	509	E	1.7	494	512
2H4M	A C	A	685	Q	1.0	681	698
2H4M	A C	A	726	N	1.1	722	740
2H4M	A C	A	727	N	1.0	722	740

2H4M	A C	A	730	W	3.5	722	740
2H4M	A C	A	770	N	1.3	765	782
2H4M	B D	B	509	E	1.3	494	512
2H4M	B D	B	543	D	1.2	535	553
2H4M	B D	B	584	F	1.0	583	597
2H4M	B D	B	653	E	1.5	639	656
2H4M	B D	B	730	W	2.7	722	739
2H4M	B D	B	770	N	1.0	765	782
2H4M	B D	B	880	L	4.8	878	888
2H4P	A B	A	16	F	3.7	-3	23
2H4P	A B	A	32	P	1.6	32	45
2H4P	A B	A	105	F	1.9	92	106
2H4P	A B	A	274	L	1.1	272	277
2H4P	A B	A	283	L	1.2	280	288
2H4Q	A B	A	16	F	2.9	-8	23
2H4Q	A B	A	32	P	1.7	32	46
2H4Q	A B	A	105	F	1.6	94	106
2H4Q	A B	A	275	E	2.2	272	277
2H4Q	A B	A	283	L	1.0	280	288
2H61	A C	C	15	H	1.2	2	19
2H61	A D	D	87	F	1.0	70	88
2H61	B D	B	15	H	1.0	2	19
2H61	E C	E	87	F	2.2	70	90
2H61	E C	E	88	F	2.0	70	90
2H61	E C	C	87	F	3.1	70	89
2H61	F G	F	88	F	1.0	70	89
2H61	H G	H	3	L	2.0	2	19
2H61	H G	H	4	E	3.2	2	19
2H61	H G	H	7	M	2.2	2	19
2H61	H G	H	11	I	1.7	2	19
2H61	H G	H	70	F	3.2	70	88
2H61	H G	H	74	M	1.3	70	88
2H61	H G	H	85	H	2.5	70	88
2H61	H G	G	3	L	2.1	2	19
2H61	H G	G	4	E	2.5	2	19
2H61	H G	G	7	M	1.4	2	19
2H61	H G	G	11	I	2.2	2	19
2H61	H G	G	70	F	3.4	70	88
2H61	H G	G	74	M	1.3	70	88
2H61	H G	G	85	H	1.9	70	88
2H62	A C	C	85	F	2.5	83	89
2H62	B C	B	66	L	1.1	59	71
2H62	B C	B	70	V	1.0	59	71
2H62	B C	C	86	Q	2.8	83	89
2H67	A B	A	3	V	3.4	2	9
2H67	A B	A	6	C	17.1	2	9
2H67	A B	A	17	E	3.1	13	18
2H67	A B	B	11	L	1.5	9	20
2H7D	A B	A	396	I	1.2	385	403
2H7D	A B	B	730	F	1.7	721	736
2H7V	A C	A	62	E	1.2	62	70
2H7V	A C	A	64	Y	1.5	62	70
2H7V	A C	A	66	R	1.2	62	70
2H7V	A C	A	67	L	2.7	62	70
2H7V	A C	C	574	E	1.1	556	581
2H7V	A C	C	591	Y	1.5	588	632
2H7V	A D	A	141	Q	1.3	139	149
2H7V	B D	B	64	Y	1.0	64	73
2H7V	B D	B	66	R	1.0	64	73
2H7V	B D	B	67	L	2.0	64	73

2H7V	B D	B	70	L	1.5	64	73
2H7V	B D	D	574	E	1.4	556	583
2H8B	B A	B	14	F	7.2	12	23
2H8P	A B	B	123	E	1.1	122	127
2H8P	A B	B	124	Q	1.3	122	127
2H8P	A C	C	49	L	2.3	24	52
2H8P	C D	C	36	L	1.3	24	52
2H8P	C D	C	39	V	1.2	24	52
2H8P	C D	C	43	G	3.2	24	52
2H8P	C D	C	51	E	2.3	24	52
2H8P	C D	C	68	W	2.4	62	74
2H8P	C D	D	88	G	6.6	86	121
2H8P	C D	D	91	V	1.5	86	121
2H8P	C D	D	95	V	2.0	86	121
2H8P	C D	D	99	G	109.0	86	121
2H8P	C D	D	103	F	1.5	86	121
2H9A	A B	A	84	H	1.4	83	87
2H9A	A B	A	250	L	1.5	237	254
2H9A	A B	A	273	Y	4.0	272	285
2H9A	A B	A	274	Q	1.2	272	285
2H9A	A B	A	277	M	1.0	272	285
2H9A	A B	A	299	D	1.0	297	311
2H9A	A B	A	301	L	2.9	297	311
2H9A	A B	A	306	L	1.4	297	311
2H9A	A B	A	344	L	1.1	343	356
2H9A	A B	A	352	D	1.1	343	356
2H9A	A B	B	229	L	1.6	217	233
2H9A	A B	B	270	R	1.1	267	286
2H9A	A B	B	273	H	2.5	267	286
2H9A	A B	B	274	W	2.4	267	286
2H9A	A B	B	277	V	1.4	267	286
2H9A	A B	B	300	E	2.3	295	309
2H9A	A B	B	303	E	1.4	295	309
2H9A	A B	B	304	H	2.2	295	309
2H9A	A B	B	308	I	1.2	295	309
2H9E	H C	H	237	W	2.1	235	242
2H9E	H C	C	71	E	1.6	67	74
2H9E	H L	H	127	W	4.4	125	132
2H9G	A B	A	124	Q	1.2	122	127
2H9G	L H	L	124	Q	1.4	122	127
2HAN	A B	B	54	Y	1.7	53	59
2HD5	A B	A	298	E	2.9	296	311
2HD5	A B	A	302	F	1.2	296	311
2HDI	A B	B	362	D	1.9	359	384
2HDN	A B	A	27	L	2.6	24	39
2HDN	A B	A	28	T	1.4	24	39
2HDN	A B	A	31	I	1.4	24	39
2HDN	A B	A	34	V	2.2	24	39
2HDN	A B	A	35	L	1.8	24	39
2HDN	A B	B	178	L	1.4	174	180
2HDN	A B	B	188	I	2.1	182	199
2HDN	A B	B	189	L	1.7	182	199
2HDN	C D	C	27	L	2.6	24	39
2HDN	C D	C	28	T	1.3	24	39
2HDN	C D	C	31	I	1.4	24	39
2HDN	C D	C	34	V	2.2	24	39
2HDN	C D	C	35	L	1.6	24	39
2HDN	C D	D	118	H	1.3	113	125
2HDN	C D	D	178	L	1.4	174	180
2HDN	C D	D	188	I	2.2	182	199

2HDN	C D	D	189	L	1.5	182	199
2HDN	E F	E	26	T	1.0	24	39
2HDN	E F	E	27	L	2.7	24	39
2HDN	E F	E	28	T	1.4	24	39
2HDN	E F	E	31	I	1.6	24	39
2HDN	E F	E	34	V	2.2	24	39
2HDN	E F	E	35	L	1.6	24	39
2HDN	E F	F	178	L	1.5	174	180
2HDN	E F	F	188	I	2.1	182	199
2HDN	E F	F	189	L	1.4	182	199
2HDN	G H	G	27	L	2.8	24	39
2HDN	G H	G	28	T	1.4	24	39
2HDN	G H	G	31	I	1.3	24	39
2HDN	G H	G	34	V	2.2	24	39
2HDN	G H	G	35	L	1.6	24	39
2HDN	G H	H	87	Y	1.8	84	93
2HDN	G H	H	178	L	1.4	174	180
2HDN	G H	H	185	E	1.0	182	199
2HDN	G H	H	188	I	2.1	182	199
2HDN	G H	H	189	L	1.4	182	199
2HDN	I J	I	26	T	1.0	24	39
2HDN	I J	I	27	L	2.8	24	39
2HDN	I J	I	28	T	1.4	24	39
2HDN	I J	I	31	I	1.5	24	39
2HDN	I J	I	34	V	2.3	24	39
2HDN	I J	I	35	L	1.7	24	39
2HDN	I J	J	178	L	1.4	174	180
2HDN	I J	J	188	I	2.3	182	199
2HDN	I J	J	189	L	1.4	182	199
2HDN	K L	K	27	L	2.7	24	39
2HDN	K L	K	28	T	2.1	24	39
2HDN	K L	K	31	I	2.2	24	39
2HDN	K L	K	34	V	2.2	24	39
2HDN	K L	K	35	L	1.7	24	39
2HDN	K L	L	118	H	1.2	113	125
2HDN	K L	L	178	L	1.5	174	180
2HDN	K L	L	185	E	1.1	182	199
2HDN	K L	L	188	I	2.2	182	199
2HDN	K L	L	189	L	1.4	182	199
2HFG	L H	L	123	Q	1.2	121	127
2HGI	I U	U	72	R	19.3	60	77
2HGI	I U	U	75	I	18.7	60	77
2HGI	M Q	Q	45	R	1.1	45	51
2HGJ	E S	S	6	L	1.1	6	16
2HGJ	E S	S	7	I	3.3	6	16
2HGJ	E S	S	10	V	1.4	6	16
2HGJ	F O	F	34	W	3.7	30	45
2HGJ	T U	T	50	R	1.8	34	62
2HGP	F Q	F	30	R	9.1	29	39
2HGP	M Q	Q	45	R	2.2	45	51
2HGP	P V	P	87	Y	1.6	87	95
2HGR	F Q	F	30	R	1.7	29	39
2HGR	F Q	Q	49	H	1.0	41	51
2HGR	G H	G	53	D	3.2	53	67
2HGR	G H	G	201	Q	2.3	201	208
2HGR	G H	G	205	E	1.7	201	208
2HGR	G H	H	107	R	2.7	104	114
2HGR	G H	H	111	E	2.3	104	114
2HGR	I U	U	75	I	1.2	60	77
2HGR	J N	N	59	Y	1.1	58	75

2HGR	M Q	Q	42	I	1.5	41	51
2HH0	L H	L	168	Q	1.0	166	175
2HHF	A B	A	69	H	2.4	66	70
2HHF	A B	A	106	R	2.0	93	107
2HHF	A B	A	204	G	9.9	204	219
2HHF	A B	A	208	G	32.3	204	219
2HHF	A B	A	209	P	2.7	204	219
2HHF	A B	A	211	V	1.4	204	219
2HHF	A B	B	568	L	2.0	566	570
2HHF	A B	B	569	H	2.5	566	570
2HHF	A B	B	606	R	1.8	601	607
2HHF	A B	B	704	G	9.1	704	720
2HHF	A B	B	708	G	8.8	704	720
2HHF	A B	B	709	P	1.6	704	720
2HHF	A B	B	711	V	1.3	704	720
2HHH	C E	C	131	R	1.5	130	144
2HHH	C E	C	135	K	1.4	130	144
2HHH	C N	C	9	G	23.0	7	12
2HHH	C N	C	29	Y	1.7	26	47
2HHH	C N	N	49	H	1.3	42	50
2HHH	D E	D	205	E	1.6	200	207
2HHH	D E	E	107	R	1.5	104	114
2HHH	J N	N	42	I	1.1	42	50
2HHH	J N	N	49	H	1.6	42	50
2HHH	L Q	L	11	V	1.1	7	14
2HHH	M S	M	88	R	1.1	87	95
2HII	A B	A	145	V	1.1	140	154
2HII	A B	A	152	L	1.3	140	154
2HII	A C	C	138	G	11.1	136	149
2HII	X Y	X	145	V	1.2	140	154
2HII	X Y	X	152	L	1.0	140	154
2HII	X Z	Z	138	G	1.2	136	149
2HII	X Z	Z	145	E	1.1	136	149
2HII	Y Z	Z	80	V	3.0	77	81
2HIK	L M	L	145	V	1.1	140	149
2HIK	L N	N	145	E	1.4	136	148
2HIO	A B	A	20	R	1.6	17	21
2HIO	A B	A	49	V	1.8	45	74
2HIO	A B	A	50	Y	1.9	45	74
2HIO	A B	A	51	L	1.2	45	74
2HIO	A B	A	54	V	1.4	45	74
2HIO	A B	A	57	Y	2.7	45	74
2HIO	A B	A	58	L	1.3	45	74
2HIO	A B	A	59	T	2.3	45	74
2HIO	A B	A	63	L	2.4	45	74
2HIO	A B	A	67	G	21.2	45	74
2HIO	A B	A	80	P	1.0	80	90
2HIO	A B	A	83	L	1.4	80	90
2HIO	A B	A	96	L	1.9	91	97
2HIO	A B	B	44	V	1.2	37	49
2HIO	A B	B	61	I	1.1	56	84
2HIO	A B	B	62	M	1.3	56	84
2HIO	A B	B	65	F	1.4	56	84
2HIO	A B	B	66	V	1.1	56	84
2HIO	A B	B	70	F	2.5	56	84
2HIO	A B	B	94	I	2.0	91	102
2HIO	A B	B	106	L	1.2	105	124
2HIO	A B	B	114	G	57.7	105	124
2HIO	A B	B	120	K	1.1	105	124
2HIO	A B	B	121	Y	3.8	105	124

2HIO	B D	B	80	L	1.0	56	84
2HIO	B D	B	83	Y	1.0	56	84
2HIO	B D	B	96	T	1.0	91	102
2HIO	B D	B	100	L	1.9	91	102
2HIO	B D	D	72	Y	2.2	48	74
2HIO	B D	D	92	R	1.0	83	93
2HIO	C D	C	50	E	1.9	44	54
2HIO	C D	C	51	I	2.2	44	54
2HIO	C D	C	67	F	1.1	64	73
2HIO	C D	C	70	L	2.0	64	73
2HIO	C D	C	74	I	2.7	74	79
2HIO	C D	C	78	F	2.3	74	79
2HIO	C D	C	92	L	1.9	86	114
2HIO	C D	C	97	E	1.2	86	114
2HIO	C D	C	99	Y	2.0	86	114
2HIO	C D	C	100	L	1.4	86	114
2HIO	C D	C	104	F	3.5	86	114
2HIO	C D	C	121	P	1.3	121	131
2HIO	C D	C	124	I	1.2	121	131
2HIO	C D	D	37	L	2.3	31	41
2HIO	C D	D	39	R	3.1	31	41
2HIO	C D	D	50	I	1.9	48	74
2HIO	C D	D	58	L	1.0	48	74
2HIO	C D	D	61	F	3.6	48	74
2HIO	C D	D	62	L	1.2	48	74
2HIO	C D	D	66	I	3.4	48	74
2HIO	C D	D	86	V	1.9	83	93
2HJ9	A C	A	138	T	1.4	138	149
2HJ9	A C	A	143	F	2.5	138	149
2HJ9	A C	A	146	H	2.3	138	149
2HJ9	A C	A	148	L	1.2	138	149
2HJ9	A C	C	94	D	1.0	93	107
2HJ9	A C	C	131	H	1.1	129	133
2HJ9	A C	C	132	F	5.0	129	133
2HJ9	A C	C	196	F	3.0	196	205
2HL5	A C	A	218	F	3.5	195	231
2HL5	A C	A	222	R	1.5	195	231
2HL5	A C	A	225	E	1.7	195	231
2HL5	A C	A	229	Q	1.0	195	231
2HL5	B D	B	218	F	3.0	197	231
2HL5	B D	B	222	R	1.6	197	231
2HL5	B D	B	229	Q	1.0	197	231
2HLD	A D	A	212	R	4.1	212	225
2HLD	A D	A	285	L	1.5	273	287
2HLD	A D	A	360	Y	1.2	356	362
2HLD	A D	D	290	G	114.0	285	296
2HLD	A D	D	294	E	1.1	285	296
2HLD	A D	D	379	Q	1.1	365	384
2HLD	A E	E	192	R	1.3	191	205
2HLD	A E	E	193	E	1.0	191	205
2HLD	A E	E	194	G	1.9	191	205
2HLD	A E	E	195	N	1.2	191	205
2HLD	A E	E	196	D	1.6	191	205
2HLD	A E	E	199	R	1.1	191	205
2HLD	A E	E	271	L	1.2	258	272
2HLD	A G	G	270	I	1.0	210	274
2HLD	B E	B	212	R	2.0	212	225
2HLD	B E	B	217	Q	1.0	212	225
2HLD	B E	B	285	L	1.6	273	287
2HLD	B E	E	290	G	94.1	285	296

2HLD	B E	E	294	E	1.1	285	296
2HLD	B F	B	301	F	1.4	300	311
2HLD	B F	B	306	R	1.3	300	311
2HLD	B F	F	192	R	1.0	191	204
2HLD	B F	F	194	G	2.1	191	204
2HLD	B G	G	257	R	1.3	210	274
2HLD	C D	C	301	F	1.2	300	311
2HLD	C D	C	302	Y	3.0	300	311
2HLD	C D	D	194	G	4.9	191	205
2HLD	C F	C	212	R	1.8	212	225
2HLD	C F	C	217	Q	1.4	212	225
2HLD	C F	C	285	L	1.5	273	287
2HLD	C F	C	286	L	1.0	273	287
2HLD	C F	F	290	G	59.4	285	296
2HLD	C F	F	326	F	1.0	320	328
2HLD	C F	F	379	Q	1.0	365	384
2HLD	D G	D	390	I	1.1	385	391
2HLD	D G	G	19	I	1.4	3	55
2HLD	D G	G	273	G	10.5	210	274
2HLD	E G	G	260	Q	1.3	210	274
2HLD	E G	G	264	T	1.0	210	274
2HLD	E G	G	271	I	1.2	210	274
2HLD	F G	F	390	I	1.8	385	392
2HLD	G H	G	51	F	2.8	3	55
2HLD	G H	G	205	V	1.8	205	209
2HLD	G H	G	212	Y	2.3	210	274
2HLD	G I	G	140	F	1.6	140	155
2HLD	G I	G	149	K	1.4	140	155
2HLD	G I	I	10	Y	1.9	10	21
2HLD	H I	I	14	L	1.0	10	21
2HLD	J M	J	212	R	2.7	212	225
2HLD	J M	J	285	L	1.6	273	287
2HLD	J M	J	286	L	1.4	273	287
2HLD	J M	J	360	Y	1.1	356	362
2HLD	J M	M	290	G	104.3	285	296
2HLD	J M	M	326	F	1.5	320	328
2HLD	J M	M	379	Q	1.0	365	384
2HLD	J N	J	301	F	2.8	300	310
2HLD	J N	J	302	Y	1.6	300	310
2HLD	J N	J	309	E	1.1	300	310
2HLD	J N	N	192	R	2.0	191	205
2HLD	J N	N	194	G	6.9	191	205
2HLD	J N	N	195	N	1.2	191	205
2HLD	J N	N	196	D	1.2	191	205
2HLD	J N	N	271	L	1.2	258	272
2HLD	J P	P	270	I	1.3	231	276
2HLD	K N	K	212	R	1.1	212	225
2HLD	K N	K	217	Q	1.1	212	225
2HLD	K N	K	285	L	1.0	273	287
2HLD	K N	K	286	L	1.3	273	287
2HLD	K N	N	290	G	20.6	285	296
2HLD	K O	K	301	F	1.5	300	311
2HLD	K O	K	302	Y	1.8	300	311
2HLD	K O	K	339	Y	1.1	339	346
2HLD	K O	O	194	G	3.7	191	204
2HLD	K O	O	337	R	1.3	337	342
2HLD	K O	O	424	F	1.2	422	426
2HLD	K P	P	253	I	1.7	231	276
2HLD	K P	P	257	R	1.4	231	276
2HLD	K X	X	464	E	15.2	463	475

2HLD	L M	L	301	F	1.7	300	311
2HLD	L M	L	302	Y	4.3	300	311
2HLD	L M	L	398	Q	1.2	392	407
2HLD	L M	L	405	F	2.5	392	407
2HLD	L M	M	192	R	1.3	191	205
2HLD	L M	M	194	G	1.1	191	205
2HLD	L M	M	196	D	1.3	191	205
2HLD	L M	M	199	R	1.6	191	205
2HLD	L M	M	337	R	2.2	337	342
2HLD	L M	M	408	R	1.2	398	415
2HLD	L M	M	424	F	1.2	422	426
2HLD	L O	L	212	R	1.8	212	225
2HLD	L O	L	285	L	1.4	273	287
2HLD	L O	L	286	L	1.2	273	287
2HLD	L O	L	360	Y	2.1	356	362
2HLD	L O	O	290	G	165.1	285	296
2HLD	M P	P	273	G	61.1	231	276
2HLD	N P	P	259	R	3.3	231	276
2HLD	N P	P	271	I	1.3	231	276
2HLD	O P	O	390	I	1.3	385	392
2HLD	P Q	P	212	Y	1.8	212	230
2HLD	S V	S	212	R	2.9	212	225
2HLD	S V	S	214	T	2.4	212	225
2HLD	S V	S	217	Q	1.1	212	225
2HLD	S V	S	285	L	1.4	273	287
2HLD	S V	S	286	L	2.0	273	287
2HLD	S V	S	360	Y	1.0	356	362
2HLD	S V	V	290	G	79.6	285	296
2HLD	S V	V	379	Q	1.1	365	384
2HLD	S V	V	387	I	1.0	385	392
2HLD	S W	S	302	Y	2.2	300	311
2HLD	S W	W	191	T	1.6	191	205
2HLD	S W	W	192	R	1.1	191	205
2HLD	S W	W	199	R	1.0	191	205
2HLD	S W	W	271	L	1.1	258	273
2HLD	T W	T	212	R	2.2	212	225
2HLD	T W	T	217	Q	1.2	212	225
2HLD	T W	T	285	L	1.5	273	287
2HLD	T W	W	290	G	39.5	285	296
2HLD	T X	T	301	F	1.2	300	311
2HLD	T X	T	302	Y	1.3	300	311
2HLD	T X	T	309	E	2.1	300	311
2HLD	T X	X	194	G	2.4	191	204
2HLD	T X	X	229	R	1.0	226	247
2HLD	T X	X	337	R	1.2	337	341
2HLD	U V	U	302	Y	3.8	300	311
2HLD	U V	U	306	R	1.4	300	311
2HLD	U V	V	194	G	4.5	191	205
2HLD	U V	V	199	R	1.3	191	205
2HLD	U V	V	337	R	1.0	337	342
2HLD	U X	U	212	R	1.2	212	225
2HLD	U X	U	285	L	1.4	273	287
2HLD	U X	X	290	G	118.7	285	296
2HLD	U X	X	326	F	1.0	320	327
2HLD	V Y	V	391	L	1.1	385	392
2HLD	V Y	Y	19	I	1.2	3	40
2HLD	W Y	Y	271	I	1.0	211	273
2HLD	X Y	X	390	I	1.4	385	392
2HLF	E F	F	123	Q	1.2	121	125
2HNT	C F	F	242	I	1.6	235	243

2HNT	E F	E	129	L	1.9	126	130
2HNT	E F	F	237	W	6.8	235	243
2HNT	E F	F	238	I	1.4	235	243
2HNT	E F	F	241	V	1.0	235	243
2HNT	L E	L	14	E	3.8	14	14
2HNT	L E	L	14	L	1.5	14	14
2HNT	L E	L	14	S	2.7	14	14
2HNT	L E	E	129	L	4.1	126	130
2HNT	L F	L	14	L	1.1	14	14
2HOD	A B	A	148	K	1.1	137	152
2HOD	A B	B	168	L	1.4	167	172
2HOD	A B	B	171	I	1.0	167	172
2HOD	A C	A	157	K	1.0	153	160
2HOD	B C	C	114	Y	3.6	114	124
2HOD	D E	D	133	I	1.0	123	160
2HOD	D E	D	149	R	1.0	123	160
2HOD	D E	D	156	I	1.1	123	160
2HOD	D E	D	185	L	1.0	178	190
2HOD	D E	E	178	K	1.8	178	192
2HOD	D F	D	136	L	1.8	123	160
2HOD	D F	F	107	I	1.1	105	134
2HOD	E F	E	179	I	1.0	178	192
2HOD	E F	E	186	V	1.4	178	192
2HOD	E F	F	110	L	1.3	105	134
2HOD	E F	F	124	L	1.4	105	134
2HOD	E F	F	131	L	2.0	105	134
2HOD	G H	G	140	V	3.0	138	148
2HOD	G H	G	147	M	1.4	138	148
2HOD	G H	G	149	R	1.9	149	160
2HOD	G H	G	152	V	1.1	149	160
2HOD	G H	G	155	D	2.5	149	160
2HOD	G H	G	156	I	1.1	149	160
2HOD	G H	G	159	R	1.1	149	160
2HOD	G H	G	181	Q	3.2	180	185
2HOD	G H	H	171	I	2.4	170	174
2HOD	G H	H	175	L	1.8	175	179
2HOD	G H	H	178	K	1.7	175	179
2HOD	G I	G	157	K	1.1	149	160
2HOD	H I	H	161	I	1.5	160	165
2HOD	J K	J	140	V	1.2	135	160
2HOD	J K	J	153	D	1.0	135	160
2HOD	J K	K	168	L	2.1	165	177
2HOD	J K	K	171	I	1.2	165	177
2HOD	J K	K	178	K	1.3	178	192
2HOD	J L	J	136	L	1.0	135	160
2HOD	J L	J	139	N	1.1	135	160
2HOD	J L	L	107	I	1.3	102	134
2HOD	K L	K	172	L	1.1	165	177
2HOD	K L	K	179	I	2.4	178	192
2HOD	K L	K	183	E	1.2	178	192
2HOD	K L	K	186	V	1.2	178	192
2HOD	K L	K	190	M	1.2	178	192
2HOD	K L	L	103	H	1.1	102	134
2HOD	K L	L	110	L	1.3	102	134
2HOD	K L	L	120	K	1.1	102	134
2HOD	K L	L	124	L	2.2	102	134
2HOD	K L	L	127	K	1.2	102	134
2HOD	K L	L	131	L	2.1	102	134
2HP0	A B	A	44	H	1.2	44	57
2HP0	A B	A	48	V	1.5	44	57

2HP0	A B	A	52	Y	2.5	44	57
2HP0	A B	A	214	W	2.5	202	216
2HP0	A B	B	44	H	1.2	44	57
2HP0	A B	B	48	V	1.6	44	57
2HP0	A B	B	214	W	2.3	202	216
2HPP	L H	L	7	F	1.5	7	11
2HPP	L H	L	8	E	2.4	7	11
2HPP	L H	L	14	E	1.5	14	14
2HPP	L H	L	14	L	2.0	14	14
2HPP	L H	L	14	L	1.0	14	14
2HQS	A H	H	115	P	4.0	115	136
2HQS	A H	H	116	E	3.1	115	136
2HQS	A H	H	117	Y	3.3	115	136
2HQS	A H	H	119	I	1.2	115	136
2HQS	A H	H	120	S	1.1	115	136
2HQS	A H	H	123	E	1.2	115	136
2HQS	A H	H	127	N	1.0	115	136
2HQS	B C	C	115	P	2.3	115	136
2HQS	B C	C	116	E	3.2	115	136
2HQS	B C	C	117	Y	2.4	115	136
2HQS	B C	C	119	I	1.2	115	136
2HQS	D E	E	115	P	1.1	115	136
2HQS	D E	E	116	E	3.1	115	136
2HQS	D E	E	117	Y	2.3	115	136
2HQS	D E	E	119	I	1.4	115	136
2HQS	F G	G	115	P	1.3	115	136
2HQS	F G	G	116	E	3.3	115	136
2HQS	F G	G	117	Y	2.5	115	136
2HQS	F G	G	119	I	1.5	115	136
2HQW	A B	A	18	L	1.3	6	20
2HQW	A B	A	47	E	1.2	45	56
2HQW	A B	A	51	M	1.2	45	56
2HQW	A B	A	87	E	2.2	82	93
2HQW	A B	A	88	A	2.2	82	93
2HQW	A B	A	92	F	2.2	82	93
2HQW	A B	A	105	L	1.2	102	112
2HQW	A B	A	120	E	1.3	118	129
2HQW	A B	A	124	M	2.0	118	129
2HQW	A B	A	141	F	4.8	138	146
2HQW	A B	A	144	M	2.0	138	146
2HQW	A B	B	879	T	1.5	877	892
2HQW	A B	B	880	F	5.0	877	892
2HQW	A B	B	887	L	4.6	877	892
2HQW	A B	B	888	A	1.8	877	892
2HQW	A B	B	890	S	1.5	877	892
2HRK	A B	A	166	R	1.5	162	174
2HRK	A B	A	170	L	1.6	162	174
2HRK	A B	B	54	R	2.9	46	55
2HRK	A B	B	102	R	2.2	98	111
2HRK	A B	B	106	Y	3.1	98	111
2HRP	L H	L	123	E	1.1	122	128
2HRP	L H	L	124	Q	1.6	122	128
2HRP	M N	M	124	Q	1.5	122	127
2HSN	A B	A	69	Y	1.9	63	71
2HSN	A B	A	86	L	1.1	80	94
2HSN	A B	B	25	E	1.3	24	39
2HSN	A B	B	55	D	1.1	46	56
2HT9	A X	A	48	H	2.1	38	51
2HT9	A X	X	-2	F	1.7	-8	2
2HTM	A E	A	85	L	2.1	76	91

2HTM	A E	A	89	L	2.3	76	91
2HTM	A E	A	207	N	1.4	207	212
2HTM	B F	B	25	F	1.5	25	36
2HTM	B F	B	88	L	1.0	76	91
2HTM	B F	B	89	L	2.9	76	91
2HTM	C G	C	81	R	1.0	76	91
2HTM	C G	C	88	L	2.0	76	91
2HTM	C G	C	89	L	3.2	76	91
2HTM	D H	D	85	L	1.5	76	91
2HTM	D H	D	89	L	2.4	76	91
2HUE	A B	B	113	H	2.9	86	114
2HUE	A B	B	126	L	2.5	121	131
2HUE	A B	B	130	I	1.7	121	131
2HUE	A C	C	72	Y	1.2	50	76
2HUE	B C	B	67	F	4.9	64	79
2HUE	B C	B	74	I	1.4	64	79
2HUE	B C	B	78	F	3.0	64	79
2HUE	B C	B	92	L	2.8	86	114
2HUE	B C	B	99	Y	2.1	86	114
2HUE	B C	B	100	L	2.0	86	114
2HUE	B C	B	101	V	1.5	86	114
2HUE	B C	B	104	F	1.9	86	114
2HUE	B C	B	121	P	1.6	121	131
2HUE	B C	C	36	R	1.8	31	41
2HUE	B C	C	37	L	2.7	31	41
2HUE	B C	C	50	I	2.7	50	76
2HUE	B C	C	58	L	1.3	50	76
2HUE	B C	C	59	K	1.0	50	76
2HUE	B C	C	61	F	2.8	50	76
2HUE	B C	C	63	E	4.9	50	76
2HUE	B C	C	66	I	3.3	50	76
2HUE	B C	C	70	V	1.2	50	76
2HUE	B C	C	86	V	1.8	83	94
2HV8	A D	A	76	I	1.2	75	82
2HV8	A D	D	735	Q	1.0	717	747
2HV8	A D	D	739	D	4.0	717	747
2HV8	A D	D	746	M	2.2	717	747
2HV8	B E	E	739	D	2.9	717	749
2HV8	B E	E	743	V	1.5	717	749
2HV8	B E	E	746	M	2.3	717	749
2HV8	C E	E	737	Y	1.1	717	749
2HV8	C F	F	735	Q	1.2	717	747
2HV8	C F	F	739	D	4.2	717	747
2HV8	C F	F	742	I	1.1	717	747
2HV8	C F	F	746	M	2.3	717	747
2HVY	A B	A	188	H	1.2	183	195
2HVY	A B	A	189	H	2.9	183	195
2HVY	A B	A	192	L	2.5	183	195
2HVY	A C	A	68	W	2.7	62	73
2HVY	A C	A	221	H	2.6	220	234
2HVY	A C	A	225	D	4.9	220	234
2HVY	A C	A	229	F	5.7	220	234
2HVY	A C	A	233	D	1.5	220	234
2HVY	A C	A	238	Y	1.5	236	243
2HVY	A C	C	42	G	3.1	42	54
2HVY	A C	C	45	R	3.5	42	54
2HVY	A C	C	46	R	3.6	42	54
2HVY	A C	C	49	K	2.5	42	54
2HVY	A C	C	50	R	6.3	42	54
2HVY	A C	C	53	L	1.5	42	54

2HVY	C D	C	44	Y	3.1	42	54
2HVY	C D	C	47	R	1.4	42	54
2HVY	C D	C	48	W	2.6	42	54
2HVY	C D	D	66	H	1.3	65	74
2HVY	C D	D	73	E	1.3	65	74
2HWN	A E	A	13	L	1.2	9	24
2HWN	A E	A	18	V	1.0	9	24
2HWN	A E	A	21	L	1.6	9	24
2HWN	A E	E	13	V	2.8	4	20
2HWN	A E	E	17	M	1.3	4	20
2HWN	B E	E	8	I	1.1	4	20
2HWN	B E	E	12	I	1.2	4	20
2HWN	B E	E	16	V	1.9	4	20
2HWN	C F	C	9	L	1.2	9	24
2HWN	C F	C	13	L	1.4	9	24
2HWN	C F	C	18	V	1.0	9	24
2HWN	C F	C	21	L	1.6	9	24
2HWN	C F	F	13	V	2.7	4	21
2HWN	C F	F	17	M	1.9	4	21
2HWN	D F	F	12	I	1.0	4	21
2HWN	D F	F	16	V	1.7	4	21
2HWZ	L H	L	122	E	1.4	121	126
2HWZ	L H	L	123	Q	1.9	121	126
2HY5	A B	A	112	L	1.0	112	122
2HY5	A B	A	113	G	4.8	112	122
2HY5	A B	A	115	L	1.0	112	122
2HY5	A B	A	116	V	1.7	112	122
2HY5	A B	A	120	I	1.2	112	122
2HY5	A B	B	224	E	1.3	221	234
2HY5	A B	B	228	V	1.3	221	234
2HY5	A B	B	231	I	1.0	221	234
2HY5	A C	A	19	S	1.1	15	30
2HY5	A C	A	23	F	3.6	15	30
2HY5	A C	C	485	Y	1.7	485	495
2HY5	A C	C	488	F	1.9	485	495
2HY5	A C	C	489	V	2.5	485	495
2HY5	B C	B	285	D	1.1	284	290
2HY5	B C	C	423	F	2.8	416	424
2HYB	A B	A	115	L	1.0	112	122
2HYB	A B	A	116	V	1.8	112	122
2HYB	A B	A	120	I	1.3	112	122
2HYB	A B	B	231	I	1.2	220	235
2HYB	A B	B	232	G	4.5	220	235
2HYB	A C	A	23	F	3.4	15	30
2HYB	A C	C	485	Y	1.3	485	495
2HYB	A C	C	488	F	1.8	485	495
2HYB	A C	C	489	V	2.6	485	495
2HYB	B C	B	285	D	1.4	284	290
2HYB	B C	B	323	V	1.2	320	330
2HYB	B C	C	423	F	1.7	416	424
2HYB	B F	B	249	Y	2.4	247	251
2HYB	D E	D	1113	G	3.9	1112	1122
2HYB	D E	D	1116	V	1.5	1112	1122
2HYB	D E	D	1120	I	1.2	1112	1122
2HYB	D E	E	1220	I	1.0	1220	1235
2HYB	D E	E	1228	V	1.0	1220	1235
2HYB	D F	D	1023	F	3.4	1015	1030
2HYB	D F	F	1485	Y	1.0	1485	1495
2HYB	D F	F	1488	F	1.8	1485	1495
2HYB	D F	F	1489	V	3.1	1485	1495

2HYB	E C	E	1249	Y	5.8	1247	1251
2HYB	E C	C	438	Y	1.3	436	440
2HYB	E F	E	1328	N	2.1	1320	1330
2HYB	E F	F	1419	S	1.0	1416	1424
2HYB	E F	F	1423	F	3.1	1416	1424
2HYB	G H	G	2112	L	1.5	2112	2122
2HYB	G H	G	2113	G	3.6	2112	2122
2HYB	G H	G	2116	V	2.0	2112	2122
2HYB	G H	G	2120	I	1.1	2112	2122
2HYB	G H	H	2231	I	1.0	2221	2235
2HYB	G I	G	2023	F	3.4	2015	2030
2HYB	G I	I	2485	Y	1.3	2485	2495
2HYB	G I	I	2488	F	1.9	2485	2495
2HYB	G I	I	2489	V	2.6	2485	2495
2HYB	H I	H	2285	D	1.4	2284	2290
2HYB	H I	I	2422	K	1.5	2416	2424
2HYB	H I	I	2423	F	4.0	2416	2424
2HYB	H L	L	3438	Y	2.5	3436	3440
2HYB	J K	J	3084	R	1.2	3079	3086
2HYB	J K	J	3112	L	1.2	3112	3122
2HYB	J K	J	3113	G	1.7	3112	3122
2HYB	J K	J	3116	V	1.5	3112	3122
2HYB	J K	J	3120	I	1.3	3112	3122
2HYB	J K	K	3224	E	1.0	3221	3235
2HYB	J K	K	3227	E	1.0	3221	3235
2HYB	J K	K	3228	V	3.5	3221	3235
2HYB	J K	K	3232	G	3.7	3221	3235
2HYB	J L	J	3023	F	3.1	3015	3030
2HYB	J L	L	3485	Y	1.3	3485	3495
2HYB	J L	L	3488	F	1.9	3485	3495
2HYB	J L	L	3489	V	3.5	3485	3495
2HYB	K I	K	3249	Y	2.0	3247	3251
2HYB	K I	I	2438	Y	1.1	2435	2440
2HYB	M N	M	4115	L	1.0	4112	4122
2HYB	M N	M	4116	V	1.5	4112	4122
2HYB	M N	M	4120	I	1.2	4112	4122
2HYB	M N	N	4232	G	14.2	4220	4235
2HYB	M O	M	4023	F	3.3	4015	4031
2HYB	M O	O	4485	Y	1.2	4485	4495
2HYB	M O	O	4488	F	2.0	4485	4495
2HYB	M O	O	4489	V	2.4	4485	4495
2HYB	N O	N	4327	M	1.1	4320	4330
2HYB	N O	O	4416	S	1.2	4415	4424
2HYB	N O	O	4423	F	2.3	4415	4424
2HYB	N R	N	4249	Y	2.7	4246	4251
2HYB	P Q	P	5112	L	1.7	5112	5122
2HYB	P Q	P	5115	L	1.0	5112	5122
2HYB	P Q	P	5116	V	1.8	5112	5122
2HYB	P Q	P	5120	I	1.3	5112	5122
2HYB	P Q	Q	5220	I	1.7	5220	5235
2HYB	P Q	Q	5224	E	1.6	5220	5235
2HYB	P Q	Q	5228	V	2.9	5220	5235
2HYB	P Q	Q	5232	G	1.4	5220	5235
2HYB	P R	P	5023	F	3.3	5015	5030
2HYB	P R	R	5485	Y	1.0	5485	5495
2HYB	P R	R	5488	F	1.7	5485	5495
2HYB	P R	R	5489	V	2.2	5485	5495
2HYB	Q R	Q	5327	M	1.1	5320	5330
2HYB	Q R	R	5423	F	2.4	5416	5424
2HYE	A B	B	24	V	1.6	23	33

2HYE	A B	B	27	F	2.5	23	33
2HYE	A B	B	32	V	1.2	23	33
2HYE	A B	B	127	Y	2.6	127	138
2HYE	A C	C	84	E	1.2	84	94
2HYE	A C	C	88	Q	1.2	84	94
2HYE	C D	C	551	Q	2.1	545	560
2HYE	C D	C	694	Y	2.1	691	707
2HYI	A B	A	124	Y	2.7	118	142
2HYI	A B	A	128	D	2.0	118	142
2HYI	A B	A	135	S	1.8	118	142
2HYI	A B	A	139	L	1.0	118	142
2HYI	A B	A	140	H	1.9	118	142
2HYI	A C	A	134	F	1.5	118	142
2HYI	A C	C	358	R	3.1	358	366
2HYI	A C	C	390	R	2.6	384	396
2HYI	A C	C	393	E	2.2	384	396
2HYI	C D	C	154	D	1.5	146	156
2HYI	C D	C	155	Y	1.2	146	156
2HYI	C D	C	171	I	1.1	164	173
2HYI	C D	C	202	Y	1.6	197	207
2HYI	C D	C	205	Y	3.2	197	207
2HYI	C D	C	289	K	1.1	287	299
2HYI	C D	C	292	W	2.0	287	299
2HYI	C D	C	388	I	1.2	384	396
2HYI	C D	C	391	D	1.5	384	396
2HYI	G H	G	55	S	1.0	54	68
2HYI	G H	G	56	V	1.0	54	68
2HYI	G H	G	128	D	1.4	116	142
2HYI	G H	G	135	S	1.6	116	142
2HYI	G H	G	140	H	4.6	116	142
2HYI	G I	G	134	F	2.2	116	142
2HYI	G I	I	223	H	1.3	223	228
2HYI	G I	I	358	R	3.3	358	366
2HYI	G I	I	390	R	2.9	384	396
2HYI	G I	I	391	D	1.0	384	396
2HYI	G I	I	395	Y	1.6	384	396
2HYI	I J	I	155	Y	1.4	146	156
2HYI	I J	I	202	Y	1.3	197	207
2HYI	I J	I	205	Y	3.1	197	207
2HYI	I J	I	292	W	2.6	287	300
2HZE	A B	A	3	E	1.2	2	9
2HZE	A B	B	84	S	1.0	83	92
2HZM	A B	A	91	L	1.5	89	94
2HZM	A B	A	93	F	2.2	89	94
2HZM	A B	A	107	I	1.5	104	112
2HZM	A B	A	111	K	1.7	104	112
2HZM	C B	C	93	F	1.8	89	94
2HZM	C D	C	91	L	1.5	89	94
2HZM	C D	C	93	F	2.1	89	94
2HZM	C D	D	203	L	1.4	200	208
2HZM	C D	D	207	L	1.2	200	208
2HZM	E F	E	91	L	2.0	89	94
2HZM	E F	E	93	F	2.1	89	94
2HZM	E F	E	108	L	1.8	104	112
2HZM	E F	E	111	K	1.9	104	112
2HZM	E F	F	203	L	1.0	200	207
2HZM	G H	G	91	L	1.5	89	94
2HZM	G H	G	93	F	2.1	89	94
2HZM	G H	G	107	I	1.3	104	111
2HZS	A B	A	91	L	1.9	89	94

2HZS	A B	A	93	F	2.0	89	94
2HZS	A B	A	107	I	1.2	104	112
2HZS	A B	A	111	K	2.2	104	112
2HZS	A B	B	203	L	1.2	200	208
2HZS	A D	A	93	F	1.8	89	94
2HZS	B I	I	198	V	1.3	198	208
2HZS	B I	I	199	D	1.9	198	208
2HZS	B I	I	201	V	1.3	198	208
2HZS	B I	I	202	L	2.3	198	208
2HZS	B I	I	204	F	3.5	198	208
2HZS	B I	I	206	F	2.9	198	208
2HZS	C B	C	93	F	1.6	89	94
2HZS	C D	C	91	L	1.1	89	94
2HZS	C D	C	93	F	1.6	89	94
2HZS	C D	C	111	K	2.1	104	112
2HZS	C D	D	203	L	1.1	200	207
2HZS	D J	J	198	V	1.3	198	207
2HZS	D J	J	199	D	1.2	198	207
2HZS	D J	J	201	V	1.1	198	207
2HZS	D J	J	202	L	1.7	198	207
2HZS	D J	J	204	F	4.0	198	207
2HZS	D J	J	206	F	1.3	198	207
2HZS	E F	E	91	L	1.4	89	94
2HZS	E F	E	93	F	1.7	89	94
2HZS	E F	E	111	K	2.0	104	112
2HZS	E F	F	203	L	1.1	200	207
2HZS	F I	I	203	K	1.7	198	208
2HZS	F K	K	202	L	1.1	198	208
2HZS	F K	K	204	F	3.5	198	208
2HZS	F K	K	205	T	1.1	198	208
2HZS	F K	K	206	F	1.4	198	208
2HZS	G H	G	91	L	1.3	89	94
2HZS	G H	G	93	F	2.4	89	94
2HZS	G H	G	107	I	1.7	104	112
2HZS	G H	G	111	K	2.1	104	112
2HZS	G H	H	203	L	1.6	200	207
2HZS	H L	L	198	V	1.4	198	208
2HZS	H L	L	199	D	1.4	198	208
2HZS	H L	L	201	V	1.2	198	208
2HZS	H L	L	202	L	2.3	198	208
2HZS	H L	L	203	K	1.7	198	208
2HZS	H L	L	204	F	2.8	198	208
2HZS	H L	L	206	F	3.5	198	208
2I0Q	A B	B	143	E	1.8	142	164
2I0Q	A B	B	149	Q	1.0	142	164
2I0Q	A B	B	156	L	1.0	142	164
2I0Q	A B	B	157	Q	1.6	142	164
2I0Q	A B	B	160	I	1.4	142	164
2I26	O M	M	62	W	3.1	60	64
2I26	O M	M	63	W	2.4	60	64
2I26	O M	M	112	R	1.9	109	116
2I2P	C N	C	30	D	2.5	25	46
2I2P	C N	C	32	L	2.4	25	46
2I2P	C N	C	33	D	2.9	25	46
2I2P	C N	C	35	D	2.1	25	46
2I2P	C N	C	36	F	1.4	25	46
2I2P	C N	C	39	R	1.5	25	46
2I2P	C N	N	89	R	1.4	80	90
2I2P	D E	D	201	E	1.2	198	203
2I2P	D E	E	111	R	1.5	109	113

2I2P	G K	K	60	F	1.3	59	71
2I2P	M S	M	87	G	1.8	85	90
2I2R	A E	A	8	W	5.9	8	15
2I2R	A E	E	56	L	1.0	50	64
2I2R	A E	E	58	R	1.0	50	64
2I2R	A E	E	60	F	1.1	50	64
2I2R	A E	E	77	I	1.5	71	82
2I2R	A E	E	78	Y	2.4	71	82
2I2R	A E	E	111	F	2.5	108	121
2I2R	A E	E	155	Y	1.9	144	159
2I2R	A E	E	174	H	1.0	174	181
2I2R	A H	A	70	E	1.6	69	73
2I2R	A H	H	57	Y	4.7	50	64
2I2R	A H	H	61	K	1.8	50	64
2I2R	B E	B	120	F	1.3	111	121
2I2R	B E	E	54	Q	1.2	50	64
2I2R	B E	E	57	Y	3.7	50	64
2I2R	B E	E	61	K	1.7	50	64
2I2R	B F	B	8	W	5.0	8	15
2I2R	B F	B	11	F	1.7	8	15
2I2R	B F	F	77	I	1.7	71	82
2I2R	B F	F	81	F	1.1	71	82
2I2R	B F	F	90	Y	1.2	88	96
2I2R	B F	F	111	F	6.2	108	121
2I2R	B F	F	118	L	1.1	108	121
2I2R	B F	F	134	Y	1.8	123	135
2I2R	B F	F	151	V	2.2	144	158
2I2R	B F	F	174	H	1.8	174	181
2I2R	B F	F	178	F	1.1	174	181
2I2R	B O	O	43	E	1.0	39	45
2I2R	C F	F	57	Y	3.3	50	64
2I2R	C F	F	61	K	1.2	50	64
2I2R	C G	C	8	W	2.8	8	15
2I2R	C G	C	11	F	2.2	8	15
2I2R	C G	G	77	I	1.4	71	82
2I2R	C G	G	81	F	1.0	71	82
2I2R	C G	G	90	Y	1.1	88	96
2I2R	C G	G	134	Y	1.3	123	135
2I2R	C N	N	43	E	1.0	39	45
2I2R	D G	D	70	E	1.3	69	73
2I2R	D G	G	54	Q	1.2	50	64
2I2R	D G	G	57	Y	4.5	50	64
2I2R	D G	G	61	K	1.6	50	64
2I2R	D H	D	8	W	4.1	8	15
2I2R	D H	D	9	L	1.1	8	15
2I2R	D H	D	11	F	1.2	8	15
2I2R	D H	H	77	I	1.2	71	82
2I2R	D H	H	81	F	1.4	71	82
2I2R	D H	H	111	F	1.6	108	121
2I2R	I M	I	8	W	5.7	8	15
2I2R	I M	M	77	I	1.2	71	82
2I2R	I M	M	134	Y	1.7	123	135
2I2R	I M	M	151	V	1.0	144	169
2I2R	I P	P	39	L	1.0	39	45
2I2R	I P	P	57	Y	3.4	50	64
2I2R	I P	P	61	K	1.0	50	64
2I2R	J M	M	54	Q	1.0	50	64
2I2R	J M	M	57	Y	2.6	50	64
2I2R	J M	M	58	R	1.0	50	64
2I2R	J N	J	8	W	5.6	8	15

2I2R	J N	J	11	F	2.3	8	15
2I2R	J N	N	77	I	1.3	71	82
2I2R	J N	N	111	F	2.6	108	121
2I2R	J N	N	118	L	2.2	108	121
2I2R	J N	N	134	Y	1.7	123	135
2I2R	J N	N	151	V	1.0	144	169
2I2R	J N	N	178	F	1.4	174	181
2I2R	K N	K	120	F	1.0	111	121
2I2R	K N	N	57	Y	3.4	50	64
2I2R	K N	N	58	R	1.3	50	64
2I2R	K N	N	61	K	1.2	50	64
2I2R	K O	K	8	W	5.5	8	15
2I2R	K O	O	77	I	1.5	71	82
2I2R	K O	O	94	L	1.1	88	96
2I2R	K O	O	111	F	2.2	108	121
2I2R	L O	L	120	F	1.1	111	121
2I2R	L O	O	54	Q	1.1	50	64
2I2R	L O	O	57	Y	4.1	50	64
2I2R	L O	O	58	R	1.0	50	64
2I2R	L O	O	61	K	1.5	50	64
2I2R	L P	L	8	W	3.0	8	15
2I2R	L P	L	9	L	359.5	8	15
2I2R	L P	P	77	I	1.5	71	82
2I2R	L P	P	78	Y	1.0	71	82
2I2R	L P	P	81	F	1.4	71	82
2I2R	L P	P	134	Y	1.0	123	135
2I2R	L P	P	151	V	1.0	144	159
2I2T	D P	P	7	L	2.7	6	11
2I2T	D P	P	10	E	1.0	6	11
2I2T	E L	E	32	V	3.5	30	37
2I2T	E L	E	178	V	3.5	177	182
2I2T	Q R	Q	42	G	79.0	37	53
2I2T	T Y	Y	26	F	1.0	25	33
2I2X	A B	A	174	Y	1.5	169	177
2I2X	A B	A	229	I	1.1	220	231
2I2X	A B	A	358	L	2.8	349	360
2I2X	A B	A	416	R	1.3	416	432
2I2X	A B	A	417	F	1.6	416	432
2I2X	A B	A	418	E	3.3	416	432
2I2X	A B	B	9	L	1.8	6	13
2I2X	A B	B	88	Y	1.5	75	90
2I2X	A B	B	103	D	1.3	95	114
2I2X	A B	B	138	I	1.3	137	150
2I2X	A D	A	116	Y	1.0	95	117
2I2X	A D	A	345	E	1.8	325	346
2I2X	A D	D	8	S	1.4	6	13
2I2X	A D	D	16	Y	3.8	16	20
2I2X	C B	C	345	E	2.1	325	346
2I2X	C B	B	8	S	1.5	6	13
2I2X	C B	B	16	Y	4.1	16	21
2I2X	C D	C	358	L	3.3	349	360
2I2X	C D	C	417	F	4.4	416	432
2I2X	C D	C	418	E	3.0	416	432
2I2X	C D	D	9	L	1.0	6	13
2I2X	C D	D	88	Y	2.3	69	90
2I2X	C D	D	96	P	1.1	95	113
2I2X	C D	D	103	D	1.4	95	113
2I2X	E F	E	358	L	2.9	349	360
2I2X	E F	E	417	F	4.9	416	431
2I2X	E F	E	418	E	2.9	416	431

2I2X	E F	F	9	L	1.3	6	13
2I2X	E F	F	26	P	2.6	26	34
2I2X	E F	F	88	Y	1.5	71	90
2I2X	E F	F	96	P	1.1	95	115
2I2X	E F	F	138	I	1.1	137	150
2I2X	E H	E	345	E	1.5	325	346
2I2X	E H	H	8	S	1.0	6	13
2I2X	E H	H	16	Y	4.8	16	21
2I2X	G F	G	345	E	1.3	325	346
2I2X	G F	F	8	S	1.3	6	13
2I2X	G F	F	16	Y	3.4	16	21
2I2X	G H	G	225	T	1.0	220	231
2I2X	G H	G	229	I	1.5	220	231
2I2X	G H	G	358	L	2.4	349	362
2I2X	G H	G	417	F	3.9	416	432
2I2X	G H	G	418	E	2.1	416	432
2I2X	G H	H	9	L	1.6	6	13
2I2X	G H	H	88	Y	1.1	69	91
2I2X	G H	H	103	D	1.0	95	110
2I2X	G H	H	138	I	1.6	137	150
2I2X	I J	I	358	L	1.6	349	362
2I2X	I J	I	417	F	4.3	416	432
2I2X	I J	I	418	E	5.6	416	432
2I2X	I J	J	18	V	1.0	16	21
2I2X	I J	J	96	P	1.0	95	110
2I2X	I J	J	138	I	1.0	137	150
2I2X	I L	I	64	R	1.1	55	76
2I2X	I L	I	345	E	1.3	325	346
2I2X	I L	L	12	V	1.0	6	13
2I2X	I L	L	16	Y	3.2	16	21
2I2X	K J	K	116	Y	1.0	95	117
2I2X	K J	K	345	E	2.1	325	346
2I2X	K J	J	8	S	1.6	6	13
2I2X	K J	J	12	V	1.0	6	13
2I2X	K J	J	16	Y	4.6	16	21
2I2X	K L	K	358	L	3.2	349	360
2I2X	K L	K	417	F	3.3	416	431
2I2X	K L	K	418	E	5.2	416	431
2I2X	K L	L	9	L	1.7	6	13
2I2X	K L	L	88	Y	1.0	75	91
2I2X	K L	L	96	P	1.0	95	113
2I2X	K L	L	138	I	1.6	137	150
2I2X	M N	M	358	L	3.1	349	360
2I2X	M N	M	417	F	2.8	416	432
2I2X	M N	M	418	E	3.5	416	432
2I2X	M N	N	9	L	1.2	6	13
2I2X	M N	N	88	Y	1.3	73	90
2I2X	M N	N	96	P	1.0	95	115
2I2X	M N	N	138	I	1.3	137	151
2I2X	M P	M	345	E	1.7	325	346
2I2X	M P	P	8	S	1.2	6	13
2I2X	M P	P	16	Y	4.6	16	20
2I2X	O N	O	345	E	1.8	325	346
2I2X	O N	N	8	S	1.1	6	13
2I2X	O N	N	16	Y	3.2	16	21
2I2X	O P	O	358	L	3.0	349	360
2I2X	O P	O	416	R	1.0	416	432
2I2X	O P	O	417	F	1.8	416	432
2I2X	O P	O	418	E	3.1	416	432
2I2X	O P	P	9	L	1.4	6	13

2I3S	A B	B	325	L	1.2	323	327
2I3S	A B	B	337	E	2.8	336	344
2I3S	A B	B	338	E	1.7	336	344
2I3S	A B	B	340	L	2.6	336	344
2I3S	A B	B	343	I	1.2	336	344
2I3S	C D	D	323	F	1.0	323	327
2I3S	C D	D	325	L	1.9	323	327
2I3S	C D	D	337	E	3.5	336	344
2I3S	C D	D	338	E	1.9	336	344
2I3S	C D	D	340	L	3.0	336	344
2I3S	E F	F	323	F	1.0	323	327
2I3S	E F	F	325	L	1.6	323	327
2I3S	E F	F	337	E	3.0	336	344
2I3S	E F	F	338	E	2.4	336	344
2I3S	E F	F	340	L	3.2	336	344
2I3S	E F	F	343	I	1.1	336	344
2I3T	A B	B	383	E	1.9	381	388
2I3T	A B	B	384	V	2.5	381	388
2I3T	A B	B	385	L	1.5	381	388
2I3T	A B	B	387	I	1.2	381	388
2I3T	C D	D	362	F	1.6	362	366
2I3T	C D	D	383	E	2.3	381	389
2I3T	C D	D	385	L	3.2	381	389
2I3T	E F	F	362	F	1.3	362	366
2I3T	E F	F	364	L	1.2	362	366
2I3T	E F	F	383	E	2.7	381	389
2I3T	E F	F	385	L	3.0	381	389
2I3T	G H	H	382	E	3.3	381	389
2I3T	G H	H	383	E	2.6	381	389
2I3T	G H	H	385	L	1.8	381	389
2I94	A B	A	38	E	4.0	25	39
2I94	A B	B	15	F	1.2	5	16
2I9L	A B	A	129	Q	1.5	127	133
2I9L	B I	I	63	A	1.0	61	79
2I9L	C D	C	129	Q	1.5	127	133
2I9L	E F	E	129	Q	1.4	127	133
2I9L	G H	G	129	Q	1.7	127	133
2IAE	A B	A	141	F	1.6	141	150
2IAE	A B	A	257	W	2.8	257	265
2IAE	A B	A	258	R	1.1	257	265
2IAE	A B	B	162	K	1.0	161	169
2IAE	A B	B	203	Q	1.5	194	204
2IAE	A C	A	417	W	2.0	417	431
2IAE	A C	A	418	R	1.7	417	431
2IAE	A C	A	456	Y	1.2	456	469
2IAE	A C	A	495	Y	2.0	495	506
2IAE	A C	A	498	R	2.0	495	506
2IAE	A C	A	499	M	1.0	495	506
2IAE	A C	C	67	E	1.4	62	72
2IAE	B C	C	131	D	1.2	128	136
2IAE	D B	B	93	P	1.6	91	104
2IAE	D E	D	257	W	3.2	257	266
2IAE	D E	E	256	K	1.9	241	257
2IAE	D F	D	418	R	1.7	417	432
2IAE	D F	D	538	F	2.5	534	539
2IAE	D F	D	574	D	1.7	573	581
2IAE	D F	D	577	Y	4.3	573	581
2IAE	D F	D	578	F	2.2	573	581
2IAE	E F	E	298	S	1.2	298	313
2IAE	E F	E	340	F	1.0	340	346

2IAE	E F	F	122	Q	2.1	121	125
2IAE	E F	F	130	Y	2.8	128	138
2IAE	E F	F	131	D	1.0	128	138
2IAM	A B	A	48	F	2.8	46	51
2IAM	A B	A	70	L	1.4	57	77
2IAM	B P	B	60	Y	1.4	52	63
2IAM	B P	B	61	W	3.6	52	63
2IAM	B P	B	82	N	1.5	73	87
2IAM	C D	D	133	H	1.2	128	135
2IAN	A B	A	48	F	3.0	46	51
2IAN	A B	A	70	L	2.1	57	77
2IAN	A B	B	57	D	1.1	55	64
2IAN	A C	A	58	G	1.3	57	77
2IAN	A C	A	65	V	1.3	57	77
2IAN	A D	A	58	G	2.1	57	77
2IAN	B C	B	60	Y	1.9	55	64
2IAN	B C	B	61	W	1.9	55	64
2IAN	B C	B	78	Y	4.6	65	89
2IAN	B C	B	81	H	1.1	65	89
2IAN	B S	B	72	R	1.6	65	89
2IAN	B T	B	55	R	1.8	55	64
2IAN	D E	E	129	A	1.4	128	133
2IAN	F G	F	48	F	2.4	46	50
2IAN	F G	F	70	L	1.4	57	77
2IAN	F H	F	65	V	1.2	57	77
2IAN	F J	F	57	Q	1.1	57	77
2IAN	G H	G	61	W	1.3	52	64
2IAN	G H	G	71	R	1.8	65	86
2IAN	G H	G	78	Y	5.8	65	86
2IAN	G H	G	81	H	1.1	65	86
2IAN	G H	G	82	N	1.2	65	86
2IAN	G I	G	76	D	1.1	65	86
2IAN	G I	G	81	H	1.2	65	86
2IAN	K L	K	48	F	2.1	46	52
2IAN	K L	K	70	L	1.2	57	77
2IAN	K L	K	73	M	1.1	57	77
2IAN	K M	K	58	G	2.6	57	77
2IAN	K M	K	62	N	1.3	57	77
2IAN	K M	K	65	V	1.2	57	77
2IAN	K M	K	72	I	1.2	57	77
2IAN	L I	L	72	R	1.1	65	73
2IAN	L J	L	55	R	1.3	55	63
2IAN	L M	L	60	Y	1.3	55	63
2IAN	L M	L	61	W	1.3	55	63
2IAN	L M	L	71	R	2.4	65	73
2IAN	L M	L	78	Y	9.1	74	87
2IAN	L M	L	85	V	1.1	74	87
2IAN	L N	L	81	H	1.7	74	87
2IAN	P Q	P	48	F	2.3	46	52
2IAN	P Q	P	70	L	1.4	56	77
2IAN	P R	P	65	V	1.5	56	77
2IAN	P S	P	58	G	1.7	56	77
2IAN	Q E	Q	55	R	1.0	52	62
2IAN	Q R	Q	60	Y	1.6	52	62
2IAN	Q R	Q	61	W	3.2	52	62
2IAN	Q R	Q	78	Y	2.7	74	89
2IAN	Q R	Q	82	N	1.4	74	89
2IAN	Q R	Q	85	V	1.3	74	89
2IAN	S T	T	130	E	2.0	128	134
2IAN	S T	T	133	H	1.4	128	134

2IBF	A B	A	12	I	1.9	7	13
2IBF	A B	A	19	Q	1.0	14	30
2IBF	A B	A	47	V	1.1	41	65
2IBF	A B	A	54	L	1.9	41	65
2IBF	A B	A	57	V	3.6	41	65
2IBF	A B	A	61	T	3.3	41	65
2IBF	A B	A	74	M	8.9	73	98
2IBF	A B	A	115	I	1.2	102	148
2IBF	A B	A	123	L	1.7	102	148
2IBF	A B	A	126	F	2.5	102	148
2IBF	A B	B	566	I	2.4	565	582
2IBF	A B	B	567	Y	10.2	565	582
2IBF	A B	B	571	K	1.2	565	582
2IBF	A B	B	577	L	3.2	565	582
2IBF	A B	B	578	S	1.1	565	582
2IBF	A B	B	581	L	1.7	565	582
2IBF	A D	A	155	E	1.4	154	182
2IBF	A D	A	165	G	31.9	154	182
2IBF	A D	D	581	L	1.2	569	585
2IBG	B E	E	219	G	3.0	215	229
2IBG	D G	G	219	G	3.4	215	229
2IBI	A B	A	360	E	1.5	358	373
2IBX	A B	B	93	T	1.2	75	126
2IBX	A B	B	100	V	1.2	75	126
2IBX	A B	B	104	N	2.3	75	126
2IBX	A B	B	108	L	1.7	75	126
2IBX	A B	B	111	H	3.1	75	126
2IBX	A D	A	104	E	2.5	102	111
2IBX	A D	A	107	H	1.4	102	111
2IBX	A D	D	76	R	1.9	75	126
2IBX	C B	B	50	N	1.2	38	59
2IBX	C D	C	107	H	1.2	102	111
2IBX	C D	D	89	L	1.0	75	126
2IBX	C D	D	93	T	1.3	75	126
2IBX	C D	D	104	N	2.5	75	126
2IBX	C D	D	108	L	1.9	75	126
2IBX	C D	D	111	H	3.5	75	126
2IBX	C D	D	115	V	1.0	75	126
2IBX	E F	F	48	V	1.0	38	59
2IBX	E F	F	55	I	1.0	38	59
2IBX	E F	F	93	T	1.3	75	126
2IBX	E F	F	100	V	1.6	75	126
2IBX	E F	F	104	N	2.4	75	126
2IBX	E F	F	108	L	1.8	75	126
2IBX	E F	F	111	H	3.7	75	126
2IBX	E F	F	115	V	1.1	75	126
2IBX	E F	F	118	L	2.2	75	126
2IBZ	A B	A	369	L	1.4	360	379
2IBZ	A B	A	372	L	1.0	360	379
2IBZ	A B	A	375	G	75.7	360	379
2IBZ	A B	A	376	Q	1.1	360	379
2IBZ	A B	B	320	Y	1.0	318	325
2IBZ	A B	B	323	L	2.1	318	325
2IBZ	A C	A	341	D	1.3	340	357
2IBZ	A C	A	342	D	1.9	340	357
2IBZ	A C	A	447	R	1.9	445	451
2IBZ	A C	C	4	R	1.1	3	7
2IBZ	A E	A	152	E	1.3	135	155
2IBZ	A E	A	163	H	2.3	156	169
2IBZ	A I	I	18	V	1.3	18	44

2IBZ	A I	I	19	G	1.2	18	44
2IBZ	C D	C	70	R	1.8	58	72
2IBZ	C D	C	224	Y	1.8	224	247
2IBZ	C D	C	225	F	1.0	224	247
2IBZ	C D	C	231	V	1.7	224	247
2IBZ	C D	C	234	F	2.4	224	247
2IBZ	C D	C	235	L	1.1	224	247
2IBZ	C D	C	238	L	2.0	224	247
2IBZ	C D	C	245	F	2.4	224	247
2IBZ	C D	C	246	Y	1.1	224	247
2IBZ	C D	D	270	G	78.6	263	292
2IBZ	C D	D	274	V	1.2	263	292
2IBZ	C D	D	277	L	2.0	263	292
2IBZ	C D	D	280	L	1.3	263	292
2IBZ	C D	D	281	Y	2.2	263	292
2IBZ	C D	D	288	K	1.7	263	292
2IBZ	C D	D	295	I	1.2	293	297
2IBZ	C E	C	49	F	3.1	32	53
2IBZ	C E	C	67	H	1.1	58	72
2IBZ	C E	E	78	F	1.9	51	82
2IBZ	C F	C	375	N	1.2	346	381
2IBZ	C F	C	376	V	1.2	346	381
2IBZ	C F	C	377	L	1.5	346	381
2IBZ	C F	C	378	F	3.6	346	381
2IBZ	C F	C	379	Y	3.7	346	381
2IBZ	C F	C	380	I	1.6	346	381
2IBZ	C F	F	8	I	1.6	5	18
2IBZ	C F	F	12	G	167.0	5	18
2IBZ	C F	F	16	L	2.1	5	18
2IBZ	C F	F	32	F	4.5	19	37
2IBZ	C F	F	33	I	6.9	19	37
2IBZ	C F	F	45	F	2.0	45	49
2IBZ	C F	F	46	D	1.2	45	49
2IBZ	C F	F	48	L	1.2	45	49
2IBZ	C F	F	75	I	1.3	65	84
2IBZ	C F	F	76	I	1.4	65	84
2IBZ	C F	F	79	H	2.5	65	84
2IBZ	C G	C	324	F	2.1	320	341
2IBZ	C G	C	327	F	2.1	320	341
2IBZ	C G	C	328	I	1.2	320	341
2IBZ	C G	C	331	F	2.4	320	341
2IBZ	C G	C	346	V	1.3	346	381
2IBZ	C G	C	347	P	1.1	346	381
2IBZ	C G	C	351	M	1.7	346	381
2IBZ	C G	G	58	Y	1.7	52	81
2IBZ	C G	G	62	P	1.2	52	81
2IBZ	C G	G	66	Y	1.9	52	81
2IBZ	C G	G	69	W	3.3	52	81
2IBZ	C G	G	73	G	2.5	52	81
2IBZ	D E	D	280	L	1.2	263	292
2IBZ	D E	D	283	L	1.3	263	292
2IBZ	D E	D	287	V	1.4	263	292
2IBZ	D E	E	66	L	3.0	51	82
2IBZ	D F	F	73	Y	1.2	65	84
2IBZ	D G	D	289	K	1.1	263	292
2IBZ	D G	D	290	F	2.3	263	292
2IBZ	D H	D	192	F	1.3	188	196
2IBZ	D H	D	246	Q	1.6	244	260
2IBZ	D H	D	249	K	1.1	244	260
2IBZ	D H	H	98	Y	1.8	89	110

2IBZ	D H	H	124	V	3.1	124	140
2IBZ	D H	H	127	F	2.3	124	140
2IBZ	D H	H	128	F	3.8	124	140
2IBZ	D H	H	143	F	6.0	141	146
2IBZ	D I	D	87	H	1.5	87	105
2IBZ	D I	D	272	K	1.3	263	292
2IBZ	D I	I	33	D	1.3	18	44
2IBZ	D I	I	40	Y	2.9	18	44
2IBZ	D I	I	49	W	3.6	49	55
2IBZ	D I	I	52	V	1.0	49	55
2IBZ	E G	E	51	K	2.0	51	82
2IBZ	E I	E	57	Y	2.2	51	82
2IBZ	E I	E	64	G	1.0	51	82
2IBZ	E I	E	65	L	1.6	51	82
2IBZ	E I	I	7	Y	2.1	6	11
2IBZ	E I	I	28	F	1.1	18	44
2IBZ	E X	E	127	Q	1.4	123	130
2IBZ	E X	E	143	D	3.8	143	147
2IBZ	F G	F	69	Y	1.9	65	84
2IBZ	H G	H	125	E	1.5	124	140
2ICE	A B	A	581	F	1.1	578	584
2ICE	A B	A	594	I	1.3	591	601
2ICE	A C	C	1410	Y	1.1	1409	1413
2ICE	D E	D	581	F	1.5	578	584
2ICE	D E	D	594	I	1.1	591	601
2ICW	A B	A	48	F	1.2	46	52
2ICW	A B	B	57	D	1.4	55	63
2ICW	A C	A	58	G	7.5	56	72
2ICW	A C	A	62	N	1.4	56	72
2ICW	A C	A	65	V	1.0	56	72
2ICW	A G	A	65	V	1.0	56	72
2ICW	A G	G	102	R	2.1	97	123
2ICW	A G	G	109	E	1.1	97	123
2ICW	A H	H	101	K	1.6	97	123
2ICW	B C	B	61	W	3.0	55	63
2ICW	B C	B	85	V	1.5	74	86
2ICW	D E	D	48	F	1.3	46	52
2ICW	D E	D	70	L	2.0	56	72
2ICW	D E	E	57	D	1.9	55	63
2ICW	D F	D	58	G	18.5	56	72
2ICW	D F	D	62	N	1.0	56	72
2ICW	D H	D	60	L	2.4	56	72
2ICW	D H	H	102	R	1.4	97	123
2ICW	E F	E	61	W	3.3	55	63
2ICW	E F	E	67	L	1.0	65	73
2ICW	E F	E	78	Y	1.3	74	86
2ICW	E F	E	81	H	2.0	74	86
2ICW	E F	E	82	N	1.5	74	86
2ICW	E F	E	85	V	1.7	74	86
2ICW	F G	G	208	K	1.0	205	211
2ICW	G I	G	56	Y	1.6	39	66
2ICW	G I	G	60	F	1.5	39	66
2ICW	G J	G	180	R	1.1	177	195
2ICW	G J	G	188	Y	2.0	177	195
2ICW	H L	H	60	F	1.1	39	66
2ICW	H L	H	76	F	1.0	72	93
2ICW	H L	H	188	Y	1.9	177	194
2IDO	A B	A	63	F	2.9	60	67
2IDO	A B	A	71	E	4.4	70	75
2IDO	A B	A	72	F	2.9	70	75

2IDO	A B	A	74	L	1.1	70	75
2IDO	A B	A	85	E	1.3	83	91
2IDO	A B	B	21	L	1.4	11	32
2IDO	A B	B	28	Y	2.8	11	32
2IDO	A B	B	31	R	3.5	11	32
2IDO	A B	B	64	S	1.2	50	66
2IDO	C D	C	63	F	2.5	60	67
2IDO	C D	C	71	E	4.1	70	75
2IDO	C D	C	72	F	3.3	70	75
2IDO	C D	C	74	L	1.2	70	75
2IDO	C D	C	85	E	1.2	83	91
2IDO	C D	D	21	L	2.1	11	32
2IDO	C D	D	28	Y	2.6	11	32
2IDO	C D	D	31	R	3.4	11	32
2IDO	C D	D	64	S	1.2	50	67
2IE3	A C	A	418	R	1.3	417	432
2IE3	A C	A	495	Y	3.0	495	511
2IE3	A C	A	535	N	1.3	534	547
2IE3	A C	A	538	F	4.4	534	547
2IE3	A C	A	574	D	1.6	573	587
2IFG	A E	E	7	F	1.1	5	9
2IFQ	A B	B	63	Q	1.1	63	69
2IFQ	C B	B	43	H	1.1	33	49
2IFQ	C B	B	48	K	1.4	33	49
2IFQ	C B	B	98	E	1.4	94	105
2IHB	A B	A	213	H	1.4	205	214
2IHB	A B	B	129	L	1.3	120	140
2IHB	A B	B	132	Y	1.5	120	140
2IHB	A B	B	133	D	1.8	120	140
2IHB	A B	B	137	R	1.0	120	140
2IHS	B D	D	196	E	2.1	195	200
2IHS	B D	D	199	R	1.1	195	200
2IJ0	A E	A	135	H	1.1	126	141
2IJ0	B C	B	139	Q	1.9	126	141
2IK8	A B	A	210	K	1.0	205	214
2IK8	A B	B	134	H	1.0	134	146
2IK8	A B	B	135	E	1.0	134	146
2IK8	A B	B	137	R	1.0	134	146
2IK8	A B	B	166	D	1.8	153	173
2IK8	C D	D	134	H	1.0	134	146
2IK8	C D	D	135	E	1.3	134	146
2IK8	C D	D	162	L	1.3	153	173
2IK8	C D	D	166	D	1.6	153	173
2INN	A C	A	33	I	1.2	30	34
2INN	A C	A	61	Y	1.5	60	81
2INN	A C	A	62	W	4.1	60	81
2INN	A C	A	109	H	2.2	102	119
2INN	A C	A	112	F	1.4	102	119
2INN	A C	A	117	K	1.0	102	119
2INN	A C	A	136	I	1.8	135	148
2INN	A C	A	142	S	1.2	135	148
2INN	A C	A	147	H	2.1	135	148
2INN	A C	A	180	D	3.3	174	185
2INN	A C	A	181	D	2.1	174	185
2INN	A C	A	447	Y	1.8	444	450
2INN	A C	C	19	H	1.0	18	24
2INN	A C	C	84	Y	1.1	81	90
2INN	A C	C	88	R	1.0	81	90
2INN	A C	C	147	T	1.2	147	151
2INN	A C	C	162	G	3.9	160	172

2INN	A C	C	203	E	1.2	200	207
2INN	A F	A	379	Y	1.2	368	386
2INN	A F	A	445	E	1.0	444	450
2INN	A F	A	458	Y	2.9	453	459
2INN	B D	B	33	I	1.2	30	34
2INN	B D	B	61	Y	1.0	60	82
2INN	B D	B	62	W	4.0	60	82
2INN	B D	B	63	K	1.0	60	82
2INN	B D	B	109	H	3.3	91	122
2INN	B D	B	139	L	32.9	135	148
2INN	B D	B	147	H	2.4	135	148
2INN	B D	D	31	R	1.0	31	35
2INN	B D	D	82	G	34.4	81	90
2INN	B D	D	84	Y	1.2	81	90
2INN	B D	D	88	R	1.1	81	90
2INN	B D	D	139	K	1.5	137	144
2INN	B D	D	147	T	1.3	147	151
2INN	B D	D	162	G	10.8	160	172
2INN	B D	D	166	Y	1.9	160	172
2INN	B D	D	169	R	1.0	160	172
2INN	B E	B	379	Y	1.1	366	387
2INN	B E	B	448	I	1.1	444	450
2INN	B E	B	455	H	2.1	453	459
2INN	B E	B	458	Y	3.5	453	459
2INN	B L	B	64	Y	2.5	60	82
2INN	B L	B	223	V	1.6	222	229
2INN	B L	B	227	F	3.3	222	229
2INP	A C	A	20	D	1.9	18	22
2INP	A C	A	33	I	1.8	30	34
2INP	A C	A	63	K	1.0	58	82
2INP	A C	A	73	Y	1.3	58	82
2INP	A C	A	109	H	2.5	91	119
2INP	A C	A	112	F	1.5	91	119
2INP	A C	A	132	Q	1.3	125	155
2INP	A C	A	139	L	1.0	125	155
2INP	A C	A	143	Q	1.2	125	155
2INP	A C	A	147	H	2.0	125	155
2INP	A C	A	167	D	1.2	162	169
2INP	A C	A	180	D	3.0	173	185
2INP	A C	A	447	Y	1.5	444	449
2INP	A C	C	18	G	19.4	18	24
2INP	A C	C	19	H	1.1	18	24
2INP	A C	C	22	R	1.0	18	24
2INP	A C	C	84	Y	1.8	81	105
2INP	A C	C	85	V	1.3	81	105
2INP	A C	C	88	R	1.4	81	105
2INP	A C	C	128	H	1.0	113	144
2INP	A C	C	131	L	1.4	113	144
2INP	A C	C	132	G	1.0	113	144
2INP	A C	C	142	G	2.7	113	144
2INP	A C	C	147	T	1.5	147	175
2INP	A C	C	154	I	1.8	147	175
2INP	A C	C	155	Y	1.0	147	175
2INP	A C	C	162	G	20.0	147	175
2INP	A C	C	164	G	3.7	147	175
2INP	A C	C	165	Q	2.0	147	175
2INP	A C	C	183	D	2.2	180	192
2INP	A C	C	189	W	1.5	180	192
2INP	A D	A	216	Y	1.7	203	217
2INP	A D	A	226	G	2.4	220	251

2INP	A D	A	227	F	1.8	220	251
2INP	A F	A	379	Y	1.7	368	386
2INP	A F	A	448	I	1.1	444	449
2INP	A F	A	458	Y	2.4	453	459
2INP	B D	B	16	Y	1.6	10	17
2INP	B D	B	20	D	1.6	18	22
2INP	B D	B	33	I	1.6	30	34
2INP	B D	B	59	D	1.7	58	82
2INP	B D	B	62	W	4.4	58	82
2INP	B D	B	109	H	2.6	91	119
2INP	B D	B	112	F	1.2	91	119
2INP	B D	B	139	L	1.2	125	155
2INP	B D	B	140	R	4.8	125	155
2INP	B D	B	143	Q	1.7	125	155
2INP	B D	B	147	H	2.2	125	155
2INP	B D	D	18	G	2.0	18	25
2INP	B D	D	19	H	1.1	18	25
2INP	B D	D	31	R	1.3	31	37
2INP	B D	D	81	Y	1.5	81	105
2INP	B D	D	84	Y	2.0	81	105
2INP	B D	D	85	V	1.4	81	105
2INP	B D	D	127	R	1.8	113	142
2INP	B D	D	134	N	1.8	113	142
2INP	B D	D	147	T	1.5	147	175
2INP	B D	D	154	I	1.7	147	175
2INP	B D	D	158	M	4.8	147	175
2INP	B D	D	161	L	2.5	147	175
2INP	B D	D	162	G	22.8	147	175
2INP	B D	D	164	G	7.7	147	175
2INP	B D	D	165	Q	1.8	147	175
2INP	B D	D	166	Y	1.9	147	175
2INP	B D	D	169	R	1.6	147	175
2INP	B D	D	172	L	1.1	147	175
2INP	B D	D	189	W	1.5	180	192
2INP	B D	D	203	E	1.2	196	206
2INP	B E	B	379	Y	1.4	366	386
2INP	B E	B	458	Y	2.5	453	459
2INP	B L	B	64	Y	1.0	58	82
2INP	B L	B	71	K	1.4	58	82
2INP	B L	B	231	S	9.1	230	251
2INP	B L	B	241	L	1.0	230	251
2IO1	A B	A	401	D	1.6	399	405
2IO1	A B	A	441	F	2.1	440	449
2IO1	A B	A	445	K	1.0	440	449
2IO1	C D	C	445	K	1.3	442	449
2IO1	E F	E	445	K	1.1	442	450
2IO5	A B	B	106	D	1.3	86	114
2IO5	A B	B	129	R	1.1	121	132
2IO5	A B	B	130	I	1.9	121	132
2IO5	B C	B	67	F	1.3	64	79
2IO5	B C	B	70	L	1.1	64	79
2IO5	B C	B	71	V	1.1	64	79
2IO5	B C	B	74	I	1.6	64	79
2IO5	B C	B	78	F	1.9	64	79
2IO5	B C	B	92	L	1.5	86	114
2IO5	B C	B	99	Y	1.4	86	114
2IO5	B C	B	100	L	1.9	86	114
2IO5	B C	B	104	F	3.0	86	114
2IO5	B C	B	121	P	1.3	121	132
2IO5	B C	C	36	R	1.0	31	41

2IO5	B C	C	37	L	1.1	31	41
2IO5	B C	C	58	L	1.3	50	76
2IO5	B C	C	59	K	1.5	50	76
2IO5	B C	C	61	F	2.7	50	76
2IO5	B C	C	62	L	1.8	50	76
2IO5	B C	C	66	I	2.4	50	76
2IO5	B C	C	70	V	1.3	50	76
2IO5	B C	C	86	V	1.4	83	94
2IOF	A K	A	164	W	1.9	164	174
2IOF	A K	A	167	Y	2.2	164	174
2IOF	A K	A	171	M	1.5	164	174
2IOF	A K	K	164	W	3.0	164	174
2IPA	A B	A	65	G	16.7	62	68
2IPK	A B	A	70	L	1.9	56	77
2IPK	A B	A	76	R	2.7	56	77
2IPK	A B	B	57	D	1.8	55	63
2IPK	A C	A	58	G	73.8	56	77
2IPK	A C	A	65	V	1.1	56	77
2IPK	A C	A	72	I	1.5	56	77
2IPK	A D	D	215	M	1.1	210	217
2IPK	B C	B	61	W	3.9	55	63
2IPK	B C	B	78	Y	1.4	74	86
2IPK	B C	B	82	N	5.4	74	86
2IPU	K G	K	123	Q	1.9	121	126
2IPU	L H	L	123	Q	1.4	121	126
2ISS	A D	A	10	I	4.8	8	19
2ISS	A D	A	13	G	15.1	8	19
2ISS	A D	A	17	M	1.2	8	19
2ISS	A D	A	36	E	2.6	29	39
2ISS	A D	A	37	E	1.5	29	39
2ISS	A D	A	250	K	1.8	245	258
2ISS	A D	A	253	V	2.2	245	258
2ISS	A D	A	254	L	2.5	245	258
2ISS	A D	D	49	T	1.2	48	58
2ISS	A D	D	50	T	1.8	48	58
2ISS	A D	D	53	R	3.0	48	58
2ISS	A D	D	54	I	2.9	48	58
2ISS	A D	D	57	E	1.0	48	58
2ISS	B E	B	10	I	1.9	8	19
2ISS	B E	B	13	G	8.6	8	19
2ISS	B E	B	17	M	2.6	8	19
2ISS	B E	E	53	R	1.3	48	58
2ISS	B E	E	54	I	1.2	48	58
2ISS	C F	C	10	I	1.8	8	19
2ISS	C F	C	13	G	14.8	8	19
2ISS	C F	C	17	M	1.2	8	19
2ISS	C F	C	36	E	1.1	29	39
2ISS	C F	F	53	R	1.1	48	58
2ISS	C F	F	54	I	1.1	48	58
2IUC	A B	A	47	L	1.8	47	56
2IUC	A B	A	54	F	2.1	47	56
2IUC	A B	A	55	Y	1.3	47	56
2IUC	A B	B	47	L	2.3	47	56
2IUC	A B	B	54	F	2.1	47	56
2IUC	A B	B	55	Y	2.1	47	56
2IV8	A P	A	834	R	1.8	834	844
2IV8	A P	P	3	D	1.5	2	13
2IV8	A P	P	6	F	3.9	2	13
2IVF	A B	A	68	Y	3.0	66	72
2IVF	A B	A	69	R	2.5	66	72

2IVF	A B	A	135	N	1.4	133	138
2IVF	A B	A	265	Y	1.7	265	275
2IVF	A B	A	270	E	2.9	265	275
2IVF	A B	A	272	R	1.1	265	275
2IVF	A B	A	273	Y	2.4	265	275
2IVF	A B	A	427	L	1.3	425	437
2IVF	A B	A	430	E	1.9	425	437
2IVF	A B	B	36	V	1.7	33	40
2IVF	A B	B	99	H	3.5	99	104
2IVF	A B	B	103	F	2.7	99	104
2IVF	A B	B	217	R	3.5	215	220
2IVF	A B	B	228	R	2.3	225	229
2IVF	A B	B	317	R	3.5	306	322
2IVF	A B	B	333	I	1.9	327	334
2IVF	A B	B	337	W	2.8	337	341
2IVF	B C	B	192	E	1.7	189	194
2IVF	B C	C	45	F	6.6	44	48
2IX2	A B	A	145	V	1.1	140	154
2IX2	A B	A	152	L	1.6	140	154
2IX2	A C	C	153	G	7.5	151	165
2IX2	A C	C	160	E	2.0	151	165
2IX2	B C	B	142	I	3.8	136	148
2IX2	B C	B	145	E	2.2	136	148
2IX7	C A	C	772	R	1.0	765	819
2IX7	C A	C	773	I	3.6	765	819
2IX7	C A	C	777	I	1.1	765	819
2IX7	C A	C	780	W	3.7	765	819
2IX7	C A	C	781	L	1.1	765	819
2IX7	C A	C	783	R	1.5	765	819
2IX7	C A	C	786	Y	2.2	765	819
2IX7	C A	A	37	R	1.3	32	39
2IX7	C A	A	45	E	1.0	45	54
2IX7	C A	A	89	F	2.0	82	92
2IX7	C A	A	91	V	1.2	82	92
2IX7	C A	A	109	M	1.3	102	110
2IX7	C A	A	123	E	1.5	118	128
2IX7	C B	C	794	I	1.0	765	819
2IX7	C B	C	796	V	2.3	765	819
2IX7	C B	C	797	Q	2.0	765	819
2IX7	C B	C	798	R	12.7	765	819
2IX7	C B	C	799	Y	4.1	765	819
2IX7	C B	C	801	R	2.4	765	819
2IX7	C B	C	802	G	3.9	765	819
2IX7	C B	C	803	Y	1.5	765	819
2IX7	C B	C	812	L	1.6	765	819
2IX7	C B	B	18	L	1.1	6	19
2IX7	C B	B	37	R	2.3	32	39
2IX7	C B	B	45	E	1.9	45	55
2IX7	C B	B	85	I	2.0	82	92
2IX7	C B	B	89	F	1.3	82	92
2IX7	C B	B	91	V	1.0	82	92
2IX7	C B	B	108	V	1.8	102	110
2IY0	A B	A	468	D	3.7	468	482
2IY0	A B	A	469	E	4.8	468	482
2IY1	A B	A	456	D	1.1	454	461
2IY1	A B	A	468	D	6.3	468	482
2IY1	A B	A	469	E	2.7	468	482
2IY1	A B	A	472	N	3.1	468	482
2IY1	A B	A	496	F	2.5	496	504
2IY1	C D	C	496	F	3.8	496	504

2IZO	A C	A	335	G	7.1	316	339
2IZO	A C	A	338	R	1.9	316	339
2IZO	B C	C	152	L	1.1	140	154
2IZV	A B	A	405	G	8.4	403	408
2IZV	A C	A	389	L	3.5	389	401
2IZV	A C	A	390	Q	1.8	389	401
2IZV	A C	A	392	I	1.0	389	401
2IZV	A C	A	396	V	1.3	389	401
2IZV	A C	A	419	L	2.6	413	420
2IZV	A C	C	76	Y	2.1	67	83
2IZV	A C	C	101	L	1.2	100	110
2IZV	A C	C	104	L	2.0	100	110
2IZV	B C	B	34	I	1.6	24	35
2IZV	B C	C	67	S	1.3	67	83
2IZV	B C	C	68	H	3.6	67	83
2IZV	B C	C	82	R	1.2	67	83
2IZX	A C	A	21	L	2.0	9	24
2IZX	A C	C	5	I	1.9	5	21
2IZX	A C	C	13	V	1.7	5	21
2IZX	A C	C	17	I	1.6	5	21
2IZX	B C	B	13	L	1.1	9	24
2IZX	B C	B	21	L	1.0	9	24
2IZX	B C	C	8	L	1.0	5	21
2IZX	B C	C	12	I	1.4	5	21
2J01	F P	F	187	V	1.0	183	189
2J01	U V	U	39	L	1.0	32	55
2J01	U V	U	40	F	1.1	32	55
2J01	U V	U	43	G	1.0	32	55
2J03	F P	F	34	W	3.3	30	41
2J03	F P	F	187	V	1.0	183	189
2J03	U V	U	39	L	1.3	32	55
2J03	U V	U	40	F	1.5	32	55
2J0M	A B	A	197	L	1.0	191	202
2J0M	A B	B	636	E	2.2	628	637
2J0Q	A C	A	223	H	1.8	223	228
2J0Q	A C	A	358	R	3.0	358	366
2J0Q	A C	A	390	R	1.5	385	396
2J0Q	A C	A	395	Y	1.1	385	396
2J0Q	A C	C	134	F	1.8	116	140
2J0Q	A G	G	125	K	1.6	124	135
2J0Q	A T	A	150	I	1.7	146	156
2J0Q	A T	A	155	Y	3.1	146	156
2J0Q	A T	A	202	Y	1.2	195	208
2J0Q	A T	A	205	Y	2.6	195	208
2J0Q	A T	A	207	Y	1.4	195	208
2J0Q	A T	A	232	F	1.8	229	233
2J0Q	A T	A	289	K	2.7	287	300
2J0Q	A T	A	292	W	2.0	287	300
2J0Q	A T	A	385	D	2.7	385	396
2J0Q	B D	B	54	Y	2.0	49	57
2J0Q	B D	D	124	Y	1.6	124	135
2J0Q	B D	D	125	K	1.7	124	135
2J0Q	B F	B	223	H	1.7	223	228
2J0Q	B F	B	358	R	3.0	358	366
2J0Q	B F	B	359	E	1.2	358	366
2J0Q	B F	B	395	Y	1.0	385	396
2J0Q	B F	F	134	F	6.4	116	140
2J0Q	B I	B	155	Y	1.5	146	156
2J0Q	B I	B	202	Y	1.4	195	208
2J0Q	B I	B	205	Y	2.0	195	208

2J0Q	B I	B	207	Y	1.4	195	208
2J0Q	B I	B	232	F	1.8	229	233
2J0Q	B I	B	289	K	1.8	287	300
2J0Q	B I	B	292	W	1.1	287	300
2J0Q	B I	B	388	I	1.4	385	396
2J0Q	C D	C	56	V	1.1	54	68
2J0Q	C D	C	124	Y	2.0	116	140
2J0Q	C D	C	128	D	1.6	116	140
2J0Q	F G	F	56	V	1.1	54	68
2J0Q	F G	F	124	Y	1.8	116	140
2J0Q	F G	F	128	D	1.3	116	140
2J0Q	F G	F	131	C	2.4	116	140
2J0Q	F G	F	135	S	1.8	116	140
2J0S	A C	A	223	H	1.2	223	232
2J0S	A C	A	224	E	1.0	223	232
2J0S	A C	A	358	R	4.2	358	366
2J0S	A C	A	390	R	3.1	384	396
2J0S	A C	A	395	Y	2.9	384	396
2J0S	A C	C	123	Y	1.1	116	142
2J0S	A C	C	130	K	1.1	116	142
2J0S	A C	C	134	F	2.9	116	142
2J0S	A T	A	202	Y	3.0	195	207
2J0S	A T	A	205	Y	3.2	195	207
2J0S	A T	A	261	E	1.1	261	276
2J0S	A T	A	288	R	1.2	287	300
2J0S	A T	A	289	K	2.3	287	300
2J0S	A T	A	292	W	1.1	287	300
2J0S	A T	A	388	I	2.0	384	396
2J0S	C D	C	56	V	1.2	54	68
2J0S	C D	C	124	Y	1.8	116	142
2J0S	C D	C	135	S	2.0	116	142
2J0S	C D	C	139	L	2.5	116	142
2J0S	C D	C	140	H	3.9	116	142
2J0T	A D	A	218	H	1.1	212	225
2J0T	C F	C	218	H	1.2	212	224
2J0T	C F	C	222	H	1.2	212	224
2J0U	A B	B	56	Y	1.3	47	57
2J1K	I B	I	461	K	1.5	458	463
2J28	D P	P	8	E	1.6	5	10
2J28	J Q	Q	99	V	5.4	95	100
2J28	Q R	Q	46	Y	1.1	42	51
2J28	T X	X	26	F	1.5	22	28
2J37	W S	S	57	L	1.1	51	65
2J37	W S	S	63	V	18.6	51	65
2J3R	A B	A	18	L	2.1	16	34
2J3R	A B	A	19	F	2.0	16	34
2J3R	A B	A	21	L	1.0	16	34
2J3R	A B	A	26	L	1.1	16	34
2J3R	A B	A	33	D	1.5	16	34
2J3R	A B	A	50	N	1.2	37	62
2J3R	A B	A	51	I	1.4	37	62
2J3R	A B	A	86	Y	1.0	71	87
2J3R	A B	B	29	F	1.7	26	43
2J3R	A B	B	31	L	1.4	26	43
2J3R	A B	B	32	L	1.8	26	43
2J3R	A B	B	35	E	1.2	26	43
2J3R	A B	B	36	M	1.7	26	43
2J3R	A B	B	39	Y	1.2	26	43
2J3R	A B	B	142	F	1.2	138	153
2J3W	C F	C	103	Y	2.9	92	112

2J3W	C F	C	107	I	1.2	92	112
2J3W	C F	F	67	D	1.1	47	73
2J3W	C F	F	181	R	1.3	176	186
2J3W	C F	F	185	L	1.2	176	186
2J55	H M	H	15	G	26.2	9	28
2J55	J L	J	26	L	1.7	10	28
2J57	G K	G	15	G	17.9	9	28
2J57	G K	G	26	L	1.4	9	28
2J57	H M	H	15	G	18.5	9	28
2J57	H M	H	26	L	1.7	9	28
2J57	I N	I	15	G	6.0	9	28
2J57	I N	I	26	L	1.4	9	28
2J57	J L	J	15	G	1.6	9	28
2J57	J L	J	26	L	1.4	9	28
2J59	A M	A	35	Y	2.7	30	39
2J59	A M	A	77	L	1.2	75	81
2J59	A M	M	1053	I	2.0	1042	1063
2J59	A M	M	1057	I	2.2	1042	1063
2J59	B N	B	35	Y	2.6	30	40
2J59	B N	B	77	L	1.1	75	81
2J59	B N	N	1028	L	1.2	1024	1038
2J59	B N	N	1053	I	1.9	1042	1063
2J59	B N	N	1057	I	1.7	1042	1063
2J59	C O	C	35	Y	2.6	30	39
2J59	C O	C	77	L	1.2	75	80
2J59	C O	O	1053	I	2.3	1042	1061
2J59	C O	O	1057	I	1.2	1042	1061
2J59	C O	O	1060	Y	1.8	1042	1061
2J59	D P	D	35	Y	2.4	30	39
2J59	D P	P	1053	I	2.0	1042	1062
2J59	D P	P	1057	I	1.8	1042	1062
2J59	D P	P	1060	Y	1.1	1042	1062
2J59	E Q	E	35	Y	2.4	30	39
2J59	E Q	E	77	L	1.1	75	81
2J59	E Q	Q	1050	R	1.1	1042	1063
2J59	E Q	Q	1053	I	1.9	1042	1063
2J59	E Q	Q	1057	I	1.8	1042	1063
2J59	E Q	Q	1060	Y	1.0	1042	1063
2J59	F R	F	35	Y	2.5	30	39
2J59	F R	F	77	L	1.0	75	81
2J59	F R	R	1053	I	1.1	1042	1063
2J59	F R	R	1057	I	1.5	1042	1063
2J59	F R	R	1060	Y	1.1	1042	1063
2J5G	A D	A	47	P	4.3	40	56
2J5G	A D	A	51	Y	2.1	40	56
2J5G	A D	A	55	R	4.1	40	56
2J5G	A D	A	90	D	1.8	86	105
2J5G	A D	A	94	W	2.2	86	105
2J5G	A D	A	215	L	1.6	214	224
2J5G	A D	A	219	Y	1.0	214	224
2J5G	A D	D	48	D	2.6	40	56
2J5G	A D	D	90	D	2.3	86	105
2J5G	A D	D	94	W	2.9	86	105
2J5G	A D	D	215	L	1.5	214	224
2J5G	C D	C	237	G	4.1	226	252
2J5G	C D	C	238	Y	2.4	226	252
2J5G	C D	C	242	L	1.9	226	252
2J5G	C D	C	245	I	1.3	226	252
2J5G	C D	D	237	G	10.5	226	252
2J5G	C D	D	238	Y	2.4	226	252

2J5G	C D	D	245	I	1.3	226	252
2J5G	E D	E	166	Y	4.1	166	174
2J5G	E D	E	169	R	3.7	166	174
2J5G	E D	E	170	Y	2.6	166	174
2J5G	E D	E	173	F	3.2	166	174
2J5G	E D	E	234	E	1.1	226	235
2J5G	E D	E	242	L	2.2	236	251
2J5G	E D	E	246	T	1.4	236	251
2J5G	E D	D	201	R	1.0	198	212
2J5G	E D	D	219	Y	2.3	214	224
2J5G	E D	D	227	R	1.3	226	252
2J5G	F D	F	201	R	1.1	198	212
2J5G	F D	F	219	Y	1.9	214	224
2J5G	F D	F	227	R	1.3	226	235
2J5G	F D	D	166	Y	4.0	166	174
2J5G	F D	D	169	R	3.9	166	174
2J5G	F D	D	170	Y	2.6	166	174
2J5G	F D	D	173	F	3.9	166	174
2J5G	F D	D	234	E	1.9	226	252
2J5G	F D	D	242	L	2.2	226	252
2J5G	F D	D	246	T	1.4	226	252
2J5L	B C	B	124	Q	1.0	122	126
2J7A	A C	A	318	D	2.1	316	320
2J7A	A F	F	40	R	1.0	40	44
2J7A	A F	F	56	H	1.1	50	58
2J7A	B C	B	221	R	1.8	221	230
2J7A	D F	D	221	R	1.2	221	225
2J7A	D F	D	318	D	1.2	316	321
2J7A	E F	E	221	R	2.2	221	225
2J7A	E F	F	41	P	1.4	40	44
2J7A	E F	F	42	F	1.1	40	44
2J7A	G I	G	318	D	1.9	316	321
2J7A	G I	I	117	K	1.1	106	120
2J7A	G L	L	40	R	1.1	40	44
2J7A	G L	L	57	K	1.1	50	58
2J7A	H I	H	221	R	1.4	221	230
2J7A	J I	I	35	K	1.2	25	37
2J7A	K L	L	41	P	1.1	40	44
2J7A	M O	M	222	N	1.4	221	225
2J7A	M O	M	318	D	1.7	316	321
2J7A	M O	O	131	E	1.0	129	133
2J7A	N O	N	221	R	1.6	221	230
2J7A	N O	N	225	R	5.5	221	230
2J7A	N O	O	54	V	1.9	50	59
2J7A	P R	P	222	N	1.2	221	225
2J7A	P R	P	318	D	1.5	316	320
2J7A	P R	R	131	E	1.9	129	133
2J7A	Q R	Q	221	R	3.0	221	225
2J7A	Q R	Q	222	N	1.5	221	225
2J7A	Q R	R	40	R	1.9	40	44
2J7A	Q R	R	41	P	1.3	40	44
2J7Q	B C	B	33	K	2.1	23	34
2J7Q	D A	D	33	K	2.0	23	35
2J88	A H	A	148	R	2.6	146	176
2J8S	A E	A	734	E	1.4	733	740
2J8S	A E	E	56	Y	14.1	50	57
2J8S	B D	D	23	R	1.4	13	25
2J8X	A B	A	113	P	1.3	113	126
2J8X	A B	A	217	L	3.5	216	220
2J8X	A B	B	4	L	3.0	4	13

2J8X	A B	B	28	E	2.1	26	34
2J8X	A B	B	31	E	1.0	26	34
2J8X	A B	B	32	V	1.9	26	34
2J8X	C D	C	116	R	1.2	113	126
2J8X	C D	C	216	P	1.8	216	220
2J8X	C D	C	217	L	3.2	216	220
2J8X	C D	D	28	E	1.8	26	34
2J8X	C D	D	32	V	1.9	26	34
2J98	A B	A	96	G	119.8	92	106
2J98	A B	A	99	L	1.1	92	106
2J98	A B	A	100	G	120.7	92	106
2J98	A B	A	103	G	167.2	92	106
2J98	A B	B	96	G	149.0	92	106
2J98	A B	B	100	G	104.4	92	106
2J9D	B E	B	18	K	1.5	13	23
2J9D	F E	F	74	I	1.0	70	82
2J9D	F E	F	79	E	1.3	70	82
2J9U	A B	A	178	H	1.6	174	192
2J9U	A B	A	186	I	1.1	174	192
2J9U	A B	A	190	R	2.3	174	192
2J9U	A B	B	154	L	1.8	152	158
2J9U	C D	C	178	H	1.7	174	192
2J9U	C D	C	190	R	2.2	174	192
2J9U	C D	D	154	L	2.0	152	158
2JBA	A B	A	13	P	1.4	12	25
2JBA	A B	A	17	M	1.1	12	25
2JBA	A B	A	20	F	2.9	12	25
2JBA	A B	A	109	P	1.7	109	121
2JBA	A B	B	20	F	2.8	12	25
2JBA	A B	B	109	P	1.4	109	122
2JBL	C L	C	178	K	1.2	172	180
2JBL	C L	C	234	M	1.7	223	240
2JBL	C L	L	159	N	1.2	150	164
2JBL	C L	L	162	Y	2.1	150	164
2JBL	C L	L	163	Q	2.2	150	164
2JBL	C L	L	261	E	1.1	259	263
2JBL	C M	C	227	Y	1.6	223	240
2JBL	C M	C	230	F	1.3	223	240
2JBL	C M	C	262	P	1.7	262	280
2JBL	C M	C	268	W	4.3	262	280
2JBL	C M	C	269	W	1.2	262	280
2JBL	C M	M	189	I	1.1	177	191
2JBL	C M	M	293	Y	1.6	292	299
2JBL	H L	H	247	L	1.1	232	248
2JBL	H L	L	8	K	2.1	6	10
2JBL	H M	H	12	I	1.0	12	37
2JBL	H M	H	17	W	1.4	12	37
2JBL	H M	H	24	I	1.3	12	37
2JBL	H M	H	32	L	2.9	12	37
2JBL	H M	H	35	E	1.4	12	37
2JBL	H M	H	36	D	1.4	12	37
2JBL	H M	M	199	W	2.3	198	224
2JBL	H M	M	202	F	1.2	198	224
2JBL	H M	M	245	R	2.7	241	254
2JBL	H M	M	262	S	1.1	260	285
2JBL	H M	M	266	W	4.6	260	285
2JBL	H M	M	269	F	1.8	260	285
2JBL	H M	M	284	L	1.6	260	285
2JBL	H M	M	295	W	2.4	292	299
2JBL	L M	L	6	E	2.1	6	10

2JBL	L M	L	9	Y	1.7	6	10
2JBL	L M	L	100	W	1.1	84	111
2JBL	L M	L	103	R	1.6	84	111
2JBL	L M	L	107	I	1.6	84	111
2JBL	L M	L	116	H	3.3	116	139
2JBL	L M	L	117	V	1.7	116	139
2JBL	L M	L	180	L	1.2	171	199
2JBL	L M	L	187	L	3.2	171	199
2JBL	L M	L	188	G	15.3	171	199
2JBL	L M	L	190	H	2.0	171	199
2JBL	L M	L	191	G	3.8	171	199
2JBL	L M	L	192	G	4.6	171	199
2JBL	L M	L	194	I	1.4	171	199
2JBL	L M	L	195	L	2.5	171	199
2JBL	L M	L	197	V	1.0	171	199
2JBL	L M	L	211	H	1.1	209	220
2JBL	L M	L	214	Q	1.5	209	220
2JBL	L M	L	215	Y	1.7	209	220
2JBL	L M	L	217	R	1.6	209	220
2JBL	L M	L	218	D	2.5	209	220
2JBL	L M	L	227	L	1.4	226	251
2JBL	L M	L	231	R	1.3	226	251
2JBL	L M	L	233	G	158.7	226	251
2JBL	L M	L	234	L	1.4	226	251
2JBL	L M	L	267	L	1.4	264	268
2JBL	L M	M	5	T	1.6	3	7
2JBL	L M	M	82	L	1.3	81	87
2JBL	L M	M	83	Q	1.2	81	87
2JBL	L M	M	86	R	3.8	81	87
2JBL	L M	M	130	R	2.5	111	138
2JBL	L M	M	134	R	1.5	111	138
2JBL	L M	M	143	H	1.8	143	167
2JBL	L M	M	144	I	2.5	143	167
2JBL	L M	M	178	W	5.0	177	191
2JBL	L M	M	214	F	4.2	198	224
2JBL	L M	M	217	H	1.3	198	224
2JBL	L M	M	218	G	9.7	198	224
2JBL	L M	M	222	L	1.5	198	224
2JBL	L M	M	233	I	1.9	232	238
2JBL	L M	M	244	E	1.9	241	254
2JBL	L M	M	245	R	2.1	241	254
2JBL	L M	M	248	L	2.1	241	254
2JBL	L M	M	249	F	3.3	241	254
2JBL	L M	M	252	W	5.8	241	254
2JBL	L M	M	261	E	1.2	260	285
2JBL	L M	M	264	H	1.7	260	285
2JBL	L M	M	265	R	1.0	260	285
2JBL	L M	M	267	G	6.2	260	285
2JBL	L M	M	268	W	2.2	260	285
2JBY	A B	A	48	L	2.1	42	52
2JBY	A B	A	51	I	1.2	42	52
2JBY	A B	A	67	T	1.0	61	72
2JBY	A B	A	79	V	1.2	77	98
2JBY	A B	A	86	L	2.0	77	98
2JBY	A B	B	74	V	1.5	70	82
2JBY	A B	B	78	L	2.4	70	82
2JBY	A B	B	81	I	1.6	70	82
2JDQ	A E	A	149	W	3.2	141	156
2JDQ	A E	A	191	W	3.7	183	198
2JDQ	A E	A	195	N	1.3	183	198

2JDQ	A E	A	234	W	1.4	226	240
2JDQ	A E	A	276	W	1.1	268	282
2JDQ	A E	A	286	N	1.0	286	296
2JDQ	A E	A	318	R	1.0	310	324
2JDQ	A E	A	360	W	3.4	352	367
2JDQ	A E	A	399	E	2.8	394	411
2JDQ	A E	A	402	W	2.9	394	411
2JDQ	B D	B	149	W	1.2	141	156
2JDQ	B D	B	191	W	3.3	183	198
2JDQ	B D	B	234	W	1.5	226	241
2JDQ	B D	B	360	W	1.8	352	367
2JDQ	B D	B	364	N	1.7	352	367
2JDQ	B D	B	399	E	3.2	394	410
2JDQ	B D	B	402	W	4.7	394	410
2JDQ	B D	B	445	N	1.0	437	461
2JE6	A B	A	105	E	2.0	105	122
2JE6	A B	A	108	I	1.9	105	122
2JE6	A B	A	109	E	2.4	105	122
2JE6	A B	A	112	R	2.0	105	122
2JE6	A B	A	116	R	2.1	105	122
2JE6	A B	A	120	D	1.5	105	122
2JE6	A B	A	251	I	2.5	248	274
2JE6	A B	B	101	I	2.3	98	115
2JE6	A B	B	102	E	3.8	98	115
2JE6	A B	B	105	K	1.8	98	115
2JE6	A B	B	108	R	1.0	98	115
2JE6	A B	B	109	E	1.2	98	115
2JE6	A B	B	214	F	1.9	211	240
2JE6	A I	A	14	I	1.1	13	20
2JEA	A B	A	105	E	1.3	105	122
2JEA	A B	A	116	R	2.1	105	122
2JEA	A B	A	251	I	2.7	248	274
2JEA	A B	B	102	E	3.4	98	115
2JEA	A B	B	112	E	2.9	98	115
2JEA	A B	B	214	F	2.0	211	239
2JEL	H P	P	70	E	2.9	70	82
2JEL	H P	P	71	Q	1.7	70	82
2JEL	L H	L	124	Q	1.5	122	128
2JET	B C	C	235	M	1.2	235	243
2JF9	A P	A	354	L	1.3	339	363
2JF9	A P	A	372	L	1.5	372	395
2JF9	A P	A	376	V	1.9	372	395
2JF9	A P	A	380	E	1.7	372	395
2JF9	A P	A	383	W	1.3	372	395
2JF9	A P	P	5	R	1.7	5	12
2JF9	A P	P	7	W	1.6	5	12
2JF9	A P	P	8	F	1.8	5	12
2JF9	B Q	B	354	L	1.2	342	363
2JF9	B Q	B	358	I	2.3	342	363
2JF9	B Q	B	372	L	2.0	372	395
2JF9	B Q	B	376	V	1.8	372	395
2JF9	B Q	B	379	L	1.0	372	395
2JF9	B Q	B	380	E	1.0	372	395
2JF9	B Q	Q	5	R	1.0	5	13
2JF9	B Q	Q	7	W	2.8	5	13
2JF9	B Q	Q	8	F	4.0	5	13
2JF9	B Q	Q	9	K	1.0	5	13
2JF9	B Q	Q	12	L	2.1	5	13
2JF9	C R	C	354	L	1.3	339	363
2JF9	C R	C	372	L	1.3	372	394

2JF9	C R	C	376	V	1.3	372	394
2JF9	C R	C	379	L	1.1	372	394
2JF9	C R	C	383	W	1.1	372	394
2JF9	C R	R	7	W	1.6	5	12
2JF9	C R	R	11	M	1.2	5	12
2JFA	A B	A	497	L	1.0	497	529
2JFA	A B	A	501	H	1.2	497	529
2JFA	A B	A	504	L	1.2	497	529
2JFA	A B	A	509	L	2.1	497	529
2JFA	A B	A	523	E	1.4	497	529
2JFA	A B	B	484	D	1.3	466	493
2JFA	A B	B	497	L	1.0	497	528
2JFA	A B	B	502	Q	1.2	497	528
2JFA	A B	B	504	L	1.0	497	528
2JFA	A B	B	508	L	1.2	497	528
2JFA	A B	B	509	L	1.7	497	528
2JFA	A B	B	513	H	1.6	497	528
2JFA	A B	B	523	E	1.5	497	528
2JFA	A P	A	358	I	1.6	339	363
2JFA	A P	A	372	L	1.1	372	395
2JFA	A P	A	376	V	1.3	372	395
2JFA	A P	P	5	L	1.2	2	14
2JFA	A P	P	9	I	3.5	2	14
2JFA	A P	P	12	G	105.2	2	14
2JFA	A P	P	13	L	2.1	2	14
2JFA	B Q	B	376	V	1.1	372	395
2JFA	B Q	Q	6	R	1.4	2	15
2JFA	B Q	Q	9	I	1.8	2	15
2JFA	B Q	Q	12	G	109.1	2	15
2JFA	B Q	Q	13	L	2.6	2	15
2JGB	A B	A	92	E	1.2	91	100
2JGB	A B	A	95	W	3.6	91	100
2JGB	A B	A	153	L	1.3	143	157
2JGB	A B	B	59	L	1.5	56	64
2JGD	A B	A	689	F	2.4	687	693
2JGD	A B	A	691	N	2.3	687	693
2JGD	A B	A	692	G	1.0	687	693
2JGD	A B	A	694	Q	1.1	694	708
2JGD	A B	A	698	D	3.5	694	708
2JGD	A B	A	703	S	3.5	694	708
2JGD	A B	A	707	K	1.2	694	708
2JGD	A B	A	736	R	5.3	734	741
2JGD	A B	A	739	Q	3.2	734	741
2JGD	A B	A	883	Y	2.8	881	885
2JGD	A B	A	884	C	2.5	881	885
2JGD	A B	B	364	G	45.2	364	373
2JGD	A B	B	367	Q	1.4	364	373
2JGD	A B	B	689	F	1.2	687	693
2JGD	A B	B	691	N	1.4	687	693
2JGD	A B	B	698	D	4.8	694	703
2JGD	A B	B	699	Q	1.6	694	703
2JGD	A B	B	736	R	3.6	734	741
2JGD	A B	B	883	Y	3.5	881	892
2JGZ	A B	B	174	I	1.8	171	185
2JGZ	A B	B	258	Y	1.1	244	260
2JGZ	A B	B	283	R	1.0	279	293
2JGZ	A B	B	286	E	2.4	279	293
2JIY	L H	L	7	R	1.4	6	10
2JIY	L H	L	8	K	2.8	6	10
2JIY	L H	H	242	M	1.3	227	243

2JIY	L M	L	6	E	2.0	6	10
2JIY	L M	L	8	K	1.2	6	10
2JIY	L M	L	9	Y	2.0	6	10
2JIY	L M	L	103	R	1.9	84	111
2JIY	L M	L	107	I	1.7	84	111
2JIY	L M	L	116	H	3.1	116	139
2JIY	L M	L	117	I	2.9	116	139
2JIY	L M	L	154	L	1.1	150	164
2JIY	L M	L	187	L	3.8	171	199
2JIY	L M	L	190	H	1.9	171	199
2JIY	L M	L	191	G	12.8	171	199
2JIY	L M	L	194	V	1.6	171	199
2JIY	L M	L	195	L	3.2	171	199
2JIY	L M	L	211	H	2.7	209	220
2JIY	L M	L	214	T	1.7	209	220
2JIY	L M	L	215	F	2.5	209	220
2JIY	L M	L	218	D	2.6	209	220
2JIY	L M	L	219	L	1.5	209	220
2JIY	L M	L	228	G	3.7	226	250
2JIY	L M	L	230	H	1.3	226	250
2JIY	L M	L	231	R	4.6	226	250
2JIY	L M	L	233	G	297.6	226	250
2JIY	L M	L	234	L	1.1	226	250
2JIY	L M	L	263	W	2.1	259	268
2JIY	L M	M	87	R	3.4	82	88
2JIY	L M	M	129	W	1.4	113	140
2JIY	L M	M	132	R	1.9	113	140
2JIY	L M	M	145	H	1.9	145	168
2JIY	L M	M	149	W	1.1	145	168
2JIY	L M	M	180	F	2.7	179	193
2JIY	L M	M	183	L	1.3	179	193
2JIY	L M	M	184	D	1.3	179	193
2JIY	L M	M	209	L	1.6	200	226
2JIY	L M	M	216	F	4.0	200	226
2JIY	L M	M	219	H	1.6	200	226
2JIY	L M	M	220	G	4.9	200	226
2JIY	L M	M	224	L	1.1	200	226
2JIY	L M	M	235	L	2.7	234	240
2JIY	L M	M	246	E	2.0	243	256
2JIY	L M	M	247	R	3.6	243	256
2JIY	L M	M	250	L	2.2	243	256
2JIY	L M	M	251	F	3.4	243	256
2JIY	L M	M	253	R	1.7	243	256
2JIY	L M	M	254	W	6.4	243	256
2JIY	L M	M	270	I	1.0	262	287
2JIY	M H	M	201	F	2.7	200	226
2JIY	M H	M	204	L	1.5	200	226
2JIY	M H	M	208	F	1.2	200	226
2JIY	M H	M	236	E	1.9	234	240
2JIY	M H	M	264	G	254.7	262	287
2JIY	M H	M	268	W	2.6	262	287
2JIY	M H	M	271	W	2.5	262	287
2JIY	M H	M	275	L	1.2	262	287
2JIY	M H	M	286	L	1.0	262	287
2JIY	M H	M	297	W	2.4	294	301
2JIY	M H	H	17	I	2.1	12	35
2JIY	M H	H	20	F	1.5	12	35
2JIY	M H	H	27	L	2.4	12	35
2JIY	M H	H	31	L	2.4	12	35
2JIY	M H	H	34	E	1.4	12	35

2JIY	M H	H	231	D	2.7	227	243
2JIZ	A D	A	210	R	2.5	210	223
2JIZ	A D	A	211	S	1.0	210	223
2JIZ	A D	A	212	T	1.3	210	223
2JIZ	A D	A	283	L	1.4	271	285
2JIZ	A D	A	284	L	1.0	271	285
2JIZ	A D	A	358	Y	1.8	354	360
2JIZ	A D	D	290	G	215.6	285	296
2JIZ	A D	D	326	F	3.1	320	328
2JIZ	A E	A	300	Y	1.2	298	309
2JIZ	A E	E	191	R	1.9	190	204
2JIZ	A E	E	271	L	1.0	258	272
2JIZ	A G	G	19	I	1.5	3	40
2JIZ	A G	G	30	K	1.0	3	40
2JIZ	B E	B	210	R	2.6	210	223
2JIZ	B E	B	218	K	1.5	210	223
2JIZ	B E	B	283	L	1.3	271	285
2JIZ	B E	E	290	G	140.4	285	296
2JIZ	B E	E	294	E	1.7	285	296
2JIZ	B F	B	300	Y	1.3	298	309
2JIZ	B F	B	307	E	2.2	298	309
2JIZ	B F	F	191	R	2.2	190	204
2JIZ	B F	F	229	R	1.2	226	246
2JIZ	B G	G	252	R	2.0	203	272
2JIZ	B G	G	263	I	1.4	203	272
2JIZ	C D	C	299	F	1.9	298	309
2JIZ	C D	C	300	Y	2.1	298	309
2JIZ	C D	C	392	L	1.3	390	404
2JIZ	C D	C	396	Q	1.8	390	404
2JIZ	C D	C	399	E	4.2	390	404
2JIZ	C D	C	403	F	1.6	390	404
2JIZ	C D	D	191	R	1.1	190	204
2JIZ	C D	D	192	E	1.0	190	204
2JIZ	C D	D	337	R	1.5	337	342
2JIZ	C D	D	408	R	3.1	399	415
2JIZ	C D	D	424	F	1.1	422	426
2JIZ	C F	C	210	R	1.0	210	223
2JIZ	C F	C	283	L	1.2	271	285
2JIZ	C F	C	284	L	3.8	271	285
2JIZ	C F	C	355	E	1.3	354	360
2JIZ	C F	C	358	Y	1.7	354	360
2JIZ	C F	C	359	K	1.5	354	360
2JIZ	C F	F	290	G	208.8	285	296
2JIZ	C F	F	294	E	1.2	285	296
2JIZ	C F	F	372	R	1.4	365	384
2JIZ	C F	F	379	Q	1.7	365	384
2JIZ	C G	G	264	E	1.4	203	272
2JIZ	D G	D	387	I	1.2	365	391
2JIZ	D G	G	16	I	1.3	3	40
2JIZ	D G	G	265	I	1.3	203	272
2JIZ	D G	G	268	G	39.0	203	272
2JIZ	E G	E	386	D	1.0	365	392
2JIZ	E G	E	390	I	1.2	365	392
2JIZ	E G	G	266	I	1.3	203	272
2JIZ	F G	F	390	I	1.7	385	392
2JIZ	H K	H	210	R	3.0	210	223
2JIZ	H K	H	283	L	1.4	271	285
2JIZ	H K	H	284	L	1.0	271	285
2JIZ	H K	H	358	Y	1.9	354	360
2JIZ	H K	K	287	T	1.0	285	296

2JIZ	H K	K	290	G	188.5	285	296
2JIZ	H K	K	294	E	1.5	285	296
2JIZ	H K	K	326	F	2.8	320	328
2JIZ	H K	K	376	K	1.0	365	391
2JIZ	H K	K	380	D	1.0	365	391
2JIZ	H L	H	299	F	1.2	298	309
2JIZ	H L	H	300	Y	2.0	298	309
2JIZ	H L	H	304	R	1.4	298	309
2JIZ	H L	L	271	L	1.1	258	272
2JIZ	H N	N	19	I	1.0	3	40
2JIZ	H N	N	258	I	2.6	203	271
2JIZ	H N	N	266	I	2.3	203	271
2JIZ	I L	I	210	R	1.7	210	223
2JIZ	I L	I	218	K	1.6	210	223
2JIZ	I L	I	283	L	1.4	271	285
2JIZ	I L	L	290	G	144.9	285	296
2JIZ	I M	I	300	Y	1.3	298	309
2JIZ	I M	I	307	E	1.1	298	309
2JIZ	I M	M	191	R	2.9	190	204
2JIZ	I N	N	263	I	1.4	203	271
2JIZ	J K	J	299	F	1.2	298	309
2JIZ	J K	J	300	Y	2.2	298	309
2JIZ	J K	J	307	E	1.3	298	309
2JIZ	J K	J	392	L	1.1	390	404
2JIZ	J K	J	396	Q	5.7	390	404
2JIZ	J K	J	399	E	3.8	390	404
2JIZ	J K	J	400	V	5.8	390	404
2JIZ	J K	J	403	F	5.5	390	404
2JIZ	J K	K	191	R	1.9	190	204
2JIZ	J K	K	195	D	1.0	190	204
2JIZ	J K	K	337	R	1.3	337	342
2JIZ	J K	K	408	R	5.5	402	415
2JIZ	J K	K	412	R	5.7	402	415
2JIZ	J K	K	424	F	1.3	422	426
2JIZ	J M	J	210	R	2.6	210	223
2JIZ	J M	J	211	S	1.1	210	223
2JIZ	J M	J	212	T	1.6	210	223
2JIZ	J M	J	218	K	1.1	210	223
2JIZ	J M	J	219	R	1.1	210	223
2JIZ	J M	J	283	L	1.2	272	285
2JIZ	J M	J	284	L	1.0	272	285
2JIZ	J M	J	358	Y	3.2	354	360
2JIZ	J M	M	290	G	191.4	285	296
2JIZ	J M	M	294	E	1.1	285	296
2JIZ	J N	N	264	E	1.0	203	271
2JIZ	K N	N	16	I	1.1	3	40
2JIZ	K N	N	265	I	1.8	203	271
2JIZ	K N	N	268	G	46.4	203	271
2JIZ	L N	L	390	I	1.2	365	392
2JIZ	L N	N	254	R	1.8	203	271
2JIZ	L N	N	255	Q	2.5	203	271
2JIZ	L N	N	259	T	1.0	203	271
2JIZ	L N	N	266	I	1.3	203	271
2JIZ	M N	M	390	I	1.9	385	392
2JJ0	L H	L	7	R	1.8	6	10
2JJ0	L H	L	8	K	2.0	6	10
2JJ0	L H	H	242	M	1.2	227	245
2JJ0	L M	L	6	E	1.6	6	10
2JJ0	L M	L	9	Y	5.6	6	10
2JJ0	L M	L	100	W	1.0	84	111

2JJ0	L M	L	103	R	1.4	84	111
2JJ0	L M	L	116	H	3.6	116	140
2JJ0	L M	L	117	I	2.6	116	140
2JJ0	L M	L	154	L	1.2	150	164
2JJ0	L M	L	187	L	2.4	171	199
2JJ0	L M	L	190	H	3.0	171	199
2JJ0	L M	L	191	G	12.9	171	199
2JJ0	L M	L	194	V	1.2	171	199
2JJ0	L M	L	195	L	2.3	171	199
2JJ0	L M	L	211	H	2.4	209	220
2JJ0	L M	L	214	T	1.6	209	220
2JJ0	L M	L	215	F	2.8	209	220
2JJ0	L M	L	218	D	1.5	209	220
2JJ0	L M	L	219	L	1.3	209	220
2JJ0	L M	L	228	G	7.7	226	251
2JJ0	L M	L	231	R	4.8	226	251
2JJ0	L M	L	233	G	326.8	226	251
2JJ0	L M	L	234	L	1.7	226	251
2JJ0	L M	M	42	F	2.9	37	43
2JJ0	L M	M	87	R	2.1	82	88
2JJ0	L M	M	145	H	1.9	145	161
2JJ0	L M	M	180	F	2.4	179	193
2JJ0	L M	M	184	D	1.2	179	193
2JJ0	L M	M	209	L	1.6	200	226
2JJ0	L M	M	216	F	3.5	200	226
2JJ0	L M	M	219	H	1.8	200	226
2JJ0	L M	M	220	G	14.7	200	226
2JJ0	L M	M	224	L	1.6	200	226
2JJ0	L M	M	234	E	1.7	234	240
2JJ0	L M	M	235	L	2.4	234	240
2JJ0	L M	M	246	E	2.2	243	256
2JJ0	L M	M	247	R	1.9	243	256
2JJ0	L M	M	250	L	6.1	243	256
2JJ0	L M	M	251	F	4.1	243	256
2JJ0	L M	M	253	R	1.3	243	256
2JJ0	L M	M	254	W	5.5	243	256
2JJ0	L M	M	266	H	2.6	262	287
2JJ0	M H	M	41	W	1.0	37	43
2JJ0	M H	M	236	E	2.4	234	240
2JJ0	M H	M	264	G	221.0	262	287
2JJ0	M H	M	267	R	1.1	262	287
2JJ0	M H	M	268	W	1.4	262	287
2JJ0	M H	M	271	W	2.1	262	287
2JJ0	M H	M	297	W	2.5	294	300
2JJ0	M H	H	27	L	1.3	12	35
2JJ0	M H	H	31	L	2.4	12	35
2JJ0	M H	H	34	E	1.1	12	35
2JJ0	M H	H	230	E	4.5	227	245
2JJ0	M H	H	231	D	2.3	227	245
2JJZ	A B	A	31	R	2.6	17	35
2JJZ	A B	B	34	L	1.1	18	35
2JJZ	A B	B	46	P	1.2	45	59
2JKI	A S	A	88	K	1.9	88	95
2JKI	A S	A	90	D	1.8	88	95
2JKI	A S	A	92	V	1.6	88	95
2JKI	A S	A	93	N	1.1	88	95
2JKI	B S	B	191	R	1.3	189	200
2JKI	B S	B	198	R	1.1	189	200
2JKI	C T	C	191	R	1.4	189	200
2JKI	C T	C	198	R	1.4	189	200

2JKI	C U	C	88	K	2.9	88	95
2JKR	A B	A	583	Y	2.0	574	590
2JKR	A B	A	585	R	1.3	574	590
2JKR	A B	A	598	V	1.5	592	599
2JKR	A B	B	482	L	2.1	478	495
2JKR	A B	B	486	T	1.1	478	495
2JKR	A B	B	525	I	3.6	517	532
2JKR	A B	B	540	V	1.1	534	542
2JKR	A E	E	527	W	2.0	517	532
2JKR	A S	A	13	L	1.0	11	22
2JKR	A S	A	17	I	1.9	11	22
2JKR	A S	A	64	F	1.1	52	67
2JKR	A S	A	96	L	1.6	88	101
2JKR	A S	A	167	S	1.1	162	179
2JKR	A S	A	170	L	1.7	162	179
2JKR	A S	A	347	Y	1.1	343	358
2JKR	A S	S	78	L	1.3	77	96
2JKR	A S	S	82	E	1.8	77	96
2JKR	A S	S	105	F	3.6	100	106
2JKR	A S	S	107	F	3.4	107	118
2JKR	A S	S	108	Y	1.6	107	118
2JKR	A S	S	111	Y	1.1	107	118
2JKR	A S	S	130	K	1.1	128	138
2JKR	B M	B	108	R	1.9	100	113
2JKR	B M	B	139	K	2.1	135	151
2JKR	B M	B	179	N	1.3	174	191
2JKR	B M	B	300	Y	1.2	296	313
2JKR	B M	B	301	V	1.2	296	313
2JKR	B M	B	333	Y	1.2	332	345
2JKR	B M	B	570	L	1.3	570	574
2JKR	B M	M	79	F	2.1	75	93
2JKR	B M	M	80	E	2.6	75	93
2JKR	B M	M	105	F	2.4	105	113
2JKR	E M	E	527	W	1.5	517	532
2JKR	E U	E	108	R	1.2	100	112
2JKR	E U	E	179	N	1.6	174	191
2JKR	E U	E	300	Y	1.3	296	313
2JKR	E U	E	301	V	1.2	296	313
2JKR	E U	E	333	Y	2.4	332	345
2JKR	E U	E	368	D	1.3	367	384
2JKR	E U	E	570	L	1.7	570	574
2JKR	E U	U	77	M	1.0	75	93
2JKR	E U	U	79	F	2.1	75	93
2JKR	E U	U	80	E	2.6	75	93
2JKR	E U	U	109	Y	1.6	105	113
2JKR	L B	B	471	E	6.2	460	472
2JKR	L B	B	505	Q	5.3	500	514
2JKR	L B	B	527	W	1.1	517	532
2JKR	L E	L	502	Y	1.2	494	507
2JKR	L E	L	589	V	1.1	574	590
2JKR	L E	L	598	V	1.8	592	599
2JKR	L E	E	486	T	2.4	478	495
2JKR	L E	E	521	D	1.2	517	532
2JKR	L E	E	524	Y	3.7	517	532
2JKR	L E	E	528	R	1.0	517	532
2JKR	L E	E	540	V	1.1	534	542
2JKR	L I	L	13	L	1.0	11	22
2JKR	L I	L	17	I	1.9	11	22
2JKR	L I	L	64	F	1.1	52	67
2JKR	L I	L	88	Y	1.1	88	101

2JKR	L I	L	96	L	1.8	88	101
2JKR	L I	L	133	H	1.1	125	139
2JKR	L I	L	167	S	1.1	162	179
2JKR	L I	L	170	L	1.8	162	179
2JKR	L I	L	177	R	1.0	162	179
2JKR	L I	L	344	N	1.2	343	358
2JKR	L I	L	347	Y	4.2	343	358
2JKR	L I	I	78	L	1.5	77	96
2JKR	L I	I	105	F	3.2	100	106
2JKR	L I	I	107	F	3.5	107	118
2JKR	L I	I	108	Y	1.8	107	118
2JKR	L I	I	111	Y	1.2	107	118
2JKR	L I	I	130	K	1.3	128	138
2JKR	M S	S	27	E	1.2	25	41
2JKR	M S	S	30	K	1.1	25	41
2JM6	A B	A	71	L	1.1	71	94
2JM6	A B	A	78	L	1.7	71	94
2JM6	A B	A	81	I	1.0	71	94
2JM6	A B	A	82	G	202.9	71	94
2JM6	A B	A	85	V	1.1	71	94
2JM6	A B	B	209	F	3.4	206	216
2JM6	A B	B	229	R	1.0	221	235
2JM6	A B	B	243	G	139.1	242	262
2JM6	A B	B	244	R	1.7	242	262
2JMF	A B	B	2328	Y	1.1	2328	2332
2JND	A B	B	235	R	1.2	230	237
2JQ9	A B	A	57	R	1.0	50	75
2JQ9	A B	A	68	E	2.0	50	75
2JQ9	A B	B	121	R	1.0	116	127
2JQ9	A B	B	126	R	1.3	116	127
2JQK	A B	A	62	R	1.3	55	81
2JQK	A B	B	122	Q	1.2	117	127
2JQK	A B	B	126	L	1.4	117	127
2JRI	A C	A	31	V	1.4	30	51
2JRI	A C	A	34	S	1.5	30	51
2JRI	A C	A	38	H	3.1	30	51
2JRI	A C	A	87	W	1.6	77	88
2JSS	A B	A	84	R	1.3	73	93
2JSS	A B	A	109	G	33.4	108	120
2JSS	A B	A	147	L	1.0	129	157
2JTT	A C	A	10	G	56.9	3	24
2JTT	A C	A	13	I	1.1	3	24
2JTT	A C	A	14	G	77.4	3	24
2JTT	A C	A	18	K	2.5	3	24
2JTT	A C	A	21	G	4.3	3	24
2JTT	A C	C	211	I	1.8	205	218
2JTT	A C	C	215	W	3.2	205	218
2JTT	A D	A	56	L	1.3	50	64
2JTT	A D	A	76	F	2.8	70	85
2JTT	A D	A	80	L	1.3	70	85
2JTT	A D	A	83	I	1.9	70	85
2JTT	A D	A	84	Y	3.7	70	85
2JTT	A D	D	195	V	1.6	192	201
2JTT	A D	D	196	L	1.4	192	201
2JTT	A D	D	199	I	1.6	192	201
2JTT	A D	D	200	Y	2.7	192	201
2JTT	A D	D	207	M	1.4	206	218
2JTT	A D	D	208	K	1.1	206	218
2JTT	B C	B	80	L	1.1	70	84
2JTT	B C	B	83	I	2.4	70	84

2JTT	B C	C	195	V	1.1	192	201
2JTT	B C	C	196	L	3.4	192	201
2JTT	B C	C	200	Y	1.3	192	201
2JTT	B D	B	6	D	1.9	2	21
2JTT	B D	B	10	G	69.1	2	21
2JTT	B D	B	14	G	136.0	2	21
2JTT	B D	D	211	I	1.6	206	218
2JTT	B D	D	215	W	1.1	206	218
2JU0	A B	A	30	W	1.0	26	38
2JU0	A B	A	51	I	1.8	45	55
2JU0	A B	A	85	F	1.5	82	93
2JU0	A B	A	107	L	1.8	99	108
2JU0	A B	B	135	L	2.1	125	136
2JU0	A B	B	160	L	1.6	155	170
2JXC	A B	A	148	G	347.7	148	156
2JXC	A B	A	153	P	1.4	148	156
2JXC	A B	A	166	G	49.8	162	173
2JXC	A B	A	169	W	1.3	162	173
2JXC	A B	A	170	E	1.2	162	173
2JXC	A B	A	196	L	1.4	182	197
2JXM	A B	B	3	F	1.2	2	9
2JY6	A B	B	584	L	1.7	576	586
2JZB	A B	A	290	L	1.0	286	291
2JZB	A B	A	297	K	2.1	297	310
2JZB	A B	A	300	L	1.2	297	310
2JZB	A B	B	479	G	72.8	475	491
2K03	A B	A	59	Q	1.1	56	67
2K1R	A B	B	87	G	3.1	86	100
2K2F	C A	C	8	L	1.0	2	12
2K2F	D B	D	9	L	2.1	2	12
2K2I	A B	A	112	L	1.3	102	114
2K2I	A B	A	113	F	2.4	102	114
2K2I	A B	A	129	V	1.2	123	134
2K2I	A B	A	130	A	2.0	123	134
2K2I	A B	A	133	L	1.2	123	134
2K2I	A B	A	145	M	1.7	140	149
2K2I	A B	A	146	I	1.2	140	149
2K2I	A B	A	162	F	1.8	159	167
2K2I	A B	A	165	I	1.6	159	167
2K2I	A B	B	651	L	2.2	651	660
2K2I	A B	B	658	W	7.0	651	660
2K2Q	A B	B	218	F	3.8	218	223
2K3S	A B	A	102	Q	1.0	94	111
2K3S	A B	A	106	R	1.6	94	111
2K3W	A B	A	73	Y	1.1	50	75
2K42	A B	A	35	R	2.3	27	37
2K42	A B	A	52	I	1.0	46	59
2K42	A B	A	68	E	1.8	62	70
2K42	A B	B	87	L	1.8	79	89
2K5B	A B	A	120	E	1.1	113	125
2K5B	A B	B	205	L	1.1	203	211
2K6Q	A B	A	69	R	1.0	60	72
2K6T	A B	B	42	L	1.8	36	47
2K7L	B A	A	474	L	1.1	470	478
2K7L	B A	A	487	E	1.0	486	501
2K7W	A B	A	21	K	1.3	16	37
2K7W	A B	A	138	G	6.5	130	155
2K7W	A B	A	141	L	1.1	130	155
2K7W	A B	B	153	R	1.2	146	161
2K7W	A B	B	159	F	1.7	146	161

2K8B	A B	B	105	M	1.4	104	120
2K8B	A B	B	106	F	2.3	104	120
2K8B	A B	B	109	Q	2.7	104	120
2K8F	A B	A	42	V	2.2	34	49
2K8F	A B	A	45	H	1.1	34	49
2K8F	A B	A	48	G	25.7	34	49
2K8M	A B	B	58	E	1.7	56	61
2K91	A B	B	18	V	1.3	9	19
2K9F	A B	A	37	P	1.2	37	51
2K9F	A B	A	38	L	1.0	37	51
2K9J	A B	A	976	G	94.4	966	991
2K9J	A B	B	700	V	1.2	693	725
2K9J	A B	B	704	I	1.2	693	725
2K9J	A B	B	708	G	1.5	693	725
2K9J	A B	B	712	L	1.5	693	725
2K9J	A B	B	723	D	1.1	693	725
2KA4	A B	A	350	R	2.6	347	373
2KA4	A B	A	352	L	2.0	347	373
2KA4	A B	A	353	I	2.4	347	373
2KA4	A B	A	354	Q	5.2	347	373
2KA4	A B	A	356	Q	9.3	347	373
2KA4	A B	A	357	L	3.4	347	373
2KA4	A B	A	362	H	1.0	347	373
2KA4	A B	A	364	H	2.5	347	373
2KA4	A B	A	391	L	1.0	384	397
2KA4	A B	A	407	H	1.8	406	421
2KA4	A B	A	414	I	2.9	406	421
2KA4	A B	A	418	W	4.4	406	421
2KA4	A B	A	427	P	1.9	427	436
2KA4	A B	A	428	V	3.8	427	436
2KA4	A B	A	431	P	2.0	427	436
2KA4	A B	B	795	L	2.6	793	798
2KA4	A B	B	806	F	1.7	801	808
2KA6	A B	A	6	R	1.6	2	23
2KA6	A B	A	7	R	2.4	2	23
2KA6	A B	A	10	I	2.7	2	23
2KA6	A B	A	56	V	1.1	55	71
2KA6	A B	A	59	Q	2.2	55	71
2KA6	A B	A	66	Y	1.8	55	71
2KA6	A B	A	80	F	1.5	79	91
2KA6	A B	A	84	I	1.3	79	91
2KA6	A B	A	87	K	2.9	79	91
2KA6	A B	B	730	E	1.8	728	739
2KA6	A B	B	731	F	4.5	728	739
2KA6	A B	B	733	E	3.0	728	739
2KA6	A B	B	734	V	1.2	728	739
2KBC	B A	B	15	V	3.2	9	24
2KBR	A B	A	5	V	2.3	3	18
2KBR	A B	A	10	R	1.0	3	18
2KBR	A B	A	34	H	1.1	20	37
2KBR	A B	A	65	L	2.2	56	66
2KBR	A B	B	104	Y	1.8	103	116
2KBR	A B	B	111	E	1.5	103	116
2KC8	A B	A	27	K	1.0	20	36
2KC8	A B	B	54	E	1.3	54	68
2KC8	A B	B	55	D	1.7	54	68
2KC8	A B	B	58	L	2.0	54	68
2KC8	A B	B	65	R	1.4	54	68
2KIN	A B	A	22	E	1.6	20	25
2KIN	A B	A	73	D	1.5	59	75

2KIN	A B	B	258	S	1.0	257	272
2KIN	A B	B	259	L	1.1	257	272
2KIN	A B	B	262	L	1.0	257	272
2KIN	A B	B	283	K	2.0	283	288
2KIN	A B	B	284	M	1.8	283	288
2KIN	A B	B	287	I	1.9	283	288
2KIN	A B	B	313	E	1.2	311	326
2KIN	A B	B	320	F	1.8	311	326
2KIN	A B	B	321	G	33.7	311	326
2KIN	A B	B	325	K	1.8	311	326
2KIN	A B	B	341	E	1.2	339	351
2NGR	A B	A	67	L	2.5	65	70
2NGR	A B	B	342	K	1.0	334	347
2NGR	A B	B	417	V	1.1	412	424
2NGR	A B	B	433	L	1.2	429	435
2NLA	A B	A	231	M	1.9	225	235
2NLA	A B	A	253	V	1.0	240	254
2NLA	A B	A	262	G	107.7	261	281
2NLA	A B	A	263	R	1.9	261	281
2NLA	A B	A	267	L	1.9	261	281
2NLA	A B	B	78	L	2.8	77	91
2NLA	A B	B	81	I	1.6	77	91
2NLA	A B	B	82	G	163.3	77	91
2NLA	A B	B	83	D	2.8	77	91
2NLA	A B	B	85	V	1.4	77	91
2NN6	B H	B	235	V	1.1	209	240
2NN6	E F	E	111	R	1.7	101	117
2NN6	E F	E	249	P	1.2	249	266
2NN6	E F	F	121	E	1.9	116	134
2NN6	E H	H	238	R	3.1	228	247
2NNA	A B	A	47	L	1.0	46	52
2NNA	A B	A	70	L	1.8	56	77
2NNA	A B	A	73	V	1.2	56	77
2NNA	A B	A	74	I	1.5	56	77
2NNA	A C	A	72	I	2.4	56	77
2NNA	B C	B	60	Y	1.3	52	63
2NNA	B C	B	61	W	2.6	52	63
2NNA	B C	B	78	V	1.8	65	88
2NNA	B C	B	81	H	1.3	65	88
2NNU	A B	A	37	R	2.4	26	49
2NNU	A B	A	44	Y	2.0	26	49
2NNU	A B	A	45	K	1.2	26	49
2NNU	A B	A	66	K	1.4	62	84
2NNU	A B	A	73	I	1.6	62	84
2NNU	A B	B	1345	I	2.2	1345	1355
2NNU	A B	B	1349	F	3.3	1345	1355
2NNU	A B	B	1352	D	2.3	1345	1355
2NNU	A B	B	1353	L	2.4	1345	1355
2NNW	A B	A	43	L	1.7	35	44
2NNW	A B	A	109	F	1.6	108	124
2NNW	A B	A	112	Y	1.8	108	124
2NNW	A B	A	116	G	32.0	108	124
2NNW	A B	A	120	T	1.6	108	124
2NNW	A B	B	109	R	1.5	108	118
2NNW	A B	B	112	R	1.0	108	118
2NNW	C D	C	43	L	1.0	35	44
2NNW	C D	C	109	F	3.5	108	124
2NNW	C D	C	112	Y	1.8	108	124
2NNW	C D	C	116	G	22.8	108	124
2NNW	C D	C	120	T	2.1	108	124

2NNW	C D	C	123	R	2.0	108	124
2NNW	C D	D	112	R	1.2	108	118
2NOJ	A B	A	1035	E	1.2	1034	1038
2NOJ	A B	A	1098	Q	1.9	1097	1107
2NOJ	A B	B	74	H	1.7	71	84
2NOJ	A B	B	75	R	1.3	71	84
2NOJ	A B	B	82	N	3.1	71	84
2NOJ	C D	C	1026	H	1.1	1018	1032
2NOJ	C D	C	1030	E	1.1	1018	1032
2NOJ	C D	C	1042	R	1.9	1041	1058
2NOJ	C D	D	74	H	2.5	71	84
2NOJ	C D	D	75	R	1.1	71	84
2NOJ	E F	E	1042	R	1.2	1041	1059
2NOJ	E F	F	74	H	1.7	71	84
2NOJ	E F	F	75	R	1.6	71	84
2NOJ	E F	F	103	L	1.2	90	105
2NOJ	G H	G	1030	E	1.0	1011	1032
2NOJ	G H	H	71	V	3.0	71	83
2NOJ	G H	H	74	H	1.3	71	83
2NOJ	G H	H	75	R	1.9	71	83
2NOJ	G H	H	82	N	1.7	71	83
2NOJ	G H	H	103	L	1.1	90	105
2NP0	A B	B	50	L	1.6	47	59
2NP0	A B	B	51	K	1.6	47	59
2NP0	A B	B	53	K	1.6	47	59
2NP0	A B	B	54	F	3.5	47	59
2NP0	A B	B	55	F	1.2	47	59
2NP0	A B	B	57	E	2.1	47	59
2NPI	A C	A	236	R	1.0	219	240
2NPI	A C	C	489	W	5.8	486	492
2NPI	B D	B	236	R	1.6	219	240
2NPI	B D	D	489	W	4.4	486	492
2NPP	A B	A	141	F	2.0	141	149
2NPP	A B	A	180	M	1.6	179	194
2NPP	A B	A	183	R	1.0	179	194
2NPP	A B	A	257	W	2.5	257	266
2NPP	A C	A	417	W	1.1	417	435
2NPP	A C	A	418	R	2.3	417	435
2NPP	A C	A	495	Y	2.7	495	511
2NPP	A C	A	538	F	2.4	534	547
2NPP	B C	B	288	S	2.0	288	304
2NPP	B C	C	131	D	2.6	129	136
2NPP	D E	D	141	F	1.9	141	150
2NPP	D E	D	257	W	1.8	257	266
2NPP	D E	E	199	Y	1.4	186	203
2NPP	D F	D	417	W	1.0	417	435
2NPP	D F	D	418	R	2.4	417	435
2NPP	D F	D	495	Y	2.9	495	511
2NPP	D F	D	538	F	1.2	534	547
2NPP	E F	F	131	D	1.2	129	136
2NPS	A B	A	61	V	1.2	60	111
2NPS	A B	A	82	L	1.2	60	111
2NPS	A B	A	107	R	1.0	60	111
2NPS	A B	B	188	I	1.6	184	246
2NPS	A B	B	191	L	1.7	184	246
2NPS	A B	B	198	V	1.2	184	246
2NPS	A B	B	219	I	2.0	184	246
2NPS	A B	B	222	N	1.9	184	246
2NPS	A B	B	239	R	1.0	184	246
2NPS	A B	B	243	Y	2.2	184	246

2NPS	A D	A	63	E	1.3	60	111
2NPS	A D	A	67	V	1.1	60	111
2NPS	A D	A	74	K	1.8	60	111
2NPS	A D	A	81	R	1.8	60	111
2NPS	A D	A	99	F	1.9	60	111
2NPS	A D	A	106	L	2.1	60	111
2NPS	A D	D	180	I	1.2	173	230
2NPS	A D	D	184	K	1.3	173	230
2NPS	A D	D	188	Q	1.0	173	230
2NPS	A D	D	191	G	3.2	173	230
2NPS	A D	D	194	L	1.0	173	230
2NPS	A D	D	195	E	1.8	173	230
2NPS	A D	D	201	L	1.2	173	230
2NPS	A D	D	218	V	1.0	173	230
2NPS	A D	D	219	M	1.6	173	230
2NPS	A D	D	222	L	2.6	173	230
2NPS	A D	D	225	V	1.0	173	230
2NPS	B C	B	188	I	1.1	184	246
2NPS	B C	B	195	I	1.2	184	246
2NPS	B C	B	202	F	1.3	184	246
2NPS	B C	B	209	I	1.6	184	246
2NPS	B C	B	216	I	1.2	184	246
2NPS	B C	B	220	E	1.1	184	246
2NPS	B C	B	223	V	1.4	184	246
2NPS	B C	B	237	L	1.0	184	246
2NPS	B C	C	138	I	3.5	131	187
2NPS	B C	C	145	I	1.1	131	187
2NPS	B C	C	146	G	105.2	131	187
2NPS	B C	C	149	M	1.6	131	187
2NPS	B C	C	153	L	1.0	131	187
2NPS	B C	C	180	I	2.1	131	187
2NPS	B C	C	184	M	1.4	131	187
2NPS	C D	C	136	Y	1.6	131	187
2NPS	C D	C	143	E	1.1	131	187
2NPS	C D	C	146	G	1.6	131	187
2NPS	C D	C	150	L	2.4	131	187
2NPS	C D	C	157	R	1.8	131	187
2NPS	C D	C	164	R	1.2	131	187
2NPS	C D	C	167	L	1.0	131	187
2NPS	C D	C	174	L	2.1	131	187
2NPS	C D	D	176	V	1.0	173	230
2NPS	C D	D	183	L	1.3	173	230
2NPS	C D	D	186	M	1.3	173	230
2NPS	C D	D	190	I	1.7	173	230
2NPS	C D	D	193	E	1.4	173	230
2NPS	C D	D	204	F	2.1	173	230
2NPS	C D	D	207	E	1.3	173	230
2NPS	C D	D	214	R	1.2	173	230
2NPS	C D	D	218	V	1.8	173	230
2NPT	A D	A	77	E	1.3	75	95
2NPT	C B	C	77	E	2.7	75	95
2NQB	A B	A	450	E	1.0	445	457
2NQB	A B	A	451	I	1.9	445	457
2NQB	A B	A	454	Y	1.1	445	457
2NQB	A B	A	467	F	1.0	464	479
2NQB	A B	A	470	L	2.1	464	479
2NQB	A B	A	474	I	2.4	464	479
2NQB	A B	A	478	F	3.1	464	479
2NQB	A B	A	499	Y	2.9	486	514
2NQB	A B	A	500	L	2.0	486	514

2NQB	A B	A	501	V	1.7	486	514
2NQB	A B	A	504	F	3.2	486	514
2NQB	A B	A	521	P	1.4	521	532
2NQB	A B	A	528	R	1.1	521	532
2NQB	A B	B	36	R	2.9	31	41
2NQB	A B	B	37	L	1.9	31	41
2NQB	A B	B	39	R	2.2	31	41
2NQB	A B	B	40	R	3.2	31	41
2NQB	A B	B	50	I	2.4	48	76
2NQB	A B	B	53	E	1.2	48	76
2NQB	A B	B	57	V	1.5	48	76
2NQB	A B	B	58	L	1.2	48	76
2NQB	A B	B	61	F	3.5	48	76
2NQB	A B	B	62	L	1.7	48	76
2NQB	A B	B	66	I	2.7	48	76
2NQB	A B	B	70	V	1.3	48	76
2NQB	A B	B	86	V	1.1	83	93
2NQB	A G	A	448	L	1.3	445	457
2NQB	A G	A	494	E	1.3	486	514
2NQB	A G	A	512	I	1.1	486	514
2NQB	B D	B	72	Y	3.3	48	76
2NQB	B D	B	75	H	3.3	48	76
2NQB	B D	B	88	Y	2.1	83	93
2NQB	B D	D	1280	Y	5.0	1253	1281
2NQB	B D	D	1290	E	1.9	1288	1299
2NQB	B D	D	1293	T	2.0	1288	1299
2NQB	B D	D	1296	R	1.6	1288	1299
2NQB	B D	D	1297	L	2.1	1288	1299
2NQB	C D	C	820	R	1.2	817	822
2NQB	C D	C	849	V	1.6	845	873
2NQB	C D	C	850	Y	4.4	845	873
2NQB	C D	C	851	L	1.3	845	873
2NQB	C D	C	854	V	1.7	845	873
2NQB	C D	C	857	Y	2.0	845	873
2NQB	C D	C	858	L	2.1	845	873
2NQB	C D	C	863	L	2.5	845	873
2NQB	C D	C	867	G	77.3	845	873
2NQB	C D	C	880	P	1.0	880	889
2NQB	C D	C	883	L	2.1	880	889
2NQB	C D	C	896	L	1.1	891	897
2NQB	C D	D	1237	Y	1.5	1235	1246
2NQB	C D	D	1241	V	1.4	1235	1246
2NQB	C D	D	1242	L	1.0	1235	1246
2NQB	C D	D	1258	I	1.6	1253	1281
2NQB	C D	D	1259	M	1.9	1253	1281
2NQB	C D	D	1262	F	3.4	1253	1281
2NQB	C D	D	1266	I	1.3	1253	1281
2NQB	C D	D	1267	F	3.2	1253	1281
2NQB	C D	D	1291	I	2.0	1288	1299
2NQB	C D	D	1303	L	2.4	1302	1321
2NQB	C D	D	1311	G	141.0	1302	1321
2NQB	C D	D	1315	V	1.1	1302	1321
2NQB	C D	D	1317	K	1.5	1302	1321
2NQB	C D	D	1318	Y	3.6	1302	1321
2NQB	E C	E	648	L	1.4	645	657
2NQB	E C	E	694	E	1.0	686	714
2NQB	E F	E	651	I	2.4	645	657
2NQB	E F	E	654	Y	1.8	645	657
2NQB	E F	E	667	F	1.0	664	679
2NQB	E F	E	670	L	2.6	664	679

2NQB	E F	E	673	E	2.2	664	679
2NQB	E F	E	674	I	2.1	664	679
2NQB	E F	E	678	F	1.8	664	679
2NQB	E F	E	692	L	1.8	686	714
2NQB	E F	E	697	E	1.1	686	714
2NQB	E F	E	699	Y	2.4	686	714
2NQB	E F	E	700	L	1.6	686	714
2NQB	E F	E	701	V	1.7	686	714
2NQB	E F	E	704	F	3.3	686	714
2NQB	E F	E	721	P	1.4	721	732
2NQB	E F	F	236	R	3.1	231	241
2NQB	E F	F	237	L	2.3	231	241
2NQB	E F	F	239	R	2.2	231	241
2NQB	E F	F	240	R	4.3	231	241
2NQB	E F	F	250	I	2.8	250	276
2NQB	E F	F	258	L	3.0	250	276
2NQB	E F	F	259	K	1.2	250	276
2NQB	E F	F	261	F	3.2	250	276
2NQB	E F	F	262	L	1.6	250	276
2NQB	E F	F	263	E	2.1	250	276
2NQB	E F	F	266	I	3.3	250	276
2NQB	E F	F	270	V	1.0	250	276
2NQB	E F	F	286	V	1.9	283	293
2NQB	F H	F	272	Y	1.4	250	276
2NQB	F H	F	275	H	2.5	250	276
2NQB	F H	F	288	Y	1.6	283	293
2NQB	F H	H	1480	Y	2.1	1453	1481
2NQB	F H	H	1497	L	1.3	1488	1499
2NQB	G H	G	1029	R	1.8	1027	1036
2NQB	G H	G	1049	V	1.7	1045	1073
2NQB	G H	G	1050	Y	4.8	1045	1073
2NQB	G H	G	1051	L	1.4	1045	1073
2NQB	G H	G	1054	V	1.8	1045	1073
2NQB	G H	G	1056	E	1.0	1045	1073
2NQB	G H	G	1057	Y	2.7	1045	1073
2NQB	G H	G	1058	L	2.0	1045	1073
2NQB	G H	G	1063	L	3.0	1045	1073
2NQB	G H	G	1067	G	75.3	1045	1073
2NQB	G H	G	1080	P	1.4	1080	1089
2NQB	G H	G	1083	L	1.7	1080	1089
2NQB	G H	G	1096	L	1.4	1091	1097
2NQB	G H	H	1437	Y	1.7	1435	1446
2NQB	G H	H	1441	V	1.5	1435	1446
2NQB	G H	H	1442	L	1.1	1435	1446
2NQB	G H	H	1458	I	1.6	1453	1481
2NQB	G H	H	1459	M	2.1	1453	1481
2NQB	G H	H	1462	F	4.0	1453	1481
2NQB	G H	H	1466	I	1.4	1453	1481
2NQB	G H	H	1467	F	3.5	1453	1481
2NQB	G H	H	1475	S	1.1	1453	1481
2NQB	G H	H	1491	I	2.1	1488	1499
2NQB	G H	H	1503	L	1.3	1502	1520
2NQB	G H	H	1510	E	1.5	1502	1520
2NQB	G H	H	1511	G	135.7	1502	1520
2NQB	G H	H	1512	T	1.0	1502	1520
2NQB	G H	H	1515	V	2.2	1502	1520
2NQB	G H	H	1517	K	1.1	1502	1520
2NQB	G H	H	1518	Y	3.3	1502	1520
2NQD	A B	B	144	L	1.9	141	145
2NS8	A H	A	113	L	1.5	107	123

2NS8	A H	A	138	G	119.3	127	157
2NS8	B H	B	148	D	1.1	127	157
2NS8	B H	B	155	K	1.4	127	157
2NS8	B H	B	170	L	1.0	168	181
2NS8	B H	B	174	I	1.6	168	181
2NS8	B H	B	177	F	1.8	168	181
2NS8	C F	C	113	L	1.3	107	124
2NS8	C F	C	138	G	115.7	127	157
2NS8	C F	C	139	H	1.5	127	157
2NS8	D F	D	148	D	1.4	127	156
2NS8	D F	D	155	K	1.1	127	156
2NS8	D F	D	174	I	1.2	168	181
2NS8	D F	D	177	F	1.7	168	181
2NTF	L H	L	124	E	1.3	122	126
2NTI	A B	A	145	V	1.0	140	154
2NTI	A B	A	152	L	1.5	140	154
2NTI	A C	A	81	K	1.0	73	83
2NTI	A C	C	138	G	1.7	136	150
2NTI	B C	C	80	V	2.4	71	81
2NTI	D E	D	145	V	1.2	140	154
2NTI	D E	D	152	L	1.3	140	154
2NTI	D F	D	78	I	1.3	73	83
2NTI	D F	F	138	G	1.0	136	149
2NTI	D F	F	145	E	1.2	136	149
2NTI	G H	G	152	L	1.4	140	154
2NTI	G I	G	81	K	1.5	73	83
2NTI	H I	H	142	D	1.7	137	149
2NTS	P A	A	4	I	1.4	4	14
2NTS	P A	A	8	N	2.5	4	14
2NTS	P A	A	12	F	1.4	4	14
2NTY	A C	A	45	T	1.8	36	52
2NTY	A C	A	46	N	2.6	36	52
2NTY	A C	A	65	R	1.4	63	82
2NTY	A C	A	250	H	1.4	249	267
2NTY	A C	A	335	R	1.4	325	354
2NTY	A C	C	106	H	1.3	90	108
2NTY	A D	D	26	Y	1.0	21	28
2NTY	A D	D	167	K	1.3	166	179
2NTY	B C	C	26	Y	1.2	19	29
2NTY	B C	C	167	K	1.8	166	178
2NTY	B D	B	45	T	1.5	36	55
2NTY	B D	B	342	Y	1.1	325	362
2NTY	B D	D	95	N	1.7	90	108
2NTY	B D	D	106	H	1.0	90	108
2NU9	A B	A	101	T	1.3	101	114
2NU9	A B	A	102	L	2.0	101	114
2NU9	A B	A	103	D	1.5	101	114
2NU9	A B	A	105	L	1.8	101	114
2NU9	A B	A	108	K	1.0	101	114
2NU9	A B	A	155	T	1.1	154	167
2NU9	A B	B	267	G	21.7	266	279
2NU9	A B	B	268	L	1.3	266	279
2NU9	A B	B	270	M	1.8	266	279
2NU9	A B	B	271	G	19.2	266	279
2NU9	A B	B	274	D	3.8	266	279
2NU9	A B	B	275	I	1.0	266	279
2NU9	A G	A	82	L	1.0	77	88
2NU9	A G	A	110	K	1.0	101	114
2NU9	A G	G	158	Y	2.6	157	167
2NU9	A G	G	165	F	1.9	157	167

2NU9	D E	D	101	T	1.2	101	114
2NU9	D E	D	102	L	1.9	101	114
2NU9	D E	D	103	D	1.9	101	114
2NU9	D E	D	105	L	2.0	101	114
2NU9	D E	D	155	T	1.0	154	167
2NU9	D E	D	156	L	1.1	154	167
2NU9	D E	E	267	G	57.1	266	279
2NU9	D E	E	268	L	1.4	266	279
2NU9	D E	E	270	M	1.3	266	279
2NU9	D E	E	271	G	16.8	266	279
2NU9	D E	E	274	D	4.2	266	279
2NU9	D I	D	79	D	1.5	77	88
2NU9	D I	I	158	Y	3.4	157	167
2NU9	D I	I	165	F	2.3	157	167
2NU9	F B	F	79	D	1.3	77	88
2NU9	F B	B	165	F	2.2	157	167
2NU9	F G	F	101	T	1.4	101	114
2NU9	F G	F	102	L	1.7	101	114
2NU9	F G	F	103	D	1.8	101	114
2NU9	F G	F	105	L	1.8	101	114
2NU9	F G	F	155	T	1.2	154	167
2NU9	F G	F	156	L	1.3	154	167
2NU9	F G	G	267	G	47.8	266	279
2NU9	F G	G	268	L	1.4	266	279
2NU9	F G	G	270	M	1.3	266	279
2NU9	F G	G	271	G	46.0	266	279
2NU9	F G	G	274	D	3.4	266	279
2NU9	H E	E	158	Y	3.0	157	167
2NU9	H E	E	165	F	1.8	157	167
2NU9	H I	H	101	T	1.4	101	114
2NU9	H I	H	102	L	1.9	101	114
2NU9	H I	H	103	D	1.8	101	114
2NU9	H I	H	105	L	1.9	101	114
2NU9	H I	I	134	E	1.0	133	140
2NU9	H I	I	267	G	69.4	266	279
2NU9	H I	I	268	L	2.1	266	279
2NU9	H I	I	270	M	2.0	266	279
2NU9	H I	I	271	G	29.1	266	279
2NU9	H I	I	274	D	3.6	266	279
2NUD	A C	A	187	L	1.0	184	199
2NUD	A C	A	188	R	1.5	184	199
2NUD	A C	A	204	K	2.3	200	210
2NUD	B D	B	204	K	2.3	200	210
2NUD	B D	B	207	L	1.6	200	210
2NUP	B C	C	116	D	6.6	116	125
2NUP	B C	C	120	Q	1.2	116	125
2NUP	B C	C	121	K	1.2	116	125
2NUP	B C	C	124	K	1.1	116	125
2NUU	A I	A	392	E	1.5	387	393
2NUU	B G	B	391	R	1.5	387	393
2NUU	B H	B	253	R	1.0	225	254
2NUU	B H	B	259	L	2.1	258	277
2NUU	B H	B	263	S	1.6	258	277
2NUU	C H	C	388	E	1.5	387	393
2NUU	C I	C	259	L	1.3	258	272
2NUU	C I	C	263	S	2.1	258	272
2NUU	D J	D	259	L	3.2	258	277
2NUU	D L	D	391	R	1.2	387	392
2NUU	E J	E	391	R	1.8	387	393
2NUU	E J	E	392	E	1.2	387	393

2NUU	E K	E	259	L	1.4	258	277
2NUU	F K	F	391	R	1.4	387	393
2NV2	A B	A	8	R	2.2	7	16
2NV2	A B	A	9	V	1.0	7	16
2NV2	A B	A	12	G	4.1	7	16
2NV2	A B	B	54	R	1.2	49	59
2NV2	A B	B	55	L	1.1	49	59
2NV2	C D	C	9	V	1.3	7	16
2NV2	C D	C	12	G	4.5	7	16
2NV2	C D	C	35	E	1.0	28	38
2NV2	C D	C	71	M	1.2	64	74
2NV2	C D	D	54	R	1.7	49	59
2NV2	C D	D	55	L	1.0	49	59
2NV2	E F	E	8	R	2.5	7	17
2NV2	E F	E	9	V	1.1	7	17
2NV2	E F	E	12	G	4.3	7	17
2NV2	E F	E	16	M	1.4	7	17
2NV2	E F	F	54	R	1.2	49	59
2NV2	E F	F	55	L	1.2	49	59
2NV2	G H	G	8	R	1.3	7	16
2NV2	G H	G	12	G	18.7	7	16
2NV2	G H	G	15	E	1.9	7	16
2NV2	G H	G	35	E	1.9	28	38
2NV2	G H	H	14	R	2.3	13	23
2NV2	G H	H	55	L	1.1	49	59
2NV2	I J	I	8	R	1.5	7	16
2NV2	I J	I	12	G	4.8	7	16
2NV2	I J	I	35	E	1.1	28	38
2NV2	I J	J	55	L	1.1	49	59
2NV2	K L	K	8	R	1.8	7	16
2NV2	K L	K	9	V	1.0	7	16
2NV2	K L	K	12	G	6.6	7	16
2NV2	K L	K	35	E	1.0	28	38
2NV2	K L	L	54	R	1.4	49	59
2NV2	K L	L	55	L	1.1	49	59
2NV2	M N	M	9	V	1.5	7	18
2NV2	M N	M	12	G	16.5	7	18
2NV2	M N	M	16	M	1.0	7	18
2NV2	M N	M	35	E	1.4	28	38
2NV2	M N	N	54	R	1.9	49	59
2NV2	M N	N	55	L	1.0	49	59
2NV2	O P	O	8	R	1.6	7	16
2NV2	O P	O	12	G	6.2	7	16
2NV2	O P	O	35	E	1.0	28	38
2NV2	O P	O	256	T	1.3	244	257
2NV2	O P	P	54	R	1.0	49	59
2NV2	O P	P	55	L	1.1	49	59
2NV2	Q R	Q	9	V	1.0	7	16
2NV2	Q R	Q	12	G	6.3	7	16
2NV2	Q R	Q	13	M	1.2	7	16
2NV2	Q R	R	54	R	1.6	49	59
2NV2	Q R	R	55	L	1.0	49	59
2NV2	S T	S	8	R	2.4	7	16
2NV2	S T	S	9	V	1.2	7	16
2NV2	S T	S	12	G	4.1	7	16
2NV2	S T	S	15	E	1.1	7	16
2NV2	S T	T	14	R	1.3	13	23
2NV2	S T	T	54	R	1.5	49	59
2NV2	S T	T	55	L	1.0	49	59
2NV2	U V	U	8	R	2.2	7	16

2NV2	U V	V	54	R	1.4	49	59
2NV2	U V	V	55	L	1.0	49	59
2NV2	W X	W	8	R	1.0	7	16
2NV2	W X	W	12	G	3.6	7	16
2NV2	W X	W	13	M	1.9	7	16
2NV2	W X	W	267	L	1.1	261	268
2NV2	W X	X	54	R	1.5	49	59
2NV2	W X	X	55	L	1.4	49	59
2NVU	A B	A	16	Q	1.2	14	20
2NVU	A B	A	18	R	1.4	14	20
2NVU	A B	A	19	L	3.1	14	20
2NVU	A B	A	67	G	125.4	67	72
2NVU	A B	A	71	G	72.0	67	72
2NVU	A B	A	340	I	1.4	336	359
2NVU	A B	A	480	H	1.3	476	486
2NVU	A B	A	492	T	1.6	491	511
2NVU	A B	A	496	F	1.4	491	511
2NVU	A B	A	499	G	40.2	491	511
2NVU	A B	A	507	K	2.0	491	511
2NVU	A B	B	2019	H	2.2	2018	2026
2NVU	A B	B	2062	E	1.3	2059	2069
2NVU	A B	B	2114	R	1.9	2103	2115
2NVU	A B	B	2227	H	1.7	2225	2234
2NVU	A B	B	2279	R	1.2	2278	2287
2NVU	A B	B	2283	G	1.7	2278	2287
2NVU	A B	B	2302	V	1.4	2293	2313
2NVU	A B	B	2306	E	2.0	2293	2313
2NVU	A J	A	263	E	1.7	263	271
2NVU	B C	B	2041	S	1.0	2040	2049
2NVU	B C	B	2044	F	1.9	2040	2049
2NVU	B C	B	2132	D	2.6	2132	2138
2NVU	B C	B	2153	W	1.5	2148	2162
2NVU	B C	B	2239	K	1.0	2235	2241
2NVU	B C	B	2400	I	2.0	2398	2403
2NVU	B C	C	147	K	1.0	147	156
2NVU	B I	B	2151	R	1.0	2148	2162
2NVU	C J	C	130	Y	2.0	125	138
2NVU	C J	C	134	Y	1.3	125	138
2NX5	F I	F	163	L	1.3	162	175
2NX5	K N	K	62	R	1.7	57	85
2NX5	K N	K	163	L	1.2	163	175
2NX5	K P	K	76	E	1.4	57	85
2NX5	Q T	Q	163	L	1.1	163	175
2NXX	A E	A	302	K	1.0	292	305
2NXX	A E	A	340	E	1.2	332	354
2NXX	A E	A	343	Y	2.9	332	354
2NXX	A E	A	361	F	1.7	358	366
2NXX	A E	A	372	R	2.7	367	377
2NXX	A E	A	376	L	1.4	367	377
2NXX	A E	E	441	H	1.1	433	449
2NXX	A E	E	445	T	1.1	433	449
2NXX	A E	E	478	E	1.3	474	495
2NXX	A E	E	501	G	64.5	500	531
2NXX	A E	E	502	T	1.0	500	531
2NXX	A E	E	504	F	1.0	500	531
2NXX	A E	E	506	K	1.0	500	531
2NXX	A E	E	508	L	1.0	500	531
2NXX	A E	E	511	L	1.0	500	531
2NXX	A E	E	513	E	1.2	500	531
2NXX	A E	E	515	R	1.6	500	531

2NXX	B F	B	343	Y	3.0	332	354
2NXX	B F	B	361	F	1.8	358	366
2NXX	B F	B	372	R	2.5	367	377
2NXX	B F	B	376	L	1.3	367	377
2NXX	B F	F	501	G	51.0	500	531
2NXX	B F	F	513	E	1.2	500	531
2NXX	B F	F	515	R	1.0	500	531
2NXX	C G	C	340	E	1.0	332	354
2NXX	C G	C	365	L	1.9	358	366
2NXX	C G	C	372	R	1.4	367	377
2NXX	C G	C	376	L	1.4	367	377
2NXX	D H	D	340	E	1.0	332	354
2NXX	D H	D	343	Y	2.8	332	354
2NXX	D H	D	361	F	1.8	358	366
2NXX	D H	D	372	R	1.3	367	377
2NXX	D H	D	376	L	1.5	367	377
2NXX	D H	H	501	G	58.5	500	531
2NXX	D H	H	508	L	1.0	500	531
2NXX	D H	H	515	R	1.3	500	531
2NY7	G H	G	369	P	1.9	369	373
2NY7	H L	L	124	Q	1.6	122	127
2NYL	A B	A	141	F	1.6	141	149
2NYL	A B	A	257	W	1.6	257	261
2NYL	A B	B	159	E	1.2	151	161
2NYL	A B	B	203	Y	1.5	187	204
2NYL	A C	A	418	R	1.2	417	426
2NYL	A C	A	535	N	1.3	534	547
2NYL	A C	A	538	F	1.7	534	547
2NYL	B C	B	288	S	1.2	288	292
2NYL	B C	C	131	D	2.9	129	137
2NYL	D E	D	141	F	2.1	141	150
2NYL	D E	D	257	W	2.6	257	261
2NYL	D E	E	199	Y	1.5	187	204
2NYL	D E	E	200	R	1.3	187	204
2NYL	D E	E	203	Y	2.7	187	204
2NYL	D F	D	538	F	1.2	534	547
2NYL	E F	E	288	S	2.3	288	292
2NYL	E F	F	125	Q	1.0	121	127
2NYL	E F	F	130	Y	2.1	129	137
2NYL	E F	F	131	D	3.0	129	137
2NZ0	A B	A	74	F	1.1	71	82
2NZ0	A B	A	77	I	1.7	71	82
2NZ0	A B	A	81	F	2.2	71	82
2NZ0	A B	A	111	F	2.1	108	121
2NZ0	A B	A	115	L	1.2	108	121
2NZ0	A B	A	118	L	2.0	108	121
2NZ0	A B	A	129	W	1.0	125	135
2NZ0	A B	A	151	V	1.0	144	158
2NZ0	A B	A	178	F	1.0	175	181
2NZ0	A B	B	8	W	5.6	8	15
2NZ0	A B	B	9	L	1.1	8	15
2NZ0	A B	B	11	F	4.3	8	15
2NZ0	A D	A	39	L	1.1	39	45
2NZ0	A D	A	50	K	1.3	50	64
2NZ0	A D	A	54	Q	2.1	50	64
2NZ0	A D	D	73	F	4.6	70	74
2NZ0	C D	C	77	I	1.5	71	82
2NZ0	C D	C	81	F	1.5	71	82
2NZ0	C D	C	94	L	1.0	88	98
2NZ0	C D	C	111	F	2.8	108	121

2NZ0	C D	C	115	L	1.4	108	121
2NZ0	C D	C	118	L	1.9	108	121
2NZ0	C D	C	129	W	1.1	125	135
2NZ0	C D	C	134	Y	2.2	125	135
2NZ0	C D	C	178	F	1.2	174	181
2NZ0	C D	D	8	W	4.4	7	15
2NZ0	C D	D	11	F	3.8	7	15
2NZ1	A D	A	266	Y	1.5	261	269
2NZ1	B E	B	266	Y	1.5	261	269
2NZ1	X Y	X	266	Y	1.4	261	269
2NZ8	A B	A	67	L	2.2	65	73
2NZ8	A B	A	70	L	1.4	65	73
2NZ8	A B	B	1236	F	2.2	1232	1265
2NZ8	A B	B	1240	E	2.9	1232	1265
2NZ8	A B	B	1364	I	1.5	1359	1383
2NZ8	A B	B	1367	V	1.0	1359	1383
2NZ8	A B	B	1375	L	1.1	1359	1383
2NZD	A B	A	50	E	1.3	45	57
2NZD	A B	A	51	I	1.7	45	57
2NZD	A B	A	54	Y	1.4	45	57
2NZD	A B	A	67	F	1.1	64	79
2NZD	A B	A	70	L	1.9	64	79
2NZD	A B	A	74	I	2.3	64	79
2NZD	A B	A	78	F	3.6	64	79
2NZD	A B	A	92	L	1.3	86	114
2NZD	A B	A	97	E	1.2	86	114
2NZD	A B	A	99	Y	2.3	86	114
2NZD	A B	A	100	L	1.9	86	114
2NZD	A B	A	101	V	1.6	86	114
2NZD	A B	A	103	L	1.5	86	114
2NZD	A B	A	104	F	3.1	86	114
2NZD	A B	A	121	P	1.5	121	131
2NZD	A B	A	128	R	1.0	121	131
2NZD	A B	B	28	G	3.5	25	29
2NZD	A B	B	36	R	2.7	31	41
2NZD	A B	B	37	L	2.4	31	41
2NZD	A B	B	39	R	2.5	31	41
2NZD	A B	B	40	R	3.5	31	41
2NZD	A B	B	50	I	1.2	50	76
2NZD	A B	B	53	E	1.0	50	76
2NZD	A B	B	57	V	1.0	50	76
2NZD	A B	B	58	L	1.4	50	76
2NZD	A B	B	61	F	2.5	50	76
2NZD	A B	B	62	L	1.9	50	76
2NZD	A B	B	66	I	2.8	50	76
2NZD	A B	B	67	R	1.8	50	76
2NZD	A B	B	70	V	1.4	50	76
2NZD	A B	B	86	V	1.2	83	93
2NZD	A G	A	94	E	1.3	86	114
2NZD	A G	A	112	I	1.0	86	114
2NZD	B D	B	72	Y	3.1	50	76
2NZD	B D	B	75	H	3.5	50	76
2NZD	B D	B	88	Y	1.2	83	93
2NZD	B D	B	92	R	2.1	83	93
2NZD	B D	D	73	E	1.4	53	81
2NZD	B D	D	80	Y	1.3	53	81
2NZD	B D	D	89	R	1.8	88	99
2NZD	B D	D	97	L	1.8	88	99
2NZD	C D	C	29	R	1.3	27	37
2NZD	C D	C	49	V	1.8	45	72

2NZD	C D	C	50	Y	3.1	45	72
2NZD	C D	C	51	L	1.7	45	72
2NZD	C D	C	54	V	1.1	45	72
2NZD	C D	C	55	L	2.0	45	72
2NZD	C D	C	57	Y	2.2	45	72
2NZD	C D	C	58	L	2.1	45	72
2NZD	C D	C	63	L	1.8	45	72
2NZD	C D	C	67	G	111.5	45	72
2NZD	C D	C	80	P	1.2	80	89
2NZD	C D	C	83	L	1.4	80	89
2NZD	C D	C	96	L	1.9	91	97
2NZD	C D	D	37	Y	1.3	35	46
2NZD	C D	D	41	V	1.3	35	46
2NZD	C D	D	59	M	1.1	53	81
2NZD	C D	D	67	F	3.0	53	81
2NZD	C D	D	75	S	1.0	53	81
2NZD	C D	D	91	I	2.1	88	99
2NZD	C D	D	103	L	2.5	102	120
2NZD	C D	D	106	H	1.4	102	120
2NZD	C D	D	111	G	209.2	102	120
2NZD	C D	D	115	V	1.3	102	120
2NZD	C D	D	118	Y	2.9	102	120
2NZD	E C	E	48	L	1.5	45	57
2NZD	E F	E	50	E	1.1	45	57
2NZD	E F	E	51	I	1.8	45	57
2NZD	E F	E	54	Y	1.4	45	57
2NZD	E F	E	67	F	1.3	64	79
2NZD	E F	E	70	L	2.2	64	79
2NZD	E F	E	73	E	2.1	64	79
2NZD	E F	E	74	I	2.0	64	79
2NZD	E F	E	78	F	3.0	64	79
2NZD	E F	E	99	Y	2.3	86	114
2NZD	E F	E	100	L	1.8	86	114
2NZD	E F	E	101	V	1.7	86	114
2NZD	E F	E	104	F	3.1	86	114
2NZD	E F	E	121	P	1.3	121	131
2NZD	E F	E	124	I	1.4	121	131
2NZD	E F	E	128	R	1.1	121	131
2NZD	E F	F	36	R	2.2	31	41
2NZD	E F	F	37	L	2.2	31	41
2NZD	E F	F	39	R	2.2	31	41
2NZD	E F	F	40	R	4.4	31	41
2NZD	E F	F	50	I	1.7	50	77
2NZD	E F	F	53	E	1.4	50	77
2NZD	E F	F	57	V	1.6	50	77
2NZD	E F	F	59	K	1.0	50	77
2NZD	E F	F	61	F	3.3	50	77
2NZD	E F	F	62	L	1.6	50	77
2NZD	E F	F	66	I	2.6	50	77
2NZD	E F	F	70	V	1.1	50	77
2NZD	E F	F	86	V	1.6	83	93
2NZD	F H	F	75	H	1.6	50	77
2NZD	F H	F	88	Y	1.7	83	93
2NZD	F H	H	97	L	1.7	88	99
2NZD	G H	G	29	R	1.1	27	36
2NZD	G H	G	32	R	1.0	27	36
2NZD	G H	G	49	V	1.8	45	73
2NZD	G H	G	50	Y	3.6	45	73
2NZD	G H	G	51	L	1.7	45	73
2NZD	G H	G	54	V	1.4	45	73

2NZD	G H	G	55	L	1.8	45	73
2NZD	G H	G	57	Y	2.3	45	73
2NZD	G H	G	58	L	1.6	45	73
2NZD	G H	G	63	L	2.5	45	73
2NZD	G H	G	67	G	77.8	45	73
2NZD	G H	G	80	P	1.2	80	89
2NZD	G H	G	83	L	1.3	80	89
2NZD	G H	G	96	L	1.4	91	97
2NZD	G H	H	37	Y	1.3	35	46
2NZD	G H	H	41	V	1.6	35	46
2NZD	G H	H	58	I	1.8	53	81
2NZD	G H	H	59	M	1.9	53	81
2NZD	G H	H	66	V	1.1	53	81
2NZD	G H	H	67	F	3.4	53	81
2NZD	G H	H	75	S	1.0	53	81
2NZD	G H	H	91	I	2.0	88	99
2NZD	G H	H	95	V	1.0	88	99
2NZD	G H	H	111	G	22.7	102	120
2NZD	G H	H	115	V	1.1	102	120
2NZD	G H	H	118	Y	1.5	102	120
2NZU	G L	G	85	I	1.0	73	89
2NZU	G L	L	47	I	1.5	47	54
2NZU	G L	L	48	M	1.4	47	54
2O01	A B	A	664	V	1.5	662	667
2O01	A B	A	666	Q	1.6	662	667
2O01	A B	A	690	L	1.4	689	695
2O01	A B	B	550	K	1.0	550	554
2O01	A B	B	581	F	1.8	581	590
2O01	A D	A	437	R	1.2	431	438
2O01	B C	B	12	I	6.0	10	15
2O01	H L	L	141	G	40.3	139	148
2O01	H L	L	145	F	1.6	139	148
2O02	A P	A	120	K	3.5	112	132
2O02	A P	A	173	N	2.0	165	182
2O02	A P	A	213	D	3.1	211	229
2O02	A P	A	217	I	1.5	211	229
2O25	A D	A	172	M	1.1	168	173
2O25	B C	C	4	I	1.0	4	19
2O26	A X	A	54	L	1.1	41	62
2O26	A X	A	84	D	1.0	72	90
2O26	B Y	B	54	L	1.7	41	62
2O26	B Y	B	57	T	2.1	41	62
2O26	B Y	B	73	Y	1.7	72	90
2O26	B Y	B	77	D	2.3	72	90
2O26	B Y	B	81	K	1.8	72	90
2O26	B Y	B	84	D	2.2	72	90
2O26	B Y	B	88	L	1.2	72	90
2O26	E U	E	54	L	1.5	41	62
2O26	E U	E	84	D	1.0	72	90
2O26	E U	E	88	L	1.4	72	90
2O26	F W	F	54	L	1.3	41	62
2O2V	A B	A	76	E	1.0	75	95
2O2V	A B	A	77	E	1.3	75	95
2O3B	A B	A	155	N	2.8	152	157
2O3B	A B	A	156	R	2.9	152	157
2O5X	L H	L	123	E	1.1	122	127
2O5X	L H	L	124	Q	1.9	122	127
2O60	A B	A	11	E	1.4	6	20
2O60	A B	A	19	F	1.0	6	20
2O60	A B	A	36	M	1.5	29	39

2O60	A B	A	51	M	1.5	45	55
2O60	A B	A	75	K	1.4	65	76
2O60	A B	A	92	F	4.8	85	93
2O60	A B	A	105	L	1.2	102	112
2O60	A B	A	124	M	1.5	118	129
2O60	A B	A	127	E	2.0	118	129
2O60	A B	A	141	F	1.3	138	146
2O60	A B	B	7	F	5.0	7	21
2O60	A B	B	8	K	1.4	7	21
2O60	A B	B	9	K	3.2	7	21
2O60	A B	B	10	L	4.5	7	21
2O60	A B	B	11	A	2.0	7	21
2O60	A B	B	12	E	1.0	7	21
2O60	A B	B	14	V	2.1	7	21
2O60	A B	B	15	K	1.0	7	21
2O60	A B	B	16	F	3.9	7	21
2O60	A B	B	19	K	1.0	7	21
2O60	A B	B	20	L	2.0	7	21
2O8A	A I	I	56	T	1.4	50	130
2O8A	A I	I	138	K	1.0	132	149
2O8A	A I	I	162	I	1.3	155	169
2O8A	B J	B	130	I	1.0	128	134
2O8A	B J	B	149	W	2.2	146	157
2O8A	B J	J	56	T	1.4	50	130
2O8A	B J	J	137	K	2.1	132	149
2O8A	B J	J	141	F	2.4	132	149
2O8A	B J	J	148	H	1.9	132	149
2O8A	B J	J	162	I	1.4	155	168
2O8F	A B	A	724	T	1.4	724	739
2O8F	A B	A	760	F	3.1	756	775
2O8F	A B	A	761	G	91.0	756	775
2O8F	A B	A	762	L	2.2	756	775
2O8F	A B	A	769	Y	1.1	756	775
2O8F	A B	A	827	G	78.7	827	834
2O8F	A B	A	830	V	1.2	827	834
2O8F	A B	A	840	V	1.0	838	847
2O8F	A B	B	471	D	1.2	463	476
2O8F	A B	B	1191	F	1.9	1189	1201
2O8F	A B	B	1194	L	1.4	1189	1201
2O8F	A B	B	1222	F	2.8	1221	1240
2O8F	A B	B	1227	I	1.4	1221	1240
2O8F	A B	B	1250	H	1.4	1250	1256
2O8F	A B	B	1299	G	29.2	1297	1306
2O8F	A B	B	1300	F	1.6	1297	1306
2O8F	A B	B	1312	V	1.8	1310	1325
2O8F	A B	B	1316	G	4.9	1310	1325
2O8F	A B	B	1319	K	1.9	1310	1325
2O8F	A B	B	1324	E	1.0	1310	1325
2O8V	A B	B	33	G	21.4	33	38
2O8V	A B	B	34	P	1.3	33	38
2O97	A B	A	13	K	2.5	3	14
2O97	A B	A	28	T	2.6	18	39
2O97	A B	A	29	L	2.0	18	39
2O97	A B	A	85	L	1.4	83	90
2O97	A B	A	89	V	1.8	83	90
2O97	A B	B	6	L	1.5	3	13
2O97	A B	B	29	I	1.5	18	38
2O97	A B	B	34	E	1.6	18	38
2O97	A B	B	85	L	1.0	83	89
2O98	A P	A	136	R	1.2	121	142

2O98	A P	A	189	E	1.2	174	192
2O98	A P	A	225	L	1.5	220	240
2O98	A P	A	229	L	2.0	220	240
2O98	A P	A	233	N	2.6	220	240
2O98	A Q	Q	943	K	1.3	932	944
2O98	B Q	B	67	R	1.1	45	78
2O98	B Q	B	75	K	2.3	45	78
2O98	B Q	B	129	K	1.3	123	142
2O98	B Q	B	181	L	1.4	174	192
2O98	B Q	B	182	N	1.1	174	192
2O98	B Q	B	229	L	2.1	217	239
2O98	B Q	B	233	N	2.1	217	239
2O98	B Q	B	237	W	1.0	217	239
2O9I	A C	A	255	I	1.9	240	261
2O9I	A C	A	259	K	1.7	240	261
2O9I	A C	A	273	I	2.9	269	278
2O9I	A C	A	424	L	1.0	423	429
2O9I	A C	A	427	E	2.3	423	429
2O9I	A C	C	633	L	2.1	631	638
2O9I	B D	B	1255	I	1.1	1240	1260
2O9I	B D	B	1269	I	1.3	1269	1277
2O9I	B D	D	1636	L	1.0	1631	1639
2O9I	B D	D	1637	L	2.4	1631	1639
2O9I	B D	D	1638	Q	1.1	1631	1639
2OBH	A C	A	112	L	1.2	86	114
2OBH	A C	A	113	F	2.9	86	114
2OBH	A C	A	126	L	1.2	123	133
2OBH	A C	A	129	V	1.1	123	133
2OBH	A C	A	145	M	1.2	139	150
2OBH	A C	C	848	W	7.7	848	862
2OBH	A C	C	851	L	1.7	848	862
2OBH	A C	C	854	G	2.2	848	862
2OBH	A C	C	855	L	3.1	848	862
2OBH	A C	C	856	L	1.9	848	862
2OBH	B D	B	112	L	1.4	86	114
2OBH	B D	B	113	F	2.8	86	114
2OBH	B D	B	126	L	1.3	123	133
2OBH	B D	B	129	V	1.3	123	133
2OBH	B D	B	145	M	1.8	139	150
2OBH	B D	B	166	M	1.1	159	167
2OBH	B D	D	848	W	7.5	848	862
2OBH	B D	D	851	L	2.4	848	862
2OBH	B D	D	855	L	3.2	848	862
2OBH	B D	D	856	L	2.0	848	862
2OCF	A D	A	372	L	1.9	372	380
2OCF	A D	A	539	L	2.2	538	546
2OCF	A D	A	543	M	1.2	538	546
2OCF	A D	D	78	L	2.3	78	84
2OCF	A D	D	82	L	2.1	78	84
2OCY	A C	A	97	L	2.7	93	114
2OCY	A C	A	100	E	1.6	93	114
2OCY	A C	A	103	D	1.4	93	114
2OCY	A C	A	104	L	1.9	93	114
2OCY	A C	A	108	L	1.1	93	114
2OCY	A C	C	49	F	2.5	49	53
2OCY	A C	C	85	I	1.7	83	91
2OCY	B C	B	109	F	6.2	105	114
2ODB	A B	A	23	Y	1.2	16	25
2ODB	A B	A	67	L	2.2	65	71
2ODB	A B	A	166	K	1.6	165	178

2ODB	A B	A	170	D	1.0	165	178
2ODB	A B	B	40	W	4.9	38	42
2ODE	A B	A	207	E	2.7	205	214
2ODE	A B	A	210	K	2.4	205	214
2ODE	A B	A	213	H	1.2	205	214
2ODE	A B	B	81	E	1.4	80	94
2ODE	A B	B	126	Q	1.3	125	137
2ODE	A B	B	153	L	1.3	144	164
2ODE	A B	B	156	K	1.1	144	164
2ODE	A B	B	157	D	2.1	144	164
2ODE	A D	D	109	F	1.7	98	114
2ODE	A D	D	135	L	1.0	125	137
2ODE	C B	B	109	F	1.1	98	114
2ODE	C B	B	110	E	1.4	98	114
2ODE	C B	B	132	R	1.0	125	137
2ODE	C D	C	207	E	1.8	205	214
2ODE	C D	C	210	K	3.0	205	214
2ODE	C D	C	213	H	1.2	205	214
2ODE	C D	D	81	E	2.3	80	94
2ODE	C D	D	153	L	1.2	144	164
2ODE	C D	D	157	D	2.4	144	164
2ODE	C D	D	161	R	1.1	144	164
2ODG	A C	C	37	K	1.1	31	47
2ODY	A B	A	1	F	1.9	1	1
2ODY	A B	A	14	E	1.2	14	14
2ODY	A B	A	14	E	1.6	14	14
2ODY	A B	A	14	L	1.6	14	14
2ODY	A B	A	14	F	1.6	14	14
2ODY	A B	A	14	Y	3.2	14	14
2ODY	A B	B	242	I	1.5	235	243
2ODY	B E	E	137	L	1.3	132	140
2ODY	C D	C	1	F	1.1	1	1
2ODY	C D	C	14	E	1.5	14	14
2ODY	C D	C	14	E	1.5	14	14
2ODY	C D	C	14	L	2.0	14	14
2ODY	C D	C	14	F	2.9	14	14
2ODY	C D	C	14	Y	4.1	14	14
2ODY	D F	F	132	E	1.3	132	139
2ODY	D F	F	133	E	2.4	132	139
2ODY	D F	F	134	E	1.0	132	139
2ODY	D F	F	138	V	1.4	132	139
2OF5	B H	B	117	D	1.3	117	126
2OF5	B H	B	165	I	1.0	156	171
2OF5	B H	H	814	Y	1.9	814	824
2OF5	C J	J	864	D	5.2	863	874
2OF5	C J	J	867	E	1.8	863	874
2OF5	D J	D	117	D	1.5	117	126
2OF5	D J	D	118	R	1.7	117	126
2OF5	D J	D	125	Q	1.0	117	126
2OF5	D J	D	165	I	1.3	156	171
2OF5	D J	J	809	H	1.5	803	810
2OF5	D J	J	814	Y	1.9	814	824
2OF5	D K	D	168	R	1.1	156	171
2OF5	D K	K	864	D	2.4	863	874
2OF5	D K	K	867	E	1.8	863	874
2OF5	E H	E	151	N	1.2	142	152
2OF5	E J	J	821	R	1.8	814	824
2OF5	E J	J	822	H	1.2	814	824
2OF5	E K	E	118	R	3.1	117	127
2OF5	E K	E	125	Q	2.4	117	127

2OF5	E K	E	165	I	1.6	156	171
2OF5	E K	E	168	R	2.2	156	171
2OF5	E K	K	814	Y	2.1	814	824
2OF5	E L	L	867	E	1.0	863	874
2OGX	A B	A	92	L	1.6	82	94
2OGX	A B	A	99	G	108.0	98	118
2OGX	A B	A	176	L	1.0	170	182
2OGX	A B	B	175	L	1.6	169	180
2OGX	A B	B	179	Q	1.2	169	180
2OGX	A B	B	233	L	1.3	228	236
2OI9	A B	A	155	Y	2.6	152	162
2OI9	A C	A	72	Q	1.2	57	85
2OI9	A C	A	75	R	1.0	57	85
2OI9	A C	A	77	N	1.2	57	85
2OJZ	L H	L	124	Q	1.2	122	127
2OJZ	L I	L	188	R	1.9	183	189
2OJZ	M H	M	188	R	2.2	183	189
2OJZ	M I	M	124	Q	1.3	122	127
2OM0	a b	a	2	I	1.5	2	6
2OM0	a b	a	16	L	1.0	13	19
2OM0	a b	b	7	C	1.1	2	20
2OM0	a b	b	11	L	1.0	2	20
2OM0	a b	b	15	L	1.6	2	20
2OM0	A B	A	2	I	1.1	2	6
2OM0	A B	A	16	L	1.3	13	19
2OM0	A B	B	11	L	1.4	3	20
2OM0	A B	B	15	L	1.6	3	20
2OM0	A B	B	18	V	1.4	3	20
2OM0	A H	A	13	L	1.3	13	19
2OM0	c d	c	2	I	1.2	2	6
2OM0	c d	c	17	E	1.6	13	19
2OM0	c d	d	15	L	1.9	3	20
2OM0	c d	d	18	V	1.5	3	20
2OM0	C D	C	2	I	1.6	2	6
2OM0	C D	C	16	L	2.0	13	19
2OM0	C D	D	11	L	1.8	2	20
2OM0	C D	D	15	L	2.3	2	20
2OM0	C D	D	18	V	1.2	2	20
2OM0	e f	e	2	I	1.2	2	6
2OM0	e f	f	11	L	1.7	3	20
2OM0	e f	f	15	L	1.2	3	20
2OM0	e f	f	18	V	1.6	3	20
2OM0	E F	E	2	I	1.6	2	6
2OM0	E F	F	11	L	1.3	2	20
2OM0	E F	F	15	L	1.6	2	20
2OM0	E F	F	18	V	1.5	2	20
2OM0	e h	e	13	L	1.5	13	19
2OM0	E J	J	2	V	1.0	2	20
2OM0	G B	G	13	L	1.0	13	19
2OM0	G D	D	2	V	1.0	2	20
2OM0	g f	g	13	L	1.6	13	19
2OM0	g h	g	2	I	2.0	2	6
2OM0	g h	g	16	L	1.0	13	19
2OM0	g h	h	11	L	2.0	3	20
2OM0	g h	h	15	L	1.5	3	20
2OM0	g h	h	18	V	1.4	3	20
2OM0	G H	G	2	I	1.6	2	6
2OM0	G H	H	11	L	1.9	3	20
2OM0	G H	H	15	L	1.7	3	20
2OM0	G H	H	18	V	1.6	3	20

2OM0	g j	j	2	V	1.2	2	20
2OM0	i b	i	13	L	1.4	13	19
2OM0	I D	I	13	L	1.5	13	19
2OM0	i j	i	2	I	2.1	2	6
2OM0	i j	i	16	L	1.0	13	19
2OM0	i j	j	11	L	2.3	2	20
2OM0	i j	j	15	L	1.8	2	20
2OM0	i j	j	18	V	1.5	2	20
2OM0	I J	I	2	I	1.3	2	6
2OM0	I J	J	11	L	2.1	2	20
2OM0	I J	J	15	L	1.4	2	20
2OM0	I J	J	18	V	1.4	2	20
2OM0	i l	l	2	V	1.3	2	20
2OM0	K F	K	13	L	1.3	13	19
2OM0	K L	K	2	I	1.6	2	6
2OM0	K L	L	11	L	2.1	3	20
2OM0	K L	L	15	L	1.6	3	20
2OM0	K L	L	18	V	1.5	3	20
2OM0	Q R	Q	2	I	1.9	2	6
2OM0	Q R	R	11	L	2.3	2	20
2OM0	Q R	R	15	L	2.0	2	20
2OM0	Q R	R	18	V	1.6	2	20
2OM0	Q T	T	5	H	1.1	3	20
2OM0	S T	S	2	I	1.5	2	6
2OM0	S T	S	16	L	1.1	13	19
2OM0	S T	T	11	L	1.0	3	20
2OM0	S T	T	15	L	1.5	3	20
2OM0	U R	R	2	V	1.0	2	20
2OM0	U V	U	2	I	1.8	2	6
2OM0	U V	U	17	E	1.2	13	19
2OM0	U V	V	11	L	2.0	3	20
2OM0	U V	V	15	L	1.5	3	20
2OM0	U V	V	18	V	1.6	3	20
2OM0	U Y	U	13	L	1.5	13	19
2OM0	X Y	X	2	I	1.6	2	6
2OM0	X Y	X	16	L	1.0	13	19
2OM0	X Y	Y	11	L	1.7	3	20
2OM0	X Y	Y	15	L	2.3	3	20
2OM0	X Y	Y	18	V	1.2	3	20
2OM7	E L	L	421	Q	1.8	419	423
2OM7	E L	L	422	E	1.6	419	423
2ONK	A C	C	158	L	1.7	156	165
2ONK	A C	C	160	H	22.9	156	165
2ONK	A C	C	176	V	1.1	169	181
2ONK	A C	C	180	L	1.0	169	181
2ONK	B D	D	158	L	2.1	156	165
2ONK	B D	D	160	H	16.6	156	165
2ONK	B D	D	180	L	1.4	169	181
2ONK	C E	C	221	Y	2.3	213	224
2ONK	D E	E	226	E	1.5	218	227
2ONK	F H	H	158	L	1.1	156	165
2ONK	F H	H	160	H	2.6	156	165
2ONK	F H	H	176	V	1.1	169	181
2ONK	F H	H	180	L	1.1	169	181
2ONK	G I	I	158	L	1.5	156	165
2ONK	G I	I	160	H	8.4	156	165
2ONK	G I	I	180	L	1.0	169	181
2ONK	H J	H	220	R	1.2	213	224
2ONL	A C	A	115	N	6.4	113	120
2ONL	A C	A	116	I	1.2	113	120

2ONL	A C	A	118	K	1.1	113	120
2ONL	A C	A	126	H	2.4	124	144
2ONL	A C	A	129	F	1.6	124	144
2ONL	A C	C	382	L	1.4	381	392
2ONL	A C	C	383	L	1.4	381	392
2ONL	B D	B	115	N	2.2	113	118
2ONL	B D	B	116	I	1.4	113	118
2ONL	B D	B	126	H	2.6	124	144
2ONL	B D	B	129	F	4.4	124	144
2ONL	B D	B	130	L	2.5	124	144
2ONL	B D	B	136	R	1.0	124	144
2ONL	B D	D	383	L	1.5	381	390
2ONL	B D	D	386	R	2.5	381	390
2OOB	A B	A	933	D	1.9	932	942
2OOB	A B	A	940	M	1.1	932	942
2OOB	A B	A	946	F	2.6	946	956
2OPL	A B	A	85	V	1.1	84	107
2OPL	A B	A	86	E	2.7	84	107
2OPL	A B	A	87	Y	4.1	84	107
2OPL	A B	A	88	L	1.3	84	107
2OPL	A B	A	90	V	2.5	84	107
2OPL	A B	A	93	S	1.3	84	107
2OPL	A B	A	94	G	119.1	84	107
2OPL	A B	A	101	V	1.3	84	107
2OPL	A B	A	103	H	1.0	84	107
2OPL	A B	A	124	L	1.5	124	128
2OPL	A B	A	125	R	1.4	124	128
2OPL	A B	A	127	F	2.2	124	128
2OPL	A B	A	160	I	1.0	153	161
2OPL	A B	A	168	P	1.1	168	175
2OPL	A B	A	169	V	1.5	168	175
2OPL	A B	A	170	Y	1.9	168	175
2OPL	A B	A	172	T	1.3	168	175
2OPL	A B	B	19	I	1.0	18	25
2OPL	A B	B	85	V	1.2	84	107
2OPL	A B	B	86	E	3.2	84	107
2OPL	A B	B	87	Y	4.4	84	107
2OPL	A B	B	88	L	2.1	84	107
2OPL	A B	B	90	V	2.6	84	107
2OPL	A B	B	93	S	1.2	84	107
2OPL	A B	B	94	G	105.0	84	107
2OPL	A B	B	101	V	1.0	84	107
2OPL	A B	B	103	H	1.1	84	107
2OPL	A B	B	125	R	1.3	124	128
2OPL	A B	B	127	F	2.5	124	128
2OPL	A B	B	160	I	1.7	153	161
2OPL	A B	B	168	P	1.1	168	175
2OPL	A B	B	169	V	1.2	168	175
2OPL	A B	B	170	Y	1.0	168	175
2OPL	A B	B	172	T	1.8	168	175
2OQ1	A B	A	19	R	1.4	19	29
2OQJ	A E	A	124	Q	1.2	122	127
2OQJ	D B	D	124	Q	1.0	122	128
2OS8	A B	A	807	G	3.1	789	824
2OS8	A B	A	808	L	1.7	789	824
2OS8	A B	A	811	I	2.0	789	824
2OS8	A B	A	815	I	1.9	789	824
2OS8	A B	A	818	W	2.0	789	824
2OS8	A B	A	830	Y	1.1	828	833
2OS8	A B	A	832	K	1.0	828	833

2OS8	A B	B	44	F	1.1	44	48
2OS8	A B	B	96	F	3.0	87	97
2OS8	A B	B	113	L	1.2	106	116
2OS8	A C	A	777	R	1.1	766	787
2OS8	A C	A	785	F	3.8	766	787
2OS8	A C	A	789	I	1.9	789	824
2OS8	A C	A	791	G	9.5	789	824
2OS8	A C	A	792	Y	3.7	789	824
2OS8	A C	A	793	L	2.0	789	824
2OS8	A C	A	798	Y	1.2	789	824
2OS8	A C	A	801	L	1.8	789	824
2OS8	A C	C	17	L	2.7	5	19
2OS8	A C	C	18	F	1.1	5	19
2OS8	A C	C	90	F	2.4	83	92
2OS8	A C	C	121	E	1.1	119	129
2OS8	A C	C	125	I	1.7	119	129
2OS8	A C	C	148	V	1.7	141	150
2OSL	L H	L	123	Q	1.2	121	125
2OT3	A B	A	303	K	1.8	284	307
2OT3	A B	A	313	D	2.4	312	327
2OT3	A B	A	316	L	1.6	312	327
2OT3	A B	A	354	Y	3.6	351	368
2OT3	A B	A	365	F	1.8	351	368
2OT3	A B	B	32	K	2.2	32	40
2OT3	A B	B	84	L	1.7	84	90
2OT3	A B	B	87	I	1.5	84	90
2OT3	A B	B	88	Y	1.1	84	90
2OT8	A C	A	460	W	1.4	452	465
2OT8	A C	A	543	D	1.0	535	551
2OT8	A C	A	685	Q	1.1	681	698
2OT8	A C	A	730	W	1.8	722	739
2OT8	B D	B	460	W	2.3	452	465
2OT8	B D	B	543	D	1.1	535	553
2OTJ	A Z	Z	29	I	1.5	20	34
2OTJ	A Z	Z	30	E	1.6	20	34
2OTJ	A Z	Z	76	G	2.7	74	82
2OTJ	A Z	Z	79	V	1.5	74	82
2OTJ	F M	F	37	T	1.0	33	43
2OTJ	F M	F	62	H	2.1	57	69
2OTJ	F M	F	66	L	1.2	57	69
2OTJ	F M	M	7	Y	2.6	4	12
2OTJ	F M	M	8	I	1.3	4	12
2OTJ	F M	M	23	L	1.4	19	33
2OTJ	K U	U	37	E	1.4	34	42
2OTJ	N Q	N	24	L	1.1	20	30
2OTJ	N Q	Q	26	P	1.1	26	30
2OTJ	S V	V	28	L	1.0	13	36
2OTK	C F	F	45	L	1.2	38	55
2OUL	A B	A	137	D	1.1	137	141
2OV2	A I	A	23	Y	1.3	16	25
2OV2	A I	A	67	L	2.1	65	73
2OV2	A I	A	70	L	2.4	65	73
2OV2	B J	B	23	Y	1.3	16	25
2OV2	B J	B	67	L	3.4	65	73
2OV2	B J	B	70	L	2.4	65	73
2OV2	B J	B	166	K	2.2	165	177
2OV2	B J	J	39	W	5.5	37	43
2OV2	C K	C	23	Y	1.3	16	25
2OV2	C K	C	67	L	1.9	65	73
2OV2	C K	C	70	L	2.0	65	73

2OV2	C K	C	166	K	1.7	165	178
2OV2	C K	C	170	D	1.1	165	178
2OV2	C K	K	39	W	5.3	37	42
2OV2	D L	D	23	Y	1.2	16	25
2OV2	D L	D	67	L	2.6	65	73
2OV2	D L	D	70	L	2.3	65	73
2OV2	D L	L	39	W	5.2	37	43
2OV2	E M	E	23	Y	1.8	16	25
2OV2	E M	E	67	L	2.4	65	73
2OV2	E M	E	70	L	2.3	65	73
2OV2	E M	M	39	W	5.4	37	41
2OV2	F N	F	23	Y	1.2	16	25
2OV2	F N	F	67	L	2.8	65	69
2OV2	F N	F	166	K	1.7	165	178
2OV2	F N	N	39	W	5.7	37	43
2OV2	G O	G	23	Y	1.4	16	25
2OV2	G O	G	67	L	3.3	65	73
2OV2	G O	G	70	L	2.6	65	73
2OV2	G O	G	166	K	1.7	165	178
2OV2	G O	G	170	D	1.3	165	178
2OV2	H N	H	147	R	1.0	139	149
2OV2	H P	H	23	Y	1.3	16	25
2OV2	H P	H	67	L	2.2	65	69
2OV2	H P	P	39	W	5.6	37	41
2OVQ	A B	A	1101	F	3.6	1097	1111
2OVQ	A B	A	1104	I	4.0	1097	1111
2OVQ	A B	A	1127	I	2.0	1113	1128
2OVQ	A B	A	1135	I	1.6	1132	1139
2OVQ	A B	A	1136	R	2.2	1132	1139
2OVQ	A B	A	1149	E	2.0	1147	1157
2OVQ	A B	B	2288	L	1.1	2286	2295
2OVQ	A B	B	2292	V	1.5	2286	2295
2OVQ	A B	B	2309	R	2.0	2309	2316
2OVQ	A B	B	2311	W	3.5	2309	2316
2OVQ	A B	B	2312	R	3.1	2309	2316
2OVQ	A B	B	2359	H	1.1	2350	2367
2OXQ	A C	C	245	V	1.1	235	246
2OXQ	B D	B	8	K	1.0	1	16
2OXQ	B D	D	245	V	1.0	235	246
2OZ4	L H	L	124	Q	1.0	122	128
2OZA	A B	A	348	R	1.0	346	364
2OZA	A B	A	351	D	1.0	346	364
2OZA	A B	A	358	S	1.3	346	364
2OZA	A B	A	386	R	3.8	381	389
2OZA	A B	B	126	H	2.6	124	144
2OZA	A B	B	129	F	1.9	124	144
2OZA	A B	B	132	Y	2.1	124	144
2OZA	A B	B	228	H	1.3	228	239
2OZB	A B	A	43	T	1.2	39	48
2OZB	A B	A	44	K	1.0	39	48
2OZB	A B	A	68	H	1.4	68	76
2OZB	A B	B	304	R	1.5	288	308
2OZB	D E	D	43	T	1.1	39	48
2OZB	D E	D	68	H	1.3	68	76
2OZB	D E	E	304	R	1.4	288	308
2OZN	A B	B	1588	I	3.1	1588	1597
2OZN	A B	B	1589	G	84.1	1588	1597
2OZN	A B	B	1591	L	1.4	1588	1597
2OZN	A B	B	1627	L	2.5	1616	1628
2P1L	A B	A	97	F	1.4	26	103

2P1L	A B	A	101	Y	3.6	26	103
2P1L	A B	A	138	G	88.6	137	157
2P1L	A B	A	139	R	1.8	137	157
2P1L	A B	B	112	L	1.6	106	126
2P1L	A B	B	116	L	2.2	106	126
2P1L	A B	B	117	K	1.3	106	126
2P1L	A B	B	120	G	28.1	106	126
2P1L	A B	B	121	D	2.0	106	126
2P1L	A B	B	123	F	3.1	106	126
2P1L	C D	C	97	F	2.2	26	105
2P1L	C D	C	101	Y	1.2	26	105
2P1L	C D	C	126	V	1.4	119	131
2P1L	C D	C	129	E	1.2	119	131
2P1L	C D	C	130	L	1.3	119	131
2P1L	C D	C	138	G	171.9	137	157
2P1L	C D	C	139	R	2.2	137	157
2P1L	C D	D	112	L	1.5	106	126
2P1L	C D	D	116	L	2.0	106	126
2P1L	C D	D	117	K	1.1	106	126
2P1L	C D	D	119	T	1.3	106	126
2P1L	C D	D	120	G	5.5	106	126
2P1L	C D	D	121	D	1.7	106	126
2P1L	C D	D	123	F	3.4	106	126
2P1L	E F	E	97	F	2.2	26	100
2P1L	E F	E	101	Y	1.4	101	105
2P1L	E F	E	126	V	1.6	119	131
2P1L	E F	E	130	L	1.0	119	131
2P1L	E F	E	138	G	111.8	137	157
2P1L	E F	E	139	R	2.0	137	157
2P1L	E F	F	112	L	1.7	106	126
2P1L	E F	F	115	R	1.4	106	126
2P1L	E F	F	116	L	2.2	106	126
2P1L	E F	F	120	G	3.6	106	126
2P1L	E F	F	121	D	1.8	106	126
2P1L	E F	F	123	F	3.7	106	126
2P1L	G H	G	97	F	2.1	26	105
2P1L	G H	G	101	Y	1.4	26	105
2P1L	G H	G	126	V	1.2	116	131
2P1L	G H	G	129	E	1.0	116	131
2P1L	G H	G	130	L	1.4	116	131
2P1L	G H	G	138	G	143.5	137	157
2P1L	G H	G	139	R	2.9	137	157
2P1L	G H	H	112	L	3.8	106	126
2P1L	G H	H	116	L	2.1	106	126
2P1L	G H	H	117	K	1.6	106	126
2P1L	G H	H	120	G	7.4	106	126
2P1L	G H	H	121	D	2.4	106	126
2P1L	G H	H	123	F	3.8	106	126
2P1N	A B	A	118	C	2.1	111	126
2P1N	A B	A	119	Q	2.1	111	126
2P1N	A B	A	121	V	1.8	111	126
2P1N	A B	A	122	A	1.5	111	126
2P1N	A B	A	125	I	1.3	111	126
2P1N	A B	A	133	I	1.3	130	134
2P1N	A B	A	151	V	1.5	146	153
2P1N	A B	A	157	W	4.1	154	159
2P1N	A B	B	17	V	2.9	13	19
2P1N	A B	B	25	K	1.7	24	32
2P1N	A B	B	26	D	1.9	24	32
2P1N	A B	B	29	S	2.5	24	32

2P1N	A B	B	30	V	1.0	24	32
2P1N	A B	B	31	S	1.0	24	32
2P1N	A B	B	37	W	1.5	35	42
2P1N	D E	D	103	L	1.0	95	108
2P1N	D E	D	119	Q	1.0	111	126
2P1N	D E	D	125	I	1.6	111	126
2P1N	D E	D	133	I	1.0	130	134
2P1N	D E	D	151	V	3.0	146	159
2P1N	D E	D	157	W	1.1	146	159
2P1N	D E	E	17	V	1.9	12	18
2P1N	D E	E	35	K	1.1	35	41
2P1N	D E	E	37	W	1.5	35	41
2P22	A B	A	324	G	233.7	323	352
2P22	A B	A	350	H	1.0	323	352
2P22	A B	A	356	L	1.2	356	383
2P22	A B	A	360	V	1.1	356	383
2P22	A B	A	368	R	1.1	356	383
2P22	A B	A	371	F	2.8	356	383
2P22	A B	A	376	H	3.0	356	383
2P22	A B	A	380	I	1.0	356	383
2P22	A B	B	37	I	1.4	31	58
2P22	A B	B	44	Y	2.0	31	58
2P22	A C	A	221	H	1.4	219	253
2P22	A C	A	225	L	1.1	219	253
2P22	A C	A	228	L	1.8	219	253
2P22	A C	A	232	V	1.7	219	253
2P22	A C	A	235	L	1.5	219	253
2P22	A C	A	236	Y	2.7	219	253
2P22	A C	A	272	L	2.0	254	287
2P22	A C	A	283	M	1.4	254	287
2P22	A C	A	286	L	1.8	254	287
2P22	A C	A	290	I	1.2	288	292
2P22	A C	A	314	V	1.8	314	318
2P22	A C	A	329	Y	9.2	323	352
2P22	A C	A	340	D	1.4	323	352
2P22	A C	A	345	L	1.0	323	352
2P22	A C	A	347	R	1.2	323	352
2P22	A C	C	64	I	1.5	62	71
2P22	A C	C	68	I	1.0	62	71
2P22	A C	C	75	L	1.4	72	82
2P22	A C	C	79	V	2.1	72	82
2P22	A C	C	88	F	1.8	86	123
2P22	A C	C	91	K	2.2	86	123
2P22	A C	C	95	F	2.0	86	123
2P22	A C	C	99	F	2.0	86	123
2P22	A C	C	116	V	1.0	86	123
2P22	A C	C	140	E	1.1	124	141
2P22	A C	C	150	L	2.6	147	171
2P22	A C	C	153	K	2.4	147	171
2P22	A C	C	154	L	1.0	147	171
2P22	A C	C	169	E	2.0	147	171
2P22	A C	C	185	I	1.7	178	206
2P22	A C	C	192	R	1.5	178	206
2P22	A C	C	196	H	2.8	178	206
2P22	A C	C	204	T	1.1	178	206
2P22	A D	A	271	H	1.2	254	287
2P22	A D	A	279	I	1.5	254	287
2P22	A D	A	286	L	1.1	254	287
2P22	A D	A	325	L	1.1	323	352
2P22	A D	A	329	Y	1.5	323	352

2P22	A D	D	9	L	2.4	4	12
2P22	C D	C	81	K	2.6	72	82
2P22	C D	C	92	I	1.7	86	123
2P22	C D	C	99	F	2.5	86	123
2P22	C D	C	106	F	1.9	86	123
2P22	C D	C	113	K	1.6	86	123
2P22	C D	C	120	L	2.2	86	123
2P22	C D	C	137	Y	1.4	124	141
2P22	C D	D	10	R	1.5	4	12
2P22	C D	D	40	L	2.4	40	66
2P22	C D	D	44	R	1.3	40	66
2P22	C D	D	47	L	1.6	40	66
2P22	C D	D	57	I	1.0	40	66
2P22	C D	D	64	H	1.5	40	66
2P22	C D	D	65	D	1.4	40	66
2P22	C D	D	71	F	1.8	67	79
2P22	C D	D	75	Y	3.0	67	79
2P24	A B	A	48	F	3.2	46	50
2P24	A B	A	62	N	1.2	56	77
2P24	A B	A	65	T	1.2	56	77
2P24	A B	A	68	H	1.5	56	77
2P24	A B	A	69	N	2.2	56	77
2P24	A B	A	70	L	1.6	56	77
2P24	A B	A	73	L	1.8	56	77
2P24	A B	A	76	R	2.5	56	77
2P24	A B	B	157	D	1.6	157	167
2P24	A B	B	186	E	2.0	168	188
2P24	A B	B	189	T	1.7	189	193
2P28	A B	A	36	D	1.2	36	40
2P2C	A B	A	18	F	2.2	16	21
2P2C	A B	A	19	Y	1.6	16	21
2P2C	A B	A	60	D	1.1	57	71
2P2C	A B	B	239	Y	2.4	238	250
2P2C	A B	B	243	L	1.6	238	250
2P2C	A B	B	256	V	2.2	256	270
2P2C	B P	P	56	K	5.0	50	58
2P2C	B P	P	122	Y	1.3	116	123
2P2C	C D	D	256	V	3.2	256	270
2P2C	D Q	D	238	W	4.2	238	250
2P2C	D Q	D	242	A	12.1	238	250
2P2C	D Q	D	266	L	2.1	256	270
2P2C	D Q	Q	89	D	2.8	83	90
2P2C	D Q	Q	122	Y	1.3	116	123
2P2C	E F	E	60	D	1.0	57	71
2P2C	E F	F	247	F	1.2	238	250
2P2C	E F	F	256	V	2.6	256	270
2P2C	F R	F	245	Q	1.9	238	250
2P2C	F R	F	266	L	3.1	256	270
2P2C	F R	R	122	Y	1.1	116	123
2P2C	G H	G	18	F	2.5	16	20
2P2C	G H	G	19	Y	2.1	16	20
2P2C	G H	H	239	Y	1.9	238	250
2P2C	G H	H	247	F	1.1	238	250
2P2C	G H	H	256	V	2.9	256	270
2P2C	H S	H	245	Q	3.9	238	250
2P2C	H S	H	266	L	3.2	256	270
2P2C	H S	S	122	Y	1.6	116	123
2P2C	I J	I	60	D	1.2	57	71
2P2C	I J	I	67	L	1.6	57	71
2P2C	I J	J	239	Y	1.0	238	250

2P2C	I J	J	256	V	2.0	256	270
2P2C	K L	K	63	T	1.0	57	71
2P2C	K L	L	240	I	4.0	238	250
2P2C	K L	L	243	L	1.7	238	250
2P2C	L U	L	266	L	5.5	256	270
2P2C	L U	U	56	K	1.1	50	58
2P2C	L U	U	89	D	1.1	83	90
2P2C	L U	U	122	Y	1.1	116	123
2P3F	H L	H	127	W	3.1	125	131
2P4N	A B	A	210	Y	1.9	209	216
2P4N	A B	A	211	D	1.7	209	216
2P4N	A B	A	406	H	1.8	405	410
2P4N	A B	A	407	W	2.1	405	410
2P4N	K A	A	415	E	1.2	415	420
2P4N	K B	B	420	E	1.4	415	437
2P4N	K B	B	430	S	3.5	415	437
2P4N	K B	B	431	E	19.1	415	437
2P58	A C	A	17	I	1.1	11	18
2P58	A C	A	57	I	4.3	38	63
2P58	A C	A	58	I	1.0	38	63
2P58	A C	A	60	Y	1.2	38	63
2P58	A C	C	5	L	1.0	5	18
2P58	A C	C	8	L	1.6	5	18
2P58	A C	C	9	L	1.4	5	18
2P58	A C	C	12	I	2.6	5	18
2P58	A C	C	16	G	16.3	5	18
2P58	A C	C	28	I	1.7	22	35
2P58	A C	C	31	W	2.8	22	35
2P58	B C	B	54	L	2.7	52	59
2P58	B C	B	71	I	1.2	69	74
2P58	B C	B	82	I	1.6	81	86
2P58	B C	B	83	L	1.1	81	86
2P58	B C	C	7	V	1.1	5	18
2P58	B C	C	8	L	1.0	5	18
2P58	B C	C	15	I	2.0	5	18
2P58	B C	C	76	L	2.0	71	82
2P58	B C	C	79	Y	1.3	71	82
2P58	B C	C	80	R	2.2	71	82
2P58	B C	C	101	R	1.7	100	108
2P5T	A B	A	70	V	1.2	69	99
2P5T	A B	A	72	D	1.3	69	99
2P5T	A B	A	73	Y	2.0	69	99
2P5T	A B	A	75	L	1.0	69	99
2P5T	A B	A	77	L	1.5	69	99
2P5T	A B	A	79	I	1.0	69	99
2P5T	A B	A	80	E	1.0	69	99
2P5T	A B	A	84	E	2.1	69	99
2P5T	A B	A	95	R	1.6	69	99
2P5T	A B	A	97	Q	1.5	69	99
2P5T	A B	A	98	D	2.6	69	99
2P5T	A B	A	112	I	2.1	110	123
2P5T	A B	A	116	D	1.0	110	123
2P5T	A B	B	18	N	1.6	8	24
2P5T	A B	B	20	R	3.1	8	24
2P5T	A B	B	46	T	1.4	45	56
2P5T	A B	B	50	R	1.5	45	56
2P5T	A B	B	157	R	2.5	147	159
2P5T	A B	B	239	M	1.4	234	252
2P5T	C D	C	76	T	1.1	69	100
2P5T	C D	C	123	H	3.5	110	127

2P5T	C D	D	21	S	1.0	8	24
2P5T	C D	D	22	L	1.0	8	24
2P5T	C D	D	49	H	1.3	45	56
2P5T	C D	D	50	R	2.4	45	56
2P5T	E F	E	70	V	1.3	69	100
2P5T	E F	E	72	D	2.3	69	100
2P5T	E F	E	73	Y	1.9	69	100
2P5T	E F	E	84	E	1.2	69	100
2P5T	E F	E	87	A	1.0	69	100
2P5T	E F	E	88	N	1.8	69	100
2P5T	E F	E	123	H	2.1	110	128
2P5T	E F	E	127	Y	2.1	110	128
2P5T	E F	F	46	T	1.5	45	56
2P5T	E F	F	49	H	1.3	45	56
2P5T	E F	F	50	R	3.5	45	56
2P5T	E F	F	235	V	1.0	234	246
2P5T	E F	F	239	M	1.6	234	246
2P5T	G H	G	95	R	1.4	69	100
2P5T	G H	G	116	D	1.2	110	128
2P5T	G H	H	20	R	2.2	8	24
2P6A	A C	C	47	F	2.0	45	53
2P6A	A C	C	51	I	1.0	45	53
2P6A	A C	C	52	F	1.4	45	53
2P6A	A D	A	58	F	1.3	57	65
2P6A	A D	D	192	R	1.0	188	199
2P6A	A D	D	195	T	1.1	188	199
2P6A	B C	B	48	I	1.0	48	53
2P6A	B C	C	47	F	1.0	45	53
2P7V	A B	A	58	C	1.5	52	78
2P7V	A B	A	62	V	1.5	52	78
2P7V	A B	A	63	D	1.0	52	78
2P7V	A B	A	70	F	1.9	52	78
2P7V	A B	A	97	E	1.0	83	114
2P7V	A B	B	595	L	2.2	584	598
2P7V	A B	B	596	R	1.1	584	598
2P80	C D	D	109	K	15.7	109	121
2P9V	A B	A	246	K	1.0	246	256
2P9V	A B	B	253	Q	1.2	246	256
2PA8	D L	D	23	E	3.1	22	35
2PA8	D L	D	24	F	2.7	22	35
2PA8	D L	D	243	L	1.3	238	264
2PA8	D L	D	246	G	72.7	238	264
2PA8	D L	D	250	I	1.5	238	264
2PA8	D L	D	252	K	1.3	238	264
2PA8	D L	D	253	I	1.8	238	264
2PA8	D L	D	256	L	1.4	238	264
2PA8	D L	D	259	K	1.1	238	264
2PA8	D L	D	260	L	1.5	238	264
2PA8	D L	L	27	L	1.9	23	34
2PA8	D L	L	30	G	10.8	23	34
2PA8	D L	L	66	K	1.0	65	91
2PA8	D L	L	70	L	1.0	65	91
2PA8	D L	L	73	I	1.6	65	91
2PA8	D L	L	79	M	1.2	65	91
2PA8	D L	L	83	Y	2.4	65	91
2PA8	D L	L	87	I	1.1	65	91
2PA8	D L	L	90	L	1.4	65	91
2PBD	A P	A	288	D	1.4	287	295
2PBD	A P	A	371	H	2.1	367	374
2PBD	A P	A	372	R	2.1	367	374

2PBD	A P	P	120	G	5.0	120	137
2PBD	A P	P	121	G	68.4	120	137
2PBD	A P	P	125	K	1.7	120	137
2PBD	A P	P	128	Y	2.4	120	137
2PBD	A V	A	345	I	1.5	338	349
2PBD	A V	V	225	L	1.2	225	231
2PBD	A V	V	229	I	2.3	225	231
2PBD	P V	P	3	W	3.6	3	11
2PBD	P V	P	6	Y	3.2	3	11
2PBD	P V	P	133	H	2.1	120	137
2PBI	A B	A	19	K	1.5	15	28
2PBI	A B	A	62	R	1.1	52	63
2PBI	A B	A	69	E	2.8	67	80
2PBI	A B	A	73	L	1.0	67	80
2PBI	A B	A	76	F	3.3	67	80
2PBI	A B	A	226	I	1.8	219	235
2PBI	A B	A	228	Y	3.2	219	235
2PBI	A B	A	229	Y	2.7	219	235
2PBI	A B	A	233	L	3.0	219	235
2PBI	A B	A	244	L	2.5	240	254
2PBI	A B	A	247	I	1.4	240	254
2PBI	A B	A	248	V	1.6	240	254
2PBI	A B	A	250	Y	2.7	240	254
2PBI	A B	A	270	W	5.0	269	273
2PBI	A B	A	278	W	3.2	276	281
2PBI	A B	A	305	R	1.3	300	306
2PBI	A B	A	393	Y	1.8	386	406
2PBI	A B	A	397	K	1.3	386	406
2PBI	A B	B	12	L	1.7	10	33
2PBI	A B	B	16	K	1.1	10	33
2PBI	A B	B	22	L	1.5	10	33
2PBI	A B	B	26	L	2.1	10	33
2PBI	A B	B	41	V	1.2	38	42
2PBI	C D	C	16	F	1.0	15	28
2PBI	C D	C	19	K	1.4	15	28
2PBI	C D	C	62	R	1.0	52	64
2PBI	C D	C	63	L	1.0	52	64
2PBI	C D	C	69	E	1.1	67	80
2PBI	C D	C	76	F	2.7	67	80
2PBI	C D	C	226	I	1.6	219	234
2PBI	C D	C	228	Y	3.3	219	234
2PBI	C D	C	229	Y	2.8	219	234
2PBI	C D	C	233	L	2.5	219	234
2PBI	C D	C	244	L	1.6	240	254
2PBI	C D	C	247	I	1.2	240	254
2PBI	C D	C	248	V	1.4	240	254
2PBI	C D	C	250	Y	3.3	240	254
2PBI	C D	C	251	S	1.3	240	254
2PBI	C D	C	270	W	5.0	269	273
2PBI	C D	C	278	W	3.6	276	281
2PBI	C D	D	12	L	1.4	12	33
2PBI	C D	D	22	L	1.0	12	33
2PBI	C D	D	26	L	1.7	12	33
2PBI	C D	D	41	V	1.1	38	42
2PCF	A B	B	3	I	1.0	2	8
2PCP	A B	A	127	S	1.1	122	128
2PCP	C D	C	124	Q	1.1	122	127
2PE6	A B	A	17	R	2.0	3	19
2PF4	A E	A	141	F	1.8	141	149
2PF4	A E	A	179	P	1.2	179	187

2PF4	A E	A	258	R	1.1	257	266
2PF4	A E	E	7	R	1.1	7	16
2PF4	A E	E	147	W	1.9	141	148
2PF4	A F	A	339	Q	10.0	339	347
2PF4	B F	B	141	F	2.0	141	149
2PF4	B F	B	179	P	3.4	179	188
2PF4	B F	B	180	M	2.3	179	188
2PF4	B F	B	218	D	2.5	218	223
2PF4	B F	B	258	R	3.4	257	266
2PF4	B F	F	7	R	1.8	7	18
2PF4	B F	F	147	W	4.3	141	148
2PF4	B H	B	417	W	1.0	417	426
2PF4	B H	B	460	E	1.4	456	474
2PF4	C E	C	496	L	2.3	495	513
2PF4	C G	C	179	P	1.2	179	188
2PF4	D F	D	417	W	1.7	417	430
2PF4	D H	H	147	W	1.3	141	148
2PG1	A L	A	36	K	1.7	35	50
2PG1	C J	C	36	K	1.4	35	50
2PG1	D K	D	35	E	1.5	35	50
2PG1	D K	D	36	K	3.1	35	50
2PG1	D K	D	37	D	1.1	35	50
2PHE	A C	C	475	F	3.0	475	480
2PHE	A C	C	476	E	1.1	475	480
2PHE	A C	C	479	F	3.5	475	480
2PHG	A B	A	191	I	2.1	188	200
2PHG	A B	A	192	G	260.5	188	200
2PHG	A B	A	195	F	2.6	188	200
2PHG	A B	A	196	K	1.5	188	200
2PHG	A B	B	480	T	1.7	477	485
2PHG	A B	B	481	D	1.7	477	485
2PHG	A B	B	483	L	1.5	477	485
2PI2	A E	A	153	N	2.1	153	173
2PI2	A E	A	155	F	1.6	153	173
2PI2	A E	A	159	I	1.8	153	173
2PI2	A E	A	160	L	1.1	153	173
2PI2	A E	A	163	I	2.7	153	173
2PI2	A E	A	167	M	1.3	153	173
2PI2	A E	E	99	Y	1.3	96	109
2PI2	B F	B	52	S	1.0	51	56
2PI2	B F	B	55	L	1.0	51	56
2PI2	B F	B	152	M	1.4	152	174
2PI2	B F	B	153	N	2.4	152	174
2PI2	B F	B	155	F	1.1	152	174
2PI2	B F	B	159	I	2.0	152	174
2PI2	B F	B	160	L	1.4	152	174
2PI2	B F	B	163	I	2.6	152	174
2PI2	B F	B	167	M	1.1	152	174
2PI2	B F	F	99	Y	1.3	96	109
2PI2	C G	C	152	M	1.3	152	173
2PI2	C G	C	153	N	2.1	152	173
2PI2	C G	C	156	T	1.0	152	173
2PI2	C G	C	159	I	1.7	152	173
2PI2	C G	C	160	L	1.3	152	173
2PI2	C G	C	163	I	2.8	152	173
2PI2	C G	C	167	M	1.1	152	173
2PI2	C G	G	99	Y	1.3	96	109
2PI2	D H	D	52	S	1.1	51	57
2PI2	D H	D	159	I	1.9	152	173
2PI2	D H	D	160	L	1.2	152	173

2PI2	D H	D	163	I	3.0	152	173
2PI2	D H	D	167	M	1.1	152	173
2PI2	D H	H	99	Y	1.1	96	109
2PJR	A B	A	292	I	2.8	290	301
2PJR	A B	A	294	Q	2.4	290	301
2PJR	A B	A	299	V	2.0	290	301
2PJR	A B	A	300	I	4.3	290	301
2PJR	A B	A	336	V	1.2	335	343
2PJR	A B	A	339	R	1.7	335	343
2PJR	A B	B	565	H	1.3	564	568
2PJR	A B	B	598	E	2.0	594	609
2PJR	A B	B	599	E	1.9	594	609
2PJR	A B	B	601	R	1.7	594	609
2PJR	A B	B	602	R	1.2	594	609
2PJR	A B	B	605	Y	3.5	594	609
2PJR	A B	B	606	V	1.1	594	609
2PJR	A B	B	607	G	16.9	594	609
2PJR	A B	B	608	I	1.8	594	609
2PJR	F G	F	992	I	2.9	990	1001
2PJR	F G	F	999	V	1.8	990	1001
2PJR	F G	F	1000	I	4.7	990	1001
2PJR	F G	F	1032	E	1.4	1029	1041
2PJR	F G	F	1035	F	1.1	1029	1041
2PJR	F G	F	1036	V	1.6	1029	1041
2PJR	F G	G	1290	E	1.9	1286	1301
2PJR	F G	G	1292	E	2.8	1286	1301
2PJR	F G	G	1297	Y	3.6	1286	1301
2PJR	F G	G	1299	G	1.7	1286	1301
2PJR	F G	G	1300	I	1.6	1286	1301
2PJW	H V	H	299	I	1.5	296	310
2PJW	H V	H	300	D	1.3	296	310
2PJW	H V	H	303	H	2.0	296	310
2PJW	H V	H	319	L	3.1	316	320
2PJW	H V	H	348	E	1.5	343	351
2PJW	H V	H	359	L	2.6	354	369
2PJW	H V	H	363	E	1.6	354	369
2PJW	H V	H	366	Y	2.4	354	369
2PJW	H V	V	365	V	1.1	362	367
2PJW	H V	V	390	F	2.1	381	412
2PJW	H V	V	393	K	1.3	381	412
2PJW	H V	V	400	L	1.3	381	412
2PJW	H V	V	407	Y	1.7	381	412
2PJW	H V	V	416	K	2.7	415	420
2PJW	H V	V	417	I	2.0	415	420
2PJW	H V	V	424	Y	2.5	423	437
2PJW	H V	V	427	L	1.6	423	437
2PJX	B D	B	119	F	1.3	117	125
2PK9	A B	A	51	I	1.6	48	59
2PK9	A B	A	52	R	1.4	48	59
2PK9	A B	A	54	I	3.1	48	59
2PK9	A B	A	56	L	1.3	48	59
2PK9	A B	A	58	K	1.2	48	59
2PK9	A B	B	163	L	1.2	152	166
2PK9	A D	D	146	K	1.1	141	149
2PK9	C B	C	214	D	1.7	214	225
2PK9	C D	C	51	I	2.0	48	60
2PK9	C D	C	54	I	1.0	48	60
2PK9	C D	C	58	K	1.0	48	60
2PK9	C D	D	163	L	1.3	152	166
2PKG	A C	A	179	P	1.2	179	187

2PKG	A C	C	147	W	2.4	141	148
2PKG	A D	A	479	H	1.8	475	480
2PKG	A D	D	102	E	1.2	100	105
2PKG	A D	D	154	E	1.8	154	169
2PKG	B C	B	476	E	1.2	475	480
2PKG	B C	B	479	H	1.7	475	480
2PKG	B C	B	520	H	1.3	520	528
2PKG	B C	C	100	W	1.7	100	105
2PKG	B C	C	102	E	1.4	100	105
2PKG	B D	B	179	P	1.2	179	196
2PKG	B D	D	147	W	2.2	141	148
2PKQ	O R	O	42	H	1.2	37	46
2PKQ	O R	R	13	R	1.5	10	20
2PKQ	O R	R	43	L	1.5	37	46
2PKQ	Q P	Q	42	H	1.1	37	46
2PKQ	Q P	Q	43	L	5.1	37	46
2PKQ	Q P	P	43	L	2.7	37	46
2PL9	A D	A	92	K	1.3	92	101
2PL9	A D	A	95	I	1.9	92	101
2PL9	A D	A	119	K	2.1	113	127
2PL9	A D	D	202	Q	2.0	202	212
2PL9	A D	D	205	V	1.0	202	212
2PL9	A D	D	206	D	2.1	202	212
2PL9	A D	D	208	L	2.0	202	212
2PL9	A D	D	209	L	1.1	202	212
2PL9	B E	B	95	I	1.6	92	101
2PL9	B E	E	205	V	1.2	202	212
2PL9	B E	E	208	L	2.3	202	212
2PL9	B E	E	209	L	1.0	202	212
2PL9	C F	C	95	I	1.7	92	101
2PL9	C F	F	205	V	1.3	202	213
2PL9	C F	F	206	D	1.0	202	213
2PL9	C F	F	208	L	1.8	202	213
2PM6	C D	C	739	R	1.6	732	745
2PMS	A C	A	21	F	2.4	14	30
2PMS	A C	C	182	E	2.8	174	192
2PMS	A C	C	183	N	1.2	174	192
2PMS	A C	C	231	D	1.8	210	249
2PMS	A D	A	324	G	30.7	323	333
2PMS	B D	B	21	F	2.3	14	30
2PMS	B D	D	182	E	3.6	174	192
2PMS	B D	D	183	N	1.1	174	192
2PMS	B D	D	186	H	1.9	174	192
2PMS	B D	D	187	R	1.0	174	192
2PMS	B D	D	227	E	1.0	212	249
2PMS	B D	D	231	D	1.3	212	249
2PMZ	A B	A	22	M	2.1	16	23
2PMZ	A B	A	277	F	2.3	262	278
2PMZ	A B	A	479	I	1.4	470	480
2PMZ	A B	A	648	L	3.0	648	652
2PMZ	A B	A	793	T	5.0	792	825
2PMZ	A B	A	795	L	1.2	792	825
2PMZ	A B	A	806	L	1.0	792	825
2PMZ	A B	B	924	I	2.0	923	932
2PMZ	A B	B	1048	R	2.0	1048	1052
2PMZ	A C	A	89	H	1.0	87	95
2PMZ	A C	A	309	F	1.4	308	312
2PMZ	A C	A	819	M	1.0	792	825
2PMZ	A C	A	823	L	1.0	792	825
2PMZ	A C	A	824	I	1.1	792	825

2PMZ	A C	C	71	G	134.5	70	75
2PMZ	A C	C	76	Q	2.1	76	83
2PMZ	A C	C	77	S	1.8	76	83
2PMZ	A C	C	78	V	2.2	76	83
2PMZ	A C	C	79	G	1.4	76	83
2PMZ	A C	C	290	R	1.3	286	296
2PMZ	A C	C	312	H	1.1	310	322
2PMZ	A C	C	354	L	1.0	350	361
2PMZ	A C	C	356	D	1.7	350	361
2PMZ	A C	C	374	I	1.7	369	376
2PMZ	A K	A	470	E	1.2	470	480
2PMZ	A K	A	479	I	1.3	470	480
2PMZ	A K	K	29	R	1.7	29	44
2PMZ	A K	K	41	L	1.9	29	44
2PMZ	B D	D	29	R	3.1	28	34
2PMZ	B D	D	60	H	1.9	55	64
2PMZ	B N	N	32	G	139.6	31	38
2PMZ	B N	N	59	V	1.4	56	61
2PMZ	C K	K	34	R	1.4	29	44
2PMZ	D L	D	30	R	1.4	28	34
2PMZ	D L	D	246	G	271.1	238	261
2PMZ	D L	D	252	K	1.4	238	261
2PMZ	D L	D	253	I	4.7	238	261
2PMZ	D L	D	256	L	1.0	238	261
2PMZ	D L	D	257	E	1.4	238	261
2PMZ	D L	D	259	K	1.2	238	261
2PMZ	D L	L	24	L	1.1	23	35
2PMZ	D L	L	27	L	1.3	23	35
2PMZ	D L	L	30	G	26.1	23	35
2PMZ	D L	L	79	M	1.3	65	86
2PMZ	D L	L	84	I	1.5	65	86
2PMZ	D N	N	56	I	1.9	56	61
2PMZ	D P	D	55	D	1.0	55	64
2PMZ	D P	D	59	A	1.4	55	64
2PMZ	D P	D	63	A	1.1	55	64
2PMZ	G R	G	342	L	1.9	341	346
2PMZ	G R	R	1097	F	2.0	1095	1107
2PMZ	G V	G	287	E	1.0	286	296
2PMZ	G W	W	18	V	3.0	16	22
2PMZ	G W	W	34	R	1.5	29	44
2PMZ	Q G	Q	89	H	1.1	87	95
2PMZ	Q G	Q	309	F	1.0	308	312
2PMZ	Q G	G	71	G	141.9	70	75
2PMZ	Q G	G	354	L	1.0	350	361
2PMZ	Q G	G	356	D	1.6	350	361
2PMZ	Q G	G	374	I	6.7	369	376
2PMZ	Q R	Q	22	M	3.0	16	23
2PMZ	Q R	Q	277	F	1.9	262	278
2PMZ	Q R	Q	342	I	6.6	341	347
2PMZ	Q R	Q	479	I	1.5	470	480
2PMZ	Q R	Q	520	E	1.0	518	524
2PMZ	Q R	Q	793	T	5.6	792	825
2PMZ	Q R	Q	795	L	1.3	792	825
2PMZ	Q R	R	1031	M	1.2	1031	1036
2PMZ	Q R	R	1048	R	1.1	1048	1052
2PMZ	Q R	R	1095	Y	2.6	1095	1107
2PMZ	Q R	R	1096	A	2.6	1095	1107
2PMZ	Q R	R	1098	K	2.4	1095	1107
2PMZ	Q R	R	1099	L	2.9	1095	1107
2PMZ	Q R	R	1100	L	3.2	1095	1107

2PMZ	Q W	Q	470	E	1.2	470	480
2PMZ	Q W	Q	477	K	1.3	470	480
2PMZ	Q W	Q	479	I	1.4	470	480
2PMZ	Q W	W	29	R	1.7	29	44
2PMZ	Q W	W	41	L	1.3	29	44
2PMZ	Q X	Q	519	E	1.0	518	524
2PMZ	Q X	X	33	R	1.0	23	35
2PMZ	R Y	Y	32	G	113.5	31	38
2PMZ	R Y	Y	58	E	1.7	56	61
2PMZ	R Y	Y	59	V	1.7	56	61
2PMZ	R Z	R	84	E	1.8	84	88
2PMZ	S X	S	30	R	1.8	28	34
2PMZ	S X	S	246	G	279.9	238	261
2PMZ	S X	S	252	K	1.5	238	261
2PMZ	S X	S	253	I	2.0	238	261
2PMZ	S X	S	256	L	1.5	238	261
2PMZ	S X	S	257	E	1.6	238	261
2PMZ	S X	S	259	K	1.1	238	261
2PMZ	S X	X	30	G	37.7	23	35
2PMZ	S X	X	79	M	1.2	65	86
2PMZ	S Y	Y	56	I	1.5	56	61
2PMZ	T U	U	20	L	4.6	18	25
2PMZ	T U	U	21	L	2.4	18	25
2PMZ	T U	U	34	L	1.5	34	38
2PO6	A C	A	147	V	4.4	141	149
2PO6	G H	H	137	E	1.2	135	141
2PO6	G H	H	140	H	1.4	135	141
2PON	A B	A	31	L	14.2	23	38
2PON	A B	A	35	G	21.5	23	38
2PON	A B	B	145	E	1.2	135	147
2PON	A B	B	146	L	1.4	135	147
2PON	A B	B	154	G	266.0	153	174
2PON	A B	B	162	F	1.4	153	174
2POP	A B	A	216	F	3.6	212	222
2POP	C D	C	2212	E	2.4	2212	2222
2POP	C D	C	2213	D	1.4	2212	2222
2POP	C D	C	2216	F	3.2	2212	2222
2PQ4	A B	B	5	R	1.8	5	21
2PQ4	A B	B	12	N	2.0	5	21
2PQA	A B	A	53	Q	1.2	51	57
2PQA	A B	A	153	N	2.0	153	172
2PQA	A B	A	159	I	1.7	153	172
2PQA	A B	A	160	L	1.2	153	172
2PQA	A B	A	166	H	1.5	153	172
2PQA	A B	B	106	I	3.0	96	109
2PQA	C D	C	152	M	1.3	152	170
2PQA	C D	C	155	F	1.9	152	170
2PQA	C D	C	156	T	1.0	152	170
2PQA	C D	C	159	I	2.0	152	170
2PQA	C D	C	163	I	1.9	152	170
2PQA	C D	C	167	M	1.1	152	170
2PQA	C D	D	99	Y	1.0	96	109
2PQK	A B	A	230	G	1.4	225	236
2PQK	A B	A	231	M	1.6	225	236
2PQK	A B	A	253	V	1.5	244	254
2PQK	A B	A	262	G	125.8	261	282
2PQK	A B	A	263	R	3.5	261	282
2PQK	A B	A	318	F	1.3	312	319
2PQK	A B	B	3	E	1.8	1	22
2PQK	A B	B	5	W	1.0	1	22

2PQK	A B	B	6	I	2.0	1	22
2PQK	A B	B	10	L	2.2	1	22
2PQK	A B	B	11	R	3.2	1	22
2PQK	A B	B	13	I	2.2	1	22
2PQK	A B	B	14	G	120.2	1	22
2PQK	A B	B	15	D	2.7	1	22
2PQK	A B	B	17	F	2.7	1	22
2PQK	A B	B	21	Y	2.2	1	22
2PQN	A B	A	24	I	1.4	19	32
2PQN	A B	A	43	F	3.0	39	52
2PQN	A B	A	47	W	1.6	39	52
2PQN	A B	B	148	L	1.6	148	163
2PQN	A B	B	149	F	4.0	148	163
2PQN	A B	B	152	F	3.9	148	163
2PQN	A B	B	155	Y	1.5	148	163
2PQN	A B	B	156	L	1.2	148	163
2PQR	A C	A	25	L	1.0	19	32
2PQR	A C	A	43	F	2.7	39	52
2PQR	A C	A	47	W	1.0	39	52
2PQR	A C	A	63	K	1.4	55	72
2PQR	A C	A	66	T	1.2	55	72
2PQR	A C	A	69	Y	1.6	55	72
2PQR	A C	A	70	K	1.7	55	72
2PQR	A C	A	78	E	1.6	76	90
2PQR	A C	A	82	Y	1.1	76	90
2PQR	A C	C	101	F	4.0	99	105
2PQR	A C	C	126	L	2.3	126	140
2PQR	A C	C	127	F	4.6	126	140
2PQR	A C	C	130	F	4.0	126	140
2PQR	A C	C	137	I	1.7	126	140
2PQR	B D	B	25	L	1.0	19	32
2PQR	B D	B	43	F	3.1	39	52
2PQR	B D	B	47	W	1.7	39	52
2PQR	B D	B	59	R	1.4	55	72
2PQR	B D	B	69	Y	1.1	55	72
2PQR	B D	B	70	K	1.1	55	72
2PQR	B D	B	76	R	2.2	76	90
2PQR	B D	B	77	R	1.3	76	90
2PQR	B D	B	78	E	1.5	76	90
2PQR	B D	B	82	Y	1.0	76	90
2PQR	B D	B	99	Y	1.1	93	107
2PQR	B D	D	101	F	3.8	97	105
2PQR	B D	D	102	R	1.9	97	105
2PQR	B D	D	126	L	2.7	126	138
2PQR	B D	D	127	F	4.5	126	138
2PQR	B D	D	130	F	3.2	126	138
2PQR	B D	D	137	I	1.3	126	138
2PRG	A C	A	297	T	1.8	277	303
2PRG	A C	A	318	L	1.1	311	333
2PRG	A C	A	468	L	1.4	467	474
2PRG	A C	C	632	K	1.1	631	638
2PRG	A C	C	633	L	2.3	631	638
2PRG	A C	C	636	L	1.5	631	638
2PRG	A C	C	637	L	3.2	631	638
2PRG	B C	B	315	V	1.9	311	333
2PRG	B C	C	690	L	1.3	688	696
2PRG	B C	C	691	H	1.3	688	696
2PRG	B C	C	693	L	1.2	688	696
2PSM	A F	A	46	E	1.5	36	54
2PSM	A F	A	49	V	1.0	36	54

2PSM	A F	A	53	E	1.0	36	54
2PSM	B C	B	46	E	4.6	36	54
2PSM	B C	B	48	Q	1.1	36	54
2PSM	B C	B	49	V	2.4	36	54
2PSM	B C	B	52	H	2.0	36	54
2PSM	B C	B	53	E	3.4	36	54
2PT7	A G	A	10	D	1.2	7	36
2PT7	A G	A	12	K	1.0	7	36
2PT7	A G	A	13	F	3.1	7	36
2PT7	A G	A	15	E	1.4	7	36
2PT7	A G	A	20	L	1.9	7	36
2PT7	A G	G	166	R	2.0	165	182
2PT7	A G	G	170	L	1.3	165	182
2PT7	A G	G	173	L	1.7	165	182
2PT7	A G	G	177	W	1.1	165	182
2PT7	B G	B	86	R	1.8	78	92
2PT7	B G	G	165	Y	1.0	165	182
2PT7	D H	D	10	D	1.0	7	36
2PT7	D H	D	13	F	3.4	7	36
2PT7	D H	D	15	E	1.4	7	36
2PT7	D H	D	20	L	1.8	7	36
2PT7	D H	H	126	L	1.0	116	127
2PT7	D H	H	166	R	1.9	165	183
2PT7	D H	H	170	L	1.2	165	183
2PT7	D H	H	173	L	1.3	165	183
2PT7	D H	H	177	W	1.5	165	183
2PT7	E H	E	86	R	1.0	78	92
2PT7	E H	H	165	Y	2.0	165	183
2PT7	E H	H	172	Y	1.8	165	183
2PUK	A B	A	64	E	1.5	63	70
2PUK	A B	A	81	E	1.4	77	82
2PUK	A C	A	35	V	1.6	33	51
2PUK	A C	A	42	G	51.1	33	51
2PUK	A C	C	38	G	108.5	38	54
2PUK	A C	C	39	P	1.3	38	54
2PUK	A C	C	41	K	1.3	38	54
2PUK	A C	C	42	L	1.5	38	54
2PUK	E F	E	66	E	1.4	63	70
2PUK	E F	E	81	E	1.6	77	82
2PUK	E G	E	35	V	1.0	33	51
2PUK	E G	E	42	G	33.3	33	51
2PUK	E G	E	45	R	1.3	33	51
2PUK	E G	G	38	G	28.3	38	54
2PUK	E G	G	39	P	1.3	38	54
2PUK	E G	G	42	L	1.5	38	54
2PUQ	L H	H	268	F	1.5	266	274
2PUQ	L H	H	272	T	1.3	266	274
2PV2	A E	A	243	F	1.2	241	249
2PV2	A E	E	6	F	4.6	3	10
2PV2	A E	E	9	I	1.0	3	10
2PV2	B E	B	243	F	1.3	241	247
2PV2	B E	E	3	T	1.2	3	10
2PV2	B E	E	4	L	1.8	3	10
2PV2	B E	E	7	W	5.5	3	10
2PV2	C F	C	243	F	1.4	241	247
2PV2	C F	F	6	F	4.6	3	11
2PV2	C F	F	9	I	1.3	3	11
2PV2	C F	F	10	F	2.6	3	11
2PV2	D F	D	243	F	1.2	241	247
2PV2	D F	F	3	T	1.2	3	11

2PV2	D F	F	4	L	1.6	3	11
2PV2	D F	F	7	W	5.2	3	11
2PV2	D F	F	8	D	1.3	3	11
2PV2	D F	F	10	F	1.1	3	11
2PV9	A B	A	14	E	2.5	14	14
2PV9	A B	A	14	L	1.9	14	14
2PVG	A B	A	81	E	2.1	77	82
2PVG	A C	A	17	F	1.1	9	25
2PVG	A C	A	24	R	1.8	9	25
2PVO	A B	A	81	E	2.2	77	82
2PVO	A C	A	42	G	223.0	33	45
2PVO	A C	C	47	G	108.9	47	63
2PVO	A C	C	48	P	1.4	47	63
2PVO	A D	A	20	Q	2.4	9	25
2PVO	A D	A	24	R	1.9	9	25
2PVO	A D	D	68	Q	1.6	66	71
2PXY	A C	C	58	G	17.0	56	70
2PXY	A D	D	81	Y	1.4	68	88
2PXY	C D	C	48	F	3.0	46	52
2PXY	C D	C	73	L	2.3	72	77
2PXY	C D	C	76	R	2.6	72	77
2PXY	C D	D	57	D	1.2	55	67
2PXY	C D	D	86	E	2.1	68	88
2Q0O	A C	A	65	G	33.1	57	66
2Q0O	A C	A	178	P	1.6	178	189
2Q0O	A C	A	181	M	1.1	178	189
2Q0O	A C	A	186	W	2.0	178	189
2Q0O	A C	A	199	L	1.8	193	201
2Q0O	A C	C	40	R	1.8	25	57
2Q0O	A C	C	50	Y	2.6	25	57
2Q0O	A C	C	53	W	3.8	25	57
2Q0O	A C	C	54	L	1.2	25	57
2Q0O	A C	C	71	Q	1.3	64	96
2Q0O	A C	C	74	Y	2.5	64	96
2Q0O	A C	C	80	R	1.7	64	96
2Q0O	A C	C	86	E	1.0	64	96
2Q0O	B D	B	178	P	1.1	178	189
2Q0O	B D	B	199	L	1.8	193	201
2Q0O	B D	D	40	R	2.0	25	58
2Q0O	B D	D	47	Q	1.0	25	58
2Q0O	B D	D	50	Y	1.6	25	58
2Q0O	B D	D	53	W	3.7	25	58
2Q0O	B D	D	86	E	1.1	64	96
2Q26	A B	A	350	V	1.2	341	354
2Q26	A B	B	370	V	1.4	366	372
2Q26	C D	C	350	V	2.2	341	352
2Q26	C D	D	370	V	1.4	370	375
2Q26	E F	E	350	V	1.2	342	354
2Q3N	A B	A	169	Y	1.8	168	181
2Q3N	A B	A	176	I	1.8	168	181
2Q6W	D F	D	62	N	1.5	56	77
2Q6W	D F	D	65	V	1.2	56	77
2Q6W	D F	D	69	N	1.4	56	77
2Q6W	D F	D	72	I	1.0	56	77
2Q6W	E F	E	81	H	1.1	78	86
2Q7N	A B	B	156	F	3.9	155	177
2Q7N	C D	D	156	F	1.3	155	178
2Q86	A B	B	130	E	1.2	128	135
2Q86	A B	B	134	K	1.1	128	135
2Q86	C D	D	130	E	1.6	128	134

2Q8A	A H	A	197	E	2.0	195	202
2Q8A	A H	A	200	H	1.8	195	202
2Q8A	A H	A	201	F	3.5	195	202
2Q8A	A H	A	219	R	1.1	213	222
2Q8A	A L	A	197	E	2.2	195	202
2Q8A	A L	A	200	H	2.2	195	202
2Q8A	L H	L	124	Q	1.1	122	126
2Q97	A T	A	143	Y	1.6	137	145
2Q97	A T	A	215	K	1.2	205	217
2Q97	A T	A	341	I	1.0	338	349
2Q97	A T	T	111	L	1.6	104	118
2Q97	A T	T	112	L	1.7	104	118
2Q97	A T	T	114	E	1.4	104	118
2Q97	A T	T	115	I	2.4	104	118
2Q97	A T	T	133	E	1.3	132	148
2Q97	A T	T	134	Q	1.1	132	148
2Q97	A T	T	138	Y	1.7	132	148
2Q97	A T	T	141	V	1.3	132	148
2Q97	A T	T	145	L	1.2	132	148
2Q9Q	A B	A	5	E	1.1	3	13
2Q9Q	A B	A	8	F	2.8	3	13
2Q9Q	A B	A	9	L	1.7	3	13
2Q9Q	A B	A	12	K	1.1	3	13
2Q9Q	A B	A	47	W	1.9	46	52
2Q9Q	A B	A	48	L	1.1	46	52
2Q9Q	A B	A	164	L	1.3	157	172
2Q9Q	A B	A	168	Y	1.3	157	172
2Q9Q	A B	B	23	P	6.3	23	40
2Q9Q	A B	B	31	E	1.4	23	40
2Q9Q	A B	B	34	W	2.8	23	40
2Q9Q	A B	B	35	M	1.0	23	40
2Q9Q	A B	B	73	L	1.5	72	103
2Q9Q	A B	B	77	I	1.0	72	103
2Q9Q	A B	B	84	R	3.7	72	103
2Q9Q	A D	A	97	K	1.0	92	102
2Q9Q	A D	A	121	W	1.1	110	138
2Q9Q	A D	A	136	V	1.7	110	138
2Q9Q	A D	A	159	F	3.5	157	172
2Q9Q	A D	A	170	L	2.6	157	172
2Q9Q	A D	D	139	L	1.9	131	154
2Q9Q	A D	D	142	F	1.3	131	154
2Q9Q	A D	D	143	I	2.3	131	154
2Q9Q	A D	D	146	F	3.6	131	154
2Q9Q	A D	D	175	L	2.0	170	191
2Q9Q	A D	D	179	G	9.5	170	191
2Q9Q	A D	D	182	G	31.5	170	191
2Q9Q	A D	D	186	F	1.7	170	191
2Q9Q	A D	D	189	W	4.7	170	191
2Q9Q	A G	A	134	S	2.2	110	138
2Q9Q	A G	A	137	R	2.3	110	138
2Q9Q	A G	G	90	L	3.1	59	95
2Q9Q	A G	G	94	Y	1.2	59	95
2Q9Q	A G	G	102	L	3.2	100	104
2Q9Q	B C	B	55	M	1.6	48	65
2Q9Q	B C	B	86	R	1.2	72	103
2Q9Q	B C	B	87	Y	4.0	72	103
2Q9Q	B C	B	89	L	1.1	72	103
2Q9Q	B C	B	93	L	1.0	72	103
2Q9Q	B C	B	97	L	1.6	72	103
2Q9Q	B C	B	101	E	1.1	72	103

2Q9Q	B C	B	129	F	2.3	124	148
2Q9Q	B C	B	133	F	1.3	124	148
2Q9Q	B C	B	137	T	1.2	124	148
2Q9Q	B C	B	140	Y	3.2	124	148
2Q9Q	B C	C	33	L	1.8	26	52
2Q9Q	B C	C	36	M	1.2	26	52
2Q9Q	B C	C	40	Y	1.7	26	52
2Q9Q	B C	C	80	L	1.1	58	95
2Q9Q	B C	C	84	L	1.8	58	95
2Q9Q	B C	C	113	W	3.9	108	129
2Q9Q	B C	C	117	Y	3.2	108	129
2Q9Q	B C	C	124	Y	2.9	108	129
2Q9Q	C D	C	10	I	2.5	4	15
2Q9Q	C D	C	68	S	6.5	58	95
2Q9Q	C D	C	74	R	5.0	58	95
2Q9Q	C D	C	86	R	1.0	58	95
2Q9Q	C D	D	22	L	1.7	22	28
2Q9Q	C D	D	25	I	1.5	22	28
2Q9Q	C D	D	75	G	8.1	70	77
2Q9Q	C D	D	76	L	1.2	70	77
2Q9Q	E F	E	5	E	1.1	3	12
2Q9Q	E F	E	8	F	1.8	3	12
2Q9Q	E F	E	9	L	1.0	3	12
2Q9Q	E F	E	47	W	3.2	46	52
2Q9Q	E F	E	48	L	1.1	46	52
2Q9Q	E F	E	164	L	1.2	150	171
2Q9Q	E F	F	34	W	1.9	23	40
2Q9Q	E F	F	73	L	2.2	73	103
2Q9Q	E F	F	77	I	2.1	73	103
2Q9Q	E F	F	84	R	2.8	73	103
2Q9Q	E F	F	88	V	1.4	73	103
2Q9Q	E H	E	97	K	1.2	92	103
2Q9Q	E H	E	121	W	2.9	110	138
2Q9Q	E H	E	128	L	1.4	110	138
2Q9Q	E H	E	129	R	1.6	110	138
2Q9Q	E H	E	151	M	1.5	150	171
2Q9Q	E H	E	155	T	1.9	150	171
2Q9Q	E H	E	156	S	1.4	150	171
2Q9Q	E H	E	159	F	4.4	150	171
2Q9Q	E H	E	166	H	2.9	150	171
2Q9Q	E H	E	170	L	3.0	150	171
2Q9Q	E H	H	142	F	1.6	131	154
2Q9Q	E H	H	143	I	1.1	131	154
2Q9Q	E H	H	146	F	2.9	131	154
2Q9Q	E H	H	150	M	2.2	131	154
2Q9Q	E H	H	175	L	1.3	170	191
2Q9Q	E H	H	179	G	18.1	170	191
2Q9Q	E H	H	182	G	35.6	170	191
2Q9Q	E H	H	183	L	1.2	170	191
2Q9Q	E H	H	185	D	1.2	170	191
2Q9Q	E H	H	186	F	2.6	170	191
2Q9Q	E H	H	189	W	3.3	170	191
2Q9Q	F G	F	86	R	1.1	73	103
2Q9Q	F G	F	87	Y	4.0	73	103
2Q9Q	F G	F	94	R	3.7	73	103
2Q9Q	F G	F	97	L	1.6	73	103
2Q9Q	F G	F	101	E	1.2	73	103
2Q9Q	F G	F	104	F	1.0	104	113
2Q9Q	F G	F	129	F	2.1	124	148
2Q9Q	F G	F	133	F	1.4	124	148

2Q9Q	F G	F	140	Y	3.6	124	148
2Q9Q	F G	F	141	L	1.1	124	148
2Q9Q	F G	G	33	L	1.6	26	51
2Q9Q	F G	G	36	M	1.2	26	51
2Q9Q	F G	G	40	Y	1.9	26	51
2Q9Q	F G	G	77	V	1.1	59	95
2Q9Q	F G	G	80	L	1.0	59	95
2Q9Q	F G	G	84	L	1.9	59	95
2Q9Q	F G	G	92	W	1.0	59	95
2Q9Q	F G	G	113	W	2.3	108	126
2Q9Q	F G	G	117	Y	1.8	108	126
2Q9Q	F G	G	124	Y	2.9	108	126
2Q9Q	F H	F	102	K	1.5	73	103
2Q9Q	G H	G	7	M	1.2	4	15
2Q9Q	G H	G	10	I	3.1	4	15
2Q9Q	G H	G	71	R	1.2	59	95
2Q9Q	G H	G	74	R	1.5	59	95
2Q9Q	G H	G	85	L	1.0	59	95
2Q9Q	G H	G	86	R	1.2	59	95
2Q9Q	G H	H	22	L	1.6	22	30
2Q9Q	G H	H	25	I	3.1	22	30
2Q9Q	G H	H	26	L	1.3	22	30
2Q9Q	G H	H	29	H	1.0	22	30
2Q9Q	G H	H	75	G	8.1	70	76
2QA4	A Z	Z	76	G	6.1	76	82
2QA4	A Z	Z	79	V	1.7	76	82
2QA4	F M	F	38	K	1.0	33	43
2QA4	F M	F	59	I	1.0	57	69
2QA4	F M	F	62	H	1.9	57	69
2QA4	F M	M	7	Y	2.7	4	12
2QA4	F M	M	24	Q	2.5	19	34
2QA4	N Q	Q	26	P	1.0	26	30
2QAC	A T	A	147	M	1.2	141	151
2QAC	A T	A	168	L	1.3	161	169
2QAC	A T	A	179	E	1.3	177	188
2QAC	A T	A	202	I	1.2	195	204
2QAC	A T	T	806	R	4.3	805	817
2QAC	A T	T	807	V	1.7	805	817
2QAC	A T	T	808	Q	2.2	805	817
2QAC	A T	T	810	H	3.4	805	817
2QAC	A T	T	811	I	2.3	805	817
2QAC	A T	T	812	R	1.1	805	817
2QAC	A T	T	813	K	2.0	805	817
2QAC	A T	T	816	V	1.0	805	817
2QAD	A B	A	371	I	1.4	369	373
2QAG	A B	B	193	E	1.3	191	206
2QAG	B C	B	31	Q	1.0	30	34
2QAG	B C	B	287	R	9.7	283	307
2QAG	B C	C	276	Q	1.4	275	286
2QAG	B C	C	279	K	1.3	275	286
2QAR	A B	A	64	L	1.3	59	65
2QAR	A B	A	69	D	1.1	67	74
2QAR	A B	A	73	R	3.2	67	74
2QAR	A B	B	71	R	2.5	67	74
2QAR	A B	B	79	D	2.4	78	107
2QAR	A B	B	80	V	1.3	78	107
2QAR	D E	D	64	L	2.0	59	65
2QAR	D E	D	68	E	2.4	67	74
2QAR	D E	D	69	D	2.4	67	74
2QAR	D E	D	72	Y	1.3	67	74

2QAR	D E	D	73	R	2.8	67	74
2QAR	D E	E	71	R	1.8	67	74
2QAR	D E	E	79	D	1.0	78	97
2QAR	D E	E	80	V	1.9	78	97
2QB0	A D	A	68	E	1.3	67	74
2QB0	A D	A	72	Y	3.4	67	74
2QB0	A D	A	73	R	4.3	67	74
2QB0	A D	D	71	R	1.2	67	74
2QB0	A D	D	79	D	2.4	78	91
2QB0	A D	D	80	V	1.8	78	91
2QB0	C B	B	80	V	1.8	78	91
2QBE	E L	E	25	E	1.7	25	30
2QBE	E L	E	29	H	2.2	25	30
2QBE	H Z	Z	59	I	3.9	55	63
2QBE	Q R	Q	42	G	171.9	35	53
2QBE	X T	X	30	M	1.2	24	34
2QBY	A B	A	103	R	1.3	101	109
2QBY	A B	B	162	D	1.9	161	170
2QBY	A B	B	193	R	1.0	192	197
2QCD	A B	A	319	G	72.1	319	328
2QCD	A B	A	349	G	2.3	348	361
2QCD	A B	A	382	Y	1.8	381	392
2QCD	A B	B	319	G	93.5	319	328
2QCD	A B	B	349	G	1.6	348	361
2QCD	A B	B	382	Y	1.8	381	393
2QCS	A B	A	129	F	2.1	128	136
2QCS	A B	A	230	E	3.2	217	234
2QCS	A B	A	244	I	2.7	243	253
2QCS	A B	A	247	Y	1.3	243	253
2QCS	A B	B	143	E	1.5	141	151
2QCS	A B	B	201	L	2.8	200	205
2QCS	A B	B	204	I	1.0	200	205
2QCS	A B	B	240	K	1.1	226	250
2QCS	A B	B	267	D	1.0	259	269
2QCS	A B	B	355	R	2.7	350	357
2QE7	A D	A	204	T	1.3	202	215
2QE7	A D	D	279	G	223.6	274	285
2QE7	A D	D	317	H	1.8	309	318
2QE7	A E	A	292	Y	1.5	290	298
2QE7	A E	E	185	T	7.9	185	195
2QE7	A E	E	188	G	2.9	185	195
2QE7	B E	E	279	G	115.8	274	285
2QE7	B F	B	292	Y	1.4	290	298
2QE7	B F	F	186	R	3.1	185	195
2QE7	B F	F	188	G	3.0	185	195
2QE7	B G	G	20	I	1.3	12	24
2QE7	C D	C	292	Y	1.5	290	298
2QE7	C D	D	186	R	1.4	185	195
2QE7	C D	D	190	D	1.2	185	195
2QE7	C D	D	256	E	1.2	247	261
2QE7	C F	F	279	G	94.5	274	285
2QEJ	A D	A	258	L	1.8	253	259
2QEX	A Z	Z	29	I	1.3	20	34
2QEX	A Z	Z	76	G	1.4	74	82
2QEX	A Z	Z	79	V	1.4	74	82
2QEX	F M	F	62	H	2.1	57	69
2QEX	F M	M	7	Y	2.8	4	12
2QEX	F M	M	8	I	1.2	4	12
2QEX	N Q	N	24	L	1.3	20	30
2QEX	N Q	Q	26	P	1.0	26	30

2QFA	A B	A	10	W	1.1	8	12
2QFA	A B	A	98	L	2.5	98	140
2QFA	A B	A	101	F	2.7	98	140
2QFA	A B	A	106	R	2.7	98	140
2QFA	A B	A	110	K	3.0	98	140
2QFA	A B	A	113	I	1.2	98	140
2QFA	A B	A	121	K	2.0	98	140
2QFA	A B	A	124	F	2.5	98	140
2QFA	A B	B	21	L	1.4	16	61
2QFA	A B	B	25	L	1.5	16	61
2QFA	A B	B	28	F	2.4	16	61
2QFA	A B	B	36	I	1.1	16	61
2QFA	A B	B	39	I	1.1	16	61
2QFA	A B	B	47	L	1.8	16	61
2QFA	A B	B	51	D	2.0	16	61
2QFA	A B	B	54	Y	4.2	16	61
2QFA	A B	B	58	I	1.6	16	61
2QFA	A B	B	74	F	1.8	70	76
2QFA	A C	A	10	W	1.9	8	12
2QFA	A C	A	120	K	2.6	98	140
2QFA	A C	A	124	F	1.0	98	140
2QFA	A C	A	131	V	1.7	98	140
2QFA	A C	A	138	L	1.5	98	140
2QFA	A C	C	12	L	2.2	8	46
2QFA	A C	C	19	L	1.4	8	46
2QFA	A C	C	22	F	1.6	8	46
2QFA	A C	C	23	L	2.0	8	46
2QFA	A C	C	27	D	1.6	8	46
2QFA	A C	C	31	L	1.2	8	46
2QFA	A C	C	34	L	2.2	8	46
2QFA	A C	C	45	F	1.8	8	46
2QFA	B C	B	24	F	3.1	16	61
2QFA	B C	B	28	F	1.3	16	61
2QFA	B C	B	46	L	1.6	16	61
2QFA	B C	B	54	Y	1.6	16	61
2QFA	B C	B	57	E	1.2	16	61
2QFA	B C	C	11	L	3.2	8	46
2QFA	B C	C	22	F	1.7	8	46
2QFA	B C	C	33	W	2.2	8	46
2QFA	B C	C	44	M	1.5	8	46
2QFA	B C	C	45	F	2.9	8	46
2QHO	A B	B	196	V	1.6	187	197
2QHO	A B	B	224	L	1.0	216	225
2QHO	C B	B	194	Q	1.1	187	197
2QHO	C B	B	202	R	1.0	202	212
2QHO	C D	D	196	V	1.7	187	197
2QHO	C D	D	224	L	1.7	216	226
2QHO	E F	F	196	V	1.5	187	197
2QHO	E F	F	224	L	2.5	216	228
2QHO	G H	H	196	V	1.5	187	197
2QHO	G H	H	224	L	1.5	216	226
2QHR	H L	L	125	E	1.5	123	128
2QI9	A C	A	223	Q	3.3	218	224
2QI9	A C	C	91	W	2.7	90	97
2QI9	A C	C	92	H	1.4	90	97
2QI9	A C	C	143	Q	1.3	129	144
2QI9	A F	A	55	I	1.3	55	76
2QI9	A F	A	170	V	1.5	169	175
2QI9	A F	F	93	Q	1.5	91	101
2QI9	A F	F	99	S	1.0	91	101

2QI9	B D	B	4	L	1.1	3	22
2QI9	B D	B	223	Q	1.5	218	224
2QI9	B F	F	203	Q	1.1	202	206
2QIE	A B	A	55	M	2.7	53	71
2QIE	A B	B	11	D	1.8	8	13
2QIE	E D	E	55	M	2.8	53	71
2QIE	E D	E	59	K	1.0	53	71
2QIE	E D	D	11	D	2.2	8	13
2QIE	H G	H	55	M	2.5	53	71
2QIE	K J	K	55	M	2.6	53	71
2QIE	K J	J	11	D	1.4	8	13
2QIY	A C	A	17	Y	1.1	5	23
2QIY	A C	C	216	E	1.8	214	229
2QIY	A C	C	217	F	2.4	214	229
2QIY	A C	C	224	R	2.9	214	229
2QIY	B D	D	217	F	2.4	215	229
2QIY	B D	D	224	R	3.0	215	229
2QJ9	A D	D	85	F	3.2	83	89
2QJ9	B C	C	85	F	3.0	83	88
2QJ9	B D	B	66	L	1.4	59	71
2QJ9	B D	D	85	F	1.0	83	89
2QJK	A B	A	77	F	1.1	77	87
2QJK	A B	A	85	R	1.5	77	87
2QJK	A B	A	247	Y	2.7	247	270
2QJK	A B	A	254	F	1.4	247	270
2QJK	A B	A	261	L	1.4	247	270
2QJK	A B	A	269	F	3.0	247	270
2QJK	A B	A	428	F	2.7	424	430
2QJK	A B	B	226	R	2.7	223	254
2QJK	A B	B	237	L	3.2	223	254
2QJK	A B	B	244	L	1.1	223	254
2QJK	A B	B	251	L	2.3	223	254
2QJK	A B	B	252	W	5.3	223	254
2QJK	A C	C	34	L	1.0	11	39
2QJK	A F	A	157	W	1.4	153	169
2QJK	A F	A	164	G	5.8	153	169
2QJK	A F	A	179	W	1.9	174	182
2QJK	A F	F	38	M	1.6	11	39
2QJK	B C	B	236	F	1.0	223	254
2QJK	B C	B	240	L	1.1	223	254
2QJK	B C	B	243	L	1.0	223	254
2QJK	B C	C	15	L	1.7	11	39
2QJK	D C	D	157	W	1.5	153	169
2QJK	D C	D	164	G	11.2	153	169
2QJK	D C	D	179	W	1.6	174	182
2QJK	D C	C	38	M	1.2	11	39
2QJK	D E	D	85	R	2.0	77	87
2QJK	D E	D	91	F	1.2	90	118
2QJK	D E	D	95	Y	1.9	90	118
2QJK	D E	D	247	Y	3.0	247	270
2QJK	D E	D	248	F	1.0	247	270
2QJK	D E	D	250	I	1.0	247	270
2QJK	D E	D	254	F	1.7	247	270
2QJK	D E	D	264	F	1.1	247	270
2QJK	D E	D	269	F	2.7	247	270
2QJK	D E	D	428	F	1.7	424	430
2QJK	D E	E	226	R	1.6	223	254
2QJK	D E	E	237	L	1.5	223	254
2QJK	D E	E	251	L	1.9	223	254
2QJK	D E	E	252	W	5.4	223	254

2QJK	E F	E	240	L	1.0	223	254
2QJK	E F	E	243	L	1.0	223	254
2QJK	E F	F	15	L	1.8	11	39
2QJK	G H	G	85	R	1.7	77	87
2QJK	G H	G	91	F	1.1	90	118
2QJK	G H	G	95	Y	3.2	90	118
2QJK	G H	G	247	Y	2.7	247	270
2QJK	G H	G	248	F	12.9	247	270
2QJK	G H	G	254	F	1.9	247	270
2QJK	G H	G	268	G	1.1	247	270
2QJK	G H	G	269	F	2.4	247	270
2QJK	G H	H	226	R	2.8	223	254
2QJK	G H	H	230	G	2.3	223	254
2QJK	G H	H	237	L	1.5	223	254
2QJK	G H	H	244	L	1.5	223	254
2QJK	G H	H	251	L	2.2	223	254
2QJK	G H	H	252	W	5.0	223	254
2QJK	G L	G	157	W	1.5	153	169
2QJK	G L	G	164	G	10.7	153	169
2QJK	G L	G	179	W	2.5	174	182
2QJK	G L	L	38	M	1.5	11	39
2QJK	H I	H	243	L	1.2	223	254
2QJK	H I	I	15	L	1.8	11	39
2QJK	J I	J	157	W	1.2	153	169
2QJK	J I	J	164	G	1.2	153	169
2QJK	J I	J	179	W	1.4	174	182
2QJK	J I	I	38	M	1.7	11	39
2QJK	J K	J	85	R	2.2	77	87
2QJK	J K	J	91	F	2.6	90	118
2QJK	J K	J	247	Y	2.6	247	270
2QJK	J K	J	248	F	1.0	247	270
2QJK	J K	J	254	F	3.1	247	270
2QJK	J K	J	261	L	1.5	247	270
2QJK	J K	J	268	G	1.0	247	270
2QJK	J K	J	269	F	3.4	247	270
2QJK	J K	J	379	W	1.0	361	382
2QJK	J K	K	231	F	1.1	223	254
2QJK	J K	K	237	L	2.3	223	254
2QJK	J K	K	244	L	1.2	223	254
2QJK	J K	K	245	Y	1.0	223	254
2QJK	J K	K	251	L	2.3	223	254
2QJK	J K	K	252	W	4.9	223	254
2QJK	K L	K	243	L	1.0	223	254
2QJK	K L	L	15	L	1.7	11	39
2QJK	M N	M	81	E	1.0	77	87
2QJK	M N	M	85	R	2.1	77	87
2QJK	M N	M	91	F	2.1	90	118
2QJK	M N	M	95	Y	2.8	90	118
2QJK	M N	M	247	Y	2.5	247	270
2QJK	M N	M	248	F	12.7	247	270
2QJK	M N	M	254	F	1.5	247	270
2QJK	M N	M	261	L	1.5	247	270
2QJK	M N	M	269	F	2.6	247	270
2QJK	M N	M	428	F	2.5	424	430
2QJK	M N	N	219	A	2.5	204	220
2QJK	M N	N	226	R	1.1	223	254
2QJK	M N	N	230	G	1.1	223	254
2QJK	M N	N	237	L	2.7	223	254
2QJK	M N	N	244	L	1.4	223	254
2QJK	M N	N	251	L	2.2	223	254

2QJK	M N	N	252	W	4.7	223	254
2QJK	M O	M	68	H	1.4	46	69
2QJK	M R	M	157	W	1.2	153	169
2QJK	M R	M	164	G	2.6	153	169
2QJK	M R	M	179	W	1.2	174	182
2QJK	M R	M	302	Y	1.1	298	306
2QJK	M R	R	38	M	1.3	11	39
2QJK	N O	N	236	F	1.0	223	254
2QJK	N O	N	240	L	1.0	223	254
2QJK	N O	O	15	L	1.9	11	39
2QJK	P O	P	157	W	1.4	153	169
2QJK	P O	P	164	G	5.1	153	169
2QJK	P O	P	179	W	1.2	174	182
2QJK	P O	O	38	M	1.1	11	39
2QJK	P Q	P	85	R	2.0	77	87
2QJK	P Q	P	91	F	2.3	90	118
2QJK	P Q	P	95	Y	1.5	90	118
2QJK	P Q	P	254	F	1.5	247	270
2QJK	P Q	P	261	L	1.1	247	270
2QJK	P Q	P	269	F	2.9	247	270
2QJK	P Q	P	428	F	3.6	424	430
2QJK	P Q	Q	226	R	1.8	223	254
2QJK	P Q	Q	230	G	1.1	223	254
2QJK	P Q	Q	237	L	1.8	223	254
2QJK	P Q	Q	244	L	1.4	223	254
2QJK	P Q	Q	251	L	2.0	223	254
2QJK	Q R	Q	236	F	1.0	223	254
2QJK	Q R	R	15	L	1.5	11	39
2QJP	A B	A	77	F	1.1	73	87
2QJP	A B	A	85	R	1.4	73	87
2QJP	A B	A	91	F	2.8	90	118
2QJP	A B	A	95	Y	2.5	90	118
2QJP	A B	A	247	Y	2.8	247	270
2QJP	A B	A	248	F	11.3	247	270
2QJP	A B	A	250	I	1.0	247	270
2QJP	A B	A	254	F	2.8	247	270
2QJP	A B	A	261	L	1.3	247	270
2QJP	A B	A	268	G	49.6	247	270
2QJP	A B	A	269	F	3.1	247	270
2QJP	A B	A	379	W	1.1	361	382
2QJP	A B	B	226	R	1.9	223	254
2QJP	A B	B	230	G	19.6	223	254
2QJP	A B	B	237	L	1.9	223	254
2QJP	A B	B	251	L	2.2	223	254
2QJP	A B	B	252	W	4.9	223	254
2QJP	A C	C	34	L	1.0	11	38
2QJP	A F	A	157	W	1.6	153	167
2QJP	A F	A	164	G	1.1	153	167
2QJP	A F	A	179	W	2.5	172	182
2QJP	B C	B	240	L	1.0	223	254
2QJP	B C	B	243	L	1.3	223	254
2QJP	B C	C	15	L	1.6	11	38
2QJP	D C	D	157	W	1.3	153	167
2QJP	D C	D	179	W	2.6	172	182
2QJP	D E	D	85	R	1.8	73	87
2QJP	D E	D	91	F	1.8	90	118
2QJP	D E	D	95	Y	1.0	90	118
2QJP	D E	D	248	F	2.2	247	270
2QJP	D E	D	254	F	2.8	247	270
2QJP	D E	D	261	L	1.5	247	270

2QJP	D E	D	268	G	55.2	247	270
2QJP	D E	D	269	F	3.3	247	270
2QJP	D E	E	226	R	2.0	223	254
2QJP	D E	E	230	G	18.3	223	254
2QJP	D E	E	237	L	2.8	223	254
2QJP	D F	F	34	L	1.2	11	38
2QJP	E F	E	243	L	1.2	223	254
2QJP	E F	F	15	L	1.4	11	38
2QJP	G H	G	85	R	1.8	73	87
2QJP	G H	G	91	F	2.9	90	118
2QJP	G H	G	250	I	1.1	247	270
2QJP	G H	G	254	F	2.8	247	270
2QJP	G H	G	268	G	52.0	247	270
2QJP	G H	G	269	F	6.3	247	270
2QJP	G H	G	379	W	1.0	361	382
2QJP	G H	H	226	R	2.2	223	254
2QJP	G H	H	230	G	24.9	223	254
2QJP	G H	H	237	L	1.4	223	254
2QJP	G H	H	251	L	1.9	223	254
2QJP	G I	I	34	L	1.1	11	38
2QJP	G L	G	157	W	1.2	153	167
2QJP	G L	G	160	T	1.6	153	167
2QJP	G L	G	179	W	2.4	172	182
2QJP	H I	H	243	L	1.1	223	254
2QJP	J I	J	157	W	1.3	153	167
2QJP	J I	J	164	G	1.0	153	167
2QJP	J I	J	179	W	2.4	172	182
2QJP	J I	J	329	K	1.1	328	345
2QJP	J K	J	77	F	1.1	73	87
2QJP	J K	J	85	R	1.4	73	87
2QJP	J K	J	91	F	2.2	90	118
2QJP	J K	J	95	Y	2.1	90	118
2QJP	J K	J	247	Y	2.9	247	270
2QJP	J K	J	248	F	1.3	247	270
2QJP	J K	J	254	F	3.1	247	270
2QJP	J K	J	261	L	1.4	247	270
2QJP	J K	J	268	G	61.1	247	270
2QJP	J K	J	269	F	4.4	247	270
2QJP	J K	J	379	W	1.0	361	382
2QJP	J K	K	226	R	2.6	223	254
2QJP	J K	K	230	G	28.1	223	254
2QJP	J K	K	237	L	3.0	223	254
2QJP	J K	K	244	L	1.0	223	254
2QJP	J K	K	251	L	2.0	223	254
2QJP	J K	K	252	W	3.9	223	254
2QJP	J L	L	34	L	1.1	11	38
2QJP	K L	K	243	L	1.2	223	254
2QJP	K L	L	15	L	1.3	11	38
2QJY	A B	A	77	F	1.2	73	87
2QJY	A B	A	85	R	2.0	73	87
2QJY	A B	A	91	F	2.4	90	118
2QJY	A B	A	248	F	1.1	247	270
2QJY	A B	A	250	I	1.0	247	270
2QJY	A B	A	254	F	2.7	247	270
2QJY	A B	A	261	L	1.4	247	270
2QJY	A B	A	264	F	1.0	247	270
2QJY	A B	A	268	G	20.6	247	270
2QJY	A B	A	269	F	3.3	247	270
2QJY	A B	B	226	R	1.5	223	254
2QJY	A B	B	230	G	17.2	223	254

2QJY	A B	B	237	L	1.8	223	254
2QJY	A B	B	244	L	1.0	223	254
2QJY	A B	B	251	L	2.1	223	254
2QJY	A B	B	252	W	3.7	223	254
2QJY	A F	A	157	W	1.5	153	169
2QJY	A F	A	179	W	2.5	172	182
2QJY	A F	A	329	K	1.2	328	345
2QJY	A F	F	38	M	1.7	11	39
2QJY	B C	B	240	L	1.1	223	254
2QJY	B C	B	243	L	1.2	223	254
2QJY	B C	C	15	L	2.3	11	39
2QJY	D C	D	157	W	1.6	153	169
2QJY	D C	D	179	W	2.2	172	182
2QJY	D C	C	38	M	1.6	11	39
2QJY	D E	D	85	R	1.8	73	87
2QJY	D E	D	91	F	2.5	90	118
2QJY	D E	D	95	Y	2.3	90	118
2QJY	D E	D	248	F	1.1	247	270
2QJY	D E	D	254	F	2.6	247	270
2QJY	D E	D	261	L	1.3	247	270
2QJY	D E	D	268	G	13.0	247	270
2QJY	D E	D	269	F	3.3	247	270
2QJY	D E	E	226	R	2.8	223	254
2QJY	D E	E	230	G	10.2	223	254
2QJY	D E	E	237	L	1.9	223	254
2QJY	D E	E	251	L	1.6	223	254
2QJY	D E	E	252	W	3.9	223	254
2QJY	E F	E	240	L	1.0	223	254
2QJY	E F	E	243	L	1.3	223	254
2QJY	E F	F	15	L	2.6	11	39
2QJY	G H	G	77	F	1.2	73	87
2QJY	G H	G	85	R	1.3	73	87
2QJY	G H	G	91	F	2.3	90	118
2QJY	G H	G	250	I	1.2	247	270
2QJY	G H	G	254	F	2.6	247	270
2QJY	G H	G	261	L	1.4	247	270
2QJY	G H	G	264	F	1.0	247	270
2QJY	G H	G	268	G	13.9	247	270
2QJY	G H	G	269	F	4.1	247	270
2QJY	G H	G	379	W	1.4	361	382
2QJY	G H	H	226	R	1.5	223	254
2QJY	G H	H	230	G	13.1	223	254
2QJY	G H	H	231	F	1.1	223	254
2QJY	G H	H	237	L	1.9	223	254
2QJY	G H	H	244	L	1.0	223	254
2QJY	G H	H	251	L	1.5	223	254
2QJY	G H	H	252	W	3.3	223	254
2QJY	G I	G	82	H	1.0	73	87
2QJY	G L	G	157	W	1.6	153	169
2QJY	G L	G	179	W	2.3	172	182
2QJY	G L	G	329	K	1.1	328	345
2QJY	G L	L	38	M	1.5	11	39
2QJY	H I	H	243	L	1.0	223	254
2QJY	H I	I	15	L	2.0	11	39
2QJY	J I	J	157	W	1.2	153	169
2QJY	J I	J	179	W	2.0	172	182
2QJY	J I	J	193	R	1.5	188	220
2QJY	J I	I	38	M	2.5	11	39
2QJY	J K	J	77	F	1.3	73	87
2QJY	J K	J	85	R	1.5	73	87

2QJY	J K	J	91	F	2.0	90	118
2QJY	J K	J	95	Y	1.8	90	118
2QJY	J K	J	248	F	1.1	247	270
2QJY	J K	J	254	F	2.7	247	270
2QJY	J K	J	261	L	1.2	247	270
2QJY	J K	J	264	F	1.0	247	270
2QJY	J K	J	268	G	21.2	247	270
2QJY	J K	J	269	F	4.1	247	270
2QJY	J K	J	379	W	1.0	361	382
2QJY	J K	K	226	R	1.9	223	254
2QJY	J K	K	230	G	8.7	223	254
2QJY	J K	K	231	F	1.3	223	254
2QJY	J K	K	237	L	2.5	223	254
2QJY	J K	K	244	L	1.1	223	254
2QJY	J K	K	251	L	2.0	223	254
2QJY	J K	K	252	W	3.6	223	254
2QJY	K L	K	240	L	1.1	223	254
2QJY	K L	K	243	L	1.1	223	254
2QJY	K L	L	15	L	2.2	11	39
2QJY	M N	M	77	F	1.1	73	87
2QJY	M N	M	85	R	2.1	73	87
2QJY	M N	M	91	F	1.9	90	118
2QJY	M N	M	95	Y	1.9	90	118
2QJY	M N	M	248	F	1.1	247	270
2QJY	M N	M	250	I	1.2	247	270
2QJY	M N	M	254	F	2.7	247	270
2QJY	M N	M	268	G	12.4	247	270
2QJY	M N	M	269	F	3.9	247	270
2QJY	M N	N	120	Q	1.0	118	123
2QJY	M N	N	226	R	3.0	223	254
2QJY	M N	N	230	G	7.6	223	254
2QJY	M N	N	231	F	1.0	223	254
2QJY	M N	N	237	L	1.3	223	254
2QJY	M N	N	244	L	1.3	223	254
2QJY	M N	N	251	L	2.5	223	254
2QJY	M N	N	252	W	4.6	223	254
2QJY	M O	M	64	V	1.2	46	68
2QJY	M O	M	82	H	1.0	73	87
2QJY	M R	M	157	W	1.5	153	169
2QJY	M R	M	179	W	2.0	172	182
2QJY	M R	R	38	M	1.6	11	39
2QJY	N O	N	243	L	1.2	223	254
2QJY	N O	O	15	L	2.1	11	39
2QJY	P O	P	157	W	1.6	153	169
2QJY	P O	P	179	W	2.0	172	182
2QJY	P O	P	193	R	1.5	188	220
2QJY	P O	O	38	M	1.6	11	39
2QJY	P Q	P	85	R	1.3	73	87
2QJY	P Q	P	91	F	2.2	90	118
2QJY	P Q	P	248	F	1.1	247	270
2QJY	P Q	P	250	I	1.2	247	270
2QJY	P Q	P	254	F	2.8	247	270
2QJY	P Q	P	261	L	1.4	247	270
2QJY	P Q	P	268	G	16.8	247	270
2QJY	P Q	P	269	F	4.0	247	270
2QJY	P Q	Q	226	R	2.0	223	254
2QJY	P Q	Q	230	G	9.9	223	254
2QJY	P Q	Q	231	F	1.2	223	254
2QJY	P Q	Q	237	L	1.9	223	254
2QJY	P Q	Q	244	L	1.1	223	254

2QJY	P Q	Q	251	L	2.3	223	254
2QJY	P Q	Q	252	W	4.7	223	254
2QJY	P R	P	82	H	1.0	73	87
2QJY	Q R	Q	243	L	1.2	223	254
2QJY	Q R	R	15	L	2.1	11	39
2QKH	B A	B	19	Q	1.0	6	32
2QKH	B A	B	22	F	2.4	6	32
2QKH	B A	B	23	V	1.4	6	32
2QKH	B A	B	26	L	1.7	6	32
2QKH	B A	B	27	L	1.8	6	32
2QKH	B A	A	35	L	1.4	32	53
2QKH	B A	A	39	W	1.7	32	53
2QKI	A B	A	579	G	1.1	578	584
2QKI	A B	A	594	I	1.1	591	601
2QKI	A C	C	1410	Y	1.9	1409	1413
2QKI	D E	D	594	I	1.3	591	601
2QKI	D F	F	1410	Y	1.6	1409	1413
2QKI	D H	D	462	E	1.0	459	465
2QKL	A B	A	8	R	2.6	3	20
2QKL	A B	A	12	N	1.0	3	20
2QKL	A B	A	15	V	1.3	3	20
2QKL	A B	A	19	H	1.4	3	20
2QKL	A B	B	14	D	4.2	8	22
2QKL	A B	B	18	R	3.4	8	22
2QKL	A B	B	19	F	1.3	8	22
2QKL	A B	B	44	F	2.2	31	53
2QKL	A B	B	48	F	2.0	31	53
2QKL	A B	B	78	W	2.8	73	79
2QKM	A B	A	12	N	1.0	2	20
2QKM	A B	A	18	F	1.3	2	20
2QKM	A B	B	18	R	2.2	8	22
2QKM	A B	B	19	F	1.3	8	22
2QKM	A B	B	44	F	3.0	31	52
2QKM	A B	B	48	F	2.1	31	52
2QKM	C B	B	26	E	1.0	25	29
2QKM	C D	C	11	V	1.3	2	20
2QKM	C D	C	12	N	1.0	2	20
2QKM	C D	C	15	V	1.0	2	20
2QKM	C D	C	18	F	1.6	2	20
2QKM	C D	C	19	H	2.3	2	20
2QKM	C D	D	14	D	1.3	8	20
2QKM	C D	D	18	R	2.9	8	20
2QKM	C D	D	19	F	1.4	8	20
2QKM	C D	D	44	F	2.0	31	53
2QKM	C D	D	48	F	1.9	31	53
2QKM	E F	E	8	R	3.2	3	20
2QKM	E F	E	11	V	1.1	3	20
2QKM	E F	E	12	N	1.4	3	20
2QKM	E F	E	15	V	1.4	3	20
2QKM	E F	E	18	F	1.4	3	20
2QKM	E F	E	19	H	1.3	3	20
2QKM	E F	F	19	F	1.4	8	22
2QKM	E F	F	21	L	1.5	8	22
2QKM	E F	F	44	F	2.6	31	53
2QKM	E F	F	48	F	2.3	31	53
2QKM	G H	G	8	R	1.0	2	20
2QKM	G H	G	12	N	1.0	2	20
2QKM	G H	G	15	V	1.2	2	20
2QKM	G H	G	18	F	1.4	2	20
2QKM	G H	G	19	H	1.9	2	20

2QKM	G H	H	14	D	1.5	9	20
2QKM	G H	H	18	R	1.7	9	20
2QKM	G H	H	19	F	1.4	9	20
2QKM	G H	H	44	F	2.2	31	52
2QKM	G H	H	48	F	1.8	31	52
2QL2	A B	A	562	F	1.6	544	571
2QL2	A B	A	564	E	1.1	544	571
2QL2	A B	A	565	L	2.3	544	571
2QL2	A B	A	568	M	1.9	544	571
2QL2	A B	A	585	L	1.5	581	599
2QL2	A B	A	589	V	1.5	581	599
2QL2	A B	A	592	I	2.7	581	599
2QL2	A B	A	595	L	1.1	581	599
2QL2	A B	A	596	E	1.3	581	599
2QL2	A B	B	124	L	1.8	102	127
2QL2	A B	B	139	K	1.1	139	157
2QL2	A B	B	143	L	3.0	139	157
2QL2	A B	B	147	K	2.1	139	157
2QL2	A B	B	149	Y	1.9	139	157
2QL2	A B	B	150	I	1.9	139	157
2QL2	A B	B	153	L	2.0	139	157
2QL2	C B	C	600	R	1.6	581	601
2QL2	C B	B	141	E	2.6	139	157
2QL2	C D	C	558	I	1.3	544	573
2QL2	C D	C	562	F	2.1	544	573
2QL2	C D	C	564	E	1.1	544	573
2QL2	C D	C	565	L	2.1	544	573
2QL2	C D	C	585	L	1.9	581	601
2QL2	C D	C	589	V	1.2	581	601
2QL2	C D	C	592	I	2.8	581	601
2QL2	C D	C	599	V	1.6	581	601
2QL2	C D	D	117	L	1.2	103	127
2QL2	C D	D	124	L	1.7	103	127
2QL2	C D	D	139	K	1.1	139	158
2QL2	C D	D	140	I	1.1	139	158
2QL2	C D	D	143	L	2.7	139	158
2QL2	C D	D	147	K	1.3	139	158
2QL2	C D	D	149	Y	1.4	139	158
2QL2	C D	D	150	I	2.1	139	158
2QL2	C D	D	153	L	2.2	139	158
2QL2	C D	D	157	L	1.9	139	158
2QL5	A B	A	93	D	1.6	90	105
2QL5	A B	A	97	L	1.3	90	105
2QL5	A B	A	104	L	2.3	90	105
2QL5	A B	B	242	V	1.6	240	250
2QL5	A B	B	245	L	1.4	240	250
2QL5	A B	B	249	L	1.0	240	250
2QL5	C D	C	393	D	1.8	390	405
2QL5	C D	C	397	L	1.2	390	405
2QL5	C D	C	404	L	1.8	390	405
2QL5	C D	D	542	V	1.1	540	552
2QL5	C D	D	545	L	1.3	540	552
2QLV	A B	A	516	L	2.5	516	529
2QLV	A B	A	523	Y	2.6	516	529
2QLV	A B	A	616	L	1.9	612	630
2QLV	A B	A	623	I	1.1	612	630
2QLV	A B	B	322	Y	1.2	316	327
2QLV	A C	A	475	P	1.2	475	486
2QLV	A C	A	479	R	1.2	475	486
2QLV	A C	A	610	F	1.3	607	611

2QLV	A C	A	613	Y	3.0	612	630
2QLV	A C	C	243	G	1.0	238	245
2QLV	A C	C	259	E	1.0	257	262
2QLV	B C	C	177	N	1.8	167	178
2QLV	D E	D	520	G	2.4	516	529
2QLV	D E	D	523	Y	1.2	516	529
2QLV	D E	D	613	Y	1.1	612	630
2QLV	D E	D	615	F	1.0	612	630
2QLV	D E	D	616	L	1.4	612	630
2QLV	D F	D	478	H	1.4	475	486
2QLV	D F	D	479	R	1.2	475	486
2QLV	D F	F	243	G	21.6	238	246
2QLV	D F	F	258	G	2.8	257	264
2QLV	D F	F	262	M	2.6	257	264
2QLV	E F	F	173	F	1.4	167	177
2QM6	A B	A	68	I	1.2	61	75
2QM6	A B	A	69	G	8.0	61	75
2QM6	A B	A	72	L	1.3	61	75
2QM6	A B	A	186	R	3.7	184	190
2QM6	A B	A	187	F	2.2	184	190
2QM6	A B	A	193	S	1.7	191	197
2QM6	A B	A	196	Y	2.4	191	197
2QM6	A B	A	239	L	1.0	235	247
2QM6	A B	A	240	I	1.0	235	247
2QM6	A B	A	243	D	1.9	235	247
2QM6	A B	A	285	G	60.5	285	299
2QM6	A B	A	289	L	1.4	285	299
2QM6	A B	A	293	L	1.8	285	299
2QM6	A B	A	312	I	2.6	309	330
2QM6	A B	A	313	H	2.1	309	330
2QM6	A B	A	319	M	1.9	309	330
2QM6	A B	A	320	R	2.4	309	330
2QM6	A B	A	323	Y	3.1	309	330
2QM6	A B	B	420	M	1.9	419	423
2QM6	A B	B	422	D	1.1	419	423
2QM6	A B	B	477	I	2.1	476	490
2QM6	A B	B	481	L	1.1	476	490
2QM6	A B	B	484	I	1.2	476	490
2QM6	A B	B	488	I	2.8	476	490
2QM6	A B	B	489	D	1.2	476	490
2QM6	A B	B	527	L	2.0	521	531
2QM6	A B	B	530	M	1.6	521	531
2QM6	C D	C	69	G	4.4	61	76
2QM6	C D	C	72	L	1.2	61	76
2QM6	C D	C	186	R	3.5	184	190
2QM6	C D	C	193	S	1.4	191	197
2QM6	C D	C	196	Y	3.6	191	197
2QM6	C D	C	240	I	1.1	235	247
2QM6	C D	C	243	D	1.1	235	247
2QM6	C D	C	285	G	59.3	285	299
2QM6	C D	C	289	L	1.5	285	299
2QM6	C D	C	293	L	2.3	285	299
2QM6	C D	C	312	I	2.6	309	329
2QM6	C D	C	319	M	1.9	309	329
2QM6	C D	C	320	R	2.1	309	329
2QM6	C D	C	323	Y	3.1	309	329
2QM6	C D	D	420	M	1.8	419	423
2QM6	C D	D	477	I	1.9	476	490
2QM6	C D	D	481	L	1.8	476	490
2QM6	C D	D	484	I	1.3	476	490

2QM6	C D	D	488	I	2.8	476	490
2QM6	C D	D	527	L	2.0	521	531
2QM6	C D	D	530	M	1.2	521	531
2QMB	A B	B	34	V	1.5	20	35
2QMB	A D	A	95	P	1.4	95	113
2QMB	A D	D	37	W	3.1	36	42
2QMB	C B	C	95	P	1.8	95	112
2QMB	C B	B	37	W	6.9	36	42
2QMB	C B	B	39	Q	1.4	36	42
2QMB	C B	B	102	N	1.7	100	117
2QMB	C D	C	34	I	1.0	22	36
2QMB	C D	C	119	P	1.2	119	137
2QMB	C D	C	122	H	3.2	119	137
2QMB	C D	D	30	R	2.1	20	35
2QMB	C D	D	34	V	1.7	20	35
2QMB	C D	D	112	I	1.5	103	117
2QME	A I	A	23	Y	1.3	16	26
2QME	A I	A	166	K	2.1	165	178
2QMU	A B	B	193	V	1.2	193	201
2QMU	A B	B	200	I	1.0	193	201
2QMU	A C	A	156	K	1.4	156	171
2QMU	A C	C	7	Y	3.2	4	16
2QNA	A B	A	585	C	1.1	578	595
2QNA	A B	A	630	M	1.4	622	640
2QNA	A B	A	719	D	1.1	707	725
2QNA	A B	A	820	G	3.2	812	830
2QNA	A B	A	824	D	4.1	812	830
2QNA	A B	A	857	K	1.2	856	874
2QNA	A B	A	864	W	2.9	856	874
2QNA	A B	B	51	Q	1.1	38	64
2QNA	A B	B	52	K	1.2	38	64
2QNA	A B	B	55	R	1.4	38	64
2QNA	A B	B	56	L	2.2	38	64
2QNA	A B	B	63	R	2.9	38	64
2QOG	A C	C	3	L	2.3	2	14
2QOG	A C	C	4	Q	2.5	2	14
2QOG	A C	C	10	K	1.3	2	14
2QOG	D B	D	52	Y	1.3	40	55
2QOG	D B	B	4	Q	1.0	2	14
2QOU	C N	C	28	F	1.9	27	46
2QOU	C N	C	32	L	1.3	27	46
2QOU	E H	E	149	P	8.5	149	156
2QOU	E H	E	151	M	8.0	149	156
2QOU	E H	E	154	A	8.1	149	156
2QOU	G K	K	60	F	2.1	59	71
2QOU	J N	N	80	R	9.2	80	90
2QOU	M S	M	82	L	1.0	66	83
2QOW	C N	C	28	F	1.1	26	46
2QOW	C N	C	32	L	1.8	26	46
2QOW	C N	C	36	F	1.7	26	46
2QOW	C N	C	39	R	1.2	26	46
2QOW	E H	E	149	P	12.6	149	156
2QOW	E H	E	151	M	12.1	149	156
2QOW	E H	E	154	A	12.2	149	156
2QOW	K G	K	59	P	1.1	59	71
2QOW	K G	K	60	F	1.5	59	71
2QOY	C N	C	28	F	1.3	26	46
2QOY	C N	C	32	L	2.1	26	46
2QOY	F R	R	63	Y	1.4	48	64
2QOY	G K	K	60	F	1.4	59	72

2QOY	J N	N	80	R	2.0	80	89
2QOY	K U	U	32	R	1.2	27	33
2QOY	M S	M	78	R	1.1	66	83
2QP0	E H	E	155	K	1.1	149	156
2QP0	K G	K	60	F	1.2	59	72
2QP0	M S	M	78	R	1.1	68	83
2QP0	N S	N	45	L	1.0	42	47
2QQD	A B	A	30	P	1.7	30	42
2QQD	A B	A	34	F	2.7	30	42
2QQD	A E	A	31	L	1.2	30	42
2QQD	A E	A	35	D	1.6	30	42
2QQD	A E	E	130	G	2.4	116	135
2QQD	A E	E	134	R	3.1	116	135
2QQD	B C	B	126	M	1.3	116	135
2QQD	B C	B	130	G	2.7	116	135
2QQD	B C	B	134	R	3.3	116	135
2QQD	B C	C	31	L	1.0	30	42
2QQD	B C	C	35	D	1.6	30	42
2QQD	B F	B	120	E	1.2	116	135
2QQD	D C	D	35	D	2.0	30	42
2QQD	D C	C	134	R	2.3	116	135
2QQD	D E	D	34	F	3.3	30	42
2QQK	H L	L	124	Q	1.2	122	127
2QQN	H L	L	124	Q	2.7	122	128
2QQP	A B	A	93	G	40.3	91	97
2QQP	A B	A	539	L	1.2	534	541
2QQP	A B	B	569	L	2.0	560	574
2QQP	A F	F	583	K	1.4	579	591
2QQP	C B	B	583	K	2.7	579	592
2QQP	C D	C	93	G	13.6	92	97
2QQP	C D	C	539	L	2.4	534	547
2QQP	C D	C	542	R	1.0	534	547
2QQP	C D	C	543	L	1.2	534	547
2QQP	C D	D	561	V	1.1	560	564
2QQP	C D	D	569	L	1.1	565	574
2QQP	C D	D	572	L	1.6	565	574
2QQP	C D	D	582	I	3.5	579	590
2QQP	C D	D	586	A	1.1	579	590
2QQP	E D	D	583	K	1.9	579	590
2QQP	E F	E	93	G	57.0	91	96
2QQP	E F	E	539	L	2.4	538	547
2QQP	E F	F	562	S	1.9	560	575
2QQP	E F	F	569	L	1.2	560	575
2QQP	E F	F	572	L	1.5	560	575
2QQP	G H	G	85	F	1.9	79	90
2QQP	G H	G	93	G	174.4	92	98
2QQP	G H	G	539	L	2.0	534	547
2QQP	G H	G	546	E	1.0	534	547
2QQP	G H	H	569	L	2.1	560	575
2QQP	G H	H	573	G	5.7	560	575
2QQP	G H	H	582	I	1.3	579	589
2QR0	A B	A	124	Q	1.2	122	128
2QR0	A C	C	17	F	1.8	17	24
2QR0	A C	C	18	M	1.2	17	24
2QR0	E F	E	123	E	1.8	122	128
2QR0	E F	E	124	Q	1.8	122	128
2QR0	G H	G	124	Q	1.2	122	128
2QR0	K J	J	17	F	2.1	17	24
2QR0	K J	J	21	Y	1.3	17	24
2QR0	K L	K	124	Q	1.4	122	128

2QR0	M N	M	124	Q	1.5	122	128
2QR0	M P	P	18	M	1.4	17	24
2QR0	Q R	Q	123	E	1.0	122	128
2QR0	Q R	Q	124	Q	1.0	122	128
2QR0	S T	S	124	Q	1.2	122	128
2QR0	W U	U	17	F	1.3	17	24
2QR0	W X	W	124	Q	1.7	122	128
2QR1	A B	A	470	Y	1.3	462	477
2QR1	A B	A	562	F	1.5	562	575
2QR1	A B	A	563	L	1.4	562	575
2QR1	A B	A	566	C	4.0	562	575
2QR1	A E	A	574	F	1.7	562	575
2QR1	A G	A	505	H	1.6	504	510
2QR1	A G	A	564	D	1.6	562	575
2QR1	B G	G	25	Y	2.5	24	28
2QR1	B G	G	45	T	3.2	43	53
2QR1	B G	G	49	L	1.9	43	53
2QR1	C D	C	467	L	1.3	462	476
2QR1	C D	C	470	Y	1.6	462	476
2QR1	C D	C	562	F	1.5	562	575
2QR1	C D	C	563	L	1.7	562	575
2QR1	C D	D	215	F	2.0	214	219
2QR1	C D	D	216	L	1.8	214	219
2QR1	C E	C	564	D	1.5	562	575
2QR1	C G	C	574	F	2.5	562	575
2QR1	D E	E	25	Y	2.7	24	28
2QR1	D E	E	49	L	1.8	43	53
2QR1	D G	G	99	K	1.2	93	100
2QRV	A B	A	728	F	2.4	723	738
2QRV	A B	A	729	E	1.5	723	738
2QRV	A B	A	731	Y	2.9	723	738
2QRV	A B	A	732	R	3.1	723	738
2QRV	A B	A	768	F	4.7	759	769
2QRV	A B	B	258	W	2.1	256	271
2QRV	A B	B	261	F	2.9	256	271
2QRV	A B	B	262	Q	2.1	256	271
2QRV	A B	B	264	H	1.6	256	271
2QRV	A B	B	265	R	3.3	256	271
2QRV	A B	B	269	Y	1.1	256	271
2QRV	A B	B	297	V	1.5	293	302
2QRV	D C	D	728	F	2.9	723	738
2QRV	D C	D	732	R	1.6	723	738
2QRV	D C	D	767	R	1.1	759	769
2QRV	D C	D	768	F	3.0	759	769
2QRV	D C	C	261	F	3.4	256	270
2QRV	D C	C	265	R	1.2	256	270
2QRV	E F	E	728	F	3.0	723	738
2QRV	E F	E	768	F	2.8	759	769
2QRV	E F	F	261	F	3.6	256	271
2QRV	E F	F	265	R	2.6	256	271
2QRV	E F	F	293	E	1.9	292	302
2QRV	H G	H	725	R	1.0	723	738
2QRV	H G	H	728	F	1.5	723	738
2QRV	H G	H	731	Y	2.3	723	738
2QRV	H G	H	732	R	1.7	723	738
2QRV	H G	H	767	R	1.3	759	769
2QRV	H G	H	768	F	2.0	759	769
2QRV	H G	G	261	F	2.6	256	270
2QRV	H G	G	262	Q	1.1	256	270
2QRV	H G	G	264	H	1.3	256	270

2QRV	H G	G	265	R	2.0	256	270
2QRV	H G	G	301	F	2.2	292	302
2QSH	A X	A	139	R	1.0	134	163
2QSH	A X	A	142	Y	1.7	134	163
2QSH	A X	A	146	L	1.4	134	163
2QSH	A X	A	147	Y	1.5	134	163
2QSH	A X	A	153	V	1.3	134	163
2QSH	A X	A	157	I	1.2	134	163
2QSH	A X	A	401	W	2.5	396	409
2QSH	A X	X	269	V	1.4	259	271
2QSH	A X	X	276	L	1.2	276	286
2QSH	A X	X	280	L	1.3	276	286
2QSH	A X	X	291	R	2.2	288	297
2QSH	A X	X	294	I	1.2	288	297
2QSH	A X	X	298	P	1.1	298	307
2QSH	A X	X	302	V	1.5	298	307
2QSH	A X	X	306	L	1.0	298	307
2QTV	A B	A	312	H	2.4	311	316
2QTV	A B	A	723	F	2.3	721	728
2QTV	A B	B	82	R	1.0	78	87
2QTV	A B	B	83	L	1.4	78	87
2QTV	B D	B	78	I	1.6	78	87
2QTV	B D	B	81	R	2.7	78	87
2QTV	B D	B	112	E	1.6	106	118
2QVS	E B	E	129	F	1.4	128	135
2QVS	E B	E	230	E	2.2	217	232
2QVS	E B	B	134	L	1.6	134	138
2QVS	E B	B	245	R	4.1	230	254
2QVS	E B	B	271	D	3.4	263	273
2QVS	E B	B	365	R	1.7	360	367
2QVS	E B	B	366	L	1.5	360	367
2QXV	A B	B	42	F	4.3	41	63
2QXV	A B	B	46	R	1.5	41	63
2QXV	A B	B	49	I	2.2	41	63
2QXV	A B	B	52	R	2.4	41	63
2QXV	A B	B	56	L	1.7	41	63
2QXV	A B	B	60	W	2.1	41	63
2QY0	A D	D	514	K	1.5	509	516
2QY0	C B	B	513	M	1.0	509	516
2QYF	A B	A	133	R	1.2	121	142
2QYF	A B	A	141	F	2.5	121	142
2QYF	A B	B	188	R	1.1	183	195
2QYF	A B	B	189	R	1.0	183	195
2QYF	C B	B	189	R	2.2	183	195
2QYF	C D	D	188	R	1.5	182	195
2QYF	C D	D	192	R	1.4	182	195
2R00	A C	A	85	P	2.5	77	90
2R00	A C	A	220	W	1.5	213	227
2R00	A C	C	78	E	1.2	77	90
2R00	A C	C	79	L	1.2	77	90
2R00	A C	C	86	I	1.2	77	90
2R00	A C	C	220	W	1.7	213	226
2R17	A C	A	104	R	2.3	98	107
2R17	A C	C	534	F	3.4	524	545
2R17	A C	C	541	F	1.1	524	545
2R17	A C	C	633	G	14.3	621	637
2R17	A C	C	675	H	1.1	663	677
2R17	A C	C	725	N	2.0	713	732
2R17	A C	C	729	Y	1.5	713	732
2R17	A C	C	772	N	2.4	761	777

2R17	B D	B	104	R	1.9	98	107
2R17	B D	D	492	G	69.6	485	497
2R17	B D	D	630	L	2.5	621	637
2R17	B D	D	633	G	14.0	621	637
2R17	B D	D	675	H	1.3	663	677
2R17	B D	D	725	N	2.2	713	732
2R17	B D	D	729	Y	2.3	713	732
2R17	B D	D	772	N	2.0	761	777
2R1H	A B	A	31	R	3.6	21	36
2R1H	A B	A	35	V	1.1	21	36
2R1H	A B	A	113	Y	1.1	96	114
2R1H	A B	A	120	P	1.1	120	140
2R1H	A B	A	123	H	2.9	120	140
2R1H	A B	B	30	R	4.0	20	35
2R1H	A B	B	33	I	1.0	20	35
2R1H	A B	B	34	V	1.8	20	35
2R1H	A B	B	112	V	1.3	100	119
2R1H	A D	D	37	W	2.7	36	41
2R1H	C B	C	96	P	1.1	96	114
2R1H	C B	C	98	N	1.2	96	114
2R1H	C B	B	37	W	3.5	36	41
2R1H	C D	C	31	R	3.8	21	36
2R1H	C D	C	35	V	1.0	21	36
2R1H	C D	C	113	Y	1.1	96	114
2R1H	C D	C	120	P	1.1	120	138
2R1H	C D	C	123	H	4.3	120	138
2R1H	C D	D	30	R	4.0	20	35
2R1H	C D	D	34	V	1.8	20	35
2R1H	C D	D	112	V	1.3	100	119
2R1T	A B	A	20	V	1.3	19	29
2R1T	A B	A	27	R	1.9	19	29
2R1T	A B	A	28	R	1.1	19	29
2R1T	A B	A	162	F	1.9	161	173
2R1T	A B	B	20	V	1.3	19	29
2R1T	A B	B	27	R	1.9	19	29
2R1T	A B	B	28	R	1.4	19	29
2R1T	A B	B	162	F	2.0	161	173
2R4R	L H	L	124	Q	2.0	122	128
2R5C	A B	A	111	Y	2.9	110	121
2R5C	A B	B	27	W	1.5	26	37
2R5C	A B	B	28	V	1.0	26	37
2R5C	A B	B	111	Y	2.6	111	121
2R5C	A B	B	282	Q	1.1	271	283
2R5Y	A B	B	256	Y	2.7	242	259
2R6C	A G	A	68	V	1.8	67	77
2R6C	A G	A	86	V	1.4	86	96
2R6C	A G	G	578	L	1.0	577	586
2R6C	B G	G	548	Y	1.1	542	554
2R6C	C H	C	67	L	2.4	67	77
2R6C	C H	C	68	V	1.2	67	77
2R6C	C H	C	86	V	1.1	86	96
2R6C	C H	H	585	K	2.3	577	586
2R6C	D H	H	548	Y	1.0	542	554
2R6C	E I	E	68	V	1.3	67	77
2R6C	E I	I	585	K	1.2	577	586
2R6G	A G	A	47	R	1.6	42	51
2R6G	A G	A	98	F	1.6	98	102
2R6G	A G	G	190	E	2.2	186	195
2R6G	A G	G	194	L	2.8	186	195
2R6G	A G	G	206	V	1.1	199	211

2R6G	A G	G	210	L	1.9	199	211
2R6G	B F	B	98	F	2.6	98	104
2R6G	B F	F	399	L	1.5	397	406
2R6G	B F	F	403	S	1.1	397	406
2R6G	B F	F	405	M	2.9	397	406
2R6G	B F	F	417	I	1.7	410	420
2R6G	E F	E	275	L	1.1	273	282
2R6G	E F	E	341	Y	1.5	336	353
2R6G	E F	F	104	R	1.5	102	110
2R6G	E F	F	173	L	1.8	173	179
2R6G	E F	F	180	R	1.1	180	186
2R6G	E G	E	230	W	1.5	229	239
2R6G	E G	E	234	N	1.2	229	239
2R6G	F G	F	67	Y	3.2	63	78
2R6G	F G	F	68	V	2.0	63	78
2R6G	F G	F	71	G	2.5	63	78
2R6G	F G	F	72	M	1.0	63	78
2R6G	F G	F	75	M	1.0	63	78
2R6G	F G	F	83	L	1.5	79	91
2R6G	F G	F	302	L	2.1	291	307
2R6G	F G	F	317	Y	2.1	314	327
2R6G	F G	F	318	R	1.2	314	327
2R6G	F G	F	322	I	1.2	314	327
2R6G	F G	F	325	Y	1.2	314	327
2R6G	F G	F	330	F	2.0	329	340
2R6G	F G	F	331	I	2.9	329	340
2R6G	F G	F	335	I	1.4	329	340
2R6G	F G	F	339	L	1.1	329	340
2R6G	F G	F	386	I	1.2	365	395
2R6G	F G	F	390	G	127.3	365	395
2R6G	F G	F	391	L	4.4	365	395
2R6G	F G	F	393	K	1.1	365	395
2R6G	F G	F	495	F	1.7	484	504
2R6G	F G	G	16	T	1.0	9	40
2R6G	F G	G	17	H	1.4	9	40
2R6G	F G	G	20	L	1.5	9	40
2R6G	F G	G	31	L	2.2	9	40
2R6G	F G	G	34	V	1.0	9	40
2R6G	F G	G	143	L	1.5	136	151
2R6G	F G	G	168	G	188.0	159	169
2R6G	F G	G	175	W	1.2	170	184
2R6G	F G	G	180	Y	1.5	170	184
2R6G	F G	G	199	P	1.1	199	211
2R6G	F G	G	213	P	5.4	212	228
2R6G	F G	G	217	V	1.4	212	228
2R6G	F G	G	221	L	1.5	212	228
2R6G	F G	G	260	W	1.1	260	285
2R6G	F G	G	263	F	2.7	260	285
2R6G	F G	G	278	F	2.6	260	285
2R6G	F G	G	282	Q	2.2	260	285
2R9R	A B	B	66	M	1.3	62	68
2R9R	G H	G	203	R	1.4	192	205
2R9R	G H	G	235	K	1.0	222	236
2R9R	G H	H	66	M	1.2	62	68
2RAO	A B	A	31	R	1.1	21	36
2RAO	A B	A	107	V	1.0	95	113
2RAO	A B	A	122	H	4.5	119	137
2RAO	A B	B	30	R	3.7	20	35
2RAO	A B	B	34	V	1.5	20	35
2RAO	A B	B	112	I	1.7	100	119

2RAO	A B	B	116	H	1.1	100	119
2RAO	A B	B	124	P	1.2	124	142
2RAO	A D	A	95	P	1.3	95	113
2RAO	A D	D	37	W	2.4	36	42
2RAO	A D	D	102	N	1.5	100	119
2RAO	C B	C	95	P	1.0	95	113
2RAO	C B	B	37	W	1.7	36	42
2RAO	C B	B	102	N	1.2	100	119
2RAO	C D	C	31	R	3.4	21	36
2RAO	C D	C	103	H	1.7	95	113
2RAO	C D	C	111	N	1.0	95	113
2RAO	C D	C	122	H	2.5	119	137
2RAO	C D	D	30	R	3.5	20	35
2RAO	C D	D	34	V	1.0	20	35
2RAO	C D	D	111	V	1.1	100	119
2RAO	C D	D	112	I	1.6	100	119
2RAW	A B	A	98	L	2.6	98	140
2RAW	A B	A	99	G	2.4	98	140
2RAW	A B	A	101	F	2.5	98	140
2RAW	A B	A	105	D	1.6	98	140
2RAW	A B	A	106	R	1.6	98	140
2RAW	A B	A	113	I	2.7	98	140
2RAW	A B	A	124	F	1.7	98	140
2RAW	A B	A	132	R	1.2	98	140
2RAW	A B	A	135	I	1.4	98	140
2RAW	A B	B	25	L	1.2	24	60
2RAW	A B	B	28	F	3.3	24	60
2RAW	A B	B	39	I	1.2	24	60
2RAW	A B	B	50	V	1.5	24	60
2RAW	A B	B	54	Y	3.6	24	60
2RAW	A B	B	70	W	5.4	70	75
2RAW	A B	B	71	L	1.8	70	75
2RAW	A B	B	73	Y	1.3	70	75
2RAW	A B	B	74	F	2.8	70	75
2RAX	A B	A	10	W	1.3	8	12
2RAX	A B	A	98	L	2.7	98	116
2RAX	A B	A	99	G	28.5	98	116
2RAX	A B	A	101	F	2.1	98	116
2RAX	A B	A	110	K	1.7	98	116
2RAX	A B	A	113	I	1.8	98	116
2RAX	A B	B	47	L	1.7	23	61
2RAX	A B	B	50	V	1.5	23	61
2RAX	A B	B	51	D	1.0	23	61
2RAX	A B	B	54	Y	3.6	23	61
2RAX	A B	B	58	I	1.6	23	61
2RAX	A B	B	70	W	2.9	70	74
2RAX	A B	B	71	L	1.7	70	74
2RAX	A B	B	73	Y	1.3	70	74
2RAX	A F	F	36	I	1.6	24	61
2RAX	E B	E	113	I	1.2	98	119
2RAX	E B	B	36	I	1.6	23	61
2RAX	E F	E	10	W	1.3	8	12
2RAX	E F	E	98	L	2.9	98	119
2RAX	E F	E	99	G	33.9	98	119
2RAX	E F	E	101	F	2.1	98	119
2RAX	E F	E	110	K	1.2	98	119
2RAX	E F	E	113	I	3.2	98	119
2RAX	E F	F	47	L	2.0	24	61
2RAX	E F	F	50	V	1.4	24	61
2RAX	E F	F	54	Y	1.2	24	61

2RAX	E F	F	58	I	1.2	24	61
2RAX	E F	F	70	W	3.4	70	74
2RAX	E F	F	71	L	1.6	70	74
2RAX	E F	F	73	Y	1.2	70	74
2RAX	X Y	X	98	L	2.4	98	116
2RAX	X Y	X	99	G	34.5	98	116
2RAX	X Y	X	101	F	1.8	98	116
2RAX	X Y	X	102	L	1.0	98	116
2RAX	X Y	Y	46	L	1.3	24	61
2RAX	X Y	Y	50	V	1.4	24	61
2RAX	X Y	Y	58	I	1.5	24	61
2RAX	X Y	Y	71	L	1.5	70	74
2RAX	X Y	Y	73	Y	1.5	70	74
2RD0	A B	B	467	Y	1.6	450	499
2RD0	A B	B	487	F	1.0	450	499
2RD0	A B	B	494	F	1.6	450	499
2RD0	A B	B	567	K	1.1	565	573
2RD4	A B	B	20	W	4.1	19	24
2RD7	A C	A	414	R	1.9	413	419
2RD7	A C	A	417	G	34.5	413	419
2RD7	A C	C	43	L	1.1	41	49
2RET	A B	B	41	L	1.1	33	49
2RET	C D	C	35	E	1.0	31	37
2RET	E F	F	44	L	1.6	34	49
2RET	G H	H	41	L	1.1	34	49
2REX	A B	A	1839	Y	1.4	1836	1840
2REX	A B	B	76	N	1.0	75	83
2REX	A B	B	114	Y	1.2	104	115
2REX	C D	C	1839	Y	1.5	1836	1840
2REX	C D	D	76	N	1.0	75	83
2REX	C D	D	80	L	1.1	75	83
2REX	C D	D	114	Y	1.2	104	115
2RF4	A B	B	39	F	4.1	33	49
2RF4	A B	B	43	F	2.3	33	49
2RF4	A B	B	82	L	1.5	82	99
2RF4	A B	B	89	L	1.1	82	99
2RF4	A B	B	92	I	1.7	82	99
2RF4	A B	B	96	F	1.3	82	99
2RF4	A D	D	90	K	1.2	82	99
2RF4	A D	D	91	R	1.6	82	99
2RF4	A D	D	94	R	1.4	82	99
2RF4	C B	B	90	K	1.4	82	99
2RF4	C B	B	94	R	1.0	82	99
2RF4	C D	D	39	F	3.9	33	48
2RF4	C D	D	43	F	2.6	33	48
2RF4	C D	D	82	L	1.8	82	99
2RF4	C D	D	89	L	1.1	82	99
2RF4	C D	D	91	R	1.3	82	99
2RF4	C D	D	92	I	1.6	82	99
2RF4	C D	D	96	F	1.5	82	99
2RF4	E F	F	43	F	1.8	33	48
2RF4	E F	F	82	L	1.7	82	99
2RF4	E F	F	89	L	1.1	82	99
2RF4	E F	F	92	I	1.4	82	99
2RF4	E F	F	96	F	1.3	82	99
2RF9	A C	A	904	E	1.0	897	905
2RF9	B D	B	904	E	1.2	897	905
2RF9	B D	B	924	V	2.1	918	927
2RFK	A B	A	68	W	2.3	62	73
2RFK	A B	A	221	H	2.2	220	233

2RFK	A B	A	229	F	3.2	220	233
2RFK	A B	B	46	R	1.6	42	53
2RFK	A B	B	50	R	1.4	42	53
2RFT	A B	A	109	N	1.0	107	114
2RFT	A B	B	81	D	1.3	75	127
2RFT	A B	B	96	I	2.4	75	127
2RFT	A B	B	97	E	1.0	75	127
2RFT	A B	B	100	V	1.0	75	127
2RFT	A B	B	101	L	1.2	75	127
2RFT	A B	B	122	L	1.1	75	127
2RGN	A B	A	213	R	1.1	210	219
2RGN	A B	A	218	H	1.4	210	219
2RGN	A B	A	257	T	3.2	247	261
2RGN	A B	A	354	K	1.3	334	355
2RGN	A B	B	215	E	1.4	210	219
2RGN	A B	B	216	W	1.2	210	219
2RGN	A B	B	220	Y	1.6	220	230
2RGN	A B	B	471	F	2.9	451	476
2RGN	A B	B	472	L	1.5	451	476
2RGN	A B	B	475	L	1.1	451	476
2RGN	B C	B	164	V	4.4	150	184
2RGN	B C	B	167	E	4.7	150	184
2RGN	B C	B	289	I	1.0	289	296
2RGN	B C	C	72	L	2.7	67	73
2RGN	D E	D	213	R	1.2	210	219
2RGN	D E	D	217	I	1.7	210	219
2RGN	D E	D	218	H	1.6	210	219
2RGN	D E	D	354	K	1.4	334	355
2RGN	D E	E	215	E	1.4	210	230
2RGN	D E	E	216	W	1.3	210	230
2RGN	D E	E	220	Y	3.6	210	230
2RGN	D E	E	471	F	2.0	470	476
2RGN	D E	E	472	L	1.4	470	476
2RGN	D E	E	475	L	1.7	470	476
2RGN	D E	E	478	P	1.4	478	490
2RGN	D E	E	483	R	1.0	478	490
2RGN	E F	E	163	Y	1.0	153	184
2RGN	E F	E	167	E	4.3	153	184
2RGN	E F	E	289	I	1.2	289	296
2RGN	E F	E	300	L	1.2	298	313
2RGN	E F	F	68	R	1.6	67	73
2RGN	E F	F	69	L	2.1	67	73
2RGN	E F	F	72	L	2.9	67	73
2RHK	A C	A	183	G	39.6	171	188
2RHK	A C	A	187	W	4.7	171	188
2RHK	A C	C	69	K	2.6	69	73
2RHK	A C	C	97	Y	1.7	97	102
2RHK	A C	C	98	F	2.3	97	102
2RHK	B C	C	72	L	1.4	69	73
2RHK	B D	B	183	G	28.3	171	188
2RHK	B D	B	184	G	1.9	171	188
2RHK	B D	B	187	W	3.3	171	188
2RHK	B D	D	69	K	1.2	69	73
2RHK	B D	D	97	Y	1.5	97	102
2RHK	B D	D	98	F	3.7	97	102
2RHS	A B	A	231	G	251.8	226	241
2RHS	A B	A	340	L	1.4	337	342
2RHS	A B	B	352	R	1.3	348	358
2RHS	A B	B	500	Q	1.1	498	513
2RHS	A B	B	568	N	2.3	557	571

2RHS	A D	A	90	L	1.1	88	93
2RHS	A D	A	239	K	1.5	226	241
2RHS	A D	A	324	Y	1.7	316	325
2RHS	A D	A	338	R	1.0	337	342
2RHS	A D	D	502	K	1.6	498	513
2RHS	A D	D	622	F	1.4	622	636
2RHS	A D	D	623	F	2.6	622	636
2RHS	A D	D	626	K	2.1	622	636
2RHS	A D	D	627	G	89.6	622	636
2RHS	A D	D	635	K	1.1	622	636
2RHS	C B	C	239	K	1.1	226	241
2RHS	C B	B	622	F	1.7	622	636
2RHS	C B	B	623	F	3.8	622	636
2RHS	C B	B	627	G	150.7	622	636
2RHS	C B	B	635	K	1.1	622	636
2RHS	C B	B	673	P	1.0	673	679
2RHS	C D	C	124	L	1.7	111	125
2RHS	C D	C	228	D	1.0	226	241
2RHS	C D	C	231	G	228.2	226	241
2RHS	C D	D	500	Q	1.9	498	513
2RHS	C D	D	568	N	1.6	557	571
2RI4	A B	A	107	V	1.0	99	113
2RI4	A B	A	119	P	1.1	119	137
2RI4	A B	B	30	R	2.3	20	35
2RI4	A B	B	116	R	1.8	101	118
2RI4	A D	D	102	N	1.1	100	118
2RI4	C B	B	37	W	1.6	36	40
2RI4	C B	B	102	N	1.5	101	118
2RI4	C D	C	31	R	1.0	21	36
2RI4	C D	C	122	H	1.5	119	137
2RI4	C D	D	30	R	4.5	24	35
2RI4	C D	D	116	R	1.5	100	118
2RI4	I J	I	122	H	5.0	119	137
2RI4	I J	J	34	V	1.3	20	35
2RI4	I J	J	116	R	2.6	100	118
2RI4	I L	L	40	R	1.0	38	42
2RI4	K L	K	107	V	1.2	96	113
2RI4	K L	K	122	H	2.1	119	139
2RI4	K L	L	30	R	2.5	21	35
2RI4	K L	L	34	V	1.1	21	35
2RII	A X	X	128	Y	1.1	122	130
2RII	A Y	A	163	F	1.0	153	169
2RII	A Y	A	165	F	2.0	153	169
2RII	B X	B	163	F	1.9	153	169
2RII	B X	B	165	F	5.4	153	169
2RII	B X	B	167	D	1.9	153	169
2RII	B Y	B	54	T	4.3	54	62
2RII	B Y	Y	61	K	4.4	59	72
2RII	B Y	Y	126	R	1.1	122	130
2RII	B Y	Y	127	V	1.0	122	130
2RIV	A B	A	20	Y	1.5	20	41
2RIV	A B	A	34	Y	1.8	20	41
2RIV	A B	A	50	P	1.7	50	63
2RIV	A B	A	99	L	1.2	85	100
2RIV	A B	A	257	M	1.4	257	263
2RIV	A B	A	261	E	1.6	257	263
2RMK	A B	A	70	L	1.2	70	75
2RMK	A B	B	148	M	1.0	124	154
2RMK	A B	B	161	K	1.0	160	193
2RMK	A B	B	162	L	1.5	160	193

2RMS	A B	A	152	K	1.1	142	157
2RMS	A B	A	154	F	1.0	142	157
2RMS	A B	A	165	I	1.1	161	172
2RMS	A B	B	144	M	1.7	132	147
2RMX	A B	A	15	G	4.5	15	26
2RNR	A B	A	432	R	1.2	420	435
2RNR	A B	B	100	L	5.0	85	103
2ROC	A B	A	209	F	1.9	206	216
2ROC	A B	A	230	V	1.0	221	235
2ROC	A B	A	234	V	1.1	221	235
2ROC	A B	A	242	W	2.6	242	262
2ROC	A B	A	243	G	58.0	242	262
2ROC	A B	A	244	R	1.0	242	262
2ROC	A B	A	299	F	1.4	293	301
2ROC	A B	A	300	F	2.6	293	301
2ROC	A B	B	138	G	115.4	131	155
2ROC	A B	B	141	L	3.9	131	155
2ROC	A B	B	144	I	2.1	131	155
2ROC	A B	B	146	D	1.1	131	155
2ROC	A B	B	148	L	1.8	131	155
2ROC	A B	B	152	Y	3.2	131	155
2ROD	A B	A	197	V	1.0	184	205
2ROD	A B	A	200	G	7.2	184	205
2ROD	A B	A	209	F	1.0	206	216
2ROD	A B	A	212	M	1.4	206	216
2ROD	A B	A	230	V	1.2	221	235
2ROD	A B	A	243	G	266.2	242	262
2ROD	A B	A	244	R	2.2	242	262
2ROD	A B	A	251	F	1.1	242	262
2ROD	A B	B	23	F	3.6	22	40
2ROD	A B	B	27	L	2.4	22	40
2ROD	A B	B	30	I	2.7	22	40
2ROD	A B	B	31	G	100.6	22	40
2ROD	A B	B	32	D	1.1	22	40
2ROD	A B	B	38	W	2.6	22	40
2SEB	A B	A	48	F	2.1	46	52
2SEB	A B	A	62	N	1.3	56	77
2SEB	A B	A	76	R	2.0	56	77
2SEB	A D	A	57	Q	1.1	56	77
2SEB	A D	A	67	K	1.3	56	77
2SEB	B E	B	60	Y	1.4	55	63
2SEB	B E	B	61	W	2.0	55	63
2SEB	B E	B	78	Y	2.6	65	87
2SEB	B E	B	81	H	1.0	65	87
2SEB	B E	B	82	N	1.6	65	87
2SIV	A B	A	547	G	1.2	547	581
2SIV	A B	A	558	V	1.4	547	581
2SIV	A B	A	565	L	1.6	547	581
2SIV	A B	A	571	W	2.2	547	581
2SIV	A B	A	572	G	1.6	547	581
2SIV	A B	A	576	L	2.8	547	581
2SIV	A B	A	579	R	2.2	547	581
2SIV	A B	B	631	W	1.2	629	661
2SIV	A B	B	638	L	1.1	629	661
2SIV	A B	B	642	I	1.5	629	661
2SIV	A F	F	646	L	1.4	629	659
2SIV	C B	C	549	V	1.6	547	581
2SIV	C B	C	552	Q	1.4	547	581
2SIV	C B	C	556	L	1.2	547	581
2SIV	C B	B	646	L	1.4	629	661

2SIV	C D	C	558	V	1.0	547	581
2SIV	C D	C	565	L	1.8	547	581
2SIV	C D	C	571	W	2.3	547	581
2SIV	C D	C	572	G	4.5	547	581
2SIV	C D	C	576	L	3.1	547	581
2SIV	C D	D	631	W	2.6	629	660
2SIV	C D	D	642	I	1.3	629	660
2SIV	E D	E	556	L	1.3	547	581
2SIV	E D	E	563	Q	1.0	547	581
2SIV	E D	E	567	R	1.0	547	581
2SIV	E D	E	570	V	1.4	547	581
2SIV	E D	D	646	L	2.0	629	660
2SIV	E F	E	561	R	1.2	547	581
2SIV	E F	E	565	L	2.0	547	581
2SIV	E F	E	568	L	1.3	547	581
2SIV	E F	E	572	G	1.5	547	581
2SIV	E F	F	635	V	1.0	629	659
2SIV	E F	F	638	L	1.9	629	659
2SIV	E F	F	642	I	1.0	629	659
2SNI	E I	E	104	Y	1.2	104	117
2SNI	E I	E	135	L	1.3	133	145
2UUN	A B	A	5	L	1.4	4	15
2UUN	A B	A	6	T	1.3	4	15
2UUN	A B	A	9	V	2.2	4	15
2UUN	A B	A	24	I	1.2	21	47
2UUN	A B	A	31	F	1.6	21	47
2UUN	A B	A	38	L	1.8	21	47
2UUN	A B	A	93	R	2.6	78	102
2UUN	A B	A	97	Y	3.0	78	102
2UUN	A B	A	100	I	1.5	78	102
2UUN	A B	B	5	F	2.7	4	15
2UUN	A B	B	13	D	1.6	4	15
2UUN	A B	B	24	I	1.1	21	33
2UUN	A B	B	31	V	1.9	21	33
2UUN	A B	B	38	L	1.6	34	46
2UUN	A B	B	91	R	1.8	76	100
2UUN	A B	B	95	Y	4.6	76	100
2UUN	A B	B	98	F	4.0	76	100
2UUN	A D	A	117	E	1.4	115	122
2UUN	A D	D	83	L	1.0	76	100
2UUN	C D	C	5	L	1.5	4	15
2UUN	C D	C	24	I	1.1	21	47
2UUN	C D	C	31	F	2.1	21	47
2UUN	C D	C	38	L	1.4	21	47
2UUN	C D	C	93	R	2.9	78	102
2UUN	C D	C	97	Y	2.6	78	102
2UUN	C D	C	100	I	1.5	78	102
2UUN	C D	D	5	F	2.4	4	14
2UUN	C D	D	13	D	1.2	4	14
2UUN	C D	D	24	I	1.2	21	33
2UUN	C D	D	31	V	1.3	21	33
2UUN	C D	D	38	L	1.9	34	46
2UUN	C D	D	91	R	1.8	76	100
2UUN	C D	D	95	Y	2.3	76	100
2UUN	C D	D	98	F	4.1	76	100
2UUN	C F	C	117	E	1.2	115	122
2UUN	C F	F	83	L	1.1	76	100
2UUN	E F	E	5	L	2.1	4	15
2UUN	E F	E	9	V	2.0	4	15
2UUN	E F	E	24	I	1.1	21	47

2UUN	E F	E	31	F	2.2	21	47
2UUN	E F	E	38	L	1.9	21	47
2UUN	E F	E	93	R	2.8	78	102
2UUN	E F	E	97	Y	2.4	78	102
2UUN	E F	E	100	I	1.4	78	102
2UUN	E F	F	5	F	2.1	4	15
2UUN	E F	F	13	D	1.3	4	15
2UUN	E F	F	24	I	1.3	21	33
2UUN	E F	F	31	V	1.7	21	33
2UUN	E F	F	38	L	1.6	34	46
2UUN	E F	F	91	R	1.7	76	100
2UUN	E F	F	95	Y	3.6	76	100
2UUN	E F	F	98	F	4.1	76	100
2UUN	G H	G	5	L	1.7	4	15
2UUN	G H	G	6	T	1.4	4	15
2UUN	G H	G	9	V	1.6	4	15
2UUN	G H	G	24	I	1.1	21	47
2UUN	G H	G	31	F	2.2	21	47
2UUN	G H	G	38	L	1.8	21	47
2UUN	G H	G	93	R	2.9	78	102
2UUN	G H	G	97	Y	2.9	78	102
2UUN	G H	G	100	I	1.4	78	102
2UUN	G H	G	110	Y	1.0	104	113
2UUN	G H	H	5	F	2.6	4	15
2UUN	G H	H	13	D	1.5	4	15
2UUN	G H	H	24	I	1.4	21	33
2UUN	G H	H	31	V	1.2	21	33
2UUN	G H	H	38	L	2.1	34	46
2UUN	G H	H	91	R	1.7	76	100
2UUN	G H	H	95	Y	4.0	76	100
2UUN	G H	H	98	F	3.9	76	100
2UUN	G J	G	117	E	1.4	115	122
2UUN	G J	J	83	L	1.0	76	100
2UUN	I J	I	5	L	1.4	4	15
2UUN	I J	I	6	T	1.3	4	15
2UUN	I J	I	9	V	1.9	4	15
2UUN	I J	I	23	E	1.5	21	47
2UUN	I J	I	24	I	1.1	21	47
2UUN	I J	I	31	F	2.3	21	47
2UUN	I J	I	38	L	1.8	21	47
2UUN	I J	I	93	R	2.8	78	102
2UUN	I J	I	97	Y	3.1	78	102
2UUN	I J	I	100	I	1.5	78	102
2UUN	I J	J	5	F	2.6	4	15
2UUN	I J	J	13	D	1.4	4	15
2UUN	I J	J	24	I	1.2	21	33
2UUN	I J	J	31	V	2.7	21	33
2UUN	I J	J	38	L	1.9	34	46
2UUN	I J	J	91	R	2.0	76	100
2UUN	I J	J	95	Y	4.2	76	100
2UUN	I J	J	98	F	3.9	76	100
2UUN	I L	I	117	E	1.8	115	122
2UUN	K H	K	117	E	1.3	115	122
2UUN	K L	K	5	L	1.3	4	15
2UUN	K L	K	9	V	2.1	4	15
2UUN	K L	K	31	F	2.3	21	47
2UUN	K L	K	38	L	1.6	21	47
2UUN	K L	K	93	R	3.0	78	102
2UUN	K L	K	97	Y	4.1	78	102
2UUN	K L	K	100	I	1.4	78	102

2UUN	K L	L	5	F	2.4	4	15
2UUN	K L	L	13	D	1.2	4	15
2UUN	K L	L	24	I	1.2	21	33
2UUN	K L	L	31	V	1.2	21	33
2UUN	K L	L	38	L	1.1	34	46
2UUN	K L	L	91	R	1.9	76	100
2UUN	K L	L	95	Y	1.9	76	100
2UUN	K L	L	98	F	4.0	76	100
2UUN	M N	M	5	L	3.1	4	15
2UUN	M N	M	6	T	1.6	4	15
2UUN	M N	M	9	V	1.9	4	15
2UUN	M N	M	24	I	1.1	21	47
2UUN	M N	M	30	R	1.4	21	47
2UUN	M N	M	31	F	3.5	21	47
2UUN	M N	M	38	L	1.5	21	47
2UUN	M N	M	93	R	2.5	78	102
2UUN	M N	M	97	Y	1.2	78	102
2UUN	M N	M	100	I	1.4	78	102
2UUN	M N	N	5	F	2.6	4	15
2UUN	M N	N	24	I	1.3	21	33
2UUN	M N	N	31	V	2.0	21	33
2UUN	M N	N	38	L	1.9	34	46
2UUN	M N	N	91	R	1.9	76	100
2UUN	M N	N	95	Y	2.3	76	100
2UUN	M N	N	98	F	4.2	76	100
2UUN	M P	P	83	L	1.1	76	100
2UUN	O P	O	5	L	1.5	4	15
2UUN	O P	O	6	T	1.2	4	15
2UUN	O P	O	9	V	2.1	4	15
2UUN	O P	O	31	F	2.1	21	47
2UUN	O P	O	38	L	1.7	21	47
2UUN	O P	O	93	R	2.9	78	102
2UUN	O P	O	97	Y	3.2	78	102
2UUN	O P	O	100	I	1.4	78	102
2UUN	O P	P	5	F	3.7	4	15
2UUN	O P	P	13	D	1.8	4	15
2UUN	O P	P	24	I	1.0	21	33
2UUN	O P	P	31	V	1.8	21	33
2UUN	O P	P	38	L	2.2	34	46
2UUN	O P	P	91	R	1.7	76	100
2UUN	O P	P	95	Y	1.9	76	100
2UUN	O P	P	98	F	4.1	76	100
2UUN	O R	O	90	Y	1.0	78	102
2UUN	O R	R	76	S	1.1	76	100
2UUN	O R	R	83	L	1.2	76	100
2UUN	Q N	N	83	L	1.1	76	100
2UUN	Q R	Q	5	L	1.6	4	15
2UUN	Q R	Q	6	T	3.2	4	15
2UUN	Q R	Q	9	V	2.0	4	15
2UUN	Q R	Q	24	I	1.3	21	47
2UUN	Q R	Q	31	F	1.7	21	47
2UUN	Q R	Q	38	L	1.8	21	47
2UUN	Q R	Q	93	R	2.4	78	102
2UUN	Q R	Q	97	Y	4.3	78	102
2UUN	Q R	Q	100	I	1.4	78	102
2UUN	Q R	R	5	F	2.6	4	15
2UUN	Q R	R	13	D	1.4	4	15
2UUN	Q R	R	24	I	1.1	21	33
2UUN	Q R	R	31	V	1.2	21	33
2UUN	Q R	R	38	L	1.9	34	46

2UUN	Q R	R	91	R	1.8	76	100
2UUN	Q R	R	95	Y	3.2	76	100
2UUN	Q R	R	98	F	4.0	76	100
2UUN	S T	S	5	L	1.1	4	15
2UUN	S T	S	9	V	1.8	4	15
2UUN	S T	S	24	I	1.1	21	47
2UUN	S T	S	31	F	2.0	21	47
2UUN	S T	S	38	L	1.9	21	47
2UUN	S T	S	93	R	2.7	78	102
2UUN	S T	S	97	Y	2.3	78	102
2UUN	S T	S	100	I	1.4	78	102
2UUN	S T	T	5	F	1.8	4	15
2UUN	S T	T	13	D	1.5	4	15
2UUN	S T	T	24	I	1.2	21	33
2UUN	S T	T	31	V	1.2	21	33
2UUN	S T	T	38	L	1.9	34	46
2UUN	S T	T	91	R	1.9	76	100
2UUN	S T	T	95	Y	2.8	76	100
2UUN	S T	T	98	F	4.4	76	100
2UUN	S V	S	117	E	1.2	115	122
2UUN	U V	U	5	L	1.7	4	15
2UUN	U V	U	9	V	2.1	4	15
2UUN	U V	U	24	I	1.1	21	47
2UUN	U V	U	31	F	2.2	21	47
2UUN	U V	U	38	L	1.8	21	47
2UUN	U V	U	93	R	2.6	78	102
2UUN	U V	U	97	Y	2.8	78	102
2UUN	U V	U	100	I	1.1	78	102
2UUN	U V	V	5	F	2.4	4	15
2UUN	U V	V	13	D	1.7	4	15
2UUN	U V	V	24	I	1.1	21	33
2UUN	U V	V	31	V	1.8	21	33
2UUN	U V	V	38	L	1.8	34	46
2UUN	U V	V	91	R	2.0	76	100
2UUN	U V	V	95	Y	3.8	76	100
2UUN	U V	V	98	F	3.9	76	100
2UUN	U X	U	117	E	1.3	115	122
2UUN	U X	X	83	L	1.0	76	100
2UUN	W T	T	83	L	1.2	76	100
2UUN	W X	W	5	L	1.6	4	15
2UUN	W X	W	9	V	1.8	4	15
2UUN	W X	W	24	I	1.1	21	47
2UUN	W X	W	31	F	2.2	21	47
2UUN	W X	W	38	L	1.7	21	47
2UUN	W X	W	93	R	2.8	78	102
2UUN	W X	W	97	Y	3.3	78	102
2UUN	W X	W	100	I	1.5	78	102
2UUN	W X	X	5	F	2.6	4	15
2UUN	W X	X	13	D	1.4	4	15
2UUN	W X	X	24	I	1.3	21	33
2UUN	W X	X	31	V	1.3	21	33
2UUN	W X	X	38	L	2.0	34	46
2UUN	W X	X	91	R	2.1	76	100
2UUN	W X	X	95	Y	3.8	76	100
2UUN	W X	X	98	F	4.0	76	100
2UVP	A B	A	4	F	4.3	4	22
2UVP	A B	A	5	Y	1.4	4	22
2UVP	A B	A	7	W	3.7	4	22
2UVP	A B	A	8	I	2.2	4	22
2UVP	A B	A	11	F	1.4	4	22

2UVP	A B	A	16	G	22.8	4	22
2UVP	A B	A	19	I	6.7	4	22
2UVP	A B	A	64	Y	2.1	59	70
2UVP	A B	A	156	D	2.0	155	175
2UVP	A B	A	157	Y	2.5	155	175
2UVP	A B	A	160	L	1.6	155	175
2UVP	A B	A	164	K	1.7	155	175
2UVP	A B	A	165	L	1.9	155	175
2UVP	A B	B	4	F	3.6	4	22
2UVP	A B	B	5	Y	1.2	4	22
2UVP	A B	B	7	W	3.2	4	22
2UVP	A B	B	8	I	2.1	4	22
2UVP	A B	B	12	V	1.2	4	22
2UVP	A B	B	16	G	54.9	4	22
2UVP	A B	B	60	W	2.4	59	70
2UVP	A B	B	64	Y	1.6	59	70
2UVP	A B	B	156	D	1.4	155	175
2UVP	A B	B	157	Y	2.4	155	175
2UVP	A B	B	160	L	1.9	155	175
2UVP	A B	B	164	K	2.1	155	175
2UVP	A D	A	106	T	1.4	96	107
2UW1	A B	A	71	F	1.7	71	84
2UW1	A B	A	79	R	2.8	71	84
2UW1	A B	A	132	R	2.3	126	153
2UW1	A B	A	150	Y	4.2	126	153
2UW1	A B	A	158	R	1.2	157	171
2UW1	A B	A	161	E	2.5	157	171
2UW1	A B	A	165	Q	2.4	157	171
2UW1	A B	A	166	Y	2.9	157	171
2UW1	A B	A	168	I	1.3	157	171
2UW1	A B	B	71	F	1.5	71	84
2UW1	A B	B	79	R	2.7	71	84
2UW1	A B	B	132	R	2.1	126	153
2UW1	A B	B	147	K	1.3	126	153
2UW1	A B	B	150	Y	3.9	126	153
2UW1	A B	B	158	R	1.5	157	171
2UW1	A B	B	161	E	2.6	157	171
2UW1	A B	B	165	Q	1.5	157	171
2UW1	A B	B	166	Y	1.4	157	171
2UW1	A B	B	168	I	1.2	157	171
2UWJ	E F	F	71	T	1.7	68	84
2UWJ	E F	F	75	R	1.0	68	84
2UXN	A B	A	391	Y	3.4	372	396
2UXN	A B	A	418	L	1.5	408	468
2UXN	A B	A	421	K	1.2	408	468
2UXN	A B	A	422	H	1.1	408	468
2UXN	A B	A	424	K	1.6	408	468
2UXN	A B	A	445	L	1.9	408	468
2UXN	A B	A	449	V	1.4	408	468
2UXN	A B	A	452	K	1.4	408	468
2UXN	A B	A	455	I	1.2	408	468
2UXN	A B	A	459	H	1.6	408	468
2UXN	A B	A	462	Y	1.2	408	468
2UXN	A B	A	474	I	2.4	474	513
2UXN	A B	A	478	F	3.7	474	513
2UXN	A B	A	486	D	1.5	474	513
2UXN	A B	A	494	Y	2.1	474	513
2UXN	A B	B	320	D	1.1	318	325
2UXN	A B	B	321	V	1.3	318	325
2UXN	A B	B	338	L	1.0	330	363

2UXN	A B	B	341	E	1.2	330	363
2UXN	A B	B	345	V	1.4	330	363
2UXN	A B	B	360	K	1.1	330	363
2UXN	A B	B	390	L	1.8	385	399
2UXN	A B	B	398	Y	2.0	385	399
2UXN	A B	B	408	V	1.5	402	410
2UY1	A B	A	254	L	1.0	247	256
2UY1	A B	A	298	K	1.3	282	300
2UY1	A B	A	324	Y	1.2	319	334
2UY1	A B	A	328	I	1.3	319	334
2UY1	A B	A	395	F	1.6	384	397
2UY1	A B	A	400	M	1.3	400	416
2UY1	A B	A	403	F	1.3	400	416
2UY1	A B	A	411	M	1.3	400	416
2UY1	A B	A	437	G	1.9	435	447
2UY1	A B	B	331	Y	2.6	319	334
2UY1	A B	B	395	F	2.0	384	397
2UY1	A B	B	396	M	1.4	384	397
2UY1	A B	B	400	M	1.4	400	416
2UY1	A B	B	403	F	1.5	400	416
2UY1	A B	B	437	G	17.0	435	447
2UY1	A B	B	438	R	1.0	435	447
2UY1	A B	B	442	F	1.1	435	447
2UYL	A B	A	129	Q	1.5	127	133
2UYL	M N	M	129	Q	1.4	127	132
2UYL	V W	V	128	E	1.0	127	132
2UYL	X Y	X	129	Q	1.4	127	132
2UYN	A B	A	84	F	1.2	84	98
2UYN	A B	A	91	Y	1.2	84	98
2UZ1	A B	A	31	D	1.1	31	40
2UZ1	A B	A	35	Q	3.3	31	40
2UZ1	A B	A	39	D	1.1	31	40
2UZ1	A B	A	76	G	51.6	76	81
2UZ1	A B	A	80	N	1.0	76	81
2UZ1	A B	A	82	V	1.0	82	91
2UZ1	A B	A	449	G	7.3	448	454
2UZ1	A B	A	452	G	33.8	448	454
2UZ1	A B	A	453	Y	2.6	448	454
2UZ1	A B	A	459	D	1.5	455	464
2UZ1	A B	A	484	F	2.2	479	490
2UZ1	A B	A	485	Q	2.4	479	490
2UZ1	A B	A	504	Y	2.2	504	511
2UZ1	A B	A	506	G	2.0	504	511
2UZ1	A B	A	507	V	1.5	504	511
2UZ1	A B	B	31	D	1.1	31	40
2UZ1	A B	B	35	Q	3.2	31	40
2UZ1	A B	B	39	D	1.2	31	40
2UZ1	A B	B	76	G	52.1	76	81
2UZ1	A B	B	83	T	1.2	82	91
2UZ1	A B	B	121	M	1.3	118	125
2UZ1	A B	B	449	G	9.6	448	454
2UZ1	A B	B	452	G	23.8	448	454
2UZ1	A B	B	453	Y	2.2	448	454
2UZ1	A B	B	459	D	1.6	455	464
2UZ1	A B	B	484	F	2.3	479	490
2UZ1	A B	B	485	Q	1.8	479	490
2UZ1	A B	B	504	Y	3.5	504	511
2UZ1	A B	B	506	G	3.2	504	511
2UZ1	A B	B	507	V	1.5	504	511
2UZ1	A C	A	137	H	1.5	135	151

2UZ1	A C	A	140	R	1.1	135	151
2UZ1	A C	C	140	R	1.0	138	151
2UZ1	D B	D	137	H	1.9	135	151
2UZ1	D B	D	140	R	1.2	135	151
2UZ1	D B	B	137	H	1.7	135	151
2UZ1	D B	B	140	R	1.0	135	151
2UZ1	D B	B	141	L	1.2	135	151
2UZ1	D C	D	31	D	1.1	31	40
2UZ1	D C	D	34	F	2.5	31	40
2UZ1	D C	D	35	Q	3.3	31	40
2UZ1	D C	D	39	D	1.1	31	40
2UZ1	D C	D	76	G	33.5	76	81
2UZ1	D C	D	79	T	2.3	76	81
2UZ1	D C	D	82	V	2.5	82	91
2UZ1	D C	D	449	G	6.2	448	454
2UZ1	D C	D	452	G	29.0	448	454
2UZ1	D C	D	453	Y	2.8	448	454
2UZ1	D C	D	459	D	1.4	455	464
2UZ1	D C	D	484	F	2.3	479	490
2UZ1	D C	D	485	Q	2.0	479	490
2UZ1	D C	D	504	Y	4.1	504	511
2UZ1	D C	D	506	G	2.3	504	511
2UZ1	D C	D	507	V	1.5	504	511
2UZ1	D C	C	31	D	1.2	31	40
2UZ1	D C	C	35	Q	3.2	31	40
2UZ1	D C	C	39	D	1.2	31	40
2UZ1	D C	C	50	E	1.1	50	64
2UZ1	D C	C	76	G	45.8	76	81
2UZ1	D C	C	79	T	1.6	76	81
2UZ1	D C	C	83	T	1.1	82	91
2UZ1	D C	C	121	M	2.7	118	124
2UZ1	D C	C	449	G	8.6	448	454
2UZ1	D C	C	452	G	43.6	448	454
2UZ1	D C	C	453	Y	2.5	448	454
2UZ1	D C	C	459	D	1.4	455	464
2UZ1	D C	C	484	F	2.1	479	490
2UZ1	D C	C	485	Q	1.8	479	490
2UZ1	D C	C	504	Y	3.4	504	511
2UZ1	D C	C	506	G	3.6	504	511
2UZ1	D C	C	507	V	1.6	504	511
2UZ6	A K	K	6	P	1.3	6	12
2UZ6	A K	K	7	P	1.0	6	12
2UZ6	A K	K	11	N	1.1	6	12
2UZ6	A O	O	10	L	1.5	6	12
2UZ6	B L	L	6	P	2.7	6	11
2UZ6	B L	L	7	P	2.7	6	11
2UZ6	C M	M	6	P	2.2	6	12
2UZ6	C M	M	7	P	1.2	6	12
2UZ6	C M	M	11	N	1.0	6	12
2UZ6	D N	N	6	P	3.1	6	12
2UZ6	D N	N	11	N	1.4	6	12
2UZ6	E N	N	10	L	1.7	6	12
2UZ6	E O	O	7	P	1.3	6	12
2UZ6	E O	O	8	C	7.0	6	12
2UZ6	E O	O	11	N	1.4	6	12
2UZ6	F P	P	7	P	1.4	6	12
2UZ6	F T	T	10	L	1.5	6	12
2UZ6	G P	P	10	L	1.5	6	12
2UZ6	H R	R	11	N	1.5	6	12
2UZ6	I R	R	10	L	2.0	6	12

2UZ6	I S	S	7	P	1.0	6	12
2UZ6	I S	S	11	N	1.1	6	12
2UZ6	J T	T	7	P	1.7	6	12
2UZ6	J T	T	11	N	1.0	6	12
2V17	H L	L	124	Q	1.5	122	128
2V1C	A C	A	148	D	3.4	145	161
2V1C	A C	C	86	P	1.1	86	90
2V1C	A C	C	93	H	1.1	92	103
2V1C	A C	C	97	E	153.4	92	103
2V1D	A B	A	391	Y	3.5	372	397
2V1D	A B	A	418	L	1.3	408	466
2V1D	A B	A	421	K	1.4	408	466
2V1D	A B	A	424	K	1.6	408	466
2V1D	A B	A	435	V	1.1	408	466
2V1D	A B	A	449	V	1.5	408	466
2V1D	A B	A	455	I	1.1	408	466
2V1D	A B	A	459	H	1.2	408	466
2V1D	A B	A	462	Y	1.3	408	466
2V1D	A B	A	478	F	2.8	474	507
2V1D	A B	A	485	R	1.9	474	507
2V1D	A B	A	486	D	1.2	474	507
2V1D	A B	B	321	V	1.0	318	324
2V1D	A B	B	338	L	1.0	330	363
2V1D	A B	B	339	D	1.4	330	363
2V1D	A B	B	359	L	1.1	330	363
2V1D	A B	B	390	L	1.2	385	399
2V1D	A B	B	398	Y	1.3	385	399
2V1D	A B	B	408	V	1.4	402	410
2V1D	A C	A	375	D	1.1	372	397
2V1D	A C	A	552	W	3.0	549	553
2V1S	A K	A	70	F	1.3	65	83
2V1S	A K	A	78	E	1.9	65	83
2V1S	A K	A	109	V	1.0	104	114
2V1S	A K	K	15	L	2.1	15	23
2V1S	A K	K	19	L	1.7	15	23
2V1S	C J	C	70	F	1.9	60	83
2V1S	C J	J	17	R	1.5	14	23
2V1S	C J	J	21	Y	3.2	14	23
2V1S	C L	C	78	E	1.1	60	83
2V1S	C L	C	109	V	1.0	104	114
2V1S	C L	L	15	L	2.0	15	23
2V1S	D K	D	68	K	5.1	59	83
2V1S	D K	D	70	F	2.8	59	83
2V1S	D K	K	21	Y	4.1	15	23
2V1S	E J	E	78	E	2.3	60	84
2V1S	E J	J	15	L	1.7	14	23
2V1S	E J	J	19	L	1.8	14	23
2V1S	E L	E	70	F	1.8	60	84
2V1S	E L	L	17	R	2.0	15	23
2V1S	E L	L	21	Y	3.5	15	23
2V1Y	A B	B	494	F	4.3	481	505
2V1Y	A B	B	496	E	1.0	481	505
2V1Y	A B	B	508	Y	1.3	506	513
2V1Y	A B	B	534	R	1.2	527	562
2V36	A B	A	64	L	1.9	54	66
2V36	A B	A	77	I	1.1	70	85
2V36	A B	A	78	Q	1.0	70	85
2V36	A B	A	139	V	1.0	135	141
2V36	A B	A	185	S	1.0	185	194
2V36	A B	A	197	K	1.1	195	201

2V36	A B	A	198	L	1.7	195	201
2V36	A B	A	207	F	2.0	202	208
2V36	A B	A	245	F	2.1	244	256
2V36	A B	A	249	L	1.0	244	256
2V36	A B	A	294	G	39.6	293	308
2V36	A B	A	298	L	2.0	293	308
2V36	A B	A	320	K	1.6	318	338
2V36	A B	A	321	Y	1.4	318	338
2V36	A B	A	328	M	1.2	318	338
2V36	A B	A	329	H	3.1	318	338
2V36	A B	A	332	Y	5.2	318	338
2V36	A B	B	491	S	1.0	487	503
2V36	A B	B	499	Y	1.3	487	503
2V36	A B	B	501	I	1.7	487	503
2V36	C D	C	64	L	1.1	54	66
2V36	C D	C	70	A	1.0	70	85
2V36	C D	C	77	I	1.0	70	85
2V36	C D	C	197	K	1.7	195	201
2V36	C D	C	198	L	1.8	195	201
2V36	C D	C	207	F	1.8	203	208
2V36	C D	C	245	F	2.2	244	256
2V36	C D	C	249	L	1.0	244	256
2V36	C D	C	294	G	43.9	293	308
2V36	C D	C	298	L	1.9	293	308
2V36	C D	C	320	K	1.9	318	339
2V36	C D	C	321	Y	2.4	318	339
2V36	C D	C	324	L	3.0	318	339
2V36	C D	C	328	M	1.2	318	339
2V36	C D	C	329	H	3.4	318	339
2V36	C D	C	332	Y	3.9	318	339
2V36	C D	D	490	I	1.1	487	503
2V36	C D	D	491	S	1.1	487	503
2V36	C D	D	494	L	1.5	487	503
2V36	C D	D	498	L	1.3	487	503
2V36	C D	D	499	Y	2.0	487	503
2V36	C D	D	501	I	1.6	487	503
2V3B	A B	A	290	M	1.2	289	304
2V46	C N	C	9	G	304.3	7	12
2V46	C N	N	49	H	1.6	41	50
2V46	F R	R	65	I	1.5	60	75
2V46	G I	I	41	V	2.3	41	49
2V4I	A B	B	198	D	1.2	194	207
2V4I	A B	B	201	F	2.5	194	207
2V4I	A B	B	251	L	2.8	237	258
2V4I	A D	D	311	G	2.1	303	313
2V4I	C B	B	303	W	1.1	303	313
2V4I	C B	B	304	G	17.0	303	313
2V4I	C B	B	311	G	34.6	303	313
2V4I	C D	D	198	D	1.0	194	207
2V4I	C D	D	201	F	2.5	194	207
2V4I	C D	D	251	L	3.0	237	258
2V4I	E F	F	197	Q	1.7	194	207
2V4I	E F	F	198	D	1.7	194	207
2V4I	E F	F	201	F	2.5	194	207
2V4I	E F	F	251	L	3.0	237	258
2V4I	E H	H	304	G	2.6	303	313
2V4I	E H	H	308	M	1.4	303	313
2V4I	E H	H	311	G	8.6	303	313
2V4I	G F	F	303	W	1.0	303	313
2V4I	G F	F	304	G	9.9	303	313

2V4I	G F	F	305	R	1.8	303	313
2V4I	G F	F	308	M	1.0	303	313
2V4I	G F	F	311	G	28.6	303	313
2V4I	G H	H	201	F	2.8	194	207
2V4I	G H	H	251	L	2.1	237	258
2V4I	G H	H	255	I	2.5	237	258
2V4J	A B	A	20	F	1.3	20	34
2V4J	A B	A	23	D	1.4	20	34
2V4J	A B	A	54	L	1.1	46	61
2V4J	A B	A	58	Y	3.4	46	61
2V4J	A B	A	114	Y	1.7	112	125
2V4J	A B	A	116	R	1.8	112	125
2V4J	A B	A	148	Q	1.0	146	161
2V4J	A B	A	151	E	1.5	146	161
2V4J	A B	A	154	F	2.5	146	161
2V4J	A B	A	195	Y	2.7	190	201
2V4J	A B	A	279	E	2.0	276	284
2V4J	A B	A	308	H	5.5	308	313
2V4J	A B	B	34	I	1.3	32	37
2V4J	A B	B	75	I	3.2	75	89
2V4J	A B	B	78	I	1.1	75	89
2V4J	A B	B	79	R	1.5	75	89
2V4J	A B	B	160	G	6.5	158	169
2V4J	A B	B	163	K	1.1	158	169
2V4J	A B	B	166	M	1.1	158	169
2V4J	A B	B	167	D	2.1	158	169
2V4J	A B	B	170	F	2.2	170	174
2V4J	A B	B	173	F	1.3	170	174
2V4J	A B	B	339	E	3.0	337	345
2V4J	A C	C	66	V	3.2	66	74
2V4J	A C	C	67	R	3.3	66	74
2V4J	A C	C	81	Y	1.6	77	84
2V4J	A C	C	90	K	1.2	88	97
2V4J	A E	A	388	F	1.6	388	395
2V4J	A E	A	431	Y	1.5	428	435
2V4J	A E	E	346	W	2.2	346	354
2V4J	A E	E	347	E	3.5	346	354
2V4J	A E	E	370	Y	3.7	367	371
2V4J	B C	B	225	P	1.0	224	229
2V4J	D B	D	384	K	1.0	379	386
2V4J	D B	D	388	F	1.6	388	395
2V4J	D B	D	428	I	2.5	428	435
2V4J	D B	D	431	Y	1.5	428	435
2V4J	D B	D	432	R	1.4	428	435
2V4J	D B	B	346	W	1.9	346	354
2V4J	D B	B	347	E	4.2	346	354
2V4J	D B	B	367	D	1.2	367	371
2V4J	D B	B	370	Y	4.2	367	371
2V4J	D E	D	20	F	1.7	20	34
2V4J	D E	D	58	Y	1.9	46	61
2V4J	D E	D	114	Y	1.7	112	125
2V4J	D E	D	116	R	1.3	112	125
2V4J	D E	D	120	D	1.6	112	125
2V4J	D E	D	123	D	2.2	112	125
2V4J	D E	D	151	E	2.3	146	161
2V4J	D E	D	154	F	2.4	146	161
2V4J	D E	D	195	Y	2.8	190	201
2V4J	D E	D	279	E	2.4	276	284
2V4J	D E	D	308	H	3.5	308	313
2V4J	D E	E	34	I	1.3	32	37

2V4J	D E	E	75	I	4.6	75	89
2V4J	D E	E	78	I	1.2	75	89
2V4J	D E	E	79	R	2.6	75	89
2V4J	D E	E	160	G	217.2	158	169
2V4J	D E	E	166	M	1.3	158	169
2V4J	D E	E	170	F	2.3	170	174
2V4J	D E	E	173	F	1.3	170	174
2V4J	D F	F	67	R	1.6	66	74
2V4J	D F	F	90	K	1.2	88	97
2V4Z	A B	A	207	E	1.7	205	214
2V4Z	A B	A	213	H	1.3	205	214
2V4Z	A B	B	108	E	1.1	107	120
2V4Z	A B	B	182	E	1.2	171	191
2V4Z	A B	B	183	N	1.3	171	191
2V4Z	A B	B	184	D	1.5	171	191
2V51	B F	B	143	Y	2.7	137	145
2V51	B F	F	74	L	2.6	72	80
2V51	B F	F	75	Q	1.0	72	80
2V51	B F	F	78	L	1.1	72	80
2V51	B F	F	87	L	1.3	84	91
2V51	D E	D	143	Y	1.7	137	145
2V51	D E	E	74	L	2.7	72	81
2V51	D E	E	87	L	1.1	84	90
2V52	B M	B	143	Y	1.0	137	145
2V52	B M	M	118	L	2.7	116	124
2V52	B M	M	119	K	1.6	116	124
2V52	B M	M	122	I	1.7	116	124
2V52	B M	M	131	L	2.2	128	134
2V55	A B	B	191	H	1.8	191	200
2V55	C D	C	285	G	3.3	285	292
2V55	C D	D	159	Y	1.3	159	164
2V55	C D	D	191	H	2.3	191	200
2V5H	A L	A	233	R	2.5	229	238
2V5H	B H	B	233	R	2.3	229	238
2V5H	B H	H	15	E	1.3	13	23
2V5H	C G	C	233	R	2.2	229	238
2V5H	D I	D	194	E	2.1	188	199
2V5H	D I	D	233	R	2.4	229	238
2V5H	D I	D	254	R	1.6	245	258
2V5H	E K	E	233	R	1.2	229	238
2V5H	F J	F	233	R	2.6	229	238
2V5H	F J	J	11	F	2.3	10	23
2V5P	A D	D	15	D	1.4	11	22
2V5P	A D	D	19	F	2.4	11	22
2V5P	B C	C	11	G	1.6	11	22
2V5P	B C	C	12	E	1.0	11	22
2V5P	B C	C	15	D	1.4	11	22
2V5P	B C	C	19	F	3.3	11	22
2V5Q	B C	B	319	L	1.0	316	321
2V6Q	A B	A	71	R	1.2	62	74
2V6Q	A B	A	99	G	108.6	98	118
2V6Q	A B	A	100	R	1.4	98	118
2V6Q	A B	A	107	W	2.4	98	118
2V6Q	A B	B	54	P	2.9	53	71
2V6Q	A B	B	57	W	2.2	53	71
2V6Q	A B	B	58	I	1.8	53	71
2V6Q	A B	B	61	E	3.1	53	71
2V6Q	A B	B	62	L	2.3	53	71
2V6Q	A B	B	63	R	1.4	53	71
2V6Q	A B	B	66	G	43.1	53	71

2V6Q	A B	B	69	F	1.9	53	71
2V6X	A B	A	8	T	1.0	6	23
2V6X	A B	A	11	I	1.7	6	23
2V6X	A B	A	15	Q	1.5	6	23
2V6X	A B	A	18	I	1.6	6	23
2V6X	A B	A	26	Y	1.1	26	40
2V6X	A B	A	60	F	2.1	50	80
2V6X	A B	A	64	L	1.5	50	80
2V6X	A B	A	66	R	3.2	50	80
2V6X	A B	B	190	L	1.4	188	193
2V6X	A B	B	221	L	1.3	219	230
2V6X	A B	B	224	R	1.1	219	230
2V6X	A B	B	225	L	1.8	219	230
2V6X	A B	B	228	L	2.4	219	230
2V7H	A B	A	123	E	1.0	122	127
2V7H	A B	A	124	Q	2.0	122	127
2V7H	L H	L	124	Q	2.9	122	126
2V7N	A B	A	165	Q	1.3	163	169
2V7N	C D	C	165	Q	1.1	163	169
2V7N	E F	E	165	Q	1.2	163	168
2V7N	G H	G	165	Q	1.3	163	168
2V7Q	A D	A	210	R	2.8	210	223
2V7Q	A D	A	283	L	1.3	271	285
2V7Q	A D	A	358	Y	1.7	354	360
2V7Q	A D	D	290	G	121.9	285	296
2V7Q	A D	D	372	R	1.2	365	392
2V7Q	A D	D	376	K	1.1	365	392
2V7Q	A D	D	379	Q	1.0	365	392
2V7Q	A E	A	299	F	1.0	298	307
2V7Q	A E	A	300	Y	1.6	298	307
2V7Q	A E	E	193	G	7.9	190	204
2V7Q	A G	A	403	F	1.7	401	406
2V7Q	B E	B	210	R	2.9	210	223
2V7Q	B E	B	218	K	1.6	210	223
2V7Q	B E	B	283	L	1.6	271	285
2V7Q	B E	B	284	L	1.3	271	285
2V7Q	B E	E	290	G	85.6	285	294
2V7Q	B F	B	299	F	1.3	298	309
2V7Q	B F	B	307	E	1.6	298	309
2V7Q	B F	B	399	E	1.3	394	400
2V7Q	B F	F	193	G	6.0	190	204
2V7Q	B F	F	195	D	1.1	190	204
2V7Q	B F	F	337	R	1.0	337	341
2V7Q	B F	F	424	F	1.3	422	426
2V7Q	B G	G	252	R	1.6	198	272
2V7Q	B G	G	263	I	1.8	198	272
2V7Q	C D	C	299	F	1.4	298	309
2V7Q	C D	C	300	Y	2.8	298	309
2V7Q	C D	D	191	R	2.3	190	203
2V7Q	C D	D	193	G	7.2	190	203
2V7Q	C D	D	260	R	1.3	258	268
2V7Q	C F	C	210	R	2.6	210	223
2V7Q	C F	C	212	T	1.2	210	223
2V7Q	C F	C	280	Q	2.0	271	285
2V7Q	C F	C	283	L	1.0	271	285
2V7Q	C F	C	358	Y	1.8	354	360
2V7Q	C F	F	290	G	108.3	285	296
2V7Q	C F	F	326	F	2.0	320	328
2V7Q	C F	F	379	Q	1.2	365	392
2V7Q	C G	G	115	I	2.3	110	120

2V7Q	C J	C	403	F	2.0	381	404
2V7Q	C J	C	417	L	1.0	415	428
2V7Q	D G	D	390	I	1.4	365	392
2V7Q	D G	G	19	I	1.8	3	53
2V7Q	D G	G	265	I	1.0	198	272
2V7Q	D G	G	268	G	10.5	198	272
2V7Q	D J	D	386	D	1.3	365	392
2V7Q	D J	D	408	R	2.6	398	415
2V7Q	D J	D	412	R	1.0	398	415
2V7Q	D J	J	27	Q	1.0	21	50
2V7Q	D J	J	29	E	3.3	21	50
2V7Q	D J	J	30	E	2.6	21	50
2V7Q	D J	J	31	E	1.4	21	50
2V7Q	D J	J	32	R	1.4	21	50
2V7Q	D J	J	33	Y	3.0	21	50
2V7Q	D J	J	34	F	1.6	21	50
2V7Q	D J	J	37	R	1.5	21	50
2V7Q	D J	J	42	L	2.0	21	50
2V7Q	E G	E	391	L	1.1	387	392
2V7Q	E G	G	254	R	2.2	198	272
2V7Q	E G	G	259	T	1.2	198	272
2V7Q	E G	G	266	I	1.2	198	272
2V7Q	F G	F	390	I	1.5	365	392
2V7Q	F J	F	387	I	1.4	365	392
2V7Q	F J	J	22	F	3.1	21	50
2V7Q	G H	G	44	Y	5.4	3	53
2V7Q	G H	G	204	Y	3.5	198	272
2V7Q	G H	G	207	Y	2.3	198	272
2V7Q	G H	G	214	Y	1.0	198	272
2V7Q	G I	G	146	L	1.5	138	147
2V7Q	G I	G	202	R	1.2	198	272
2V7Q	G I	G	206	E	1.9	198	272
2V7Q	G I	I	5	R	1.4	3	7
2V7Q	G I	I	11	Y	1.5	11	24
2V7Q	G I	I	12	I	3.3	11	24
2V7Q	G I	I	13	R	1.7	11	24
2V7Q	G J	G	16	I	1.3	3	53
2V7Q	G J	J	22	F	1.0	21	50
2V7Q	H I	H	133	I	2.1	125	145
2V7Q	H I	H	141	L	1.6	125	145
2V7Q	H I	I	3	Y	1.4	3	7
2V7Q	H I	I	11	Y	4.4	11	24
2V7Q	H I	I	14	Y	1.0	11	24
2V7Q	H I	I	17	I	2.1	11	24
2V7Q	H I	I	22	V	1.5	11	24
2V7Q	H I	I	23	R	1.3	11	24
2V7Q	H I	I	30	F	1.6	29	33
2V8F	A C	A	2	G	1.3	2	13
2V8F	A C	A	3	W	4.2	2	13
2V8F	A C	A	6	Y	3.2	2	13
2V8F	B C	B	3	W	4.1	3	13
2V8F	B C	B	6	Y	3.4	3	13
2V8F	B C	B	133	Y	1.6	120	137
2V8Q	A B	A	533	I	1.0	531	545
2V8Q	A B	A	536	F	5.3	531	545
2V8Q	A B	A	537	E	1.2	531	545
2V8Q	A E	A	531	H	1.2	531	545
2V8Q	A E	A	533	I	1.3	531	545
2V8S	E V	E	52	F	1.5	41	53
2V8S	E V	E	54	Y	2.3	54	69

2V8S	E V	E	95	E	1.4	95	104
2V8S	E V	V	19	R	1.0	9	27
2V8W	A B	A	69	V	1.1	69	78
2V8W	A B	A	73	W	3.1	69	78
2V8W	A B	B	56	R	1.0	56	62
2V8W	A B	B	58	F	1.1	56	62
2V8W	A B	B	59	L	1.8	56	62
2V8W	E F	E	73	W	3.1	69	79
2V8W	E F	E	135	L	1.3	125	139
2V8W	E F	F	56	R	1.4	56	64
2V8W	E F	F	59	L	2.2	56	64
2VAS	A B	A	725	K	1.1	724	729
2VAS	A B	A	789	I	1.5	785	815
2VAS	A B	A	792	R	1.7	785	815
2VAS	A B	A	793	W	5.6	785	815
2VAS	A B	A	794	K	1.8	785	815
2VAS	A B	A	795	K	2.8	785	815
2VAS	A B	A	796	V	1.0	785	815
2VAS	A B	A	798	W	1.1	785	815
2VAS	A B	A	801	L	1.0	785	815
2VAS	A B	A	803	V	2.4	785	815
2VAS	A B	A	809	K	1.9	785	815
2VAS	A B	A	810	I	1.9	785	815
2VAS	A B	A	812	Y	1.3	785	815
2VAS	A B	B	18	L	4.0	6	20
2VAS	A B	B	19	F	1.0	6	20
2VAS	A B	B	36	M	1.2	29	38
2VAS	A B	B	51	M	1.5	45	55
2VAS	A B	B	54	E	1.0	45	55
2VAS	A B	B	87	E	1.6	80	93
2VAS	A B	B	92	F	2.0	80	93
2VAS	A B	B	105	L	1.3	102	112
2VAS	A B	B	123	E	1.2	118	128
2VAS	A B	B	124	M	1.7	118	128
2VAS	A B	B	127	E	1.4	118	128
2VBL	A B	A	11	L	1.9	7	20
2VBL	A B	A	12	Y	1.8	7	20
2VBL	A B	A	15	G	83.2	7	20
2VBL	A B	A	16	F	2.2	7	20
2VBL	A B	A	19	G	113.3	7	20
2VBL	A B	A	54	F	1.8	52	63
2VBL	A B	B	11	L	1.2	7	20
2VBL	A B	B	12	Y	3.3	7	20
2VBL	A B	B	15	G	121.6	7	20
2VBL	A B	B	16	F	1.7	7	20
2VBL	A B	B	54	F	2.1	52	63
2VBN	A B	A	11	L	1.4	7	20
2VBN	A B	A	12	Y	1.3	7	20
2VBN	A B	A	15	G	150.9	7	20
2VBN	A B	A	16	F	1.9	7	20
2VBN	A B	A	19	G	6.0	7	20
2VBN	A B	A	54	F	1.3	52	63
2VBN	A B	B	11	L	1.4	7	20
2VBN	A B	B	15	G	107.2	7	20
2VBN	A B	B	16	F	2.0	7	20
2VBN	A B	B	19	G	5.8	7	20
2VBN	A B	B	54	F	2.1	52	63
2VBO	A B	A	11	L	1.1	7	20
2VBO	A B	A	12	Y	2.2	7	20
2VBO	A B	A	15	G	108.0	7	20

2VBO	A B	A	16	F	1.6	7	20
2VBO	A B	A	19	G	9.0	7	20
2VBO	A B	A	54	F	1.5	52	63
2VBO	A B	B	11	L	1.4	7	20
2VBO	A B	B	12	Y	3.0	7	20
2VBO	A B	B	15	G	76.9	7	20
2VBO	A B	B	16	F	2.0	7	20
2VBO	A B	B	19	G	8.1	7	20
2VBO	A B	B	54	F	2.4	52	63
2VDA	A B	A	236	Y	1.3	235	244
2VDA	A B	B	13	L	1.1	13	19
2VDA	A B	B	17	V	1.9	13	19
2VDB	A B	A	233	K	1.0	228	248
2VDB	A B	A	271	I	1.0	268	272
2VDB	A B	A	321	E	2.0	315	322
2VDB	A B	A	325	V	1.3	323	337
2VDB	A B	B	28	Y	1.8	26	34
2VDC	A J	J	109	V	596.7	109	113
2VDC	A J	J	111	E	638.0	109	113
2VDC	B G	B	1124	L	718.2	1122	1126
2VDC	B G	G	109	V	646.1	109	113
2VDC	B G	G	111	E	718.0	109	113
2VDC	C J	C	1445	N	1.6	1438	1446
2VDC	C J	C	1449	R	1.3	1447	1454
2VDC	C K	K	109	V	596.8	109	113
2VDC	C K	K	111	E	637.8	109	113
2VDC	D H	D	1124	L	718.2	1122	1126
2VDC	D H	H	109	V	645.9	109	113
2VDC	D H	H	111	E	717.9	109	113
2VDC	E L	L	109	V	596.9	109	113
2VDC	E L	L	111	E	638.3	109	113
2VDC	F I	F	1124	L	718.2	1122	1126
2VDC	F I	I	109	V	646.3	109	113
2VDC	F I	I	111	E	717.9	109	113
2VDN	A B	B	262	L	4.4	259	263
2VDN	A B	B	321	Y	1.3	315	324
2VDN	H L	L	124	Q	1.2	122	127
2VDO	A B	B	262	L	2.6	259	263
2VDO	A B	B	293	G	1.3	292	302
2VDO	A B	B	321	Y	1.4	315	324
2VDO	H L	L	124	Q	1.3	122	127
2VDU	B E	E	168	N	1.6	166	170
2VDU	B E	E	207	Y	2.1	199	209
2VDU	D F	F	168	N	1.7	166	170
2VDU	D F	F	207	Y	2.5	199	209
2VDW	A B	A	579	M	1.0	564	580
2VDW	A B	A	794	R	1.2	788	801
2VDW	A B	A	798	F	2.3	788	801
2VDW	A B	A	805	M	1.7	802	806
2VDW	A B	B	43	Y	1.2	43	55
2VDW	A B	B	49	R	2.5	43	55
2VDW	A B	B	257	Y	2.4	239	269
2VDW	C D	C	579	M	1.1	564	580
2VDW	C D	C	794	R	1.4	788	801
2VDW	C D	C	797	K	1.1	788	801
2VDW	C D	C	798	F	3.7	788	801
2VDW	C D	C	815	F	1.2	809	823
2VDW	C D	D	43	Y	1.0	43	55
2VDW	C D	D	44	F	1.3	43	55
2VDW	C D	D	257	Y	2.4	239	269

2VDW	E F	E	571	Y	1.1	564	580
2VDW	E F	E	575	L	1.0	564	580
2VDW	E F	E	798	F	2.8	788	801
2VDW	E F	E	815	F	1.2	809	824
2VDW	E F	F	43	Y	1.3	43	56
2VDW	E F	F	44	F	2.3	43	56
2VDW	E F	F	47	I	1.1	43	56
2VDW	E F	F	257	Y	1.8	239	268
2VDW	G H	G	791	I	1.0	788	801
2VDW	G H	G	798	F	2.8	788	801
2VDW	G H	G	815	F	1.1	809	824
2VDW	G H	H	43	Y	1.3	43	56
2VDW	G H	H	44	F	2.0	43	56
2VDW	G H	H	55	R	1.0	43	56
2VDW	G H	H	257	Y	2.6	248	268
2VE7	A C	A	187	W	2.1	177	198
2VE7	A C	A	194	I	1.9	177	198
2VE7	A C	A	228	Y	2.3	222	240
2VE7	A C	A	230	I	1.0	222	240
2VE7	A C	A	236	F	1.5	222	240
2VE7	A C	A	250	L	1.1	244	259
2VE7	A C	A	254	L	1.5	244	259
2VE7	A C	A	258	F	3.2	244	259
2VE7	A C	A	265	L	2.0	262	1123
2VE7	A C	A	1128	L	1.0	1124	1143
2VE7	A C	A	1138	Y	3.8	1124	1143
2VE7	A C	A	1142	L	2.4	1124	1143
2VE7	A C	C	81	G	4.4	79	99
2VE7	A C	C	82	F	3.5	79	99
2VE7	A C	C	98	I	1.6	79	99
2VE7	A C	C	110	L	1.2	106	111
2VE7	A C	C	127	F	1.1	114	142
2VE7	A C	C	130	F	4.2	114	142
2VE7	A C	C	131	R	1.2	114	142
2VE7	A C	C	138	Y	5.7	114	142
2VE7	A C	C	141	F	1.2	114	142
2VE7	A C	C	145	Y	3.5	144	148
2VE7	A C	C	1143	Y	3.6	1141	1148
2VE7	A C	C	1183	K	1.2	1182	1193
2VE7	A C	C	1186	S	1.0	1182	1193
2VE7	A C	C	1190	W	3.0	1182	1193
2VE7	B D	B	91	F	1.2	89	105
2VE7	B D	B	187	W	2.8	177	199
2VE7	B D	B	194	I	3.0	177	199
2VE7	B D	B	195	H	2.1	177	199
2VE7	B D	B	225	F	2.9	222	237
2VE7	B D	B	228	Y	3.3	222	237
2VE7	B D	B	229	T	1.3	222	237
2VE7	B D	B	230	I	1.0	222	237
2VE7	B D	B	233	Y	1.3	222	237
2VE7	B D	B	236	F	1.0	222	237
2VE7	B D	B	250	L	2.2	244	258
2VE7	B D	B	251	Q	1.0	244	258
2VE7	B D	B	254	L	1.7	244	258
2VE7	B D	B	265	L	1.5	264	277
2VE7	B D	B	282	L	1.0	278	1134
2VE7	B D	B	1138	Y	4.3	1135	1143
2VE7	B D	B	1142	L	2.2	1135	1143
2VE7	B D	B	1215	R	2.5	1207	1222
2VE7	B D	D	81	G	84.2	80	99

2VE7	B D	D	82	F	3.4	80	99
2VE7	B D	D	127	F	1.1	114	151
2VE7	B D	D	130	F	4.3	114	151
2VE7	B D	D	138	Y	4.7	114	151
2VE7	B D	D	141	F	1.6	114	151
2VE7	B D	D	142	L	1.5	114	151
2VE7	B D	D	145	Y	3.3	114	151
2VE7	B D	D	155	L	1.7	155	164
2VE7	B D	D	166	L	1.5	165	1123
2VE7	B D	D	1143	Y	5.2	1129	1148
2VE7	B D	D	1145	Q	1.0	1129	1148
2VE7	B D	D	1187	D	2.0	1182	1193
2VE7	B D	D	1190	W	4.9	1182	1193
2VGL	A B	A	463	Y	2.7	459	472
2VGL	A B	A	539	A	3.1	535	542
2VGL	A B	A	547	K	3.6	543	552
2VGL	A B	B	482	L	3.2	478	488
2VGL	A B	B	517	P	2.0	517	528
2VGL	A B	B	524	Y	4.2	517	528
2VGL	A B	B	525	I	2.5	517	528
2VGL	A M	A	360	E	1.0	360	369
2VGL	A M	A	391	D	1.3	383	397
2VGL	A M	A	422	E	1.3	418	436
2VGL	A M	A	426	L	1.1	418	436
2VGL	A M	M	99	E	1.2	98	104
2VGL	A S	A	17	I	1.7	11	23
2VGL	A S	A	88	Y	3.1	88	101
2VGL	A S	A	96	L	1.9	88	101
2VGL	A S	A	133	H	1.6	125	139
2VGL	A S	A	167	S	1.3	162	179
2VGL	A S	A	170	L	1.7	162	179
2VGL	A S	A	202	G	44.4	201	218
2VGL	A S	A	256	W	2.0	255	266
2VGL	A S	A	344	N	1.1	343	358
2VGL	A S	A	347	Y	1.1	343	358
2VGL	A S	A	348	L	1.2	343	358
2VGL	A S	S	105	F	2.0	100	106
2VGL	A S	S	107	F	3.4	107	118
2VGL	A S	S	108	Y	1.4	107	118
2VGL	A S	S	111	Y	1.4	107	118
2VGL	A S	S	112	T	1.1	107	118
2VGL	A S	S	130	K	1.4	128	141
2VGL	A S	S	138	L	1.6	128	141
2VGL	B M	B	38	I	1.1	27	43
2VGL	B M	B	71	L	1.9	63	76
2VGL	B M	B	217	W	2.9	216	229
2VGL	B M	B	220	I	1.3	216	229
2VGL	B M	B	300	Y	1.3	296	309
2VGL	B M	B	301	V	1.2	296	309
2VGL	B M	B	333	Y	1.5	332	345
2VGL	B M	B	405	Y	1.4	404	418
2VGL	B M	B	574	Y	1.0	570	575
2VGL	B M	M	77	M	11.6	75	91
2VGL	B M	M	79	F	1.2	75	91
2VGL	B M	M	80	E	1.2	75	91
2VGL	B M	M	84	K	1.5	75	91
2VGL	B M	M	105	F	1.5	105	116
2VGL	B M	M	106	V	1.5	105	116
2VGL	M S	S	27	E	1.4	25	41
2VGL	M S	S	31	L	1.0	25	41

2VGL	M S	S	33	E	1.7	25	41
2VGL	M S	S	36	H	1.1	25	41
2VGO	A D	D	807	L	1.2	805	817
2VGO	A D	D	815	Y	3.7	805	817
2VGO	A D	D	821	V	1.0	821	828
2VGO	A D	D	825	Y	2.0	821	828
2VGO	A D	D	833	L	1.4	833	837
2VGO	A D	D	836	L	2.5	833	837
2VGO	B C	B	139	R	1.0	135	147
2VGO	B C	C	807	L	2.1	804	817
2VGO	B C	C	811	I	2.0	804	817
2VGO	B C	C	814	Q	2.0	804	817
2VGO	B C	C	815	Y	4.7	804	817
2VGO	B C	C	833	L	1.6	833	837
2VGO	B C	C	836	L	2.5	833	837
2VGX	A B	A	65	L	1.4	59	66
2VGX	A B	B	39	L	1.6	37	49
2VGX	A B	B	65	L	1.2	59	66
2VH3	A B	A	102	T	1.3	97	107
2VH3	A B	A	104	F	2.8	97	107
2VH3	A B	A	105	Q	1.5	97	107
2VH3	A B	B	104	F	2.2	97	108
2VH3	A B	B	105	Q	1.2	97	108
2VHM	E L	E	29	H	1.9	25	36
2VHM	Q R	Q	43	Q	1.1	43	48
2VHM	Q R	Q	46	Y	1.3	43	48
2VHM	Q R	Q	111	K	1.2	102	116
2VHN	E L	E	29	H	1.1	28	38
2VHO	C N	N	89	R	2.7	84	90
2VIR	A B	A	127	E	1.0	125	130
2VJE	C B	C	462	F	1.9	462	471
2VJE	C D	D	433	L	1.5	431	435
2VJH	A B	A	5	V	1.5	4	15
2VJH	A B	A	6	T	1.3	4	15
2VJH	A B	A	9	L	2.6	4	15
2VJH	A B	A	13	D	1.1	4	15
2VJH	A B	A	24	L	3.0	21	47
2VJH	A B	A	27	V	1.8	21	47
2VJH	A B	A	31	I	1.1	21	47
2VJH	A B	A	48	H	1.1	48	63
2VJH	A B	A	87	D	1.3	76	100
2VJH	A B	A	91	R	3.4	76	100
2VJH	A B	A	94	N	2.9	76	100
2VJH	A B	A	95	Y	4.6	76	100
2VJH	A B	A	98	V	4.3	76	100
2VJH	A B	A	99	V	2.0	76	100
2VJH	A B	A	108	W	1.6	103	111
2VJH	A B	B	6	S	2.6	4	15
2VJH	A B	B	9	V	2.1	4	15
2VJH	A B	B	10	V	3.1	4	15
2VJH	A B	B	13	D	3.5	4	15
2VJH	A B	B	24	L	1.7	22	33
2VJH	A B	B	34	G	18.0	34	47
2VJH	A B	B	38	L	1.7	34	47
2VJH	A B	B	91	R	2.1	76	100
2VJH	A B	B	95	Y	3.2	76	100
2VJH	A B	B	98	L	2.1	76	100
2VJH	A D	A	153	R	1.8	146	163
2VJH	A D	A	161	N	2.0	146	163
2VJH	C B	C	153	R	1.6	146	163

2VJH	C B	C	161	N	1.1	146	163
2VJM	A B	A	142	V	1.3	140	147
2VJM	A B	A	175	H	1.0	167	191
2VJM	A B	A	178	I	3.1	167	191
2VJM	A B	A	179	G	5.5	167	191
2VJM	A B	A	181	L	1.6	167	191
2VJM	A B	A	185	E	1.7	167	191
2VJM	A B	A	186	I	1.7	167	191
2VJM	A B	A	188	H	1.9	167	191
2VJM	A B	A	205	L	1.5	200	208
2VJM	A B	A	207	L	2.0	200	208
2VJM	A B	A	209	R	1.1	209	222
2VJM	A B	A	212	L	2.4	209	222
2VJM	A B	A	213	R	1.1	209	222
2VJM	A B	A	216	Q	2.4	209	222
2VJM	A B	A	217	R	2.5	209	222
2VJM	A B	A	219	E	1.1	209	222
2VJM	A B	A	220	R	1.6	209	222
2VJM	A B	A	353	M	2.1	353	358
2VJM	A B	A	364	K	1.1	360	365
2VJM	A B	B	58	L	1.1	58	62
2VJM	A B	B	59	Y	11.8	58	62
2VJM	A B	B	142	V	1.5	141	147
2VJM	A B	B	178	I	2.9	171	191
2VJM	A B	B	179	G	5.8	171	191
2VJM	A B	B	181	L	1.4	171	191
2VJM	A B	B	185	E	1.0	171	191
2VJM	A B	B	186	I	1.3	171	191
2VJM	A B	B	188	H	2.6	171	191
2VJM	A B	B	205	L	1.7	200	208
2VJM	A B	B	207	L	1.7	200	208
2VJM	A B	B	209	R	1.6	209	222
2VJM	A B	B	212	L	2.3	209	222
2VJM	A B	B	215	Q	1.0	209	222
2VJM	A B	B	216	Q	2.3	209	222
2VJM	A B	B	217	R	1.5	209	222
2VJM	A B	B	219	E	2.0	209	222
2VJM	A B	B	220	R	1.5	209	222
2VJM	A B	B	353	M	2.3	353	358
2VJT	A B	A	8	I	2.7	3	14
2VJT	A B	A	23	L	1.1	20	32
2VJT	A B	A	33	G	99.2	33	46
2VJT	A B	A	37	L	2.3	33	46
2VJT	A B	A	90	R	2.4	75	99
2VJT	A B	A	94	Y	3.7	75	99
2VJT	A B	A	97	V	1.1	75	99
2VJT	A B	B	5	I	1.5	4	15
2VJT	A B	B	9	I	2.4	4	15
2VJT	A B	B	31	F	2.9	21	33
2VJT	A B	B	34	G	44.7	34	47
2VJT	A B	B	38	V	1.2	34	47
2VJT	A B	B	90	R	2.2	75	99
2VJT	A B	B	94	Y	1.4	75	99
2VJT	A B	B	97	L	1.2	75	99
2VL2	A C	A	119	I	1.6	117	121
2VL2	B C	B	79	F	1.6	78	88
2VL2	B C	C	79	F	2.2	78	88
2VL2	B C	C	80	V	1.3	78	88
2VL5	C D	D	128	Q	2.4	126	132
2VL5	C D	D	131	S	1.6	126	132

2VLH	A B	A	61	W	1.6	58	66
2VLH	A B	A	64	M	1.2	58	66
2VLH	A B	A	100	R	1.8	99	110
2VLH	A B	A	129	H	1.7	124	133
2VLH	A B	A	286	E	1.2	272	287
2VLH	A B	A	297	R	1.9	296	310
2VLH	A B	B	61	W	1.1	58	65
2VLH	A B	B	100	R	1.9	99	110
2VLH	A B	B	129	H	1.4	124	133
2VLH	A B	B	280	E	2.2	272	287
2VLH	A B	B	284	V	1.1	272	287
2VLH	A B	B	297	R	1.6	296	311
2VLJ	A D	A	154	E	1.2	152	162
2VLJ	D E	E	137	H	2.3	132	139
2VLR	A D	A	154	E	1.3	152	162
2VLR	A E	A	72	Q	1.1	57	85
2VLR	F I	F	154	E	1.3	152	175
2VML	A F	A	116	V	1.3	113	120
2VML	A F	F	76	N	1.0	76	100
2VML	A F	F	83	L	1.4	76	100
2VML	E D	E	115	E	1.2	113	120
2VML	E D	E	116	V	1.3	113	120
2VML	E D	D	83	L	1.5	76	100
2VML	E F	E	5	I	1.3	4	15
2VML	E F	E	6	T	1.5	4	15
2VML	E F	E	9	I	3.0	4	15
2VML	E F	E	13	D	1.0	4	15
2VML	E F	E	24	L	1.4	21	47
2VML	E F	E	31	F	2.0	21	47
2VML	E F	E	38	M	1.2	21	47
2VML	E F	E	91	R	3.5	76	100
2VML	E F	E	95	Y	3.4	76	100
2VML	E F	E	98	V	1.1	76	100
2VML	E F	F	5	F	1.9	4	15
2VML	E F	F	13	D	1.6	4	15
2VML	E F	F	38	L	1.5	34	47
2VML	E F	F	91	R	1.7	76	100
2VML	E F	F	95	Y	3.7	76	100
2VML	E F	F	98	L	2.6	76	100
2VML	G H	G	5	I	1.3	4	15
2VML	G H	G	6	T	1.4	4	15
2VML	G H	G	9	I	3.0	4	15
2VML	G H	G	13	D	1.2	4	15
2VML	G H	G	24	L	1.5	21	47
2VML	G H	G	31	F	1.9	21	47
2VML	G H	G	91	R	3.6	76	100
2VML	G H	G	95	Y	4.1	76	100
2VML	G H	H	5	F	1.3	4	15
2VML	G H	H	13	D	1.6	4	15
2VML	G H	H	38	L	1.6	34	47
2VML	G H	H	91	R	1.7	76	100
2VML	G H	H	95	Y	4.0	76	100
2VML	G H	H	98	L	2.7	76	100
2VML	G J	G	108	Y	1.0	103	111
2VML	G J	G	115	E	1.3	113	120
2VML	G J	G	116	V	1.7	113	120
2VML	G J	J	83	L	1.6	76	100
2VML	I J	I	5	I	1.2	4	15
2VML	I J	I	6	T	1.5	4	15
2VML	I J	I	9	I	4.1	4	15

2VML	I J	I	24	L	1.6	21	47
2VML	I J	I	31	F	1.9	21	47
2VML	I J	I	38	M	1.1	21	47
2VML	I J	I	91	R	3.0	76	100
2VML	I J	I	95	Y	3.7	76	100
2VML	I J	I	98	V	1.1	76	100
2VML	I J	J	5	F	1.6	4	15
2VML	I J	J	13	D	1.1	4	15
2VML	I J	J	38	L	1.6	34	47
2VML	I J	J	91	R	1.5	76	100
2VML	I J	J	95	Y	3.0	76	100
2VML	I J	J	98	L	2.6	76	100
2VML	I L	I	116	V	1.2	113	120
2VML	I L	L	83	L	1.2	76	100
2VML	K H	K	115	E	1.0	113	120
2VML	K H	K	116	V	1.2	113	120
2VML	K H	H	76	N	1.2	76	100
2VML	K H	H	83	L	1.0	76	100
2VML	K L	K	5	I	1.3	4	15
2VML	K L	K	6	T	1.3	4	15
2VML	K L	K	9	I	2.9	4	15
2VML	K L	K	24	L	1.5	21	47
2VML	K L	K	30	R	1.0	21	47
2VML	K L	K	31	F	2.0	21	47
2VML	K L	K	38	M	1.2	21	47
2VML	K L	K	91	R	3.2	76	100
2VML	K L	K	95	Y	4.8	76	100
2VML	K L	K	98	V	1.5	76	100
2VML	K L	L	5	F	2.0	4	15
2VML	K L	L	13	D	1.1	4	15
2VML	K L	L	38	L	1.7	34	47
2VML	K L	L	91	R	1.8	76	100
2VML	K L	L	95	Y	2.7	76	100
2VML	K L	L	98	L	2.4	76	100
2VN5	A B	B	17	L	1.9	16	28
2VN5	A B	B	19	F	2.1	16	28
2VN5	A B	B	23	K	1.1	16	28
2VN5	A B	B	58	L	2.3	47	59
2VN5	C D	D	17	L	2.0	16	28
2VN5	C D	D	19	F	2.1	16	28
2VOF	A B	A	48	V	1.0	32	52
2VOF	A B	A	55	Y	1.7	53	59
2VOF	A B	A	87	G	67.9	86	113
2VOF	A B	A	88	R	4.6	86	113
2VOF	A B	A	95	F	1.2	86	113
2VOF	A B	A	147	K	1.6	142	148
2VOF	A B	B	137	I	2.0	132	152
2VOF	A B	B	138	G	48.6	132	152
2VOF	A B	B	140	Q	1.0	132	152
2VOF	A B	B	141	L	1.2	132	152
2VOF	A B	B	142	R	1.5	132	152
2VOF	A B	B	144	I	1.5	132	152
2VOF	A B	B	146	D	3.8	132	152
2VOF	A B	B	148	L	2.0	132	152
2VOF	C D	C	55	Y	1.6	53	58
2VOF	C D	C	87	G	60.6	86	107
2VOF	C D	C	88	R	3.9	86	107
2VOF	C D	C	95	F	1.2	86	107
2VOF	C D	D	133	W	3.2	133	152
2VOF	C D	D	137	I	2.2	133	152

2VOF	C D	D	138	G	15.9	133	152
2VOF	C D	D	141	L	2.1	133	152
2VOF	C D	D	142	R	2.7	133	152
2VOF	C D	D	144	I	1.1	133	152
2VOF	C D	D	146	D	3.9	133	152
2VOF	C D	D	148	L	2.1	133	152
2VOG	A B	A	55	Y	1.5	53	57
2VOG	A B	A	74	V	1.5	64	79
2VOG	A B	A	77	K	1.3	64	79
2VOG	A B	A	87	G	20.9	86	106
2VOG	A B	A	91	T	1.3	86	106
2VOG	A B	A	95	F	1.2	86	106
2VOG	A B	A	148	F	1.1	143	149
2VOG	A B	B	134	I	2.4	130	149
2VOG	A B	B	137	K	1.1	130	149
2VOG	A B	B	138	L	1.8	130	149
2VOG	A B	B	139	Q	2.4	130	149
2VOG	A B	B	141	I	1.1	130	149
2VOG	A B	B	145	F	2.4	130	149
2VOH	A B	A	47	E	1.6	32	52
2VOH	A B	A	55	Y	1.6	53	58
2VOH	A B	A	56	L	4.2	53	58
2VOH	A B	A	74	V	1.2	64	79
2VOH	A B	A	78	E	1.0	64	79
2VOH	A B	A	87	G	151.7	86	108
2VOH	A B	A	88	R	4.4	86	108
2VOH	A B	A	91	T	1.1	86	108
2VOH	A B	A	95	F	1.3	86	108
2VOH	A B	A	148	F	1.5	140	149
2VOH	A B	B	68	L	1.9	67	86
2VOH	A B	B	71	V	1.9	67	86
2VOH	A B	B	72	G	50.9	67	86
2VOH	A B	B	74	Q	1.3	67	86
2VOH	A B	B	75	L	1.8	67	86
2VOH	A B	B	78	I	1.6	67	86
2VOH	A B	B	79	G	43.3	67	86
2VOH	A B	B	80	D	3.6	67	86
2VOH	A B	B	82	I	1.0	67	86
2VOH	A B	B	85	R	1.5	67	86
2VOI	A B	A	77	K	1.3	64	79
2VOI	A B	A	87	G	141.2	86	106
2VOI	A B	A	88	R	2.6	86	106
2VOI	A B	A	95	F	1.4	86	106
2VOI	A B	B	82	I	1.5	79	99
2VOI	A B	B	86	I	2.3	79	99
2VOI	A B	B	90	L	2.0	79	99
2VOI	A B	B	94	G	45.4	79	99
2VOI	A B	B	95	D	2.4	79	99
2VOL	A B	A	251	L	1.0	247	252
2VOL	A B	A	310	H	1.4	310	315
2VOL	A B	A	311	Q	1.4	310	315
2VOY	A F	A	55	S	89.9	54	65
2VOY	A J	A	17	C	55.9	15	28
2VOY	B D	D	834	F	1.2	833	854
2VOY	B D	D	850	G	87.7	833	854
2VOY	B E	E	98	L	1.7	92	101
2VOY	B F	F	217	K	52.4	216	223
2VOY	C D	C	985	K	3.3	976	987
2VOY	C D	D	835	F	2.2	833	854
2VOY	C H	C	968	L	1.5	968	972

2VOY	D E	D	850	G	24.3	833	854
2VOY	D E	E	99	I	1.1	92	101
2VOY	G H	H	295	Y	2.2	290	297
2VOY	G H	H	315	I	1.0	313	329
2VOY	G I	G	248	P	5.2	248	272
2VOY	G I	G	249	L	6.8	248	272
2VOY	G I	G	251	Q	6.9	248	272
2VOY	G I	I	413	E	12.6	411	417
2VOY	H I	H	326	M	1.2	313	329
2VOY	H I	I	412	L	1.4	411	417
2VOY	H K	K	775	I	1.6	750	780
2VOY	I K	K	750	G	66.6	750	780
2VOY	I K	K	751	R	13.1	750	780
2VOY	K L	L	807	L	1.0	790	809
2VPD	A B	A	381	L	1.5	376	385
2VPD	A B	A	396	M	1.0	393	398
2VPD	A B	B	182	T	1.2	182	194
2VPD	A B	B	186	N	2.2	182	194
2VPD	C D	C	381	L	1.0	376	385
2VPD	C D	C	396	M	1.3	393	397
2VPD	C D	D	182	T	1.1	182	194
2VPD	C D	D	186	N	1.2	182	194
2VPE	A B	A	381	L	1.5	376	385
2VPE	A B	A	382	L	1.7	376	385
2VPE	A B	A	396	M	1.2	393	398
2VPE	A B	B	182	T	1.9	182	194
2VPE	A B	B	186	N	1.1	182	194
2VPE	C D	C	381	L	1.8	376	385
2VPE	C D	C	382	L	1.2	376	385
2VPE	C D	C	396	M	1.4	393	397
2VPE	C D	D	182	T	1.8	182	194
2VPE	C D	D	186	N	1.9	182	194
2VPG	A B	A	381	L	1.6	376	385
2VPG	A B	A	382	L	1.1	376	385
2VPG	A B	A	396	M	1.2	393	398
2VPG	A B	B	182	T	2.5	182	194
2VPG	A B	B	186	N	1.5	182	194
2VPG	C D	C	381	L	1.3	376	385
2VPG	C D	C	382	L	1.5	376	385
2VPG	C D	D	182	T	1.7	182	194
2VPG	C D	D	186	N	2.1	182	194
2VQ1	A B	A	124	Q	1.7	122	127
2VQ1	E F	E	124	Q	1.7	122	128
2VR0	A C	C	130	M	1.0	129	133
2VR0	B C	C	57	K	1.1	50	59
2VR0	E F	E	222	N	1.0	221	225
2VRC	A D	A	95	R	1.0	80	97
2VRC	A D	A	96	D	1.0	80	97
2VRC	B D	B	153	R	1.1	150	159
2VRC	B D	D	244	F	2.4	242	258
2VRC	C D	C	85	V	1.0	80	97
2VRC	C D	C	92	K	1.3	80	97
2VRC	C D	C	95	R	1.5	80	97
2VRC	C D	C	119	H	1.5	116	132
2VRC	C D	C	126	Y	2.3	116	132
2VRC	C D	D	92	K	1.3	80	98
2VRC	C D	D	95	R	2.0	80	98
2VRC	C D	D	126	Y	3.4	116	132
2VRW	A B	A	65	D	1.6	65	73
2VRW	A B	A	66	R	1.5	65	73

2VRW	A B	A	67	L	3.9	65	73
2VRW	A B	B	194	K	1.6	191	226
2VRW	A B	B	201	E	2.2	191	226
2VRW	A B	B	335	K	1.0	335	347
2VRW	A B	B	337	H	1.7	335	347
2VRW	A B	B	371	N	1.5	350	389
2VRW	A B	B	375	R	1.0	350	389
2VSK	C B	B	91	R	1.3	86	92
2VSO	A E	A	35	R	5.7	31	39
2VSO	A E	A	38	F	1.0	31	39
2VSO	A E	E	628	E	1.0	622	636
2VSO	A E	E	838	F	5.5	834	851
2VSO	B F	B	35	R	3.0	31	39
2VSO	B F	B	38	F	2.8	31	39
2VSO	B F	F	615	N	1.3	603	616
2VSO	B F	F	838	F	2.5	834	851
2VT1	A B	A	245	K	1.8	242	250
2VT1	A B	A	248	I	2.5	242	250
2VT1	A B	B	292	Y	2.9	284	296
2VTB	A B	A	151	D	1.0	147	163
2VTB	A B	A	154	R	1.9	147	163
2VTB	A B	A	158	Q	2.1	147	163
2VTB	A B	B	154	R	2.0	147	164
2VTB	A B	B	157	N	1.1	147	164
2VTB	A B	B	158	Q	2.2	147	164
2VU8	E I	E	172	Y	1.0	165	173
2VUS	A I	A	333	E	1.0	331	346
2VUS	A I	A	337	E	3.2	331	346
2VUS	A I	I	699	L	1.1	695	705
2VUS	B J	B	28	V	1.1	16	29
2VUS	B J	B	198	P	2.7	196	207
2VUS	B J	B	201	L	2.6	196	207
2VUS	B J	B	337	E	1.3	331	346
2VUS	B J	J	699	L	1.1	695	704
2VUS	C K	C	28	V	1.2	16	29
2VUS	C K	C	337	E	1.0	331	346
2VUS	D L	D	28	V	1.4	16	29
2VUS	E M	M	700	F	1.9	695	705
2VUS	E M	M	704	H	1.1	695	705
2VUS	F N	N	699	L	1.0	695	705
2VUS	F N	N	700	F	1.1	695	705
2VUS	G O	G	28	V	1.4	16	29
2VUS	G O	G	337	E	1.0	331	346
2VUS	G O	O	700	F	1.5	695	705
2VVC	A L	A	127	W	3.4	125	131
2VVL	F G	F	107	T	1.6	100	109
2VVL	F G	G	101	H	1.1	100	109
2VVL	F G	G	243	D	1.2	238	246
2VWE	A C	A	18	I	1.2	17	25
2VWE	A E	A	17	W	2.0	17	25
2VWE	A E	A	21	Y	3.6	17	25
2VWE	B J	B	18	I	1.1	17	25
2VWE	B L	B	21	Y	1.3	17	25
2VXQ	H L	L	123	E	1.3	122	127
2VXQ	H L	L	124	Q	1.7	122	127
2VXS	H L	L	124	E	1.2	123	128
2VXS	H L	L	125	E	1.6	123	128
2VXS	J N	N	125	E	1.0	123	128
2VXS	K O	O	125	E	1.1	123	128
2VXT	H L	L	124	Q	1.6	122	127

2VXU	H L	L	124	Q	1.6	122	127
2VXU	I M	M	123	E	1.0	122	128
2VXU	I M	M	124	Q	2.1	122	128
2VXV	H L	L	124	Q	1.7	122	128
2VYN	D A	D	10	R	1.0	10	22
2VYN	D A	D	314	E	1.1	313	331
2VYN	D A	A	10	R	1.7	10	21
2VYN	D A	A	38	Y	6.9	36	45
2VYN	D A	A	41	Y	1.6	36	45
2VYN	D A	A	42	M	7.0	36	45
2VYN	D A	A	313	E	1.0	312	327
2VYR	A E	A	53	M	2.1	49	63
2VYR	A E	A	54	H	1.9	49	63
2VYR	A E	A	57	G	72.8	49	63
2VYR	A J	A	99	Y	1.6	96	105
2VYR	B F	B	53	M	1.0	49	63
2VYR	B F	B	57	G	80.9	49	63
2VYR	C G	C	50	K	1.5	49	63
2VYR	C G	C	53	M	2.0	49	63
2VYR	C G	C	57	G	72.9	49	63
2VYR	C G	C	58	Q	1.8	49	63
2VYR	D H	D	50	K	1.1	49	63
2VYR	D H	D	53	M	1.8	49	63
2VYR	D H	D	54	H	2.2	49	63
2VYR	D H	D	57	G	52.2	49	63
2VYR	D H	D	58	Q	1.3	49	63
2VZD	A C	A	250	F	1.2	249	257
2VZD	A C	A	365	F	1.3	354	368
2VZD	A C	C	7	L	1.2	3	11
2VZD	A C	C	8	L	1.4	3	11
2VZD	B D	B	250	F	1.4	249	257
2VZD	B D	B	362	Y	2.2	354	368
2VZD	B D	B	365	F	1.4	354	368
2VZD	B D	D	7	L	3.1	2	11
2VZD	B D	D	8	L	2.0	2	11
2VZG	A B	A	5	L	1.9	4	15
2VZG	A B	A	8	L	1.3	4	15
2VZG	A B	A	9	L	1.2	4	15
2VZG	A B	A	12	L	2.0	4	15
2VZI	A B	A	5	L	1.9	2	13
2VZI	A B	A	8	L	1.8	2	13
2VZI	A B	A	9	M	1.9	2	13
2VZI	A B	A	12	L	1.5	2	13
2VZI	A B	B	362	Y	1.6	354	368
2VZI	A B	B	365	F	1.0	354	368
2W0C	A P	A	100	Q	8.3	97	104
2W0C	B Q	Q	44	G	6.8	44	52
2W0C	D R	R	44	G	236.1	44	53
2W0C	E R	R	30	W	12.7	21	43
2W0C	G P	G	103	M	9.6	97	104
2W0C	H S	S	44	G	4.4	44	50
2W0C	I S	S	37	K	1.0	23	43
2W19	A C	A	385	D	1.1	383	402
2W19	A C	A	392	Q	1.1	383	402
2W19	A C	A	458	E	1.3	446	461
2W19	A C	C	56	H	1.8	56	66
2W19	A C	C	60	M	1.6	56	66
2W19	A C	C	63	I	1.0	56	66
2W19	B D	B	385	D	1.4	383	402
2W19	B D	B	392	Q	1.2	383	402

2W19	B D	B	458	E	1.1	446	461
2W19	B D	D	56	H	2.5	56	66
2W19	B D	D	60	M	1.4	56	66
2W19	B D	D	63	I	1.1	56	66
2W2H	A C	A	47	D	1.2	41	53
2W2H	B D	B	47	D	1.1	41	53
2W2M	P A	A	266	I	1.6	261	278
2W2M	P A	A	269	E	1.2	261	278
2W2M	P A	A	295	R	1.3	295	307
2W2X	A C	A	23	Y	1.7	16	25
2W2X	A C	A	166	K	1.4	165	171
2W2X	A D	A	67	L	1.5	65	73
2W2X	A D	D	102	F	5.4	98	113
2W2X	B C	B	67	L	2.5	65	73
2W2X	B C	B	70	L	1.6	65	73
2W2X	B C	C	98	V	2.3	98	113
2W2X	B C	C	102	F	3.5	98	113
2W65	A B	B	129	Q	1.7	127	132
2W65	C D	D	128	E	1.1	127	131
2W65	C D	D	129	Q	1.3	127	131
2W72	A B	A	31	R	3.7	21	36
2W72	A B	A	34	L	1.0	21	36
2W72	A B	A	103	H	1.2	95	112
2W72	A B	A	122	H	3.0	119	137
2W72	A B	B	30	R	4.2	20	35
2W72	A B	B	34	V	1.6	20	35
2W72	A B	B	116	H	2.3	100	119
2W72	A B	B	124	P	1.6	124	144
2W72	B C	B	37	W	2.8	36	41
2W72	B C	B	40	R	2.0	36	41
2W72	D C	D	30	R	4.1	20	35
2W72	D C	D	34	V	1.6	20	35
2W72	D C	C	31	R	3.6	21	36
2W72	D C	C	103	H	1.2	95	113
2W72	D C	C	107	V	1.0	95	113
2W72	D C	C	122	H	3.0	119	137
2W73	A K	A	92	F	1.1	65	93
2W73	A K	A	145	M	2.0	138	146
2W73	A K	K	396	I	1.7	396	409
2W73	A K	K	400	I	2.1	396	409
2W73	A K	K	401	R	1.0	396	409
2W73	A K	K	404	G	107.2	396	409
2W73	A L	A	14	E	1.0	6	20
2W73	A L	A	18	L	2.2	6	20
2W73	A L	A	19	F	1.0	6	20
2W73	A L	A	68	F	2.2	65	93
2W73	A L	A	83	E	1.5	65	93
2W73	A L	L	408	R	1.5	396	411
2W73	A L	L	410	F	2.5	396	411
2W73	B L	B	92	F	1.4	65	93
2W73	B L	B	109	M	1.0	102	112
2W73	B L	B	145	M	1.6	138	146
2W73	B L	L	397	R	1.1	396	411
2W73	B L	L	400	I	1.9	396	411
2W73	B L	L	403	I	1.7	396	411
2W73	B L	L	404	G	103.4	396	411
2W73	E M	E	92	F	1.6	65	93
2W73	E M	M	400	I	1.2	396	410
2W73	E M	M	403	I	1.9	396	410
2W73	E M	M	404	G	88.3	396	410

2W73	E O	E	11	E	2.1	6	20
2W73	E O	E	14	E	1.4	6	20
2W73	E O	E	18	L	2.1	6	20
2W73	E O	E	19	F	1.5	6	20
2W73	E O	O	403	I	1.4	396	411
2W73	E O	O	405	K	1.6	396	411
2W73	E O	O	406	M	1.1	396	411
2W73	E O	O	410	F	2.2	396	411
2W73	F M	F	11	E	1.3	6	20
2W73	F M	F	14	E	1.0	6	20
2W73	F M	F	18	L	2.4	6	20
2W73	F M	F	75	K	1.1	65	93
2W73	F M	M	403	I	1.3	396	410
2W73	F M	M	405	K	2.2	396	410
2W73	F M	M	406	M	2.5	396	410
2W73	F O	F	92	F	1.7	65	93
2W73	F O	F	108	V	4.0	102	112
2W73	F O	O	396	I	1.7	396	411
2W73	F O	O	400	I	1.6	396	411
2W73	F O	O	403	I	1.8	396	411
2W73	F O	O	404	G	82.3	396	411
2W73	F O	O	408	R	1.0	396	411
2W80	A D	A	340	M	1.3	338	343
2W80	B C	B	340	M	1.0	338	344
2W80	E F	E	340	M	1.6	338	343
2W80	G H	G	340	M	2.0	338	343
2W83	A C	A	73	L	1.8	71	76
2W83	A C	C	416	V	1.9	389	452
2W83	A C	C	423	K	1.0	389	452
2W83	A D	D	425	D	1.9	392	452
2W83	B C	C	425	D	1.2	389	452
2W83	B D	B	73	L	1.6	71	77
2W83	B D	B	76	H	1.0	71	77
2W83	B D	D	416	V	1.9	392	452
2W84	A B	A	35	F	2.4	26	37
2W84	A B	A	52	F	3.2	46	57
2W84	A B	A	56	K	2.0	46	57
2W84	A B	B	103	W	4.9	94	110
2W84	A B	B	107	F	3.2	94	110
2W85	A B	A	52	F	2.9	46	57
2W85	A B	A	56	K	1.0	46	57
2W85	A B	B	105	F	1.3	102	112
2W85	A B	B	110	F	2.7	102	112
2W96	B A	B	61	R	1.9	51	67
2W96	B A	A	138	L	1.0	134	148
2W9E	A H	A	145	Y	2.9	144	153
2W9E	A H	A	149	Y	1.4	144	153
2W9E	A L	A	148	R	4.6	144	153
2WAQ	A B	A	277	F	1.2	271	278
2WAQ	A B	A	500	Q	2.8	499	510
2WAQ	A B	A	502	Y	6.9	499	510
2WAQ	A B	A	504	S	1.4	499	510
2WAQ	A B	A	649	E	1.0	648	652
2WAQ	A B	A	728	M	4.7	724	729
2WAQ	A B	A	792	P	1.0	792	811
2WAQ	A B	A	795	L	1.2	792	811
2WAQ	A B	A	796	F	1.9	792	811
2WAQ	A B	A	802	G	144.3	792	811
2WAQ	A B	B	919	P	5.7	918	922
2WAQ	A B	B	924	L	1.5	924	940

2WAQ	A B	B	927	I	1.2	924	940
2WAQ	A B	B	1041	G	2.5	1033	1043
2WAQ	A B	B	1042	F	4.7	1033	1043
2WAQ	A B	B	1047	L	1.7	1045	1052
2WAQ	A B	B	1050	D	2.5	1045	1052
2WAQ	A B	B	1051	R	1.2	1045	1052
2WAQ	A B	B	1104	I	1.3	1098	1110
2WAQ	A C	A	89	H	1.9	87	96
2WAQ	A C	C	70	I	3.0	70	102
2WAQ	A C	C	71	G	199.2	70	102
2WAQ	A C	C	111	V	1.8	104	112
2WAQ	A C	C	312	H	1.8	310	322
2WAQ	A C	C	315	L	1.8	310	322
2WAQ	A C	C	351	V	1.3	351	361
2WAQ	A C	C	355	L	1.5	351	361
2WAQ	A C	C	356	D	1.5	351	361
2WAQ	A C	C	360	R	1.1	351	361
2WAQ	A C	C	374	I	1.1	369	376
2WAQ	A L	A	519	E	1.0	518	528
2WAQ	A L	A	526	G	10.4	518	528
2WAQ	B C	B	1048	L	1.3	1045	1052
2WAQ	B C	B	1049	K	1.0	1045	1052
2WAQ	B C	B	1100	F	1.5	1098	1110
2WAQ	B C	C	373	I	1.2	369	376
2WAQ	B D	B	961	L	1.4	953	963
2WAQ	B D	D	22	L	1.0	22	35
2WAQ	B D	D	56	E	1.9	55	65
2WAQ	B N	B	747	S	1.4	745	750
2WAQ	B N	N	32	G	50.9	31	38
2WAQ	B N	N	43	Y	2.3	43	50
2WAQ	B N	N	44	C	3.2	43	50
2WAQ	B N	N	47	R	2.9	43	50
2WAQ	C E	E	22	L	2.0	22	29
2WAQ	C H	C	287	E	1.0	286	303
2WAQ	C K	K	19	F	1.5	14	23
2WAQ	C K	K	30	Y	1.8	29	45
2WAQ	D L	D	23	E	1.0	22	35
2WAQ	D L	D	24	F	3.2	22	35
2WAQ	D L	D	28	I	1.1	22	35
2WAQ	D L	D	30	R	1.1	22	35
2WAQ	D L	D	246	G	16.5	240	263
2WAQ	D L	D	249	I	1.0	240	263
2WAQ	D L	D	250	I	1.7	240	263
2WAQ	D L	D	253	I	2.2	240	263
2WAQ	D L	D	256	L	1.0	240	263
2WAQ	D L	D	260	L	1.9	240	263
2WAQ	D L	L	27	L	1.9	22	31
2WAQ	D L	L	30	G	8.5	22	31
2WAQ	D L	L	73	I	1.7	65	86
2WAQ	D L	L	77	R	1.1	65	86
2WAQ	D L	L	79	M	1.5	65	86
2WAQ	D L	L	83	Y	2.4	65	86
2WAQ	D L	L	84	I	1.4	65	86
2WAQ	D L	L	90	L	1.3	87	91
2WAQ	E F	F	21	L	2.6	20	25
2WAQ	E F	F	33	L	1.0	32	44
2WAQ	E F	F	34	L	1.5	32	44
2WAQ	E F	F	40	Y	2.7	32	44
2WAQ	E F	F	82	E	1.3	80	84
2WAQ	H K	K	15	F	1.0	14	23

2WAQ	H Q	H	25	I	1.3	25	36
2WAQ	H Q	H	29	Y	2.2	25	36
2WAQ	H Q	Q	66	R	1.0	61	73
2WAQ	H Q	Q	67	L	1.4	61	73
2WAQ	H Q	Q	70	D	1.3	61	73
2WAX	A B	A	309	Q	1.4	307	321
2WAX	A B	A	312	H	3.7	307	321
2WAX	A B	A	316	T	1.8	307	321
2WAX	A B	A	432	R	1.2	432	443
2WAX	A B	A	433	F	3.4	432	443
2WAX	A B	A	435	L	1.2	432	443
2WAX	A B	A	436	K	2.7	432	443
2WAX	A B	A	439	E	1.1	432	443
2WAX	A B	B	206	F	2.3	206	212
2WAX	A B	B	210	L	1.6	206	212
2WAX	A B	B	215	K	1.9	215	226
2WAX	A B	B	219	F	3.4	215	226
2WAX	A B	B	222	I	1.5	215	226
2WAX	C D	C	312	H	4.7	307	320
2WAX	C D	C	316	T	1.2	307	320
2WAX	C D	C	432	R	1.2	432	443
2WAX	C D	C	433	F	1.0	432	443
2WAX	C D	C	436	K	2.1	432	443
2WAX	C D	D	206	F	3.2	206	211
2WAX	C D	D	210	L	2.4	206	211
2WAX	C D	D	215	K	1.5	215	225
2WAX	C D	D	219	F	1.5	215	225
2WAX	C D	D	222	I	3.0	215	225
2WB1	A B	A	343	I	1.1	341	347
2WB1	A B	A	520	E	1.4	518	525
2WB1	A B	A	648	L	4.1	648	652
2WB1	A B	A	651	V	4.2	648	652
2WB1	A B	A	728	M	1.4	724	729
2WB1	A B	A	743	M	4.9	740	746
2WB1	A B	A	796	F	1.3	792	802
2WB1	A B	A	820	Q	1.5	812	827
2WB1	A B	B	446	R	1.0	443	447
2WB1	A B	B	918	L	2.7	918	922
2WB1	A B	B	924	L	1.6	924	940
2WB1	A B	B	927	I	4.7	924	940
2WB1	A B	B	931	I	3.1	924	940
2WB1	A B	B	1000	V	1.3	1000	1004
2WB1	A B	B	1042	F	3.8	1033	1043
2WB1	A B	B	1103	L	1.1	1098	1110
2WB1	A B	B	1104	I	1.4	1098	1110
2WB1	A B	B	1108	M	1.0	1098	1110
2WB1	A C	A	823	L	1.2	812	827
2WB1	A C	A	824	I	1.1	812	827
2WB1	A C	C	36	I	1.8	31	43
2WB1	A C	C	71	G	296.2	70	77
2WB1	A C	C	311	R	2.3	310	321
2WB1	A C	C	315	L	3.2	310	321
2WB1	A C	C	319	V	2.9	310	321
2WB1	A C	C	354	L	1.1	353	360
2WB1	A C	C	355	L	2.3	353	360
2WB1	A C	C	374	I	1.1	369	376
2WB1	A C	C	375	I	1.0	369	376
2WB1	A K	A	479	I	1.4	470	480
2WB1	A K	K	32	I	1.0	29	45
2WB1	B D	D	60	H	1.0	55	65

2WB1	B N	N	32	G	39.7	32	38
2WB1	B N	N	47	R	1.6	46	51
2WB1	B N	N	58	E	2.0	57	61
2WB1	C B	B	1048	L	1.1	1045	1050
2WB1	C B	B	1100	F	1.3	1098	1110
2WB1	C H	C	287	E	2.2	286	304
2WB1	C K	K	30	Y	2.5	29	45
2WB1	F E	F	44	V	1.2	34	45
2WB1	H K	K	15	F	1.8	14	24
2WB1	R O	O	32	G	130.4	32	38
2WB1	R O	O	50	L	1.3	46	51
2WB1	R S	S	33	M	1.1	22	35
2WB1	R S	S	34	L	1.4	22	35
2WB1	R X	R	90	L	1.0	85	91
2WB1	S O	S	61	R	1.3	55	65
2WB1	S O	O	56	I	1.8	56	61
2WB1	U T	U	40	Y	2.1	34	45
2WB1	W I	I	66	E	1.1	63	68
2WB1	W R	W	18	E	1.5	16	21
2WB1	W R	W	500	Q	1.2	499	510
2WB1	W R	W	504	S	2.0	499	510
2WB1	W R	W	728	M	1.6	724	729
2WB1	W R	W	796	F	3.2	792	802
2WB1	W R	R	919	P	3.7	918	922
2WB1	W R	R	957	Q	1.0	955	963
2WB1	W R	R	1041	G	2.0	1033	1043
2WB1	W R	R	1042	F	3.5	1033	1043
2WB1	W R	R	1047	L	1.0	1045	1050
2WB1	W R	R	1103	L	1.6	1098	1110
2WB1	W Y	W	89	H	1.0	87	95
2WB1	W Y	W	127	S	1.4	126	130
2WB1	W Y	W	819	M	1.1	812	827
2WB1	W Y	W	820	Q	1.0	812	827
2WB1	W Y	W	823	L	1.3	812	827
2WB1	W Y	W	824	I	1.3	812	827
2WB1	W Y	Y	32	L	1.0	31	43
2WB1	W Y	Y	70	I	2.7	70	77
2WB1	W Y	Y	71	G	299.9	70	77
2WB1	W Y	Y	104	L	1.3	104	111
2WB1	W Y	Y	311	R	1.4	310	321
2WB1	W Y	Y	319	V	2.0	310	321
2WB1	W Y	Y	354	L	1.0	353	360
2WB1	W Y	Y	355	L	2.0	353	360
2WB1	W Y	Y	374	I	1.1	369	376
2WB1	Y I	I	30	Y	2.7	29	45
2WB1	Y R	Y	375	I	1.0	369	376
2WB1	Y R	R	1040	I	3.0	1033	1043
2WB1	Y R	R	1100	F	1.9	1098	1110
2WB1	Y T	T	22	L	1.2	22	29
2WB1	Y Z	Y	287	E	1.4	286	304
2WB1	Z J	J	67	L	1.1	63	73
2WBE	A B	A	72	P	3.3	72	81
2WBE	A B	A	397	L	1.0	387	401
2WBE	A C	C	278	L	1.2	275	290
2WBE	B C	B	420	E	1.4	415	437
2WBJ	A B	A	70	L	1.7	56	77
2WBJ	A D	A	58	G	88.5	56	77
2WBJ	A D	A	65	V	1.1	56	77
2WBJ	A D	A	72	I	1.1	56	77
2WBJ	B C	B	69	E	2.4	65	77

2WBJ	B C	B	81	H	2.5	78	89
2WBJ	B C	B	84	G	5.8	78	89
2WBJ	B D	B	61	W	3.2	55	63
2WBJ	B D	B	78	Y	1.7	78	89
2WBJ	B D	B	85	V	1.3	78	89
2WBJ	C D	D	160	E	1.2	158	165
2WBJ	E F	E	48	F	2.9	46	50
2WBJ	E F	E	70	L	1.5	56	77
2WBJ	E F	E	73	M	1.1	56	77
2WBJ	E F	E	76	R	2.8	56	77
2WBJ	E F	F	56	P	2.0	55	63
2WBJ	E F	F	57	D	2.5	55	63
2WBJ	E H	E	58	G	50.6	56	77
2WBJ	E H	E	65	V	1.4	56	77
2WBJ	E H	E	66	D	2.3	56	77
2WBJ	E H	E	69	N	1.4	56	77
2WBJ	F G	F	69	E	2.2	65	77
2WBJ	F G	F	81	H	2.1	78	89
2WBJ	F H	F	61	W	2.7	55	63
2WBJ	F H	F	78	Y	2.7	78	89
2WBJ	F H	F	85	V	1.4	78	89
2WC0	A D	A	108	H	2.2	106	115
2WC0	A D	D	10	H	2.0	9	19
2WC0	B F	F	10	H	1.9	10	20
2WC0	E F	F	11	L	1.1	10	20
2WD7	A B	A	243	F	3.4	234	246
2WD7	A B	B	243	F	3.4	234	246
2WD7	A C	A	132	F	1.5	116	142
2WD7	A C	A	173	L	1.5	172	195
2WD7	A C	A	176	M	1.5	172	195
2WD7	A C	A	179	H	1.0	172	195
2WD7	A C	A	183	G	60.9	172	195
2WD7	A C	A	190	L	1.1	172	195
2WD7	A C	A	191	E	1.2	172	195
2WD7	A C	C	132	F	3.0	116	141
2WD7	A C	C	173	L	1.1	172	195
2WD7	A C	C	176	M	2.1	172	195
2WD7	A C	C	179	H	1.2	172	195
2WD7	A C	C	183	G	42.6	172	195
2WD7	A C	C	191	E	1.6	172	195
2WD7	A D	D	221	W	2.0	215	225
2WDI	F P	F	31	H	1.8	30	45
2WDI	F P	F	187	V	1.0	183	189
2WDI	U V	U	40	F	1.8	33	67
2WDI	U V	U	43	G	2.4	33	67
2WEL	A D	A	297	R	1.4	296	311
2WEL	A D	A	298	R	1.0	296	311
2WEL	A D	A	299	K	3.7	296	311
2WEL	A D	A	300	L	1.1	296	311
2WEL	A D	A	302	G	7.9	296	311
2WEL	A D	A	304	I	2.0	296	311
2WEL	A D	A	305	L	1.5	296	311
2WEL	A D	A	308	M	1.5	296	311
2WEL	A D	A	309	L	1.1	296	311
2WEL	A D	D	12	E	1.2	7	21
2WEL	A D	D	15	E	1.6	7	21
2WEL	A D	D	20	F	1.0	7	21
2WEL	A D	D	93	F	1.6	79	94
2WEL	A D	D	125	M	1.5	119	130
2WEL	A D	D	128	E	1.0	119	130

2WEL	A D	D	142	F	1.4	139	146
2WG3	A C	C	380	E	1.2	376	382
2WG3	A C	C	381	E	1.5	376	382
2WG3	B D	D	380	E	1.1	376	382
2WG3	B D	D	381	E	1.0	376	382
2WG8	A B	A	59	M	1.0	53	67
2WG8	A B	A	63	H	1.1	53	67
2WG8	A B	B	63	H	1.0	53	67
2WH1	C N	C	9	G	203.0	7	11
2WH1	C N	C	33	L	2.0	27	44
2WH1	C N	C	34	L	1.2	27	44
2WH1	G K	K	59	Y	1.7	58	75
2WH1	J N	N	45	R	2.1	44	50
2WH1	J N	N	49	H	1.1	44	50
2WH2	F P	F	34	W	2.6	30	45
2WH2	N U	U	64	R	3.6	56	69
2WH2	N U	U	100	V	1.6	97	101
2WH2	U V	U	40	F	2.6	33	55
2WH2	U V	U	98	L	1.2	97	101
2WH4	F P	F	31	H	1.5	30	44
2WH4	F P	F	34	W	3.3	30	44
2WH4	N U	U	64	R	3.0	56	69
2WH4	N U	U	100	V	1.1	97	101
2WH4	U V	U	40	F	2.4	33	55
2WH4	U V	U	43	G	1.0	33	55
2WH4	U V	U	47	Y	1.4	33	55
2WH4	U V	U	98	L	1.3	97	101
2WHP	A B	A	373	L	2.0	372	382
2WHP	A B	A	534	R	1.4	526	541
2WHP	A B	A	535	F	3.1	526	541
2WHP	A B	B	373	L	1.5	372	383
2WHP	A B	B	380	L	1.7	372	383
2WHP	A B	B	535	F	3.2	526	542
2WHP	A B	B	539	L	1.5	526	542
2WII	A B	A	594	I	1.1	591	602
2WII	A B	B	1017	L	2.6	1017	1037
2WIN	A B	B	1012	W	1.4	1012	1016
2WIN	A B	B	1410	Y	4.3	1409	1413
2WIN	A N	N	39	Y	2.3	38	58
2WIN	B N	N	53	Y	1.6	38	58
2WIN	B Q	Q	10	Y	2.7	9	25
2WIN	B Q	Q	60	F	1.7	60	83
2WIN	B Q	Q	68	Y	1.9	60	83
2WIN	C D	C	578	K	1.6	578	584
2WIN	C D	C	594	I	1.0	591	601
2WIN	C D	D	1410	Y	4.1	1409	1413
2WIN	C M	M	39	Y	2.0	38	58
2WIN	D P	P	10	Y	2.0	9	25
2WIN	D P	P	60	F	1.7	60	83
2WIN	D P	P	68	Y	1.9	60	83
2WIN	E F	E	580	V	1.9	578	584
2WIN	E F	E	591	Q	1.0	591	601
2WIN	E F	F	1410	Y	3.2	1409	1413
2WIN	E P	P	39	Y	2.0	38	58
2WIN	F M	M	60	F	2.8	60	83
2WIN	F M	M	61	K	1.0	60	83
2WIN	F M	M	68	Y	1.9	60	83
2WIN	F P	P	46	I	1.0	38	58
2WIN	F P	P	53	Y	1.7	38	58
2WIN	G H	G	578	K	2.0	578	584

2WIN	G H	G	581	F	2.0	578	584
2WIN	G H	H	1410	Y	3.8	1409	1413
2WIN	G Q	Q	39	Y	2.3	38	58
2WIN	H N	N	10	Y	1.9	9	25
2WIN	H N	N	60	F	2.7	60	83
2WIN	H N	N	61	K	1.5	60	83
2WIN	H N	N	68	Y	1.9	60	83
2WIN	H Q	Q	46	I	1.0	38	58
2WIN	H Q	Q	53	Y	1.9	38	58
2WIN	I M	M	27	N	1.1	26	33
2WIN	J Q	Q	78	D	1.5	60	83
2WIN	K P	P	78	D	1.6	60	83
2WIN	L N	L	432	D	2.0	430	434
2WIN	L N	N	27	N	1.0	26	33
2WIN	L N	N	29	N	2.2	26	33
2WIU	A B	B	12	Q	1.2	10	24
2WIU	A B	B	19	L	1.9	10	24
2WIU	C B	C	283	M	1.2	275	284
2WIU	C D	D	19	L	1.7	10	24
2WJV	A D	D	1110	D	2.0	1110	1128
2WJV	A D	D	1113	F	1.9	1110	1128
2WJV	A D	D	1194	L	1.4	1193	1198
2WJV	B E	B	161	V	1.6	155	164
2WJV	B E	E	1110	D	1.6	1110	1129
2WJV	B E	E	1113	F	2.9	1110	1129
2WJV	B E	E	1117	L	1.5	1110	1129
2WJV	B E	E	1121	M	1.6	1110	1129
2WJV	B E	E	1125	L	2.8	1110	1129
2WJV	B E	E	1128	R	2.2	1110	1129
2WME	A E	E	335	E	1.0	331	347
2WME	B C	B	66	M	1.0	65	82
2WME	B C	B	70	R	2.2	65	82
2WME	B C	B	114	E	2.3	98	119
2WME	B C	B	118	G	40.7	98	119
2WME	B C	B	428	H	1.1	424	434
2WME	B C	C	70	R	2.3	65	82
2WME	B C	C	114	E	2.2	98	119
2WME	B C	C	118	G	30.9	98	119
2WME	B C	C	428	H	1.1	424	434
2WME	B C	C	433	R	1.3	424	434
2WME	D C	D	235	K	3.0	231	245
2WME	D C	D	269	R	2.8	267	277
2WME	D C	D	276	M	1.7	267	277
2WME	D C	D	428	H	1.2	424	434
2WME	D C	D	432	H	2.0	424	434
2WME	D C	C	235	K	1.3	231	245
2WME	D C	C	276	M	1.7	267	279
2WME	D C	C	428	H	1.1	424	434
2WME	D C	C	432	H	2.1	424	434
2WME	F E	F	235	K	1.7	231	245
2WME	F E	F	276	M	1.6	267	277
2WME	F E	F	428	H	1.0	424	434
2WME	F E	F	432	H	1.3	424	434
2WME	F E	E	235	K	1.5	231	245
2WME	F E	E	276	M	1.6	267	277
2WME	F E	E	428	H	1.1	424	433
2WME	F E	E	432	H	1.9	424	433
2WME	H E	H	70	R	3.3	65	82
2WME	H E	H	114	E	1.8	98	119
2WME	H E	H	118	G	30.3	98	119

2WME	H E	H	428	H	1.1	424	434
2WME	H E	E	70	R	1.1	65	82
2WME	H E	E	114	E	3.1	98	119
2WME	H E	E	118	G	53.7	98	119
2YVC	C F	C	281	L	1.5	274	294
2YVJ	A B	A	291	W	1.6	291	307
2Z0E	A B	A	146	N	2.2	145	158
2Z2L	A B	A	195	S	1.4	195	199
2Z2L	A B	A	197	F	3.1	195	199
2Z2L	A B	A	226	I	1.1	224	228
2Z2L	A B	B	270	Q	1.3	267	285
2Z2L	A B	B	274	E	3.1	267	285
2Z2L	B C	C	651	E	2.8	646	656
2Z2L	B C	C	654	R	3.1	646	656
2Z2L	D E	D	197	F	3.4	195	199
2Z2L	D E	D	198	I	1.1	195	199
2Z2L	D E	D	219	M	1.6	219	223
2Z2L	D E	D	226	I	1.3	224	229
2Z2L	D E	E	270	Q	1.3	267	285
2Z2L	D E	E	274	E	1.6	267	285
2Z2L	E F	E	414	D	1.3	409	419
2Z2L	E F	F	647	G	5.5	646	656
2Z2L	E F	F	651	E	2.5	646	656
2Z2L	E F	F	654	R	1.9	646	656
2Z2S	A B	A	30	F	3.6	23	41
2Z2S	A B	A	32	H	1.1	23	41
2Z2S	A B	A	38	K	2.4	23	41
2Z2S	A B	A	39	G	11.0	23	41
2Z2S	A B	A	52	E	2.2	48	58
2Z2S	A B	A	56	Q	1.0	48	58
2Z2S	A B	A	63	W	1.1	61	65
2Z2S	A B	A	81	F	4.4	76	86
2Z2S	A B	A	85	R	1.7	76	86
2Z2S	A B	A	162	L	1.0	162	179
2Z2S	A B	A	165	I	2.0	162	179
2Z2S	A B	A	166	K	1.3	162	179
2Z2S	A B	A	170	R	1.5	162	179
2Z2S	A B	A	173	L	1.0	162	179
2Z2S	A B	A	177	R	1.1	162	179
2Z2S	A B	B	46	D	1.6	36	52
2Z2S	A B	B	48	V	1.3	36	52
2Z2S	A B	B	49	G	287.3	36	52
2Z2S	A B	B	50	G	135.6	36	52
2Z2S	A B	B	66	L	2.6	65	69
2Z2S	A H	A	170	R	1.5	162	179
2Z2S	A H	A	171	L	1.0	162	179
2Z2S	A H	H	22	E	1.2	22	33
2Z2S	C D	C	26	F	1.2	23	41
2Z2S	C D	C	30	F	2.8	23	41
2Z2S	C D	C	32	H	1.3	23	41
2Z2S	C D	C	36	K	1.9	23	41
2Z2S	C D	C	38	K	1.9	23	41
2Z2S	C D	C	39	G	11.8	23	41
2Z2S	C D	C	52	E	1.9	48	58
2Z2S	C D	C	63	W	2.8	61	65
2Z2S	C D	C	81	F	1.6	76	86
2Z2S	C D	C	85	R	2.3	76	86
2Z2S	C D	C	126	L	1.4	121	132
2Z2S	C D	C	130	I	1.0	121	132
2Z2S	C D	D	48	V	1.6	36	52

2Z2S	C D	D	49	G	209.4	36	52
2Z2S	C D	D	50	G	127.5	36	52
2Z2S	C D	D	66	L	1.7	65	69
2Z2S	C F	C	171	L	1.2	162	179
2Z2S	E F	E	26	F	1.7	23	41
2Z2S	E F	E	30	F	3.3	23	41
2Z2S	E F	E	36	K	1.0	23	41
2Z2S	E F	E	38	K	3.2	23	41
2Z2S	E F	E	39	G	16.4	23	41
2Z2S	E F	E	40	F	1.7	23	41
2Z2S	E F	E	52	E	1.4	48	58
2Z2S	E F	E	63	W	2.5	61	65
2Z2S	E F	E	81	F	2.1	76	88
2Z2S	E F	E	126	L	1.0	121	133
2Z2S	E F	E	166	K	1.2	163	178
2Z2S	E F	E	170	R	2.4	163	178
2Z2S	E F	E	173	L	2.0	163	178
2Z2S	E F	F	15	Y	1.4	9	18
2Z2S	E F	F	37	E	1.8	36	52
2Z2S	E F	F	43	G	12.8	36	52
2Z2S	E F	F	46	D	1.0	36	52
2Z2S	E F	F	49	G	53.1	36	52
2Z2S	E F	F	50	G	139.9	36	52
2Z2S	E F	F	66	L	2.1	65	69
2Z2S	G H	G	26	F	1.7	23	41
2Z2S	G H	G	30	F	4.3	23	41
2Z2S	G H	G	36	K	1.1	23	41
2Z2S	G H	G	38	K	1.9	23	41
2Z2S	G H	G	39	G	17.2	23	41
2Z2S	G H	G	40	F	1.3	23	41
2Z2S	G H	G	52	E	2.3	48	58
2Z2S	G H	G	56	Q	1.0	48	58
2Z2S	G H	G	63	W	2.8	61	65
2Z2S	G H	G	81	F	2.0	76	87
2Z2S	G H	G	126	L	1.4	121	130
2Z2S	G H	G	145	F	3.6	135	146
2Z2S	G H	G	166	K	1.1	163	179
2Z2S	G H	G	169	I	1.0	163	179
2Z2S	G H	H	15	Y	1.2	9	18
2Z2S	G H	H	43	G	82.7	36	52
2Z2S	G H	H	48	V	1.3	36	52
2Z2S	G H	H	49	G	75.1	36	52
2Z2S	G H	H	50	G	135.6	36	52
2Z2S	G H	H	65	S	1.0	65	69
2Z2S	G H	H	66	L	2.9	65	69
2Z2T	A D	A	1551	Q	1.0	1547	1581
2Z2T	A D	A	1565	L	4.2	1547	1581
2Z2T	A D	A	1568	L	2.2	1547	1581
2Z2T	A D	A	1571	W	2.0	1547	1581
2Z2T	A D	D	1631	W	1.5	1631	1661
2Z2T	A D	D	1635	I	1.1	1631	1661
2Z2T	A D	D	1638	Y	5.7	1631	1661
2Z2T	A D	D	1642	I	1.1	1631	1661
2Z2T	A D	D	1645	L	1.1	1631	1661
2Z2T	A D	D	1652	Q	1.7	1631	1661
2Z2T	A F	A	1556	L	1.7	1547	1581
2Z2T	A F	A	1570	V	1.0	1547	1581
2Z2T	A F	F	3631	W	1.8	3631	3661
2Z2T	A F	F	3646	I	1.6	3631	3661
2Z2T	A F	F	3653	Q	1.1	3631	3661

2Z2T	B D	B	2556	L	1.5	2547	2580
2Z2T	B D	D	1646	I	1.5	1631	1661
2Z2T	B E	B	2564	H	1.0	2547	2580
2Z2T	B E	B	2565	L	2.1	2547	2580
2Z2T	B E	B	2568	L	2.2	2547	2580
2Z2T	B E	B	2571	W	2.5	2547	2580
2Z2T	B E	E	2631	W	1.6	2631	2661
2Z2T	B E	E	2635	I	1.0	2631	2661
2Z2T	B E	E	2638	Y	2.8	2631	2661
2Z2T	B E	E	2641	K	1.1	2631	2661
2Z2T	B E	E	2642	I	1.6	2631	2661
2Z2T	B E	E	2645	L	1.9	2631	2661
2Z2T	B E	E	2652	Q	1.3	2631	2661
2Z2T	C E	C	3549	V	1.2	3547	3581
2Z2T	C E	C	3556	L	2.3	3547	3581
2Z2T	C E	C	3570	V	1.5	3547	3581
2Z2T	C E	C	3573	I	1.7	3547	3581
2Z2T	C E	C	3577	Q	1.7	3547	3581
2Z2T	C E	E	2631	W	2.4	2631	2661
2Z2T	C E	E	2646	I	2.1	2631	2661
2Z2T	C E	E	2653	Q	1.2	2631	2661
2Z2T	C E	E	2660	L	1.4	2631	2661
2Z2T	C F	C	3551	Q	1.6	3547	3581
2Z2T	C F	C	3568	L	2.3	3547	3581
2Z2T	C F	C	3571	W	2.7	3547	3581
2Z2T	C F	F	3631	W	2.1	3631	3661
2Z2T	C F	F	3635	I	1.1	3631	3661
2Z2T	C F	F	3638	Y	2.4	3631	3661
2Z2T	C F	F	3641	K	1.1	3631	3661
2Z2T	C F	F	3642	I	1.1	3631	3661
2Z2T	C F	F	3645	L	1.2	3631	3661
2Z2Y	A B	A	193	Y	2.6	193	206
2Z2Y	A B	A	198	I	2.1	193	206
2Z2Y	A B	A	201	E	3.6	193	206
2Z2Y	A B	A	243	Y	1.5	243	254
2Z2Y	A B	A	247	M	1.1	243	254
2Z2Y	C D	C	193	Y	2.3	193	206
2Z2Y	C D	C	198	I	2.2	193	206
2Z2Y	C D	C	201	E	3.0	193	206
2Z2Y	C D	C	205	L	1.3	193	206
2Z2Y	C D	C	243	Y	2.0	243	254
2Z2Y	C D	C	247	M	1.3	243	254
2Z3R	A B	A	46	E	1.7	36	55
2Z3R	A D	A	60	H	1.9	57	76
2Z3R	C B	C	60	H	1.7	57	75
2Z3R	C D	C	46	E	3.6	36	55
2Z3R	C D	C	49	V	1.0	36	55
2Z3R	C D	C	53	E	3.7	36	55
2Z3R	C J	C	68	I	2.0	57	75
2Z3R	C J	C	72	N	2.2	57	75
2Z3R	E F	E	46	E	4.0	36	55
2Z3R	E F	E	49	V	1.2	36	55
2Z3R	E F	E	53	E	2.9	36	55
2Z3R	E H	E	48	Q	1.2	36	55
2Z3R	E H	E	52	L	1.3	36	55
2Z3R	E H	E	60	H	2.4	57	76
2Z3R	G F	G	60	H	1.6	57	75
2Z3R	G H	G	46	E	3.9	36	55
2Z3R	G H	G	53	E	4.7	36	55
2Z3R	I J	I	46	E	2.8	36	55

2Z3R	I J	I	53	E	3.4	36	55
2Z3R	I L	I	60	H	1.5	57	76
2Z3R	K J	K	52	L	1.2	36	55
2Z3R	K J	K	60	H	1.9	57	76
2Z3R	K J	K	64	E	1.5	57	76
2Z3R	K L	K	46	E	3.5	36	55
2Z3R	K L	K	49	V	1.4	36	55
2Z3R	K L	K	53	E	3.4	36	55
2Z3R	M N	M	46	E	2.5	36	55
2Z3R	M N	M	53	E	3.4	36	55
2Z3R	M P	M	60	H	1.7	57	75
2Z3R	O N	O	52	L	1.0	36	55
2Z3R	O N	O	60	H	2.2	57	77
2Z3R	O P	O	46	E	5.7	36	55
2Z3R	O P	O	53	E	1.1	36	55
2Z4Q	A B	A	128	E	1.2	127	133
2Z4Q	A B	A	129	Q	1.6	127	133
2Z5C	A C	C	91	H	1.1	85	104
2Z5C	A C	C	97	V	1.0	85	104
2Z5C	A C	C	101	L	1.0	85	104
2Z5C	B C	C	102	Y	2.0	85	104
2Z5C	B C	C	103	Y	1.2	85	104
2Z5C	D F	F	91	H	1.1	85	104
2Z5C	D F	F	97	V	1.0	85	104
2Z5C	E F	F	102	Y	1.9	85	104
2Z5C	E F	F	103	Y	1.3	85	104
2Z7X	A B	A	376	Y	2.7	374	381
2Z8V	A D	A	201	F	1.0	195	202
2Z91	A B	B	123	E	1.4	122	126
2Z91	A B	B	124	Q	1.6	122	126
2Z91	C D	D	124	Q	1.5	122	127
2ZAE	A B	A	23	I	1.3	20	24
2ZAE	A B	A	29	I	1.2	27	31
2ZAE	A B	A	30	F	1.0	27	31
2ZAE	A B	B	18	I	2.2	12	37
2ZAE	A B	B	21	E	1.8	12	37
2ZAE	A B	B	22	R	1.7	12	37
2ZAE	A B	B	25	T	1.6	12	37
2ZAE	A B	B	29	L	1.0	12	37
2ZAE	A B	B	32	R	1.7	12	37
2ZAE	A B	B	36	Y	1.0	12	37
2ZAE	A B	B	40	L	1.2	38	55
2ZAE	A B	B	44	Y	1.1	38	55
2ZAE	A B	B	47	L	1.7	38	55
2ZAE	C D	C	20	Y	1.3	18	24
2ZAE	C D	C	23	I	2.3	18	24
2ZAE	C D	C	29	I	1.3	27	32
2ZAE	C D	C	30	F	1.5	27	32
2ZAE	C D	C	120	L	1.2	116	121
2ZAE	C D	D	18	I	1.9	13	33
2ZAE	C D	D	22	R	1.5	13	33
2ZAE	C D	D	25	T	1.3	13	33
2ZAE	C D	D	29	L	1.8	13	33
2ZAE	C D	D	44	Y	2.7	38	56
2ZAL	A B	A	28	Y	1.6	22	45
2ZAL	A B	A	32	L	1.9	22	45
2ZAL	A B	A	36	V	1.4	22	45
2ZAL	A B	A	43	L	1.0	22	45
2ZAL	A B	A	53	V	2.0	49	63
2ZAL	A B	A	57	V	2.0	49	63

2ZAL	A B	A	61	E	1.2	49	63
2ZAL	A D	A	126	G	131.6	125	134
2ZAL	A D	D	234	E	1.8	233	239
2ZAL	A D	D	238	R	2.4	233	239
2ZAL	C B	C	126	G	144.1	125	134
2ZAL	C B	B	234	E	1.1	233	239
2ZAL	C B	B	238	R	2.5	233	239
2ZAL	C D	C	28	Y	2.3	22	45
2ZAL	C D	C	32	L	1.5	22	45
2ZAL	C D	C	36	V	1.3	22	45
2ZAL	C D	C	43	L	1.0	22	45
2ZAL	C D	C	53	V	2.0	49	63
2ZAL	C D	C	57	V	2.0	49	63
2ZAL	C D	C	61	E	1.3	49	63
2ZBK	A B	A	77	K	1.3	73	83
2ZBK	A B	A	90	Y	1.8	84	95
2ZBK	A B	B	467	K	1.1	466	486
2ZBK	A B	B	469	L	1.2	466	486
2ZBK	A B	B	473	K	2.4	466	486
2ZBK	A B	B	474	Y	2.4	466	486
2ZBK	A B	B	477	E	1.1	466	486
2ZBK	A B	B	478	V	1.2	466	486
2ZBK	A B	B	485	F	4.9	466	486
2ZBK	C D	C	90	Y	1.8	86	95
2ZBK	C D	D	467	K	1.3	458	486
2ZBK	C D	D	478	V	1.2	458	486
2ZBK	C D	D	485	F	5.1	458	486
2ZBK	E F	E	80	M	1.3	73	83
2ZBK	E F	E	90	Y	1.5	86	95
2ZBK	E F	F	473	K	1.2	466	486
2ZBK	E F	F	474	Y	1.4	466	486
2ZBK	E F	F	478	V	1.4	466	486
2ZBK	E F	F	485	F	5.3	466	486
2ZBK	G H	G	90	Y	2.1	86	95
2ZBK	G H	H	467	K	1.6	458	486
2ZBK	G H	H	471	Y	1.0	458	486
2ZBK	G H	H	474	Y	2.0	458	486
2ZBK	G H	H	477	E	1.3	458	486
2ZBK	G H	H	485	F	3.9	458	486
2ZC5	A B	B	276	L	1.9	273	284
2ZC5	C D	D	276	L	1.4	273	288
2ZCK	P L	P	237	K	1.7	236	245
2ZCY	A B	A	121	Q	1.2	109	123
2ZCY	A B	B	23	Q	2.6	22	33
2ZCY	A B	B	26	Y	3.1	22	33
2ZCY	A B	B	84	D	3.2	82	103
2ZCY	A B	B	86	E	1.1	82	103
2ZCY	A G	A	23	Q	1.5	22	34
2ZCY	A G	A	26	Y	3.3	22	34
2ZCY	A G	A	83	P	18.2	82	99
2ZCY	A G	A	84	D	1.3	82	99
2ZCY	A G	A	86	R	1.2	82	99
2ZCY	A G	G	114	K	1.8	109	126
2ZCY	A G	G	121	Q	1.1	109	126
2ZCY	A G	G	125	Q	1.0	109	126
2ZCY	A H	A	102	R	1.4	100	103
2ZCY	A H	H	61	S	1.0	49	71
2ZCY	B C	C	23	Q	1.3	22	34
2ZCY	B C	C	26	Y	1.0	22	34
2ZCY	B C	C	84	D	1.8	82	103

2ZCY	B I	B	101	K	1.2	82	103
2ZCY	B I	I	57	E	1.3	49	71
2ZCY	B I	I	61	Y	1.6	49	71
2ZCY	B I	I	64	N	1.1	49	71
2ZCY	B I	I	65	L	1.5	49	71
2ZCY	C D	D	26	Y	2.1	22	33
2ZCY	C J	J	57	E	1.0	49	70
2ZCY	C J	J	60	Q	1.3	49	70
2ZCY	C J	J	65	L	1.6	49	70
2ZCY	C K	K	81	K	1.1	76	90
2ZCY	D E	E	23	Q	1.9	22	34
2ZCY	D E	E	26	Y	3.0	22	34
2ZCY	D E	E	83	P	1.3	82	103
2ZCY	D K	D	93	R	1.3	82	103
2ZCY	D K	K	64	R	2.2	49	70
2ZCY	D K	K	68	L	1.7	49	70
2ZCY	D L	L	81	R	1.1	76	90
2ZCY	D L	L	85	H	1.3	76	90
2ZCY	E F	E	118	D	2.4	109	123
2ZCY	E F	E	121	Q	2.6	109	123
2ZCY	E F	E	177	E	1.7	169	180
2ZCY	E F	F	23	Q	2.6	22	34
2ZCY	E F	F	26	Y	3.4	22	34
2ZCY	E F	F	83	P	1.1	82	103
2ZCY	E F	F	84	D	2.2	82	103
2ZCY	E F	F	86	R	2.1	82	103
2ZCY	E L	E	86	R	1.9	82	103
2ZCY	E L	E	90	N	1.5	82	103
2ZCY	E L	E	96	C	1.5	82	103
2ZCY	E M	M	66	N	1.3	49	68
2ZCY	E M	M	78	Y	1.2	76	92
2ZCY	F G	F	121	Q	2.2	109	123
2ZCY	F G	G	23	Q	3.1	22	32
2ZCY	F G	G	26	Y	3.7	22	32
2ZCY	F G	G	82	I	1.1	82	103
2ZCY	F G	G	83	P	1.4	82	103
2ZCY	F G	G	84	D	2.2	82	103
2ZCY	F N	F	99	F	1.4	82	103
2ZCY	F N	F	102	L	1.3	82	103
2ZCY	F N	N	66	Y	1.3	49	70
2ZCY	F N	N	78	T	1.6	76	90
2ZCY	F N	N	82	V	1.1	76	90
2ZCY	G H	G	110	D	3.1	109	126
2ZCY	G H	H	66	H	2.5	49	71
2ZCY	G N	G	101	Y	1.8	82	103
2ZCY	G N	N	61	Y	2.1	49	70
2ZCY	G N	N	65	L	1.2	49	70
2ZCY	H I	H	51	D	3.9	49	71
2ZCY	H I	I	88	Y	2.4	76	90
2ZCY	H I	I	139	E	1.2	131	142
2ZCY	H I	I	141	L	1.2	131	142
2ZCY	H I	I	153	E	2.9	148	165
2ZCY	H I	I	157	Q	1.2	148	165
2ZCY	H N	H	88	F	1.9	76	90
2ZCY	H N	N	53	Q	1.1	49	70
2ZCY	H Z	H	163	I	1.0	148	166
2ZCY	H Z	H	164	W	1.5	148	166
2ZCY	H Z	Z	153	K	3.3	148	166
2ZCY	H Z	Z	157	D	1.0	148	166
2ZCY	I J	J	84	R	1.3	76	90

2ZCY	I J	J	132	F	1.6	129	141
2ZCY	I Y	Y	164	H	1.6	148	166
2ZCY	I Y	Y	193	G	1.9	192	204
2ZCY	I Y	Y	196	F	2.3	192	204
2ZCY	I Y	Y	197	W	1.8	192	204
2ZCY	I Z	I	135	F	1.0	131	142
2ZCY	I Z	I	136	G	218.2	131	142
2ZCY	I Z	I	164	D	1.0	148	165
2ZCY	J K	J	50	G	39.6	49	70
2ZCY	J K	J	57	E	1.1	49	70
2ZCY	J Y	J	133	Y	1.1	129	141
2ZCY	J Y	J	140	H	1.1	129	141
2ZCY	J Y	J	165	R	2.7	148	166
2ZCY	J Y	Y	133	F	2.0	131	140
2ZCY	J Y	Y	136	G	1.8	131	140
2ZCY	J Y	Y	139	D	2.0	131	140
2ZCY	J Y	Y	165	R	1.4	148	166
2ZCY	K L	K	51	D	3.7	49	70
2ZCY	K L	K	53	Q	1.0	49	70
2ZCY	K L	K	54	F	3.0	49	70
2ZCY	K L	K	55	W	1.4	49	70
2ZCY	K L	L	88	Y	5.9	76	90
2ZCY	L M	M	88	Y	1.7	76	92
2ZCY	L M	M	139	R	1.0	129	14
2ZCY	M N	M	53	Q	1.5	49	68
2ZCY	M N	N	88	Y	3.1	76	90
2ZCY	O P	O	121	Q	1.2	109	123
2ZCY	O P	P	23	Q	2.1	22	33
2ZCY	O P	P	26	Y	2.9	22	33
2ZCY	O P	P	84	D	1.7	82	103
2ZCY	O U	O	23	Q	1.6	22	34
2ZCY	O U	O	26	Y	3.1	22	34
2ZCY	O U	O	83	P	20.8	82	99
2ZCY	O U	O	86	R	1.4	82	99
2ZCY	O U	U	114	K	1.5	109	126
2ZCY	O U	U	121	Q	1.6	109	126
2ZCY	O V	O	94	K	1.2	82	99
2ZCY	O V	O	102	R	1.3	100	103
2ZCY	O V	V	61	S	1.0	49	70
2ZCY	O V	V	65	L	1.0	49	70
2ZCY	O V	V	68	L	1.4	49	70
2ZCY	P Q	Q	26	Y	3.2	22	34
2ZCY	P Q	Q	33	R	1.2	22	34
2ZCY	P W	P	93	R	1.0	82	103
2ZCY	P W	W	61	Y	1.3	49	71
2ZCY	P W	W	64	N	1.1	49	71
2ZCY	P W	W	65	L	1.7	49	71
2ZCY	P W	W	68	L	1.9	49	71
2ZCY	P X	P	99	Y	4.2	82	103
2ZCY	P X	X	66	Y	3.9	49	70
2ZCY	Q R	R	26	Y	2.4	22	34
2ZCY	Q X	Q	100	R	1.7	82	103
2ZCY	Q X	X	60	Q	1.0	49	70
2ZCY	Q X	X	64	Q	1.6	49	70
2ZCY	Q X	X	65	L	1.7	49	70
2ZCY	Q Y	Y	81	K	1.1	76	90
2ZCY	R S	S	23	Q	1.8	22	34
2ZCY	R S	S	26	Y	2.3	22	34
2ZCY	R S	S	83	P	1.6	82	103
2ZCY	R Y	R	93	R	2.7	82	103

2ZCY	R Y	Y	64	R	1.9	49	70
2ZCY	R Y	Y	68	L	3.1	49	70
2ZCY	R Z	R	99	H	1.0	82	103
2ZCY	R Z	Z	81	R	1.2	76	90
2ZCY	R Z	Z	85	H	1.2	76	90
2ZCY	S T	S	117	C	1.6	109	123
2ZCY	S T	S	118	D	2.0	109	123
2ZCY	S T	S	121	Q	2.5	109	123
2ZCY	S T	S	177	E	1.7	169	180
2ZCY	S T	T	23	Q	2.5	22	34
2ZCY	S T	T	26	Y	3.2	22	34
2ZCY	S T	T	83	P	1.0	82	103
2ZCY	S T	T	84	D	2.2	82	103
2ZCY	S T	T	86	R	1.6	82	103
2ZCY	S Z	S	93	R	1.9	82	103
2ZCY	S Z	S	97	N	3.7	82	103
2ZCY	S Z	Z	65	W	1.1	49	70
2ZCY	S Z	Z	68	F	2.0	49	70
2ZCY	T U	T	121	Q	2.1	109	123
2ZCY	T U	U	23	Q	3.1	22	32
2ZCY	T U	U	26	Y	3.9	22	32
2ZCY	T U	U	82	I	1.0	82	103
2ZCY	T U	U	83	P	1.4	82	103
2ZCY	T U	U	84	D	2.2	82	103
2ZCY	T U	U	86	R	1.6	82	103
2ZCY	U V	U	110	D	3.1	109	126
2ZCY	U V	V	66	H	2.6	49	70
2ZCY	V L	V	164	W	1.3	148	166
2ZCY	V L	L	153	K	1.2	148	166
2ZCY	V L	L	154	L	1.1	148	166
2ZCY	V L	L	165	R	1.2	148	166
2ZCY	V M	V	77	V	1.0	76	90
2ZCY	V M	V	132	L	1.1	131	141
2ZCY	V M	V	139	E	1.0	131	141
2ZCY	V M	M	137	L	1.3	129	14
2ZCY	V M	M	161	V	1.1	148	165
2ZCY	V M	M	199	F	1.5	197	202
2ZCY	V W	V	51	D	2.4	49	70
2ZCY	V W	W	135	F	1.2	131	142
2ZCY	V W	W	139	E	1.2	131	142
2ZCY	V W	W	141	L	1.0	131	142
2ZCY	V W	W	153	E	3.0	148	165
2ZCY	V W	W	157	Q	1.2	148	165
2ZCY	W K	K	164	H	1.7	148	166
2ZCY	W K	K	197	W	1.7	192	204
2ZCY	W L	W	136	G	243.2	131	142
2ZCY	W L	W	164	D	1.2	148	165
2ZCY	W L	L	165	R	1.0	148	166
2ZCY	W X	X	84	R	1.2	76	90
2ZCY	W X	X	132	F	1.7	129	141
2ZCY	X K	X	133	Y	1.2	129	141
2ZCY	X K	X	165	R	2.7	148	166
2ZCY	X K	K	133	F	2.1	131	140
2ZCY	X K	K	136	G	2.4	131	140
2ZCY	X K	K	139	D	1.0	131	140
2ZCY	X K	K	165	R	1.3	148	166
2ZCY	X Y	X	50	G	37.4	49	70
2ZCY	X Y	X	57	E	1.1	49	70
2ZCY	Y Z	Y	51	D	3.7	49	70
2ZCY	Y Z	Y	54	F	3.0	49	70

2ZCY	Y Z	Y	55	W	1.3	49	70
2ZCY	Y Z	Z	88	Y	5.8	76	90
2ZDI	B C	B	45	E	3.8	6	48
2ZET	A C	A	84	L	1.2	79	88
2ZET	A C	C	14	E	1.0	12	53
2ZET	A C	C	21	V	4.1	12	53
2ZET	A C	C	25	D	1.2	12	53
2ZET	A C	C	35	R	1.0	12	53
2ZET	A C	C	112	V	1.2	105	118
2ZET	A C	C	115	I	1.1	105	118
2ZET	A C	C	120	W	1.2	119	127
2ZET	A C	C	133	G	2.0	133	141
2ZET	B D	B	84	L	2.0	82	86
2ZET	B D	D	18	V	1.1	12	53
2ZET	B D	D	21	V	1.4	12	53
2ZET	B D	D	35	R	1.0	12	53
2ZET	B D	D	112	V	1.0	105	118
2ZET	B D	D	115	I	1.3	105	118
2ZET	B D	D	121	Y	3.9	119	127
2ZFB	A B	A	31	R	2.4	20	36
2ZFB	A B	A	35	T	1.3	20	36
2ZFB	A B	A	107	V	1.7	95	113
2ZFB	A B	A	111	I	1.2	95	113
2ZFB	A B	A	122	H	2.2	119	130
2ZFB	A B	B	30	R	3.2	20	35
2ZFB	A B	B	34	V	1.1	20	35
2ZFB	A B	B	108	D	1.0	100	118
2ZFB	A B	B	112	I	4.0	100	118
2ZFB	A B	B	116	G	1.0	100	118
2ZFD	A B	A	86	F	5.0	85	95
2ZFD	A B	A	131	Y	2.0	120	132
2ZFD	A B	A	148	V	1.2	141	155
2ZFD	A B	A	152	L	1.0	141	155
2ZFD	A B	A	154	E	2.2	141	155
2ZFD	A B	A	167	I	2.2	161	176
2ZFD	A B	A	171	T	2.0	161	176
2ZFD	A B	A	174	E	1.0	161	176
2ZFD	A B	A	188	W	1.5	185	195
2ZFD	A B	A	191	L	1.1	185	195
2ZFD	A B	A	206	Y	2.7	205	209
2ZFD	A B	B	313	F	5.1	312	318
2ZFD	A B	B	314	D	1.0	312	318
2ZFD	A B	B	315	I	2.1	312	318
2ZFD	A B	B	316	I	2.9	312	318
2ZHX	A B	A	93	S	1.1	92	105
2ZHX	A L	L	31	E	1.1	26	34
2ZHX	C D	C	170	R	2.1	170	175
2ZHX	E F	E	170	R	2.2	170	175
2ZHX	E F	F	31	E	1.5	26	34
2ZHX	G H	G	170	R	3.0	170	175
2ZHX	G H	G	171	D	1.4	170	175
2ZHX	G H	H	27	E	1.5	26	34
2ZHX	G H	H	28	E	2.1	26	34
2ZHX	G H	H	29	V	2.1	26	34
2ZHX	G H	H	32	V	1.0	26	34
2ZHX	I J	I	93	S	1.0	92	105
2ZHX	I J	I	170	R	2.1	170	179
2ZHX	I J	J	28	E	1.0	26	34
2ZHX	K L	K	170	R	1.5	170	179
2ZHX	K L	L	32	V	1.4	26	34

2ZHX	M N	M	194	P	1.6	194	199
2ZHX	M N	M	195	L	1.9	194	199
2ZIV	A B	A	403	I	1.0	396	405
2ZIV	A B	A	409	R	1.2	407	417
2ZIV	A B	A	410	E	1.2	407	417
2ZIV	A B	A	413	F	3.0	407	417
2ZIV	A B	A	449	V	1.0	441	456
2ZIV	A B	A	452	Q	1.5	441	456
2ZIV	A B	A	453	V	1.8	441	456
2ZIV	A B	A	478	Y	1.2	465	483
2ZIV	A B	A	532	V	1.3	532	541
2ZIV	A B	A	533	R	1.2	532	541
2ZIV	A B	A	534	E	1.2	532	541
2ZIV	A B	A	539	Q	1.2	532	541
2ZIV	A B	A	548	G	175.4	548	558
2ZIV	A B	A	555	L	1.1	548	558
2ZIV	A B	A	604	L	2.3	595	605
2ZIV	A B	B	410	E	1.8	405	419
2ZIV	A B	B	413	V	1.3	405	419
2ZIV	A B	B	417	L	2.5	405	419
2ZIV	A B	B	439	F	1.2	429	445
2ZIV	A B	B	457	F	2.0	456	462
2ZIV	A B	B	459	F	3.4	456	462
2ZIV	A B	B	461	L	1.3	456	462
2ZIV	A B	B	478	L	2.0	478	487
2ZIV	A B	B	481	V	1.3	478	487
2ZIV	A B	B	484	R	2.0	478	487
2ZIV	A B	B	507	P	1.1	507	516
2ZIV	A B	B	509	L	1.5	507	516
2ZIV	A B	B	556	Q	1.1	547	557
2ZIX	A B	A	347	G	535.2	346	354
2ZIX	A B	A	392	Q	1.1	392	396
2ZIX	A B	A	393	V	1.4	392	396
2ZIX	A B	A	407	E	1.8	405	409
2ZIX	A B	A	411	Y	1.4	410	414
2ZIX	A B	A	477	R	1.4	476	481
2ZIX	A B	B	508	Q	1.1	507	511
2ZJQ	B M	M	9	R	1.2	9	16
2ZJQ	B M	M	13	L	1.5	9	16
2ZJQ	C I	C	28	H	1.7	24	30
2ZJQ	G N	N	60	L	10.4	49	67
2ZJQ	G N	N	101	R	1.5	95	102
2ZJQ	H M	H	119	R	1.5	116	121
2ZJQ	N O	N	46	E	1.4	40	48
2ZJQ	N O	N	47	Y	1.3	40	48
2ZJQ	P Z	P	56	L	1.3	50	60
2ZJQ	P Z	P	59	F	2.5	50	60
2ZJQ	Q V	V	26	M	1.2	23	33
2ZJS	Y E	Y	5	F	1.0	2	10
2ZJS	Y E	Y	22	L	1.0	12	33
2ZJS	Y E	Y	189	F	2.3	183	195
2ZJS	Y E	Y	193	V	1.1	183	195
2ZJS	Y E	Y	412	L	1.3	399	422
2ZJS	Y E	E	27	V	1.0	26	52
2ZJS	Y E	E	34	I	2.3	26	52
2ZJS	Y E	E	37	F	3.1	26	52
2ZJS	Y E	E	41	F	1.9	26	52
2ZJS	Y E	E	42	M	1.3	26	52
2ZJS	Y E	E	45	L	1.3	26	52
2ZJS	Y E	E	46	G	1.2	26	52

2ZJS	Y E	E	48	Y	1.5	26	52
2ZKR	n q	n	32	R	1.5	29	37
2ZL1	A B	A	43	H	1.0	42	46
2ZL1	A B	B	48	I	1.5	42	61
2ZL1	A B	B	52	I	1.8	42	61
2ZL1	A B	B	56	Y	2.8	42	61
2ZL1	A B	B	60	G	42.1	42	61
2ZL1	A B	B	101	F	1.3	101	117
2ZLE	I D	I	3348	E	6.5	3348	3352
2ZLE	K D	D	1291	W	29.3	1284	1292
2ZME	A B	A	64	F	2.0	62	76
2ZME	A B	A	95	D	1.2	93	111
2ZME	A B	A	98	Y	4.0	93	111
2ZME	A B	A	154	L	4.8	141	155
2ZME	A B	A	218	K	1.6	206	219
2ZME	A B	B	178	F	1.2	173	194
2ZME	A B	B	180	D	1.4	173	194
2ZME	A B	B	181	L	1.9	173	194
2ZME	A B	B	223	S	1.0	212	224
2ZME	A B	B	270	Y	2.5	266	277
2ZME	A B	B	286	D	2.3	284	293
2ZME	B D	D	25	T	1.5	23	39
2ZNE	A C	A	122	F	1.3	112	123
2ZNE	A C	A	166	R	1.0	148	169
2ZNE	B C	B	180	Y	2.6	180	191
2ZNE	B D	B	95	W	2.0	82	103
2ZNE	B D	B	102	Y	1.9	82	103
2ZNE	B D	B	122	F	2.5	112	123
2ZNL	A B	A	411	F	1.2	405	415
2ZNL	A B	A	412	N	1.4	405	415
2ZNL	A B	A	666	L	1.8	653	674
2ZNL	A B	A	670	Q	2.3	653	674
2ZNL	A B	A	706	W	2.5	698	716
2ZNL	A B	A	710	F	2.1	698	716
2ZNV	A B	A	329	E	1.4	329	338
2ZNV	A B	A	332	F	3.0	329	338
2ZNV	A B	A	360	D	1.6	358	371
2ZNV	A B	A	363	T	1.1	358	371
2ZNV	A B	A	367	Y	3.0	358	371
2ZNV	A C	A	358	S	1.0	358	371
2ZNV	D C	C	33	K	1.4	23	35
2ZNV	D E	D	329	E	2.2	329	338
2ZNV	D E	D	332	F	3.0	329	338
2ZNV	D E	D	360	D	1.7	358	371
2ZNV	D E	D	363	T	2.4	358	371
2ZNV	D E	D	367	Y	2.8	358	371
2ZNV	D E	D	369	L	1.1	358	371
2ZNW	A Y	Y	97	K	3.9	89	100
2ZNW	A Z	Z	27	N	1.1	25	36
2ZNW	A Z	Z	121	Q	1.0	120	124
2ZNW	B Z	Z	63	W	1.4	60	64
2ZNW	B Z	Z	97	K	4.3	89	99
2ZOE	A B	A	164	Y	1.6	161	165
2ZON	A G	A	195	E	1.6	193	207
2ZON	A G	A	198	G	114.1	193	207
2ZPK	L H	L	125	E	2.1	123	128
2ZPK	M I	M	124	E	1.1	123	128
2ZPK	M I	M	125	E	2.3	123	128
2ZSH	A B	A	13	R	1.4	10	15
2ZSH	A B	A	21	W	1.9	18	35

2ZSH	A B	A	22	V	1.5	18	35
2ZSH	A B	A	23	L	1.1	18	35
2ZSH	A B	A	27	F	1.5	18	35
2ZSH	A B	A	29	V	1.2	18	35
2ZSH	A B	A	45	L	1.4	43	50
2ZSH	A B	A	48	Y	3.1	43	50
2ZSH	A B	A	49	L	1.2	43	50
2ZSH	A B	B	31	L	3.4	29	34
2ZSH	A B	B	50	L	2.1	43	58
2ZSH	A B	B	51	E	2.7	43	58
2ZSH	A B	B	80	L	1.1	80	90
2ZT9	A B	A	42	V	1.0	35	56
2ZT9	A B	A	46	I	1.1	35	56
2ZT9	A B	A	66	Y	3.8	62	76
2ZT9	A B	A	85	I	1.1	79	106
2ZT9	A B	A	88	W	4.0	79	106
2ZT9	A B	A	105	Y	1.8	79	106
2ZT9	A B	A	118	W	1.4	115	137
2ZT9	A B	A	122	V	1.6	115	137
2ZT9	A B	A	132	G	83.5	115	137
2ZT9	A B	A	145	Y	1.7	142	158
2ZT9	A B	A	146	W	4.1	142	158
2ZT9	A B	B	51	I	1.7	33	58
2ZT9	A B	B	54	L	1.4	33	58
2ZT9	A B	B	95	L	1.1	94	115
2ZT9	A B	B	98	V	1.0	94	115
2ZT9	A B	B	111	V	1.1	94	115
2ZT9	A B	B	112	P	1.3	94	115
2ZT9	A B	B	133	F	2.5	127	149
2ZT9	A D	A	82	I	1.1	79	106
2ZT9	A D	D	37	P	1.0	13	43
2ZT9	A D	D	41	Y	3.0	13	43
2ZT9	A D	D	42	F	1.2	13	43
2ZT9	A G	A	95	L	2.1	79	106
2ZT9	A G	A	99	L	1.7	79	106
2ZT9	A G	A	102	F	2.3	79	106
2ZT9	A G	G	10	V	1.1	4	31
2ZT9	A G	G	14	I	1.0	4	31
2ZT9	A G	G	18	L	1.8	4	31
2ZT9	A G	G	20	G	86.7	4	31
2ZT9	A G	G	21	L	2.0	4	31
2ZT9	A G	G	22	F	1.1	4	31
2ZT9	B C	B	38	Y	2.7	33	58
2ZT9	B C	B	42	I	1.6	33	58
2ZT9	B C	B	56	V	1.4	33	58
2ZT9	B C	C	258	L	2.6	252	286
2ZT9	B C	C	265	V	1.0	252	286
2ZT9	B C	C	272	L	1.4	252	286
2ZT9	B C	C	276	K	1.8	252	286
2ZT9	B D	B	38	Y	1.2	33	58
2ZT9	B D	D	24	F	1.3	13	43
2ZT9	B G	B	18	L	1.0	12	20
2ZT9	B G	G	22	F	1.3	4	31
2ZT9	B G	G	29	Y	1.7	4	31
2ZT9	B H	B	42	I	1.2	33	58
2ZT9	B H	B	46	G	2.0	33	58
2ZT9	B H	B	57	L	2.1	33	58
2ZT9	B H	H	7	G	2.5	2	26
2ZT9	B H	H	8	W	2.5	2	26
2ZT9	B H	H	11	L	1.1	2	26

2ZT9	B H	H	22	V	1.0	2	26
2ZT9	C D	C	261	F	1.5	252	286
2ZT9	C D	C	272	L	1.4	252	286
2ZT9	C D	D	27	V	1.1	13	43
2ZT9	C D	D	30	V	1.5	13	43
2ZT9	C H	H	4	L	1.9	2	26
2ZT9	C H	H	7	G	6.0	2	26
2ZT9	C H	H	21	M	1.8	2	26
2ZT9	C H	H	24	W	1.2	2	26
2ZT9	C H	H	25	G	30.8	2	26
2ZT9	D E	D	15	R	1.0	13	43
2ZT9	E H	E	7	Y	1.9	2	28
2ZT9	E H	E	11	L	2.0	2	28
2ZT9	E H	H	6	L	1.1	2	26
2ZT9	E H	H	13	V	2.1	2	26
2ZT9	E H	H	17	W	2.4	2	26
2ZT9	F G	F	5	L	1.3	2	29
2ZT9	F G	F	13	F	1.5	2	29
2ZT9	F G	G	8	G	136.3	4	31
2ZT9	F G	G	12	G	55.9	4	31
2ZT9	F G	G	16	V	1.0	4	31
2ZT9	F H	F	19	G	40.7	2	29
2ZT9	F H	F	23	G	74.0	2	29
2ZT9	F H	F	26	L	1.2	2	29
2ZT9	F H	F	27	L	1.9	2	29
2ZT9	F H	H	15	F	2.0	2	26
2ZT9	F H	H	23	V	1.0	2	26
2ZT9	F H	H	24	W	2.0	2	26
2ZU0	A C	A	373	F	3.3	369	378
2ZU0	A C	A	374	Y	5.1	369	378
2ZU0	A C	A	375	L	1.4	369	378
2ZU0	A C	A	376	R	2.9	369	378
2ZU0	A C	A	388	M	1.3	382	394
2ZU0	A C	C	73	E	3.6	72	79
2ZU0	A C	C	98	F	2.5	95	109
2ZU0	A C	C	155	D	1.0	148	162
2ZU0	A C	C	158	Q	1.3	148	162
2ZU0	B D	B	374	Y	1.9	369	377
2ZU0	B D	D	98	F	1.9	95	106
2ZU6	A B	A	110	R	1.5	110	128
2ZU6	A B	A	160	G	156.2	159	167
2ZU6	A B	A	161	R	3.3	159	167
2ZU6	A B	A	186	E	1.8	184	190
2ZU6	A B	A	283	R	1.8	282	291
2ZU6	A B	B	178	H	2.2	164	179
2ZU6	A B	B	183	E	1.8	181	186
2ZU6	A B	B	249	E	1.1	233	251
2ZU6	A B	B	324	V	1.0	324	332
2ZU6	A B	B	361	H	3.1	360	369
2ZU6	A B	B	403	R	1.1	403	411
2ZU6	A E	E	238	K	1.0	234	253
2ZU6	C B	C	110	R	1.0	110	122
2ZU6	C B	C	160	G	191.7	159	168
2ZU6	C B	C	282	R	1.3	282	295
2ZU6	D E	D	110	R	1.2	110	123
2ZU6	D E	D	160	G	152.5	159	168
2ZU6	D E	D	161	R	2.1	159	168
2ZU6	D E	E	177	E	1.2	164	179
2ZU6	D E	E	324	V	1.0	324	332
2ZU6	D E	E	361	H	1.6	360	369

2ZU6	F E	F	160	G	221.0	159	168
2ZU6	F E	F	283	R	1.8	282	294
2ZU6	F E	E	337	E	1.6	335	342
2ZU6	F E	E	346	E	1.7	344	355
2ZVN	A B	B	320	E	1.0	290	324
2ZVN	A D	D	304	D	2.2	291	336
2ZVN	C F	F	320	E	1.1	254	337
2ZVN	C H	H	290	T	1.8	286	336
2ZVN	C H	H	293	V	1.4	286	336
2ZVN	C H	H	301	Y	1.7	286	336
2ZVN	E B	B	286	I	1.2	259	289
2ZVN	E F	F	304	D	1.8	254	337
2ZVN	E H	H	316	V	1.1	286	336
2ZVN	G B	B	293	V	1.1	290	324
2ZVN	G D	D	305	F	1.1	291	336
2ZVN	G D	D	316	V	1.1	291	336
2ZVN	G F	F	286	I	1.7	254	337
2ZXE	A B	A	855	G	1.8	847	876
2ZXE	A B	A	856	Q	1.0	847	876
2ZXE	A B	A	863	L	1.3	847	876
2ZXE	A B	A	867	F	2.0	847	876
2ZXE	A B	A	910	Q	1.2	908	937
2ZXE	A B	A	994	Y	1.3	992	1012
2ZXE	A B	A	1016	W	1.5	1016	1022
2ZXE	A B	B	40	Y	1.0	31	61
2ZXE	A B	B	43	F	2.8	31	61
2ZXE	A B	B	44	Y	1.4	31	61
2ZXE	A B	B	47	L	1.3	31	61
2ZXE	A B	B	51	F	4.0	31	61
2ZXE	A B	B	55	I	1.1	31	61
2ZXE	A B	B	58	L	2.0	31	61
2ZXE	A G	A	959	F	2.5	952	971
2ZXE	A G	A	970	Y	2.3	952	971
2ZXE	A G	G	19	L	2.1	16	39
2ZXE	A G	G	20	R	1.4	16	39
2ZXE	A G	G	23	G	195.8	16	39
2ZXE	A G	G	24	L	2.3	16	39
2ZXE	A G	G	34	G	1.2	16	39
2ZXE	A G	G	37	I	1.8	16	39
2ZXE	A G	G	38	L	1.5	16	39
2ZXX	A C	A	104	R	1.4	95	138
2ZXX	A C	A	111	L	1.9	95	138
2ZXX	A C	C	183	Y	2.1	182	186
2ZXX	B C	B	95	Y	2.7	93	130
2ZXX	B C	B	96	W	1.3	93	130
2ZXX	B C	B	98	E	1.0	93	130
2ZXX	B F	F	304	L	1.7	300	329
2ZXX	B F	F	307	R	1.4	300	329
2ZXX	D F	D	104	R	1.3	95	137
2ZXX	D F	D	107	L	1.2	95	137
2ZXX	D F	D	111	L	2.4	95	137
2ZXX	D F	F	183	Y	2.8	182	186
2ZXX	E F	E	85	L	1.7	82	86
2ZXX	E F	E	95	Y	3.3	93	147
2ZYZ	A B	A	53	L	1.1	49	62
2ZYZ	A B	B	151	G	56.6	144	154
2ZYZ	A D	A	3	V	1.3	3	15
2ZYZ	A D	A	4	L	1.2	3	15
2ZYZ	C B	C	2	D	1.9	2	15
2ZYZ	C B	C	4	L	1.2	2	15

2ZYZ	C D	C	49	I	1.0	49	62
2ZYZ	C D	C	52	L	1.0	49	62
2ZYZ	C D	C	53	L	1.2	49	62
2ZYZ	C D	D	147	I	2.0	144	154
32C2	A B	A	127	Q	1.6	125	129
3A0B	a c	a	5145	V	1.1	5143	5147
3A0B	a c	a	5288	L	2.3	5278	5293
3A0B	a c	c	5291	W	1.7	5286	5293
3A0B	a c	c	5424	S	1.3	5422	5449
3A0B	a c	c	5435	F	1.4	5422	5449
3A0B	A C	A	164	G	8.9	158	165
3A0B	A C	C	291	W	8.4	286	293
3A0B	A C	C	317	F	1.7	306	324
3A0B	A C	C	396	M	2.2	386	398
3A0B	A C	C	424	S	1.0	422	452
3A0B	A C	C	436	F	1.3	422	452
3A0B	A C	C	442	L	1.1	422	452
3A0B	A C	C	443	W	1.3	422	452
3A0B	a d	a	5126	Y	1.5	5110	5129
3A0B	a d	a	5143	I	1.2	5143	5147
3A0B	a d	a	5178	G	1.9	5176	5190
3A0B	a d	a	5180	F	3.4	5176	5190
3A0B	a d	a	5208	G	42.6	5207	5222
3A0B	a d	a	5212	C	135.0	5207	5222
3A0B	a d	a	5216	G	159.5	5207	5222
3A0B	a d	a	5257	R	1.3	5248	5259
3A0B	a d	a	5280	V	137.2	5278	5293
3A0B	a d	a	5320	I	1.2	5319	5324
3A0B	a d	a	5321	I	1.3	5319	5324
3A0B	a d	a	5323	R	1.1	5319	5324
3A0B	a d	a	5327	G	173.2	5325	5332
3A0B	a d	a	5331	M	1.3	5325	5332
3A0B	a d	d	5129	Q	5.8	5109	5137
3A0B	a d	d	5136	V	7.9	5109	5137
3A0B	a d	d	5179	F	2.0	5175	5188
3A0B	a d	d	5210	L	2.1	5205	5216
3A0B	a d	d	5212	A	137.0	5205	5216
3A0B	a d	d	5214	H	95.8	5205	5216
3A0B	a d	d	5215	G	46.3	5205	5216
3A0B	a d	d	5247	V	1.0	5247	5254
3A0B	a d	d	5252	F	24.8	5247	5254
3A0B	a d	d	5264	K	1.3	5264	5274
3A0B	a d	d	5272	L	12.2	5264	5274
3A0B	a d	d	5275	P	7.0	5275	5291
3A0B	a d	d	5317	K	1.1	5314	5325
3A0B	a d	d	5324	G	32.1	5314	5325
3A0B	a d	d	5328	W	2.5	5326	5330
3A0B	A D	A	180	F	2.2	176	190
3A0B	A D	A	187	Q	1.1	176	190
3A0B	A D	A	208	G	34.1	207	222
3A0B	A D	A	216	G	41.7	207	222
3A0B	A D	A	258	L	2.6	248	259
3A0B	A D	A	275	L	4.5	271	294
3A0B	A D	A	319	D	3.2	319	324
3A0B	A D	A	327	G	284.6	325	332
3A0B	A D	A	328	M	21.8	325	332
3A0B	A D	A	331	M	2.2	325	332
3A0B	A D	D	125	F	1.0	114	137
3A0B	A D	D	141	Y	1.4	141	146
3A0B	A D	D	142	N	3.9	141	146

3A0B	A D	D	205	L	1.3	199	216
3A0B	A D	D	215	G	55.7	199	216
3A0B	A D	D	317	K	1.0	314	325
3A0B	A D	D	324	G	55.0	314	325
3A0B	a i	a	5032	W	1.8	5032	5054
3A0B	a i	a	5033	F	1.0	5032	5054
3A0B	a i	a	5036	I	1.5	5032	5054
3A0B	a i	i	5019	F	2.2	5019	5025
3A0B	a i	i	5022	G	76.2	5019	5025
3A0B	A I	A	14	W	1.2	13	18
3A0B	A I	A	17	F	1.5	13	18
3A0B	A I	A	33	F	2.5	32	51
3A0B	A I	A	36	I	1.1	32	51
3A0B	A I	A	131	W	1.5	131	136
3A0B	A I	A	135	Y	1.1	131	136
3A0B	A I	I	19	F	2.5	2	25
3A0B	A I	I	22	G	133.7	2	25
3A0B	A T	T	3	T	1.1	3	11
3A0B	A T	T	7	V	1.3	3	11
3A0B	A V	V	151	I	1.0	135	152
3A0B	b d	b	5254	W	1.7	5251	5255
3A0B	b d	b	5450	F	1.4	5444	5452
3A0B	b d	b	5454	V	2.1	5454	5462
3A0B	b d	b	5457	L	1.9	5454	5462
3A0B	b d	d	5144	I	1.1	5142	5146
3A0B	b d	d	5147	S	7.8	5147	5156
3A0B	b d	d	5160	Y	3.0	5157	5164
3A0B	b d	d	5299	I	1.1	5299	5307
3A0B	B D	B	460	L	1.6	457	465
3A0B	B D	B	467	I	1.0	466	470
3A0B	B D	D	280	W	1.8	275	291
3A0B	B D	D	288	G	1.6	275	291
3A0B	b h	b	5133	P	2.1	5132	5157
3A0B	b h	b	5134	K	1.3	5132	5157
3A0B	b h	b	5223	Y	2.4	5222	5226
3A0B	b h	h	5014	L	2.8	5013	5017
3A0B	B o	B	307	E	1.6	307	313
3A0B	B O	B	422	R	1.2	414	423
3A0B	b T	T	18	F	1.0	12	21
3A0B	B t	t	5018	F	1.0	5012	5020
3A0B	c i	i	5024	L	1.2	5019	5025
3A0B	c k	c	5059	L	1.4	5058	5069
3A0B	c k	c	5062	F	2.4	5058	5069
3A0B	c k	c	5063	W	1.2	5058	5069
3A0B	c k	c	5112	F	1.2	5109	5128
3A0B	C K	C	59	L	1.6	58	69
3A0B	C K	C	112	F	1.2	109	117
3A0B	C O	C	377	L	1.8	377	383
3A0B	C O	C	378	N	1.0	377	383
3A0B	C O	O	33	Y	1.1	33	37
3A0B	c u	c	5317	F	1.2	5306	5324
3A0B	C U	C	317	F	1.2	306	324
3A0B	C V	C	317	F	1.2	306	324
3A0B	c z	c	5120	I	1.0	5109	5128
3A0B	c z	z	5012	L	1.5	5011	5027
3A0B	C Z	C	120	I	1.5	118	128
3A0B	C Z	Z	47	W	1.3	45	55
3A0B	d e	d	5101	F	1.0	5101	5107
3A0B	d e	e	5047	F	2.0	5042	5048
3A0B	d e	e	5076	V	2.0	5072	5084

3A0B	D E	D	101	F	1.2	101	107
3A0B	d f	d	5042	Y	1.6	5042	5053
3A0B	D H	D	15	F	1.1	14	22
3A0B	d l	l	5030	L	1.1	5014	5031
3A0B	D L	L	30	L	1.3	16	31
3A0B	D M	D	304	R	1.0	299	307
3A0B	d x	d	5021	W	1.9	5014	5022
3A0B	d x	d	5035	I	1.0	5032	5041
3A0B	D X	D	18	L	1.8	14	22
3A0B	D X	D	21	W	1.9	14	22
3A0B	D X	D	35	I	1.0	32	41
3A0B	D X	X	37	L	1.2	14	42
3A0B	e f	e	5030	L	1.6	5030	5041
3A0B	e f	e	5034	G	214.5	5030	5041
3A0B	e f	e	5035	W	1.7	5030	5041
3A0B	e f	e	5037	F	11.4	5030	5041
3A0B	e f	e	5038	V	3.2	5030	5041
3A0B	e f	f	5031	I	1.2	5025	5041
3A0B	e f	f	5035	G	107.8	5025	5041
3A0B	e f	f	5036	A	11.1	5025	5041
3A0B	E F	E	34	G	247.0	25	41
3A0B	E F	F	31	I	1.0	25	41
3A0B	E F	F	35	G	42.4	25	41
3A0B	f j	f	5034	L	1.5	5025	5041
3A0B	f j	j	5028	F	1.6	5019	5033
3A0B	f j	j	5031	G	55.5	5019	5033
3A0B	h x	x	5019	F	3.4	5014	5038
3A0B	H X	H	47	E	1.0	33	50
3A0B	H X	X	19	F	3.2	14	42
3A0B	j k	j	5011	W	1.1	5010	5018
3A0B	J K	J	11	W	1.3	10	18
3A0B	k y	y	5014	G	86.3	5004	5016
3A0B	k y	y	5018	I	1.2	5017	5025
3A0B	k z	k	5018	F	1.4	5016	5024
3A0B	l m	l	5020	G	11.4	5014	5031
3A0B	l m	l	5024	I	1.7	5014	5031
3A0B	l m	m	5007	G	36.8	5007	5014
3A0B	l m	m	5008	F	2.4	5007	5014
3A0B	l m	m	5022	L	20.9	5016	5023
3A0B	l m	m	5026	Y	25.9	5024	5031
3A0B	L M	L	20	G	7.0	16	31
3A0B	L M	L	24	I	1.5	16	31
3A0B	L M	M	22	L	1.5	16	30
3A0B	l t	l	5018	Y	1.5	5014	5031
3A0B	l t	l	5029	L	1.5	5014	5031
3A0B	l t	t	5012	C	12.0	5012	5020
3A0B	L T	L	29	L	1.6	16	31
3A0B	L T	T	9	I	1.4	3	11
3A0B	L T	T	13	I	1.4	12	21
3A0B	L T	T	16	L	1.2	12	21
3A0B	y z	y	5021	L	1.0	5017	5025
3A0B	Y Z	Y	39	L	1.0	35	43
3A0B	Y Z	Z	21	I	1.2	13	23
3A1G	A B	A	695	L	1.5	690	700
3A1G	A B	A	698	K	1.3	690	700
3A1G	A B	A	699	F	2.6	690	700
3A1G	A B	A	725	D	2.1	720	733
3A1G	A B	A	746	I	1.2	746	756
3A1G	A B	A	750	I	1.5	746	756
3A1G	A B	B	3	R	2.8	3	10

3A1G	A B	B	4	I	2.2	3	10
3A1G	A B	B	7	L	1.4	3	10
3A1G	A B	B	17	R	1.1	14	23
3A1G	A B	B	19	I	1.1	14	23
3A1G	A D	D	17	R	1.0	14	23
3A1G	C D	C	691	R	1.0	690	700
3A1G	C D	C	695	L	1.3	690	700
3A1G	C D	C	698	K	1.3	690	700
3A1G	C D	C	699	F	3.0	690	700
3A1G	C D	C	725	D	1.7	720	733
3A1G	C D	C	746	I	1.6	746	756
3A1G	C D	C	750	I	1.7	746	756
3A1G	C D	D	3	R	3.4	3	10
3A1G	C D	D	4	I	2.2	3	10
3A1G	C D	D	7	L	1.7	3	10
3A1G	C D	D	19	I	2.0	14	23
3A1Q	A C	C	85	F	1.9	81	120
3A1Q	D F	F	81	E	1.1	81	118
3A1Q	D F	F	89	L	1.0	81	118
3A1Q	E F	F	106	E	1.2	81	118
3B2U	J I	I	349	P	1.0	349	354
3B2U	K J	K	123	E	1.2	122	126
3B2U	K J	K	124	Q	1.0	122	126
3B2U	L H	L	124	Q	1.0	122	128
3B2U	N M	M	349	P	1.0	349	354
3B2U	T S	S	349	P	1.1	349	354
3B2U	U T	U	124	Q	1.2	122	128
3B2U	W V	V	349	P	1.0	349	354
3B4V	A C	C	57	L	2.3	54	61
3B4V	A D	A	58	F	2.0	58	69
3B4V	A D	D	199	R	1.7	195	206
3B4V	B C	B	58	F	2.3	58	68
3B4V	B C	C	199	R	2.7	195	206
3B4V	B D	D	57	L	1.8	54	61
3B4V	E G	G	57	L	2.1	54	61
3B4V	E H	E	58	F	2.0	58	70
3B4V	E H	E	61	T	1.2	58	70
3B4V	E H	H	56	N	1.0	54	62
3B4V	E H	H	60	F	2.6	54	62
3B4V	E H	H	199	R	2.0	195	206
3B4V	F D	F	21	K	1.9	20	24
3B4V	F G	G	60	F	2.7	54	61
3B4V	F G	G	199	R	1.7	195	206
3B4V	F H	H	57	L	1.5	54	62
3B4V	F H	H	58	L	1.7	54	62
3B4V	F H	H	60	F	2.0	54	62
3B4V	F H	H	61	L	2.8	54	62
3B5N	A B	A	40	V	1.0	27	86
3B5N	A B	A	43	M	2.2	27	86
3B5N	A B	A	47	I	1.8	27	86
3B5N	A B	A	57	L	1.1	27	86
3B5N	A B	A	74	F	2.2	27	86
3B5N	A B	A	75	K	2.5	27	86
3B5N	A B	A	82	R	1.7	27	86
3B5N	A B	B	210	L	2.0	190	257
3B5N	A B	B	213	L	2.9	190	257
3B5N	A B	B	214	F	1.7	190	257
3B5N	A B	B	231	I	2.3	190	257
3B5N	A B	B	245	G	3.6	190	257
3B5N	A B	B	248	H	3.0	190	257

3B5N	A D	A	32	L	1.1	27	86
3B5N	A D	A	49	K	1.2	27	86
3B5N	A D	A	60	I	1.8	27	86
3B5N	A D	A	63	K	1.4	27	86
3B5N	A D	A	67	L	1.8	27	86
3B5N	A D	A	74	F	1.5	27	86
3B5N	A D	A	81	V	1.4	27	86
3B5N	A D	D	620	D	1.1	589	649
3B5N	A D	D	633	T	1.0	589	649
3B5N	A D	D	640	L	1.6	589	649
3B5N	A D	D	647	L	1.8	589	649
3B5N	A K	A	80	R	1.0	27	86
3B5N	B C	B	190	L	1.1	190	257
3B5N	B C	B	193	V	1.0	190	257
3B5N	B C	B	197	H	1.8	190	257
3B5N	B C	B	204	E	1.5	190	257
3B5N	B C	B	207	M	1.5	190	257
3B5N	B C	B	214	F	1.4	190	257
3B5N	B C	B	218	E	1.3	190	257
3B5N	B C	B	221	V	1.6	190	257
3B5N	B C	B	235	V	1.0	190	257
3B5N	B C	C	450	M	1.3	432	499
3B5N	B C	C	458	G	4.1	432	499
3B5N	B C	C	464	M	1.4	432	499
3B5N	B C	C	471	Q	1.1	432	499
3B5N	B C	C	475	V	1.4	432	499
3B5N	B C	C	479	L	1.0	432	499
3B5N	B C	C	482	M	2.0	432	499
3B5N	B C	C	492	K	1.6	432	499
3B5N	B C	C	496	L	1.6	432	499
3B5N	B D	B	200	L	1.6	190	257
3B5N	B D	B	214	F	2.3	190	257
3B5N	B D	D	601	I	1.2	589	649
3B5N	C D	C	437	K	1.1	432	499
3B5N	C D	C	444	T	1.4	432	499
3B5N	C D	C	448	L	1.3	432	499
3B5N	C D	C	455	E	1.5	432	499
3B5N	C D	C	493	V	1.4	432	499
3B5N	C D	D	590	M	1.6	589	649
3B5N	C D	D	594	I	1.5	589	649
3B5N	C D	D	601	I	2.1	589	649
3B5N	C D	D	604	V	1.0	589	649
3B5N	C D	D	607	R	1.5	589	649
3B5N	C D	D	608	L	1.6	589	649
3B5N	C D	D	611	M	1.4	589	649
3B5N	C D	D	614	T	3.4	589	649
3B5N	C D	D	629	I	1.5	589	649
3B5N	C D	D	647	L	1.0	589	649
3B5N	E F	E	36	I	1.6	30	86
3B5N	E F	E	40	V	1.2	30	86
3B5N	E F	E	43	M	1.7	30	86
3B5N	E F	E	47	I	1.6	30	86
3B5N	E F	E	54	G	1.3	30	86
3B5N	E F	E	74	F	1.7	30	86
3B5N	E F	E	75	K	2.3	30	86
3B5N	E F	E	82	R	2.5	30	86
3B5N	E F	F	203	L	1.4	190	256
3B5N	E F	F	210	L	2.3	190	256
3B5N	E F	F	213	L	2.8	190	256
3B5N	E F	F	214	F	1.2	190	256

3B5N	E F	F	231	I	2.3	190	256
3B5N	E F	F	245	G	2.3	190	256
3B5N	E F	F	248	H	1.9	190	256
3B5N	E H	E	32	L	1.7	30	86
3B5N	E H	E	49	K	1.7	30	86
3B5N	E H	E	60	I	1.2	30	86
3B5N	E H	E	63	K	1.8	30	86
3B5N	E H	E	67	L	1.5	30	86
3B5N	E H	E	74	F	1.2	30	86
3B5N	E H	E	81	V	1.5	30	86
3B5N	E H	H	609	K	1.2	589	649
3B5N	E H	H	616	G	1.5	589	649
3B5N	E H	H	619	L	1.8	589	649
3B5N	E H	H	620	D	1.1	589	649
3B5N	E H	H	626	L	1.4	589	649
3B5N	E H	H	634	D	1.1	589	649
3B5N	E H	H	640	L	1.4	589	649
3B5N	E H	H	647	L	1.7	589	649
3B5N	F G	F	190	L	1.3	190	256
3B5N	F G	F	197	H	1.9	190	256
3B5N	F G	F	207	M	1.5	190	256
3B5N	F G	F	214	F	1.2	190	256
3B5N	F G	F	221	V	1.4	190	256
3B5N	F G	F	225	Q	1.2	190	256
3B5N	F G	F	229	D	1.1	190	256
3B5N	F G	F	235	V	1.6	190	256
3B5N	F G	F	246	V	1.0	190	256
3B5N	F G	F	253	V	1.3	190	256
3B5N	F G	G	433	I	1.3	432	499
3B5N	F G	G	450	M	1.3	432	499
3B5N	F G	G	458	G	2.7	432	499
3B5N	F G	G	464	M	1.5	432	499
3B5N	F G	G	468	Q	1.0	432	499
3B5N	F G	G	471	Q	1.2	432	499
3B5N	F G	G	475	V	1.3	432	499
3B5N	F G	G	482	M	1.4	432	499
3B5N	F G	G	492	K	1.5	432	499
3B5N	F G	G	496	L	1.4	432	499
3B5N	F H	F	200	L	1.0	190	256
3B5N	F H	F	214	F	2.1	190	256
3B5N	F H	H	608	L	1.0	589	649
3B5N	G H	G	437	K	1.1	432	499
3B5N	G H	G	441	V	1.0	432	499
3B5N	G H	G	444	T	1.5	432	499
3B5N	G H	G	448	L	1.5	432	499
3B5N	G H	G	455	E	1.9	432	499
3B5N	G H	G	472	L	1.2	432	499
3B5N	G H	G	482	M	1.2	432	499
3B5N	G H	G	493	V	1.3	432	499
3B5N	G H	H	590	M	1.3	589	649
3B5N	G H	H	594	I	1.5	589	649
3B5N	G H	H	601	I	2.1	589	649
3B5N	G H	H	607	R	1.7	589	649
3B5N	G H	H	608	L	1.6	589	649
3B5N	I J	I	36	I	1.5	30	86
3B5N	I J	I	40	V	1.2	30	86
3B5N	I J	I	43	M	2.3	30	86
3B5N	I J	I	47	I	1.6	30	86
3B5N	I J	I	54	G	4.4	30	86
3B5N	I J	I	57	L	1.4	30	86

3B5N	I J	I	75	K	1.5	30	86
3B5N	I J	J	210	L	2.1	192	253
3B5N	I J	J	213	L	2.7	192	253
3B5N	I J	J	214	F	1.6	192	253
3B5N	I J	J	231	I	2.3	192	253
3B5N	I J	J	248	H	1.4	192	253
3B5N	I L	I	32	L	1.9	30	86
3B5N	I L	I	42	I	1.3	30	86
3B5N	I L	I	57	L	1.0	30	86
3B5N	I L	I	60	I	1.4	30	86
3B5N	I L	I	63	K	2.9	30	86
3B5N	I L	I	67	L	2.9	30	86
3B5N	I L	I	74	F	1.3	30	86
3B5N	I L	L	609	K	1.9	589	647
3B5N	I L	L	619	L	1.2	589	647
3B5N	I L	L	626	L	1.3	589	647
3B5N	I L	L	630	E	2.2	589	647
3B5N	I L	L	633	T	1.0	589	647
3B5N	I L	L	640	L	1.8	589	647
3B5N	J K	J	197	H	1.4	192	253
3B5N	J K	J	204	E	1.4	192	253
3B5N	J K	J	207	M	1.5	192	253
3B5N	J K	J	214	F	1.4	192	253
3B5N	J K	J	221	V	1.5	192	253
3B5N	J K	J	235	V	1.0	192	253
3B5N	J K	K	450	M	1.3	435	498
3B5N	J K	K	458	G	3.9	435	498
3B5N	J K	K	475	V	1.3	435	498
3B5N	J K	K	482	M	1.1	435	498
3B5N	J K	K	492	K	1.7	435	498
3B5N	J K	K	496	L	1.0	435	498
3B5N	J L	J	214	F	2.4	192	253
3B5N	K L	K	444	T	1.4	435	498
3B5N	K L	K	448	L	1.3	435	498
3B5N	K L	K	455	E	1.0	435	498
3B5N	K L	K	472	L	1.1	435	498
3B5N	K L	K	476	E	1.5	435	498
3B5N	K L	L	590	M	1.5	589	647
3B5N	K L	L	594	I	1.2	589	647
3B5N	K L	L	597	N	1.0	589	647
3B5N	K L	L	601	I	1.4	589	647
3B5N	K L	L	607	R	1.3	589	647
3B5N	K L	L	608	L	1.7	589	647
3B5N	K L	L	622	Q	1.1	589	647
3B5N	K L	L	625	R	1.6	589	647
3B63	A C	A	200	E	1.2	198	209
3B63	A C	C	285	R	1.2	282	290
3B63	B C	C	108	K	1.2	108	123
3B63	D E	E	108	K	1.3	108	119
3B63	D F	D	55	K	1.0	50	56
3B63	I J	I	185	M	1.1	177	187
3B63	I J	I	248	E	14.3	247	258
3B63	I J	J	110	N	7.7	108	123
3B63	J L	L	285	R	3.3	285	290
3B63	J L	L	286	K	10.3	285	290
3B63	K L	L	110	N	24.9	108	122
3B63	K L	L	112	E	1.6	108	122
3B63	K M	M	286	K	1.3	282	287
3B63	N L	N	285	R	1.3	282	291
3B63	N M	N	108	K	1.5	108	123

3B63	N M	N	183	Y	1.0	177	190
3B63	N M	N	261	F	1.1	259	264
3B63	N M	M	190	E	1.3	177	191
3B71	A D	A	1032	K	2.0	1011	1047
3B71	B E	B	958	G	4.6	949	973
3B71	B E	B	998	I	1.2	980	1007
3B71	B E	E	413	L	1.8	407	416
3B71	B E	E	414	L	2.0	407	416
3B8E	A B	A	859	F	1.1	849	868
3B8E	A B	A	994	Y	1.7	981	1005
3B8E	A B	B	42	F	1.5	39	59
3B8E	A B	B	46	L	1.0	39	59
3B8E	A B	B	50	F	2.5	39	59
3B8E	C D	C	856	L	1.3	851	859
3B8E	C D	D	42	F	2.2	38	56
3B8E	C D	D	46	L	1.7	38	56
3B9F	L H	L	14	E	1.4	14	14
3B9F	L H	L	14	E	2.9	14	14
3B9F	L H	L	14	L	2.1	14	14
3B9F	L H	L	14	Y	2.6	14	14
3B9J	A B	A	142	A	1.0	136	143
3B9J	A B	B	265	G	1.0	262	271
3B9J	A B	B	266	I	1.1	262	271
3B9J	A B	B	341	Q	2.4	340	346
3B9J	A C	A	31	R	2.4	26	35
3B9J	A C	A	115	F	3.7	115	131
3B9J	A C	C	1197	G	193.4	1188	1209
3B9J	A C	C	1204	G	3.3	1188	1209
3B9J	B C	B	269	K	1.9	262	271
3B9J	B C	B	270	F	1.5	262	271
3B9J	B C	B	507	F	3.0	505	528
3B9J	B C	B	514	S	1.1	505	528
3B9J	B C	B	517	F	2.2	505	528
3B9J	B C	C	679	E	1.4	675	683
3B9J	B C	C	680	R	1.6	675	683
3B9J	I J	I	141	D	1.1	136	143
3B9J	I J	J	270	F	1.2	262	271
3B9J	I J	J	340	K	1.4	340	346
3B9J	I J	J	341	Q	2.8	340	346
3B9J	I K	I	31	R	2.8	26	34
3B9J	I K	I	115	F	3.3	115	131
3B9J	I K	I	154	R	1.9	154	162
3B9J	I K	I	157	L	1.0	154	162
3B9J	I K	K	1197	G	51.2	1188	1207
3B9J	J K	J	269	K	1.6	262	271
3B9J	J K	J	507	F	3.9	505	528
3B9J	J K	J	511	L	1.0	505	528
3B9J	J K	J	517	F	1.8	505	528
3B9J	J K	K	679	E	1.3	675	684
3BBN	B H	B	181	I	1.0	180	184
3BBN	C N	C	33	L	2.8	29	42
3BBN	C N	C	34	Q	1.7	29	42
3BBN	C N	N	86	M	1.4	80	89
3BBN	D E	D	47	R	1.2	43	59
3BBN	D E	D	195	E	2.6	191	198
3BBN	D E	E	254	R	1.9	251	261
3BBN	D E	E	258	E	1.2	251	261
3BBN	G I	G	40	Y	1.7	36	41
3BBN	J N	N	80	G	14.4	80	89
3BBN	J N	N	83	L	1.4	80	89

3BBN	J N	N	84	R	2.1	80	89
3BBN	N S	N	45	G	2.0	42	47
3BBN	N S	N	46	K	2.0	42	47
3BBO	S T	S	47	H	1.4	43	68
3BBO	V Z	Z	90	F	1.1	88	99
3BBO	V Z	Z	93	R	1.6	88	99
3BBP	C F	F	1597	K	1.3	1579	1606
3BC1	A B	A	184	R	1.0	170	188
3BC1	A B	A	185	M	1.0	170	188
3BC1	A B	B	15	I	1.3	7	35
3BC1	A B	B	18	V	1.7	7	35
3BC1	A B	B	21	R	2.6	7	35
3BC1	A B	B	25	L	2.0	7	35
3BC1	A B	B	32	R	3.0	7	35
3BC1	A B	B	49	M	1.0	43	51
3BC1	A F	A	120	H	1.3	110	121
3BC1	A F	F	16	M	1.2	7	35
3BC1	A F	F	19	L	1.6	7	35
3BC1	E B	E	82	R	2.0	82	88
3BC1	E B	B	8	E	1.2	7	35
3BC1	E B	B	9	F	2.2	7	35
3BC1	E B	B	12	Q	1.6	7	35
3BC1	E B	B	16	M	1.6	7	35
3BC1	E B	B	19	L	1.5	7	35
3BC1	E B	B	27	R	3.0	7	35
3BC1	E F	F	15	I	1.8	7	35
3BC1	E F	F	18	V	1.8	7	35
3BC1	E F	F	21	R	2.6	7	35
3BC1	E F	F	22	D	1.3	7	35
3BC1	E F	F	25	L	1.7	7	35
3BC1	E F	F	29	E	1.1	7	35
3BC1	E F	F	32	R	2.7	7	35
3BC1	E F	F	49	M	1.0	43	50
3BCQ	A B	A	31	R	3.1	21	36
3BCQ	A B	A	107	L	2.1	96	110
3BCQ	A B	A	123	H	3.5	120	140
3BCQ	A B	B	30	R	2.3	20	35
3BCQ	A B	B	33	I	1.0	20	35
3BCQ	A B	B	34	V	1.8	20	35
3BCQ	A B	B	112	V	1.2	100	119
3BCQ	A B	B	116	M	1.9	100	119
3BCQ	A D	A	96	P	1.0	96	110
3BCQ	A D	D	37	W	2.2	36	42
3BCQ	A D	D	40	R	1.6	36	42
3BCQ	C B	C	96	P	1.5	96	114
3BCQ	C B	B	37	W	3.0	37	42
3BCQ	C D	C	104	H	1.0	96	114
3BCQ	C D	C	108	V	1.0	96	114
3BCQ	C D	C	112	Q	1.0	96	114
3BCQ	C D	C	123	H	1.1	120	138
3BCQ	C D	D	30	R	1.5	23	35
3BCQ	C D	D	34	V	1.7	23	35
3BCQ	C D	D	112	V	1.1	100	119
3BDY	H L	L	123	E	1.1	122	128
3BDY	H L	L	124	Q	1.4	122	128
3BEG	A B	A	564	D	3.6	561	573
3BEG	A B	A	571	E	3.4	561	573
3BEJ	B F	B	299	V	1.2	280	305
3BEJ	B F	B	303	K	1.3	280	305
3BEJ	B F	B	317	I	6.9	313	337

3BEJ	B F	F	690	L	1.4	688	695
3BEJ	B F	F	694	L	2.1	688	695
3BG0	A B	B	138	I	2.0	136	143
3BG0	A B	B	513	R	1.9	500	514
3BG0	A B	B	544	K	2.0	534	550
3BG0	A B	B	547	Y	1.6	534	550
3BG0	D C	C	483	F	1.1	474	484
3BG0	D C	C	543	L	1.5	534	550
3BG0	D C	C	544	K	1.7	534	550
3BG0	D C	C	547	Y	1.0	534	550
3BG0	E F	F	138	I	1.8	136	143
3BG0	E F	F	439	R	1.4	431	440
3BG0	E F	F	513	R	2.2	500	514
3BG0	E F	F	544	K	2.3	534	550
3BG0	H G	G	543	L	1.3	534	550
3BG0	H G	G	544	K	1.8	534	550
3BG0	H G	G	547	Y	5.3	534	550
3BG4	B C	C	237	W	1.8	234	244
3BG4	B C	C	241	T	1.3	234	244
3BG4	B C	C	242	L	1.4	234	244
3BGF	A B	A	427	N	3.2	426	430
3BGF	L H	L	124	Q	1.1	122	127
3BGO	P S	S	108	I	1.8	104	117
3BGO	P S	S	112	E	3.2	104	117
3BH6	A B	A	35	K	1.2	30	38
3BH6	A B	A	102	E	1.9	100	113
3BIM	A I	A	58	Y	1.6	55	61
3BIM	A I	A	116	H	1.9	115	125
3BIM	A J	A	17	D	1.1	14	28
3BIM	B J	B	55	G	14.3	55	61
3BIM	B J	B	58	Y	1.7	55	61
3BIM	B J	B	116	H	2.3	115	123
3BIM	C K	C	55	G	1.4	55	61
3BIM	C K	C	58	Y	1.8	55	61
3BIM	C K	C	116	H	1.4	115	123
3BIM	C L	C	17	D	1.6	14	28
3BIM	D K	D	17	D	1.3	14	28
3BIM	D L	D	55	G	2.2	55	61
3BIM	D L	D	58	Y	1.5	55	61
3BIM	D L	D	116	H	1.8	115	124
3BIM	E M	E	58	Y	2.1	55	63
3BIM	E M	E	116	H	2.0	115	123
3BIM	E N	E	17	D	1.3	14	28
3BIM	E N	E	21	N	1.1	14	28
3BIM	E N	E	24	R	1.2	14	28
3BIM	F M	F	17	D	1.5	14	28
3BIM	F N	F	58	Y	1.3	55	61
3BIM	F N	F	116	H	1.8	115	123
3BIM	G O	G	58	Y	1.3	55	61
3BIM	G O	G	116	H	2.3	115	125
3BIM	G P	G	17	D	1.4	14	28
3BIM	H O	H	17	D	1.1	14	28
3BIM	H P	H	116	H	2.0	115	125
3BJI	A D	A	201	E	1.7	199	219
3BJI	A D	A	330	M	1.1	322	334
3BJI	A D	A	331	Q	1.1	322	334
3BJI	A D	A	337	H	1.4	335	345
3BJI	A D	D	67	L	2.1	65	69
3BJI	B C	B	201	E	3.1	191	228
3BJI	B C	B	337	H	1.8	335	346

3BJI	B C	C	65	D	1.6	65	69
3BJI	B C	C	66	R	2.5	65	69
3BJI	B C	C	67	L	1.7	65	69
3BKJ	L H	L	123	Q	1.3	121	127
3BKY	H L	L	123	Q	1.2	121	127
3BL2	A C	A	48	F	2.5	32	56
3BL2	A C	A	51	H	2.3	32	56
3BL2	A C	A	60	Y	1.4	60	64
3BL2	A C	A	74	L	1.8	71	79
3BL2	A C	A	78	L	1.1	71	79
3BL2	A C	A	86	G	123.5	85	103
3BL2	A C	A	87	R	2.2	85	103
3BL2	A C	A	90	G	4.2	85	103
3BL2	A C	C	110	L	2.9	107	123
3BL2	A C	C	114	L	2.5	107	123
3BL2	A C	C	115	K	1.3	107	123
3BL2	A C	C	118	G	26.6	107	123
3BL2	A C	C	119	D	1.3	107	123
3BL2	A C	C	121	F	4.1	107	123
3BL2	A D	D	116	V	1.0	107	123
3BL2	B C	C	116	V	1.0	107	123
3BL2	B D	B	48	F	2.2	35	56
3BL2	B D	B	51	H	1.6	35	56
3BL2	B D	B	52	Y	1.5	35	56
3BL2	B D	B	60	Y	1.0	60	64
3BL2	B D	B	74	L	2.1	67	79
3BL2	B D	B	78	L	1.2	67	79
3BL2	B D	B	86	G	136.0	85	103
3BL2	B D	B	87	R	3.1	85	103
3BL2	B D	D	107	M	1.3	107	123
3BL2	B D	D	110	L	2.4	107	123
3BL2	B D	D	113	R	1.0	107	123
3BL2	B D	D	114	L	2.3	107	123
3BL2	B D	D	115	K	1.0	107	123
3BL2	B D	D	118	G	14.2	107	123
3BL2	B D	D	119	D	2.9	107	123
3BL2	B D	D	121	F	4.2	107	123
3BLH	A B	A	61	I	1.4	61	73
3BLH	A B	A	64	L	1.6	61	73
3BLH	A B	A	71	Q	1.2	61	73
3BLH	A B	B	89	F	2.2	80	95
3BLH	A B	B	93	K	3.1	80	95
3BLH	A B	B	137	E	1.5	124	144
3BLH	A B	B	141	L	1.2	124	144
3BLW	A B	A	189	L	1.1	188	201
3BLW	A B	A	190	G	1.4	188	201
3BLW	A B	A	221	M	2.0	216	226
3BLW	A B	A	242	I	1.6	237	251
3BLW	A B	B	195	L	1.1	194	210
3BLW	A B	B	196	A	1.0	194	210
3BLW	A B	B	199	L	1.2	194	210
3BLW	A B	B	226	L	1.9	221	231
3BLW	A B	B	229	V	1.5	221	231
3BLW	A B	B	249	I	1.5	244	259
3BLW	A B	B	256	G	55.4	244	259
3BLW	C D	C	189	L	1.3	188	201
3BLW	C D	C	190	G	2.2	188	201
3BLW	C D	C	221	M	1.1	216	226
3BLW	C D	C	242	I	1.1	237	251
3BLW	C D	D	222	D	1.0	221	231

3BLW	C D	D	226	L	2.1	221	231
3BLW	C D	D	229	V	1.6	221	231
3BLW	C D	D	256	G	27.9	244	259
3BLW	E F	E	189	L	1.2	188	201
3BLW	E F	E	190	G	1.1	188	201
3BLW	E F	E	221	M	1.0	216	226
3BLW	E F	E	242	I	1.0	237	251
3BLW	E F	F	226	L	1.7	221	231
3BLW	E F	F	229	V	1.5	221	231
3BLW	E F	F	249	I	1.2	244	259
3BLW	E F	F	256	G	95.7	244	259
3BLW	G H	G	224	V	1.9	216	226
3BLW	G H	G	242	I	1.4	237	251
3BLW	G H	H	226	L	1.3	221	231
3BLW	G H	H	229	V	2.8	221	231
3BLW	G H	H	249	I	1.5	244	259
3BLW	G H	H	253	L	1.7	244	259
3BLW	G H	H	256	G	135.1	244	259
3BLW	I J	I	189	L	2.5	188	201
3BLW	I J	I	224	V	1.2	216	226
3BLW	I J	I	242	I	1.6	237	251
3BLW	I J	J	226	L	1.7	221	231
3BLW	I J	J	229	V	1.6	221	231
3BLW	I J	J	249	I	1.7	244	259
3BLW	I J	J	256	G	107.7	244	259
3BLW	K L	K	189	L	1.1	188	201
3BLW	K L	K	224	V	1.4	216	226
3BLW	K L	K	242	I	1.3	237	251
3BLW	K L	L	226	L	2.4	221	231
3BLW	K L	L	229	V	1.5	221	231
3BLW	K L	L	249	I	1.5	244	259
3BLW	K L	L	256	G	107.6	244	259
3BLW	M N	M	189	L	1.1	188	201
3BLW	M N	M	190	G	1.8	188	201
3BLW	M N	M	221	M	1.0	216	226
3BLW	M N	M	242	I	1.4	237	251
3BLW	M N	N	222	D	1.5	221	231
3BLW	M N	N	226	L	2.8	221	231
3BLW	M N	N	229	V	1.6	221	231
3BLW	M N	N	249	I	1.2	244	259
3BLW	M N	N	256	G	54.8	244	259
3BLW	O P	O	190	G	2.6	188	201
3BLW	O P	O	221	M	1.1	216	226
3BLW	O P	O	242	I	1.5	237	251
3BLW	O P	P	222	D	1.9	221	231
3BLW	O P	P	226	L	2.3	221	231
3BLW	O P	P	229	V	1.5	221	231
3BLW	O P	P	249	I	1.2	244	259
3BLW	O P	P	256	G	51.1	244	259
3BMC	A B	A	243	F	3.4	234	246
3BMC	A B	B	243	F	3.2	234	246
3BMC	A C	A	129	I	1.2	116	142
3BMC	A C	A	132	F	2.2	116	142
3BMC	A C	A	173	L	1.4	172	192
3BMC	A C	A	176	M	1.9	172	192
3BMC	A C	A	179	H	2.1	172	192
3BMC	A C	A	183	G	13.8	172	192
3BMC	A C	A	190	L	1.0	172	192
3BMC	A C	A	191	E	1.4	172	192
3BMC	A C	C	132	F	2.4	116	142

3BMC	A C	C	173	L	1.5	172	192
3BMC	A C	C	176	M	1.6	172	192
3BMC	A C	C	179	H	2.2	172	192
3BMC	A C	C	183	G	15.9	172	192
3BMC	A C	C	191	E	1.5	172	192
3BMC	A D	D	221	W	1.9	215	225
3BN9	C D	C	123	E	1.0	122	126
3BO0	A B	A	220	F	1.8	209	225
3BO0	A B	A	418	V	1.0	411	435
3BO0	A B	A	421	V	1.2	411	435
3BO0	A B	A	425	Y	2.0	411	435
3BO0	A B	B	39	V	1.1	31	55
3BO0	A B	B	43	G	195.2	31	55
3BO0	A B	B	51	G	84.2	31	55
3BO0	A C	A	10	K	4.1	5	11
3BO0	A C	A	29	W	1.3	23	41
3BO0	A C	A	36	L	1.4	23	41
3BO0	A C	A	156	Y	10.0	137	163
3BO0	A C	A	160	I	7.2	137	163
3BO0	A C	C	30	P	3.6	30	49
3BO0	A C	C	33	V	1.5	30	49
3BO0	A C	C	34	I	1.5	30	49
3BOW	A B	A	582	D	1.1	574	584
3BOW	A B	A	642	L	1.3	640	648
3BOW	A B	A	645	V	1.7	640	648
3BOW	A B	A	691	L	1.6	691	700
3BOW	A B	A	694	W	4.2	691	700
3BOW	A B	A	695	L	1.6	691	700
3BOW	A B	B	144	D	1.3	143	154
3BOW	A B	B	218	R	1.5	209	219
3BOW	A B	B	242	F	1.0	228	249
3BOW	A B	B	245	F	3.1	228	249
3BOW	A B	B	260	I	1.4	260	270
3BOW	A B	B	263	W	4.2	260	270
3BOW	A B	B	264	L	1.3	260	270
3BOW	A B	B	268	M	1.0	260	270
3BOW	A B	B	269	Y	1.1	260	270
3BOW	A C	A	454	L	1.1	450	455
3BOW	A C	A	560	V	1.8	550	564
3BOW	A C	A	601	W	3.5	594	615
3BOW	A C	C	576	L	1.3	573	584
3BOW	A C	C	579	L	2.1	573	584
3BOW	A C	C	582	S	1.2	573	584
3BOW	A C	C	583	L	1.7	573	584
3BOW	A C	C	623	Y	1.5	621	628
3BOW	A C	C	626	L	1.9	621	628
3BOW	A C	C	627	L	1.7	621	628
3BOW	B C	B	103	F	1.4	99	112
3BOW	B C	B	106	L	2.7	99	112
3BOW	B C	B	110	L	1.8	99	112
3BOW	B C	B	129	V	1.8	119	133
3BOW	B C	B	170	W	3.7	163	183
3BOW	B C	C	653	I	2.7	652	660
3BOW	B C	C	656	L	2.7	652	660
3BOW	B C	C	659	D	1.1	652	660
3BP8	A C	A	136	F	2.0	124	139
3BP8	B D	B	136	F	1.2	124	139
3BP8	B D	B	137	I	1.4	124	139
3BPL	A B	A	5	I	1.1	5	20
3BPL	A B	A	9	E	3.1	5	20

3BPL	A B	A	12	K	1.6	5	20
3BPL	A B	A	13	T	1.2	5	20
3BPL	A B	A	56	Y	1.1	41	59
3BPL	A B	A	81	R	2.1	70	95
3BPL	A B	A	85	R	1.0	70	95
3BPL	A B	A	88	R	3.4	70	95
3BPL	A B	A	91	W	1.6	70	95
3BPL	A B	A	92	G	72.7	70	95
3BPL	A C	A	11	I	1.1	5	20
3BPL	A C	A	124	Y	2.6	109	127
3BPN	A B	A	12	K	1.5	5	20
3BPN	A B	A	81	R	1.7	70	95
3BPN	A B	A	88	R	1.6	70	95
3BPN	A B	A	92	G	13.1	70	95
3BPN	A C	A	11	I	1.5	5	20
3BPN	A C	A	19	E	1.2	5	20
3BPN	A C	A	121	R	1.4	109	127
3BPN	A C	A	124	Y	2.7	109	127
3BPO	A B	A	8	T	1.6	6	21
3BPO	A B	A	12	E	2.1	6	21
3BPO	A B	A	62	K	1.0	61	70
3BPO	A B	A	66	M	3.3	61	70
3BPO	A B	A	69	G	204.3	61	70
3BPQ	A B	A	21	E	3.0	14	35
3BPQ	A B	A	23	I	1.0	14	35
3BPQ	A B	A	24	L	2.4	14	35
3BPQ	A B	A	27	G	46.2	14	35
3BPQ	A B	A	28	L	2.6	14	35
3BPQ	A B	A	29	A	1.8	14	35
3BPQ	A B	A	32	M	2.1	14	35
3BPQ	A B	B	80	R	1.1	80	87
3BPQ	A B	B	83	I	1.7	80	87
3BPQ	A B	B	86	Y	2.1	80	87
3BPQ	C B	C	19	K	2.4	14	35
3BPQ	C B	B	84	Y	1.9	80	87
3BPQ	C B	B	85	D	1.5	80	87
3BPQ	C D	C	24	L	1.3	14	35
3BPQ	C D	C	27	G	18.9	14	35
3BPQ	C D	C	28	L	1.9	14	35
3BPQ	C D	C	32	M	2.9	14	35
3BPQ	C D	D	83	I	1.8	80	84
3BPS	P A	A	265	L	1.0	261	278
3BPS	P A	A	266	I	1.4	261	278
3BPS	P A	A	269	E	2.9	261	278
3BPS	P A	A	295	R	1.7	295	307
3BPS	P A	A	296	V	1.1	295	307
3BQO	A B	A	106	E	2.8	95	111
3BQO	A B	A	127	Q	1.3	117	134
3BQU	C D	C	123	E	1.5	122	127
3BQU	C D	C	124	Q	1.3	122	127
3BRT	A B	A	719	L	1.0	707	727
3BRT	A B	B	75	R	2.0	50	109
3BRT	A B	B	93	L	2.9	50	109
3BRT	A D	A	729	E	1.0	728	732
3BRT	A D	D	65	I	1.2	51	110
3BRT	A D	D	79	L	1.1	51	110
3BRT	A D	D	97	F	2.4	51	110
3BRT	C B	C	708	L	1.4	705	731
3BRT	C B	C	711	E	1.7	705	731
3BRT	C B	C	715	L	1.3	705	731

3BRT	C B	B	73	R	1.4	50	109
3BRT	C B	B	79	L	1.2	50	109
3BRT	C B	B	97	F	1.1	50	109
3BRT	C D	C	713	H	1.0	705	731
3BRT	C D	C	719	L	1.4	705	731
3BRT	C D	C	720	E	1.3	705	731
3BRT	C D	D	79	L	1.1	51	110
3BRT	C D	D	82	F	1.8	51	110
3BRT	C D	D	92	F	2.7	51	110
3BRT	C D	D	93	L	1.2	51	110
3BRV	A B	B	75	R	2.4	50	109
3BRV	A B	B	82	F	2.1	50	109
3BRV	A B	B	89	E	1.3	50	109
3BRV	A B	B	92	F	2.2	50	109
3BRV	A D	A	708	L	1.5	706	727
3BRV	A D	D	65	I	1.0	50	109
3BRV	A D	D	72	L	1.0	50	109
3BRV	A D	D	79	L	1.0	50	109
3BRV	A D	D	97	F	1.8	50	109
3BRV	C B	B	97	F	1.3	50	109
3BRV	C D	D	103	L	1.0	50	109
3BRW	B D	B	382	F	1.4	380	385
3BS5	A B	A	57	R	2.4	56	62
3BS5	A B	A	61	R	2.0	56	62
3BS5	A B	B	165	I	1.7	165	183
3BS5	A B	B	166	G	91.4	165	183
3BS5	A B	B	167	H	2.9	165	183
3BS5	A B	B	168	Q	1.6	165	183
3BS5	A B	B	170	L	3.2	165	183
3BS5	A B	B	173	E	2.1	165	183
3BSZ	A F	A	82	L	2.2	75	83
3BSZ	M N	M	127	E	1.0	126	130
3BT2	L H	L	123	Q	1.9	121	126
3BTP	A B	A	164	L	1.7	162	169
3BTP	A B	A	168	R	1.3	162	169
3BTP	A B	A	323	W	2.8	317	324
3BTP	A B	A	373	Y	1.1	371	378
3BTP	A B	A	382	P	2.1	382	389
3BTP	A B	A	383	W	3.6	382	389
3BTP	A B	B	40	D	1.5	38	52
3BTP	A B	B	42	E	1.0	38	52
3BTP	A B	B	43	M	1.5	38	52
3BTP	A B	B	46	L	1.9	38	52
3BTP	A B	B	48	N	3.0	38	52
3BTP	A B	B	49	F	2.4	38	52
3BU8	A C	A	84	Q	1.4	73	89
3BU8	A C	A	109	R	1.2	95	112
3BU8	B C	B	155	K	1.1	147	168
3BUA	A E	A	84	Q	1.8	73	89
3BUA	A E	A	87	L	1.5	73	89
3BUA	A E	A	94	E	1.3	94	112
3BUA	A E	A	101	L	1.6	94	112
3BUA	A E	A	102	R	1.1	94	112
3BUA	A E	A	109	R	1.4	94	112
3BUA	A E	E	503	K	1.0	499	504
3BUA	B F	B	87	L	4.6	73	89
3BUA	B F	B	98	S	2.3	97	112
3BUA	B F	B	101	L	1.0	97	112
3BUA	B F	B	102	R	2.3	97	112
3BUA	B F	B	104	M	1.3	97	112

3BUA	B F	B	109	R	1.6	97	112
3BUA	B F	B	142	E	1.5	128	143
3BUA	B F	F	503	K	2.0	499	504
3BUA	C G	C	80	R	1.0	73	89
3BUA	C G	C	84	Q	1.1	73	89
3BUA	C G	C	87	L	1.8	73	89
3BUA	C G	C	88	V	1.0	73	89
3BUA	C G	C	101	L	1.0	98	112
3BUA	C G	C	109	R	1.2	98	112
3BUA	D H	D	80	R	1.0	73	89
3BUA	D H	D	84	Q	1.9	73	89
3BUA	D H	D	87	L	1.7	73	89
3BUA	D H	D	102	R	1.1	98	112
3BUA	D H	D	142	E	1.0	128	143
3BUZ	A B	A	62	Y	1.5	61	66
3BVH	A B	A	133	I	1.0	131	138
3BVH	A B	A	147	M	1.0	139	160
3BVH	A B	A	148	K	2.0	139	160
3BVH	A B	A	149	R	1.2	139	160
3BVH	A B	A	151	E	1.5	139	160
3BVH	A B	A	152	V	1.0	139	160
3BVH	A B	A	153	D	1.5	139	160
3BVH	A B	A	155	D	1.4	139	160
3BVH	A B	A	156	I	2.9	139	160
3BVH	A B	A	157	K	1.2	139	160
3BVH	A B	A	158	I	2.3	139	160
3BVH	A B	A	159	R	2.1	139	160
3BVH	A B	A	177	D	1.1	175	190
3BVH	A B	B	172	L	3.7	171	193
3BVH	A B	B	175	L	1.5	171	193
3BVH	A B	B	178	K	1.9	171	193
3BVH	A B	B	185	D	2.0	171	193
3BVH	A B	B	192	Y	2.0	171	193
3BVH	A C	A	136	L	4.3	131	138
3BVH	A C	A	150	L	1.6	139	160
3BVH	A C	A	157	K	1.1	139	160
3BVH	A C	C	125	K	1.0	109	134
3BVH	A C	C	128	V	1.8	109	134
3BVH	B C	B	179	I	1.7	171	193
3BVH	B C	C	120	K	1.5	109	134
3BVH	B C	C	124	L	2.0	109	134
3BVH	B C	C	131	L	1.6	109	134
3BVH	D E	D	133	I	2.0	131	160
3BVH	D E	D	151	E	1.6	131	160
3BVH	D E	D	154	I	1.4	131	160
3BVH	D E	D	155	D	1.8	131	160
3BVH	D E	D	156	I	1.2	131	160
3BVH	D E	E	171	I	1.7	169	193
3BVH	D E	E	175	L	1.2	169	193
3BVH	D E	E	178	K	1.9	169	193
3BVH	D E	E	182	L	2.1	169	193
3BVH	D E	E	185	D	1.3	169	193
3BVH	D E	E	192	Y	1.7	169	193
3BVH	D F	D	136	L	1.6	131	160
3BVH	D F	D	146	D	1.1	131	160
3BVH	D F	D	147	M	1.1	131	160
3BVH	D F	D	150	L	1.4	131	160
3BVH	D F	D	157	K	2.0	131	160
3BVH	D F	F	125	K	1.0	111	133
3BVH	D F	F	128	V	1.0	111	133

3BVH	D F	F	132	E	1.0	111	133
3BVH	E F	E	169	R	2.7	169	193
3BVH	E F	E	172	L	1.1	169	193
3BVH	E F	E	179	I	1.8	169	193
3BVH	E F	E	186	V	1.1	169	193
3BVH	E F	F	113	I	2.1	111	133
3BVH	E F	F	120	K	1.6	111	133
3BVH	E F	F	124	L	1.9	111	133
3BVH	E F	F	131	L	1.4	111	133
3BVH	E F	F	210	Q	1.1	208	214
3BWN	D C	D	109	H	1.3	100	114
3BWN	D C	D	243	Y	2.5	234	248
3BWN	D C	D	246	V	1.4	234	248
3BWN	D C	C	109	H	2.1	100	115
3BWN	D C	C	246	V	1.3	234	248
3BWU	C D	D	22	F	3.4	15	24
3BX4	A B	A	30	E	1.0	26	35
3BX4	C D	C	30	E	1.1	26	35
3BXK	A B	A	14	E	1.5	6	20
3BXK	A B	B	1961	I	1.9	1961	1976
3BXK	A B	B	1962	Y	1.6	1961	1976
3BXK	A B	B	1965	M	1.0	1961	1976
3BXK	A B	B	1967	I	3.1	1961	1976
3BXK	A B	B	1971	Y	2.7	1961	1976
3BXK	A B	B	1972	R	2.0	1961	1976
3BXK	C D	C	11	E	1.0	6	20
3BXK	C D	C	18	L	1.4	6	20
3BXK	C D	C	51	M	1.1	45	56
3BXK	C D	C	68	F	6.0	65	76
3BXK	C D	C	72	M	1.4	65	76
3BXK	C D	C	75	K	1.4	65	76
3BXK	C D	C	84	E	1.9	82	93
3BXK	C D	C	120	E	1.5	118	129
3BXK	C D	D	1961	I	2.6	1961	1978
3BXK	C D	D	1962	Y	3.1	1961	1978
3BXK	C D	D	1965	M	1.3	1961	1978
3BXK	C D	D	1966	M	1.0	1961	1978
3BXK	C D	D	1967	I	2.6	1961	1978
3BXK	C D	D	1970	Y	1.1	1961	1978
3BXK	C D	D	1972	R	1.5	1961	1978
3BYH	A B	A	91	Y	8.7	79	95
3BYH	A B	B	606	Q	1.1	606	621
3BZ1	A C	A	135	Y	6.7	131	137
3BZ1	A C	A	284	W	1.4	268	293
3BZ1	A C	A	288	L	2.1	268	293
3BZ1	A C	C	291	W	1.9	268	293
3BZ1	A C	C	317	F	1.5	306	324
3BZ1	A C	C	425	W	1.4	422	454
3BZ1	A C	C	435	F	1.0	422	454
3BZ1	A C	C	436	F	1.3	422	454
3BZ1	A C	C	446	G	42.1	422	454
3BZ1	A C	C	447	R	5.3	422	454
3BZ1	A D	A	143	I	2.0	143	147
3BZ1	A D	A	180	F	1.6	176	191
3BZ1	A D	A	184	I	1.7	176	191
3BZ1	A D	A	187	Q	1.0	176	191
3BZ1	A D	A	208	G	45.1	196	222
3BZ1	A D	A	216	G	17.0	196	222
3BZ1	A D	A	254	Y	1.3	248	260
3BZ1	A D	A	258	L	1.9	248	260

3BZ1	A D	A	269	R	1.7	268	293
3BZ1	A D	A	320	I	1.4	317	332
3BZ1	A D	A	321	I	1.7	317	332
3BZ1	A D	A	323	R	1.5	317	332
3BZ1	A D	A	327	G	212.3	317	332
3BZ1	A D	A	328	M	1.0	317	332
3BZ1	A D	A	331	M	1.3	317	332
3BZ1	A D	D	132	I	1.8	109	136
3BZ1	A D	D	179	F	2.0	178	189
3BZ1	A D	D	183	L	1.0	178	189
3BZ1	A D	D	214	H	1.5	209	220
3BZ1	A D	D	215	G	75.5	209	220
3BZ1	A D	D	252	F	2.1	246	258
3BZ1	A D	D	264	K	2.4	264	291
3BZ1	A D	D	271	M	1.0	264	291
3BZ1	A D	D	301	Q	1.6	299	308
3BZ1	A D	D	314	F	2.9	314	332
3BZ1	A D	D	321	L	1.4	314	332
3BZ1	A D	D	324	G	34.4	314	332
3BZ1	A D	D	325	I	1.4	314	332
3BZ1	A D	D	328	W	2.8	314	332
3BZ1	A I	A	14	W	1.1	13	22
3BZ1	A I	A	32	W	2.6	32	54
3BZ1	A I	A	33	F	2.1	32	54
3BZ1	A I	A	35	V	1.1	32	54
3BZ1	A I	A	36	I	1.5	32	54
3BZ1	A I	A	135	Y	1.6	131	137
3BZ1	A I	A	136	R	1.3	131	137
3BZ1	A I	I	19	F	2.1	2	21
3BZ1	A T	T	6	Y	1.7	2	22
3BZ1	A V	V	151	I	1.1	135	153
3BZ1	B D	B	257	W	2.1	236	259
3BZ1	B D	B	273	Y	2.0	272	277
3BZ1	B D	B	453	F	1.4	447	472
3BZ1	B D	B	460	L	2.0	447	472
3BZ1	B D	B	464	F	1.4	447	472
3BZ1	B D	B	467	I	1.3	447	472
3BZ1	B D	D	159	I	1.0	158	164
3BZ1	B D	D	188	F	1.8	178	189
3BZ1	B D	D	280	W	2.7	264	291
3BZ1	B D	D	284	I	1.2	264	291
3BZ1	B D	D	288	G	17.6	264	291
3BZ1	B D	D	326	R	1.1	314	332
3BZ1	B H	B	226	Y	4.4	223	229
3BZ1	B L	L	34	Y	1.0	14	37
3BZ1	B M	M	21	F	1.6	5	31
3BZ1	B M	M	25	L	1.6	5	31
3BZ1	B U	U	44	D	1.1	42	47
3BZ1	C I	C	259	W	2.1	258	262
3BZ1	C K	C	59	L	1.2	50	75
3BZ1	C K	C	70	F	1.3	50	75
3BZ1	C K	C	112	F	1.8	109	134
3BZ1	C K	K	22	V	1.2	19	43
3BZ1	C K	K	26	P	1.2	19	43
3BZ1	C U	U	77	K	1.2	73	82
3BZ1	C V	C	317	F	1.2	306	324
3BZ1	C Z	C	120	I	1.0	109	134
3BZ1	C Z	Z	27	Y	2.0	2	29
3BZ1	C Z	Z	47	W	1.1	34	59
3BZ1	D E	D	54	F	2.3	32	55

3BZ1	D E	E	44	Y	1.3	42	47
3BZ1	D F	D	49	L	2.2	32	55
3BZ1	D F	D	54	F	1.1	32	55
3BZ1	D F	F	33	F	2.9	18	41
3BZ1	D F	F	37	I	1.3	18	41
3BZ1	D F	F	40	M	1.2	18	41
3BZ1	D L	L	30	L	1.1	14	37
3BZ1	D L	L	31	F	2.0	14	37
3BZ1	D L	L	34	Y	2.8	14	37
3BZ1	D O	D	320	L	1.2	314	332
3BZ1	D O	O	208	L	1.1	205	211
3BZ1	D V	D	328	W	1.9	314	332
3BZ1	D X	D	17	I	1.4	14	23
3BZ1	D X	D	21	W	2.9	14	23
3BZ1	D X	D	35	I	1.0	32	55
3BZ1	D X	X	38	I	1.3	14	42
3BZ1	D X	X	40	I	1.0	14	42
3BZ1	E F	E	30	L	1.4	17	40
3BZ1	E F	E	31	F	1.9	17	40
3BZ1	E F	E	34	G	84.1	17	40
3BZ1	E F	E	35	W	3.2	17	40
3BZ1	E F	E	38	V	1.3	17	40
3BZ1	E F	F	31	I	1.7	18	41
3BZ1	E F	F	32	F	1.4	18	41
3BZ1	E F	F	35	G	40.2	18	41
3BZ1	F J	J	24	I	2.0	10	33
3BZ1	F J	J	27	L	1.1	10	33
3BZ1	F J	J	28	F	1.9	10	33
3BZ1	F J	J	31	G	3.9	10	33
3BZ1	H X	X	19	F	1.6	14	42
3BZ1	J K	J	11	W	1.1	10	33
3BZ1	J y	J	11	W	1.1	10	33
3BZ1	K y	K	20	P	34.7	19	43
3BZ1	K y	K	21	L	1.2	19	43
3BZ1	K y	y	24	M	1.1	22	30
3BZ1	K y	y	36	I	1.1	36	42
3BZ1	L M	L	14	R	1.1	14	37
3BZ1	L M	L	20	G	3.7	14	37
3BZ1	L M	L	24	I	1.8	14	37
3BZ1	L M	L	35	F	1.4	14	37
3BZ1	L M	L	36	F	2.2	14	37
3BZ1	L M	M	7	G	39.4	5	31
3BZ1	L M	M	14	F	2.3	5	31
3BZ1	L M	M	26	Y	1.2	5	31
3BZ1	L T	L	18	Y	2.9	14	37
3BZ1	L T	L	25	L	2.1	14	37
3BZ1	L T	L	29	L	1.9	14	37
3BZ1	L T	L	36	F	1.5	14	37
3BZ1	L T	T	9	I	2.3	2	22
3BZ1	L T	T	13	I	2.0	2	22
3BZ1	L T	T	16	L	1.6	2	22
3BZ1	y Z	Z	17	F	1.2	2	29
3BZ1	y Z	Z	25	V	1.4	2	29
3BZ4	A B	A	124	Q	1.4	122	128
3BZ4	A H	A	184	D	1.1	183	187
3BZ4	C D	C	124	Q	1.7	122	128
3BZ4	E F	E	124	Q	1.5	122	127
3BZ4	G B	G	184	D	1.7	183	188
3BZ4	G H	G	123	E	1.0	122	128
3BZL	A C	A	249	L	2.2	246	253

3BZL	A C	C	290	K	1.0	289	301
3BZL	A C	C	294	I	1.6	289	301
3BZL	A C	C	297	L	1.7	289	301
3BZL	B D	B	253	I	2.9	249	255
3BZL	B D	D	295	I	1.5	289	301
3C01	A E	A	246	K	1.9	243	251
3C01	A E	A	249	I	2.2	243	251
3C01	A E	E	290	V	1.2	285	297
3C01	A E	E	293	Y	2.2	285	297
3C01	A E	E	332	L	1.1	326	343
3C01	B E	B	244	Q	1.1	243	251
3C01	B F	B	246	K	1.8	243	251
3C01	B F	B	248	D	1.2	243	251
3C01	B F	B	249	I	3.1	243	251
3C01	B F	F	293	Y	3.2	285	297
3C01	C G	C	249	I	3.3	243	251
3C01	C G	G	290	V	4.9	285	297
3C01	C G	G	293	Y	2.9	285	297
3C01	C G	G	305	I	1.1	305	314
3C01	C G	G	307	L	1.6	305	314
3C01	C G	G	332	L	1.1	326	345
3C01	D H	D	246	K	1.1	243	251
3C01	D H	D	249	I	2.8	243	251
3C01	D H	H	290	V	5.8	285	297
3C01	D H	H	293	Y	2.8	285	297
3C03	A C	A	290	K	1.2	289	301
3C03	B C	B	253	I	2.5	246	255
3C03	B C	C	294	I	1.5	289	301
3C03	B C	C	297	L	1.5	289	301
3C0R	A B	A	157	I	1.2	155	159
3C0R	A B	A	165	Y	1.2	162	171
3C0R	C D	C	157	I	2.0	155	159
3C0R	C D	C	180	E	2.3	178	188
3C0T	A B	B	187	M	1.1	184	197
3C0T	A B	B	188	L	1.7	184	197
3C0T	A B	B	192	L	1.4	184	197
3C0T	A B	B	194	F	1.6	184	197
3C0T	A B	B	195	M	1.3	184	197
3C14	A B	A	413	V	2.3	409	430
3C14	A B	B	912	L	2.8	909	927
3C14	A B	B	913	R	1.4	909	927
3C14	A B	B	917	E	1.9	909	927
3C14	A B	B	923	D	1.3	909	927
3C14	B C	B	917	E	1.1	909	927
3C14	B C	C	234	W	1.0	228	237
3C14	B C	C	235	I	1.0	228	237
3C1B	A B	A	450	E	2.0	445	457
3C1B	A B	A	451	I	1.9	445	457
3C1B	A B	A	454	Y	1.6	445	457
3C1B	A B	A	467	F	1.3	464	479
3C1B	A B	A	470	L	1.9	464	479
3C1B	A B	A	474	I	2.4	464	479
3C1B	A B	A	478	F	3.3	464	479
3C1B	A B	A	497	E	1.1	486	514
3C1B	A B	A	499	Y	2.8	486	514
3C1B	A B	A	500	L	2.7	486	514
3C1B	A B	A	501	V	1.6	486	514
3C1B	A B	A	504	F	3.2	486	514
3C1B	A B	A	521	P	1.6	521	532
3C1B	A B	A	524	I	1.3	521	532

3C1B	A B	B	28	G	1.7	25	29
3C1B	A B	B	36	R	3.8	31	41
3C1B	A B	B	37	L	2.6	31	41
3C1B	A B	B	39	R	3.1	31	41
3C1B	A B	B	40	R	3.7	31	41
3C1B	A B	B	50	I	3.0	50	76
3C1B	A B	B	53	E	1.0	50	76
3C1B	A B	B	57	V	1.4	50	76
3C1B	A B	B	58	L	1.2	50	76
3C1B	A B	B	59	K	1.0	50	76
3C1B	A B	B	61	F	3.5	50	76
3C1B	A B	B	62	L	1.5	50	76
3C1B	A B	B	66	I	2.8	50	76
3C1B	A B	B	67	R	1.6	50	76
3C1B	A B	B	70	V	1.4	50	76
3C1B	A B	B	74	E	1.1	50	76
3C1B	A G	A	448	L	1.4	445	457
3C1B	A G	A	455	Q	1.2	445	457
3C1B	A G	A	494	E	1.3	486	514
3C1B	A G	A	512	I	1.0	486	514
3C1B	B D	B	72	Y	2.0	50	76
3C1B	B D	B	75	H	1.9	50	76
3C1B	B D	B	88	Y	2.1	83	93
3C1B	B D	B	92	R	2.5	83	93
3C1B	B D	D	1273	E	1.7	1253	1281
3C1B	B D	D	1277	L	1.1	1253	1281
3C1B	B D	D	1280	Y	2.2	1253	1281
3C1B	B D	D	1293	T	1.4	1288	1299
3C1B	B D	D	1297	L	2.2	1288	1299
3C1B	C D	C	834	L	1.0	827	836
3C1B	C D	C	849	V	1.8	845	873
3C1B	C D	C	850	Y	4.2	845	873
3C1B	C D	C	851	L	1.4	845	873
3C1B	C D	C	854	V	1.5	845	873
3C1B	C D	C	855	L	2.2	845	873
3C1B	C D	C	857	Y	3.3	845	873
3C1B	C D	C	858	L	2.0	845	873
3C1B	C D	C	863	L	2.6	845	873
3C1B	C D	C	867	G	38.8	845	873
3C1B	C D	C	880	P	1.4	880	889
3C1B	C D	C	883	L	1.7	880	889
3C1B	C D	C	896	L	1.8	891	897
3C1B	C D	D	1237	Y	1.5	1235	1246
3C1B	C D	D	1241	V	1.1	1235	1246
3C1B	C D	D	1263	V	1.1	1253	1281
3C1B	C D	D	1267	F	3.3	1253	1281
3C1B	C D	D	1291	I	1.9	1288	1299
3C1B	C D	D	1295	V	1.8	1288	1299
3C1B	C D	D	1303	L	2.7	1302	1320
3C1B	C D	D	1311	G	126.5	1302	1320
3C1B	C D	D	1318	Y	3.7	1302	1320
3C1B	E C	E	648	L	1.2	645	657
3C1B	E F	E	650	E	1.9	645	657
3C1B	E F	E	651	I	1.9	645	657
3C1B	E F	E	654	Y	2.1	645	657
3C1B	E F	E	667	F	1.0	664	679
3C1B	E F	E	670	L	2.2	664	679
3C1B	E F	E	673	E	1.3	664	679
3C1B	E F	E	674	I	2.3	664	679
3C1B	E F	E	678	F	2.5	664	679

3C1B	E F	E	692	L	1.9	686	714
3C1B	E F	E	697	E	1.3	686	714
3C1B	E F	E	699	Y	2.5	686	714
3C1B	E F	E	700	L	1.7	686	714
3C1B	E F	E	701	V	1.6	686	714
3C1B	E F	E	704	F	3.2	686	714
3C1B	E F	E	721	P	1.6	721	732
3C1B	E F	F	236	R	2.8	231	241
3C1B	E F	F	237	L	2.3	231	241
3C1B	E F	F	239	R	2.9	231	241
3C1B	E F	F	240	R	4.2	231	241
3C1B	E F	F	250	I	2.0	248	276
3C1B	E F	F	257	V	1.0	248	276
3C1B	E F	F	258	L	1.0	248	276
3C1B	E F	F	261	F	3.3	248	276
3C1B	E F	F	262	L	1.4	248	276
3C1B	E F	F	266	I	2.9	248	276
3C1B	E F	F	270	V	1.1	248	276
3C1B	E F	F	286	V	1.9	283	293
3C1B	F D	D	1265	D	1.3	1253	1281
3C1B	F H	F	272	Y	1.6	248	276
3C1B	F H	F	275	H	2.8	248	276
3C1B	F H	F	288	Y	2.5	283	293
3C1B	F H	H	1480	Y	3.7	1453	1481
3C1B	F H	H	1493	T	1.4	1488	1499
3C1B	F H	H	1496	R	1.2	1488	1499
3C1B	G H	G	1029	R	2.2	1027	1036
3C1B	G H	G	1034	L	1.0	1027	1036
3C1B	G H	G	1049	V	1.8	1045	1072
3C1B	G H	G	1050	Y	4.7	1045	1072
3C1B	G H	G	1051	L	1.6	1045	1072
3C1B	G H	G	1054	V	1.6	1045	1072
3C1B	G H	G	1055	L	2.2	1045	1072
3C1B	G H	G	1057	Y	4.7	1045	1072
3C1B	G H	G	1058	L	5.2	1045	1072
3C1B	G H	G	1063	L	2.4	1045	1072
3C1B	G H	G	1067	G	46.2	1045	1072
3C1B	G H	G	1083	L	1.6	1080	1089
3C1B	G H	G	1092	E	5.2	1091	1097
3C1B	G H	G	1096	L	1.0	1091	1097
3C1B	G H	H	1437	Y	1.4	1435	1446
3C1B	G H	H	1441	V	1.6	1435	1446
3C1B	G H	H	1442	L	1.0	1435	1446
3C1B	G H	H	1458	I	1.5	1453	1481
3C1B	G H	H	1459	M	1.8	1453	1481
3C1B	G H	H	1463	V	1.1	1453	1481
3C1B	G H	H	1467	F	3.3	1453	1481
3C1B	G H	H	1470	I	1.1	1453	1481
3C1B	G H	H	1491	I	2.2	1488	1499
3C1B	G H	H	1503	L	2.3	1502	1520
3C1B	G H	H	1510	E	1.1	1502	1520
3C1B	G H	H	1511	G	117.1	1502	1520
3C1B	G H	H	1518	Y	3.3	1502	1520
3C3Q	A B	A	143	D	1.0	143	165
3C3Q	A B	A	147	K	1.3	143	165
3C3Q	A B	B	210	E	1.2	209	216
3C4M	A C	A	34	K	2.2	34	54
3C4M	A C	A	38	I	1.1	34	54
3C4M	A C	C	20	R	5.9	16	34
3C4M	A C	C	23	W	1.8	16	34

3C4M	A C	C	24	L	2.6	16	34
3C4M	A C	C	28	L	1.0	16	34
3C4M	B D	B	34	K	2.1	34	57
3C4M	B D	B	37	Q	1.1	34	57
3C4M	B D	D	20	R	5.7	16	34
3C4M	B D	D	23	W	3.8	16	34
3C4M	B D	D	24	L	2.6	16	34
3C4M	B D	D	27	K	1.3	16	34
3C4M	B D	D	28	L	1.4	16	34
3C4M	B D	D	31	V	2.2	16	34
3C59	A B	A	32	L	1.7	32	53
3C59	A B	A	39	W	2.6	32	53
3C59	A B	B	23	I	2.0	23	28
3C59	A B	B	26	L	1.8	23	28
3C59	A B	B	27	K	1.8	23	28
3C5J	A B	A	48	F	2.6	46	50
3C5J	A B	A	70	L	1.7	56	77
3C5J	A B	A	73	M	1.3	56	77
3C5J	A C	A	58	G	3.7	56	77
3C5J	A C	A	72	I	1.2	56	77
3C5J	B C	B	61	W	2.8	55	63
3C5J	B C	B	74	Q	1.6	74	89
3C5J	B C	B	78	Y	1.8	74	89
3C5J	B C	B	81	H	1.3	74	89
3C5J	B C	B	82	N	1.4	74	89
3C5W	A C	A	417	W	1.7	417	435
3C5W	A C	A	418	R	1.6	417	435
3C5W	A C	A	456	Y	1.0	456	474
3C5W	A C	A	495	Y	2.3	495	511
3C5W	A C	A	499	M	1.0	495	511
3C5W	A C	A	535	N	1.2	534	550
3C5W	A C	A	538	F	1.5	534	550
3C5W	A C	A	574	D	1.2	573	586
3C5W	A C	A	578	F	1.5	573	586
3C5W	A C	C	71	I	1.2	62	73
3C5W	A C	C	72	G	1.9	62	73
3C5W	C P	P	298	W	1.2	298	303
3C5W	C P	P	332	I	1.0	328	336
3C5W	C P	P	335	M	1.1	328	336
3C5Z	A D	D	92	E	1.0	91	111
3C5Z	C D	C	49	F	3.4	47	53
3C5Z	C D	C	66	V	1.4	57	77
3C5Z	C D	C	70	N	2.4	57	77
3C5Z	C D	C	74	L	1.8	57	77
3C5Z	C D	D	83	D	3.0	81	90
3C5Z	E F	F	130	E	1.5	128	132
3C5Z	F H	H	93	I	1.2	91	111
3C5Z	G H	G	49	F	4.3	47	53
3C5Z	G H	G	66	V	1.4	57	77
3C5Z	G H	G	70	N	2.5	57	77
3C5Z	G H	G	74	L	1.7	57	77
3C5Z	G H	H	83	D	3.0	81	90
3C60	A B	B	133	H	2.2	128	134
3C60	C D	C	49	F	2.9	47	53
3C60	C D	C	59	G	7.1	57	78
3C60	C D	C	63	N	1.2	57	78
3C60	C D	C	70	N	2.9	57	78
3C60	C D	C	71	L	1.3	57	78
3C60	C D	C	74	L	1.3	57	78
3C60	C D	C	77	R	3.9	57	78

3C60	C D	D	83	D	1.9	81	90
3C60	E F	F	130	E	1.8	128	134
3C60	E F	F	133	H	2.1	128	134
3C60	E H	H	107	H	1.0	91	111
3C60	G H	G	49	F	3.2	47	53
3C60	G H	G	59	G	2.7	57	78
3C60	G H	G	63	N	1.1	57	78
3C60	G H	G	70	N	2.7	57	78
3C60	G H	G	71	L	1.0	57	78
3C60	G H	G	74	L	1.9	57	78
3C60	G H	G	77	R	3.7	57	78
3C60	G H	H	83	D	1.9	81	90
3C66	A C	A	489	V	1.3	482	492
3C66	A C	C	97	K	1.0	96	101
3C6L	A B	B	134	K	1.3	128	135
3C6L	B D	D	92	E	3.4	91	103
3C6L	B D	D	96	R	1.1	91	103
3C6L	C D	C	63	N	1.6	60	78
3C6L	C D	C	71	L	1.1	60	78
3C6L	C D	C	75	T	1.2	60	78
3C6L	E H	H	92	E	1.3	91	111
3C6L	G H	G	49	F	2.8	47	53
3C6L	G H	G	59	G	11.6	57	78
3C6L	G H	G	63	N	1.0	57	78
3C6L	G H	G	66	V	1.2	57	78
3C6L	G H	G	77	R	1.0	57	78
3C6L	G H	H	83	D	1.3	81	88
3C72	A B	A	25	L	1.6	17	42
3C72	A B	A	67	N	1.3	63	78
3C72	A B	A	70	R	2.3	63	78
3C72	A B	A	107	Y	16.9	107	120
3C72	A B	A	147	D	1.1	143	156
3C72	A B	A	178	Y	3.3	178	192
3C72	A B	A	179	S	1.2	178	192
3C72	A B	A	230	F	3.2	226	238
3C72	A B	A	234	W	1.6	226	238
3C72	A B	A	272	W	2.0	271	285
3C72	A B	A	310	Y	2.9	308	328
3C72	A B	A	313	D	2.7	308	328
3C72	A B	B	37	Y	2.1	37	42
3C72	A B	B	213	D	1.0	212	221
3C72	A B	B	217	W	4.9	212	221
3C72	A B	B	218	W	1.1	212	221
3C75	H M	H	55	G	73.9	54	68
3C75	H M	H	58	G	16.5	54	68
3C75	H M	H	66	L	1.3	54	68
3C75	J L	J	55	G	91.3	54	68
3C75	J L	J	58	G	14.0	54	68
3C75	J L	J	66	L	1.3	54	68
3C7B	A B	A	8	E	1.7	4	9
3C7B	A B	A	17	F	2.3	17	35
3C7B	A B	A	20	E	2.6	17	35
3C7B	A B	A	55	Y	4.2	43	58
3C7B	A B	A	109	T	1.6	109	122
3C7B	A B	A	112	L	1.4	109	122
3C7B	A B	A	117	D	1.0	109	122
3C7B	A B	A	120	E	3.0	109	122
3C7B	A B	A	150	F	1.4	146	155
3C7B	A B	A	193	Y	2.6	188	199
3C7B	A B	A	196	T	2.2	188	199

3C7B	A B	A	261	E	1.6	258	265
3C7B	A B	A	366	W	3.1	361	369
3C7B	A B	B	64	I	1.3	64	78
3C7B	A B	B	65	Y	3.3	64	78
3C7B	A B	B	66	T	1.0	64	78
3C7B	A B	B	67	V	1.2	64	78
3C7B	A B	B	68	R	3.8	64	78
3C7B	A B	B	149	G	139.1	147	158
3C7B	A B	B	152	K	2.9	147	158
3C7B	A B	B	155	M	1.5	147	158
3C7B	A B	B	159	Y	2.8	159	163
3C7B	A B	B	162	F	1.4	159	163
3C7B	A B	B	355	Y	2.8	353	357
3C7B	A E	A	407	Y	2.1	406	415
3C7B	A E	E	329	W	1.8	329	337
3C7B	A E	E	331	R	1.2	329	337
3C7B	D B	D	371	R	1.1	370	377
3C7B	D B	D	407	Y	2.8	406	414
3C7B	D B	D	411	L	1.5	406	414
3C7B	D B	B	329	W	2.2	329	337
3C7B	D E	D	17	F	2.6	17	35
3C7B	D E	D	20	E	1.1	17	35
3C7B	D E	D	23	K	2.2	17	35
3C7B	D E	D	27	L	1.0	17	35
3C7B	D E	D	55	Y	4.0	43	58
3C7B	D E	D	109	T	1.6	109	123
3C7B	D E	D	112	L	1.3	109	123
3C7B	D E	D	113	R	1.3	109	123
3C7B	D E	D	120	E	1.6	109	123
3C7B	D E	D	150	F	1.3	146	155
3C7B	D E	D	193	Y	2.9	188	199
3C7B	D E	D	290	H	2.5	290	295
3C7B	D E	D	294	K	1.5	290	295
3C7B	D E	D	366	W	3.2	361	369
3C7B	D E	E	64	I	1.5	64	78
3C7B	D E	E	65	Y	4.0	64	78
3C7B	D E	E	66	T	1.3	64	78
3C7B	D E	E	67	V	1.0	64	78
3C7B	D E	E	68	R	1.9	64	78
3C7B	D E	E	69	E	1.4	64	78
3C7B	D E	E	75	D	1.1	64	78
3C7B	D E	E	149	G	162.2	147	158
3C7B	D E	E	159	Y	1.8	159	163
3C7B	D E	E	162	F	1.0	159	163
3C7B	D E	E	355	Y	2.7	353	357
3C7K	A B	A	86	R	1.0	70	92
3C7K	A B	A	211	K	1.3	208	215
3C7K	A B	B	133	H	1.6	133	144
3C7K	C D	C	86	R	1.2	68	92
3C7K	C D	D	134	E	1.2	133	145
3C7K	C D	D	165	D	1.1	164	169
3C7N	A B	A	579	Y	1.8	569	583
3C7N	A B	B	134	Y	1.7	123	136
3C7N	A B	B	262	R	2.1	257	274
3C8G	C B	C	49	I	1.8	47	54
3C8G	C B	C	73	L	1.0	67	77
3C8G	C B	C	75	Y	1.9	67	77
3C8G	C B	B	75	Y	1.6	67	77
3C8G	C D	D	154	T	2.6	153	168
3C8K	A D	D	221	K	1.2	218	226

3C91	A H	A	100	K	1.6	82	104
3C91	A H	A	101	V	1.1	82	104
3C91	A H	H	64	E	1.2	49	70
3C91	A H	H	65	L	1.4	49	70
3C91	A H	H	67	R	1.1	49	70
3C91	B I	B	101	V	1.3	82	104
3C91	C J	C	93	R	1.3	82	104
3C91	C J	C	100	K	1.4	82	104
3C91	C J	C	101	V	1.3	82	104
3C91	C J	J	65	L	1.6	49	70
3C91	D K	D	100	K	1.0	82	104
3C91	E L	E	93	R	2.6	82	104
3C91	E L	E	94	I	2.1	82	104
3C91	E L	E	100	K	2.6	82	104
3C91	E L	E	101	V	1.4	82	104
3C91	E L	L	61	A	2.2	49	70
3C91	E L	L	64	E	2.8	49	70
3C91	E L	L	67	R	1.9	49	70
3C91	F M	M	65	L	1.5	49	70
3C91	F N	N	69	Q	1.0	49	70
3C91	G H	G	99	E	102.8	82	104
3C91	G N	G	93	R	1.1	82	104
3C91	G N	G	100	K	1.0	82	104
3C91	G N	N	65	L	1.5	49	70
3C91	G N	N	67	R	1.0	49	70
3C91	G N	N	68	L	1.4	49	70
3C91	O V	O	100	K	1.6	82	104
3C91	O V	O	101	V	1.1	82	104
3C91	O V	V	65	L	1.4	49	70
3C91	O V	V	67	R	1.1	49	70
3C91	O W	O	99	E	3.4	82	104
3C91	O W	W	85	N	2.9	76	90
3C91	P W	P	93	R	2.4	82	104
3C91	P W	P	100	K	1.6	82	104
3C91	P W	P	101	V	1.3	82	104
3C91	P W	W	65	L	2.4	49	70
3C91	P X	X	62	E	6.8	49	70
3C91	P X	X	69	Q	1.0	49	70
3C91	Q X	Q	93	R	1.0	82	104
3C91	Q X	Q	100	K	1.4	82	104
3C91	Q X	X	65	L	1.5	49	70
3C91	R Y	R	100	K	1.0	82	104
3C91	S Z	S	101	V	1.4	82	104
3C91	U V	U	99	E	2.4	82	104
3C98	A B	A	38	M	1.2	35	44
3C98	A B	A	39	R	1.2	35	44
3C98	A B	A	115	F	1.4	112	120
3C98	A B	A	338	Q	1.4	338	359
3C98	A B	B	34	F	1.4	31	63
3C98	A B	B	115	I	1.0	111	157
3C98	A B	B	216	F	1.7	213	227
3C98	A B	B	220	A	1.1	213	227
3C98	A B	B	224	E	1.1	213	227
3C98	A B	B	233	I	2.8	233	239
3C98	A B	B	234	E	7.5	233	239
3C9A	A C	C	58	F	2.0	56	63
3C9A	A C	C	61	W	2.4	56	63
3C9A	B D	D	58	F	2.2	56	63
3C9A	B D	D	61	W	2.8	56	63
3CBJ	A B	A	181	L	1.1	178	182

3CDG	A J	A	65	R	1.9	57	85
3CDG	A J	A	69	D	1.4	57	85
3CDG	A K	A	162	D	1.2	152	175
3CDG	C E	C	72	Q	1.1	57	85
3CDG	C E	C	75	R	1.6	57	85
3CDG	C E	C	79	R	1.1	57	85
3CDG	E F	F	169	I	1.2	161	170
3CDK	A B	A	103	G	108.6	102	114
3CDK	A B	B	89	F	2.0	85	94
3CDK	A B	B	131	D	1.3	129	136
3CDK	A D	A	113	G	1.8	102	114
3CDK	C D	C	91	L	1.6	84	93
3CDK	C D	C	103	G	26.1	102	114
3CDK	C D	C	107	E	1.7	102	114
3CDK	C D	C	179	I	1.0	177	184
3CF4	A G	A	99	K	1.6	98	132
3CF4	A G	A	425	L	1.9	422	426
3CF4	A G	A	435	E	1.1	433	442
3CF4	A G	A	657	H	1.5	656	660
3CF4	A G	A	704	E	1.5	702	714
3CF4	A G	G	88	H	3.1	87	95
3CF4	A G	G	92	F	2.8	87	95
3CF4	A G	G	93	Y	1.8	87	95
3CF4	A G	G	119	F	2.9	118	131
3CF4	A G	G	120	Y	3.7	118	131
3CF4	A G	G	156	K	1.2	156	169
3CF6	E R	E	799	L	1.0	793	815
3CF6	E R	E	879	E	1.5	870	882
3CF6	E R	E	915	F	1.3	906	920
3CF6	E R	E	919	G	63.1	906	920
3CF6	E R	R	67	M	1.2	65	75
3CF6	E R	R	70	L	1.5	65	75
3CF6	E R	R	71	Y	1.7	65	75
3CF6	E R	R	73	K	1.4	65	75
3CFA	L A	L	55	F	3.9	55	60
3CFA	L A	L	57	I	2.2	55	60
3CFA	L A	A	81	K	1.1	79	84
3CFA	M B	M	55	F	3.8	55	60
3CFA	M B	M	57	I	2.1	55	60
3CFA	R G	R	55	F	3.8	55	60
3CFA	R G	R	57	I	1.9	55	60
3CFA	S H	S	55	F	5.3	55	60
3CFA	S H	S	57	I	2.5	55	60
3CFB	A B	A	124	Q	1.7	122	127
3CFB	L H	L	124	Q	1.0	122	127
3CFD	A B	A	123	E	1.1	122	128
3CFD	A B	A	124	Q	2.4	122	128
3CFD	L H	L	124	Q	1.1	122	128
3CFI	A B	A	38	M	1.0	35	54
3CFI	A B	A	46	N	2.1	35	54
3CFI	A B	A	53	L	1.3	35	54
3CFI	D E	D	35	E	1.4	33	54
3CFI	D E	D	39	F	2.4	33	54
3CFI	D E	D	46	N	2.6	33	54
3CFI	D E	D	53	L	1.7	33	54
3CFI	D E	E	41	L	1.9	34	57
3CFI	G H	G	35	E	2.3	33	54
3CFI	G H	G	39	F	2.0	33	54
3CFI	G H	G	46	N	2.2	33	54
3CFI	G H	H	37	R	1.0	33	57

3CFI	G H	H	41	L	1.5	33	57
3CFI	J K	J	35	E	1.6	33	54
3CFI	J K	J	38	M	1.5	33	54
3CFI	J K	J	39	F	3.2	33	54
3CFI	J K	J	42	M	2.9	33	54
3CFI	J K	J	46	N	2.1	33	54
3CFI	J K	K	41	L	1.4	33	57
3CFI	J K	K	48	L	2.4	33	57
3CFK	A B	A	124	Q	1.5	122	128
3CFK	A K	A	126	K	1.0	122	128
3CFK	E D	E	126	K	1.1	122	128
3CFK	G I	G	124	Q	1.5	122	128
3CFK	J B	J	126	K	1.6	122	128
3CFK	L H	L	124	Q	1.1	122	128
3CFV	A F	A	30	L	2.6	10	31
3CFV	A F	F	34	I	1.6	31	40
3CFV	A F	F	35	R	2.4	31	40
3CFV	A F	F	37	L	1.1	31	40
3CFV	B E	B	30	L	2.9	10	31
3CFV	B E	B	407	I	1.2	405	409
3CFV	B E	E	34	I	1.2	31	39
3CFV	B E	E	35	R	1.8	31	39
3CFV	B E	E	37	L	1.3	31	39
3CHW	A P	A	372	R	2.1	367	374
3CHW	A P	P	59	Y	1.8	56	62
3CHW	A P	P	120	G	5.4	120	137
3CHW	A P	P	121	G	3.3	120	137
3CHW	A P	P	125	K	1.7	120	137
3CHW	P V	P	3	W	3.6	3	11
3CHW	P V	P	6	Y	2.8	3	11
3CHW	P V	P	130	M	1.0	120	137
3CHW	P V	P	133	H	1.4	120	137
3CHX	A B	A	192	I	2.2	192	197
3CHX	A B	A	195	I	2.4	192	197
3CHX	A B	A	243	G	55.4	239	253
3CHX	A B	A	251	I	1.2	239	253
3CHX	A B	A	258	Y	5.5	254	261
3CHX	A B	B	31	L	1.4	25	36
3CHX	A B	B	106	W	2.3	93	110
3CHX	A B	B	131	V	1.4	129	135
3CHX	A B	B	134	L	1.1	129	135
3CHX	A B	B	166	W	1.6	166	170
3CHX	A B	B	185	L	1.5	185	192
3CHX	A B	B	188	L	6.8	185	192
3CHX	B C	B	40	G	47.2	37	50
3CHX	B C	B	43	H	1.4	37	50
3CHX	B C	B	104	G	1.8	93	110
3CHX	B C	C	131	T	2.4	130	134
3CHX	B C	C	145	S	1.4	144	148
3CHX	E F	E	192	I	2.2	192	197
3CHX	E F	E	195	I	1.3	192	197
3CHX	E F	E	243	G	55.5	239	253
3CHX	E F	E	251	I	1.2	239	253
3CHX	E F	E	258	Y	1.4	254	261
3CHX	E F	F	106	W	1.1	93	110
3CHX	E F	F	131	V	1.4	129	135
3CHX	E F	F	134	L	1.1	129	135
3CHX	E F	F	166	W	1.6	166	170
3CHX	E F	F	185	L	1.5	185	192
3CHX	F G	F	40	G	47.3	37	50

3CHX	F G	F	43	H	1.4	37	50
3CHX	F G	F	104	G	1.8	93	110
3CHX	F G	G	131	T	2.4	130	134
3CHX	F G	G	145	S	1.4	144	148
3CHX	I J	I	192	I	2.2	192	197
3CHX	I J	I	195	I	2.2	192	197
3CHX	I J	I	243	G	56.1	239	253
3CHX	I J	I	251	I	1.2	239	253
3CHX	I J	I	258	Y	1.4	254	261
3CHX	I J	J	102	L	1.5	93	110
3CHX	I J	J	106	W	2.1	93	110
3CHX	I J	J	131	V	1.4	129	135
3CHX	I J	J	134	L	1.1	129	135
3CHX	I J	J	166	W	1.6	166	170
3CHX	J K	J	40	G	47.3	37	50
3CHX	J K	J	43	H	1.4	37	50
3CHX	J K	J	104	G	1.8	93	110
3CHX	J K	K	131	T	2.4	130	134
3CHX	J K	K	133	H	1.0	130	134
3CHX	J K	K	145	S	1.4	144	148
3CI0	I J	I	42	W	2.6	32	53
3CI0	I J	I	46	N	2.1	32	53
3CI0	I J	I	52	Y	1.2	32	53
3CI0	I K	I	52	Y	2.0	32	53
3CI0	I K	K	42	W	3.5	30	59
3CI0	J K	K	155	D	1.9	155	160
3CI0	J K	K	177	E	1.4	175	180
3CI0	J K	K	179	R	1.1	175	180
3CIP	A G	A	143	Y	1.6	137	145
3CIP	A G	A	345	I	2.9	338	349
3CIP	A G	A	361	E	2.0	359	366
3CIP	A G	G	71	Q	1.9	71	88
3CIP	A G	G	75	G	55.3	71	88
3CIP	A G	G	79	I	3.4	71	88
3CIP	A G	G	80	F	2.3	71	88
3CIP	A G	G	82	V	1.1	71	88
3CJB	A G	A	143	Y	1.2	137	145
3CJB	A G	A	345	I	2.7	338	349
3CJB	A G	G	71	Q	1.8	71	88
3CJB	A G	G	75	G	26.8	71	88
3CJB	A G	G	79	I	1.7	71	88
3CJB	A G	G	82	V	1.0	71	88
3CJC	A D	D	49	G	4.4	46	56
3CJC	A D	D	53	D	1.3	46	56
3CJC	A G	A	143	Y	1.2	137	145
3CJC	A G	A	345	I	2.1	338	348
3CJH	A B	A	61	C	2.6	47	62
3CJH	A B	A	81	Y	3.0	71	96
3CJH	A B	A	87	V	1.1	71	96
3CJH	A B	A	92	Y	1.9	71	96
3CJH	A B	B	37	I	1.2	30	49
3CJH	A B	B	45	F	3.5	30	49
3CJH	A B	B	61	E	1.1	59	86
3CJH	A D	A	58	F	1.6	47	62
3CJH	A D	A	59	E	1.0	47	62
3CJH	A D	A	74	I	1.4	71	96
3CJH	A D	A	78	L	2.2	71	96
3CJH	A D	D	71	R	1.8	59	83
3CJH	A D	D	72	F	1.4	59	83
3CJH	A D	D	78	R	1.3	59	83

3CJH	A D	D	79	I	2.7	59	83
3CJH	A D	D	82	G	1.5	59	83
3CJH	C D	C	60	K	1.0	48	62
3CJH	C D	C	61	C	1.4	48	62
3CJH	C D	C	76	Q	1.8	71	94
3CJH	C D	C	81	Y	2.5	71	94
3CJH	C D	C	85	W	1.9	71	94
3CJH	C D	C	92	Y	1.6	71	94
3CJH	C D	D	37	I	2.6	30	49
3CJH	C D	D	38	H	2.0	30	49
3CJH	C D	D	45	F	3.3	30	49
3CJH	C J	C	60	K	1.6	48	62
3CJH	E B	E	50	V	1.0	47	62
3CJH	E B	E	58	F	2.6	47	62
3CJH	E B	E	74	I	1.3	71	94
3CJH	E B	E	78	L	1.8	71	94
3CJH	E B	B	47	K	1.1	30	49
3CJH	E B	B	67	N	1.5	59	86
3CJH	E B	B	72	F	2.6	59	86
3CJH	E B	B	78	R	1.0	59	86
3CJH	E B	B	79	I	2.5	59	86
3CJH	E B	B	82	G	4.7	59	86
3CJH	E B	B	83	L	1.2	59	86
3CJH	G H	G	81	Y	2.4	71	95
3CJH	G H	G	87	V	1.2	71	95
3CJH	G H	G	92	Y	2.2	71	95
3CJH	G H	H	37	I	1.6	30	49
3CJH	G H	H	45	F	3.0	30	49
3CJH	G H	H	61	E	1.0	59	86
3CJH	G J	G	54	S	1.2	47	62
3CJH	G J	G	58	F	1.7	47	62
3CJH	G J	G	74	I	1.8	71	95
3CJH	G J	G	78	L	2.2	71	95
3CJH	G J	J	47	K	1.1	30	49
3CJH	G J	J	72	F	1.7	59	84
3CJH	G J	J	76	N	1.0	59	84
3CJH	G J	J	78	R	1.2	59	84
3CJH	G J	J	79	I	2.7	59	84
3CJH	G J	J	82	G	1.7	59	84
3CJH	G J	J	83	L	1.7	59	84
3CJH	I D	I	60	K	1.3	48	62
3CJH	I J	I	81	Y	2.3	71	94
3CJH	I J	I	85	W	2.1	71	94
3CJH	I J	I	92	Y	1.6	71	94
3CJH	I J	J	37	I	2.8	30	49
3CJH	I J	J	38	H	2.1	30	49
3CJH	I J	J	45	F	3.4	30	49
3CJH	I L	I	50	V	1.4	48	62
3CJH	I L	I	53	I	1.1	48	62
3CJH	I L	I	58	F	3.3	48	62
3CJH	I L	I	71	D	1.8	71	94
3CJH	I L	I	74	I	1.2	71	94
3CJH	I L	I	78	L	1.8	71	94
3CJH	I L	L	67	N	1.9	59	86
3CJH	I L	L	72	F	3.1	59	86
3CJH	I L	L	75	T	1.2	59	86
3CJH	I L	L	78	R	1.9	59	86
3CJH	I L	L	79	I	3.1	59	86
3CJH	I L	L	82	G	6.1	59	86
3CJH	I L	L	83	L	1.4	59	86

3CJH	K H	K	50	V	1.0	47	62
3CJH	K H	K	58	F	2.7	47	62
3CJH	K H	K	74	I	1.3	71	96
3CJH	K H	K	78	L	1.7	71	96
3CJH	K H	H	67	N	1.2	59	86
3CJH	K H	H	71	R	1.7	59	86
3CJH	K H	H	72	F	2.6	59	86
3CJH	K H	H	78	R	1.5	59	86
3CJH	K H	H	79	I	2.3	59	86
3CJH	K H	H	82	G	4.3	59	86
3CJH	K H	H	83	L	1.2	59	86
3CJH	K L	K	81	Y	2.6	71	96
3CJH	K L	K	87	V	1.2	71	96
3CJH	K L	K	92	Y	2.1	71	96
3CJH	K L	L	38	H	1.1	30	49
3CJH	K L	L	41	T	1.1	30	49
3CJH	K L	L	45	F	3.8	30	49
3CJI	A B	A	33	V	2.1	33	37
3CJI	A B	A	36	L	1.0	33	37
3CJI	A B	A	108	F	1.6	108	113
3CJI	A B	B	44	L	2.2	44	50
3CJI	A C	C	168	R	1.7	165	170
3CJI	A D	A	35	F	1.0	33	37
3CJI	B D	B	46	Q	1.2	44	50
3CJK	A B	A	14	G	27.5	13	27
3CJK	A B	A	21	R	1.3	13	27
3CJS	A B	A	21	F	2.2	17	23
3CJS	A B	B	22	P	1.9	22	30
3CJT	A B	A	21	F	3.1	17	24
3CJT	A B	A	59	W	4.5	59	66
3CJT	A B	A	63	W	3.5	59	66
3CJT	A B	B	22	P	2.4	22	30
3CJT	A B	B	24	G	87.9	22	30
3CJT	A B	B	25	P	1.5	22	30
3CJT	C D	C	21	F	2.6	14	23
3CJT	C D	C	59	W	4.4	56	60
3CJT	C D	C	63	W	1.8	62	67
3CJT	C D	D	22	P	1.7	22	29
3CJT	C D	D	24	G	30.7	22	29
3CJT	C D	D	25	P	1.0	22	29
3CJT	C D	D	28	G	46.6	22	29
3CJT	E F	E	18	P	1.0	14	23
3CJT	E F	E	21	F	2.6	14	23
3CJT	E F	E	59	W	2.8	59	67
3CJT	E F	E	63	W	1.7	59	67
3CJT	E F	F	22	P	2.3	22	30
3CJT	E F	F	24	G	130.1	22	30
3CJT	E F	F	25	P	1.5	22	30
3CJT	E F	F	34	I	1.1	34	45
3CJT	G H	G	21	F	3.0	17	23
3CJT	G H	G	59	W	3.5	56	60
3CJT	G H	H	22	P	1.9	22	30
3CJT	G H	H	24	G	35.6	22	30
3CJT	G H	H	25	P	1.0	22	30
3CJT	G H	H	28	G	100.5	22	30
3CJT	I J	I	18	P	1.0	17	24
3CJT	I J	I	21	F	2.6	17	24
3CJT	I J	I	22	D	1.1	17	24
3CJT	I J	I	59	W	4.7	59	66
3CJT	I J	I	60	L	1.8	59	66

3CJT	I J	I	63	W	2.9	59	66
3CJT	I J	J	22	P	2.2	22	30
3CJT	I J	J	24	G	108.4	22	30
3CJT	I J	J	25	P	1.6	22	30
3CJT	I J	J	34	I	1.1	34	45
3CJT	I J	J	79	R	1.0	74	82
3CJT	K L	K	21	F	2.9	14	24
3CJT	K L	K	59	W	4.3	56	60
3CJT	K L	K	63	W	1.2	62	67
3CJT	K L	L	22	P	1.7	22	30
3CJT	K L	L	24	G	31.7	22	30
3CJT	K L	L	28	G	10.2	22	30
3CJT	K L	L	34	I	1.2	34	45
3CJT	M N	M	18	P	1.0	17	24
3CJT	M N	M	21	F	2.8	17	24
3CJT	M N	M	59	W	4.5	59	67
3CJT	M N	M	60	L	2.1	59	67
3CJT	M N	M	63	W	2.4	59	67
3CJT	M N	N	24	G	129.8	23	30
3CJT	M N	N	25	P	1.6	23	30
3CJT	M N	N	34	I	1.2	34	45
3CJT	O P	O	21	F	2.3	17	24
3CJT	O P	O	59	W	4.0	56	60
3CJT	O P	P	22	P	2.1	22	30
3CJT	O P	P	24	G	29.0	22	30
3CJT	O P	P	28	G	63.5	22	30
3CK4	A B	A	6	L	2.1	2	31
3CK4	A B	A	13	L	1.6	2	31
3CK4	A B	A	23	E	1.1	2	31
3CK4	A B	A	24	V	1.1	2	31
3CK4	A B	A	26	R	2.1	2	31
3CK4	A B	A	27	L	2.1	2	31
3CK4	A B	B	3	V	1.4	3	32
3CK4	A B	B	6	L	1.6	3	32
3CK4	A B	B	10	V	1.1	3	32
3CK4	A B	B	13	L	1.3	3	32
3CK4	A B	B	24	V	1.1	3	32
3CK4	A B	B	27	L	1.8	3	32
3CK4	A B	B	31	V	1.4	3	32
3CK4	D C	D	6	L	1.6	3	34
3CK4	D C	D	10	V	1.0	3	34
3CK4	D C	D	13	L	2.0	3	34
3CK4	D C	D	20	L	1.3	3	34
3CK4	D C	D	23	E	1.2	3	34
3CK4	D C	D	24	V	1.1	3	34
3CK4	D C	D	26	R	1.5	3	34
3CK4	D C	D	27	L	2.2	3	34
3CK4	D C	C	3	V	1.0	2	31
3CK4	D C	C	6	L	2.0	2	31
3CK4	D C	C	10	V	1.2	2	31
3CK4	D C	C	13	L	1.5	2	31
3CK4	D C	C	20	L	1.8	2	31
3CK4	D C	C	24	V	1.5	2	31
3CK4	D C	C	27	L	1.9	2	31
3CK4	E F	E	6	L	2.4	3	31
3CK4	E F	E	13	L	1.1	3	31
3CK4	E F	E	20	L	1.2	3	31
3CK4	E F	E	23	E	1.8	3	31
3CK4	E F	E	24	V	1.2	3	31
3CK4	E F	E	26	R	2.6	3	31

3CK4	E F	E	27	L	2.2	3	31
3CK4	E F	F	3	V	1.1	2	31
3CK4	E F	F	6	L	1.8	2	31
3CK4	E F	F	10	V	1.2	2	31
3CK4	E F	F	24	V	1.0	2	31
3CK4	E F	F	27	L	1.9	2	31
3CK4	H G	H	6	L	2.9	3	31
3CK4	H G	H	13	L	1.6	3	31
3CK4	H G	H	20	L	3.0	3	31
3CK4	H G	H	24	V	1.3	3	31
3CK4	H G	H	26	R	1.3	3	31
3CK4	H G	H	27	L	2.3	3	31
3CK4	H G	G	6	L	1.5	2	31
3CK4	H G	G	10	V	1.1	2	31
3CK4	H G	G	13	L	1.3	2	31
3CK4	H G	G	20	L	1.4	2	31
3CK4	H G	G	27	L	1.9	2	31
3CK4	I J	I	2	K	1.0	2	31
3CK4	I J	I	6	L	2.6	2	31
3CK4	I J	I	13	L	2.0	2	31
3CK4	I J	I	20	L	1.6	2	31
3CK4	I J	I	23	E	2.2	2	31
3CK4	I J	I	24	V	1.2	2	31
3CK4	I J	I	26	R	2.8	2	31
3CK4	I J	I	27	L	2.6	2	31
3CK4	I J	J	3	V	1.2	2	31
3CK4	I J	J	6	L	2.3	2	31
3CK4	I J	J	10	V	1.2	2	31
3CK4	I J	J	13	L	1.0	2	31
3CK4	I J	J	24	V	1.5	2	31
3CK4	I J	J	27	L	1.6	2	31
3CK4	I J	J	28	K	1.2	2	31
3CK4	L K	L	6	L	1.0	2	31
3CK4	L K	L	9	K	1.1	2	31
3CK4	L K	L	13	L	2.2	2	31
3CK4	L K	L	20	L	1.3	2	31
3CK4	L K	L	23	E	1.3	2	31
3CK4	L K	L	26	R	2.2	2	31
3CK4	L K	L	27	L	2.4	2	31
3CK4	L K	K	6	L	1.2	3	31
3CK4	L K	K	10	V	2.0	3	31
3CK4	L K	K	20	L	1.6	3	31
3CK4	L K	K	24	V	1.5	3	31
3CK4	L K	K	27	L	1.7	3	31
3CL3	A D	A	83	H	1.7	77	85
3CL3	A D	D	234	Y	1.4	195	247
3CL3	A D	D	238	F	2.9	195	247
3CL3	A D	D	245	I	1.0	195	247
3CL3	A E	E	226	K	1.1	197	248
3CL3	B E	E	238	F	2.4	197	248
3CLE	L H	L	124	Q	1.5	122	127
3CM8	A B	A	408	Q	2.9	405	415
3CM8	A B	A	412	N	1.8	405	415
3CM8	A B	A	636	V	1.3	633	650
3CM8	A B	A	666	L	1.6	653	674
3CM8	A B	A	706	W	2.4	698	715
3CM8	A B	A	710	F	2.3	698	715
3CM8	A B	B	6	P	1.7	6	10
3CM8	A B	B	8	L	1.6	6	10
3CM8	A B	B	9	L	2.5	6	10

3CMA	A Z	Z	49	R	1.5	48	59
3CMA	A Z	Z	54	E	1.2	48	59
3CMA	A Z	Z	100	G	103.2	98	105
3CMA	A Z	Z	103	V	1.1	98	105
3CMA	F M	F	34	N	1.3	33	42
3CMA	F M	F	57	E	1.7	57	69
3CMA	F M	F	62	H	2.0	57	69
3CMA	F M	M	7	Y	2.7	4	12
3CMA	F M	M	8	I	1.4	4	12
3CMA	F M	M	46	L	1.2	46	52
3CMA	K U	U	37	E	1.1	34	42
3CMA	N Q	N	24	L	1.0	20	30
3CMA	S V	V	28	L	1.1	13	36
3CMO	L H	L	124	Q	1.1	122	127
3CPH	G A	G	248	R	3.5	239	253
3CPH	G A	G	252	I	1.3	239	253
3CPJ	G B	G	244	Q	1.2	239	253
3CPJ	G B	B	80	S	1.1	80	84
3CQC	A B	A	897	L	1.2	894	914
3CQC	A B	A	901	L	1.7	894	914
3CQC	A B	A	902	Q	1.0	894	914
3CQC	A B	B	937	W	1.3	936	943
3CQC	A B	B	938	L	1.4	936	943
3CQC	A B	B	966	K	1.1	964	981
3CQC	A B	B	972	G	9.6	964	981
3CQC	A B	B	973	L	1.5	964	981
3CQC	A B	B	976	L	2.9	964	981
3CQG	A B	A	898	R	2.2	894	913
3CQG	A B	A	901	L	2.1	894	913
3CQG	A B	B	938	L	1.3	936	943
3CQG	A B	B	966	K	3.0	964	980
3CQG	A B	B	970	L	1.2	964	980
3CQG	A B	B	972	G	3.1	964	980
3CQG	A B	B	976	L	1.6	964	980
3CQX	A D	A	57	N	1.2	53	58
3CQX	A D	A	258	R	2.7	257	274
3CQX	A D	A	262	R	1.0	257	274
3CQX	A D	A	265	T	1.8	257	274
3CQX	A D	D	156	Q	2.1	153	161
3CQX	A D	D	160	I	1.6	153	161
3CQX	A D	D	167	Q	2.7	164	188
3CQX	B C	B	258	R	3.7	257	274
3CQX	B C	B	265	T	1.1	257	274
3CQX	B C	C	156	Q	1.6	153	162
3CQX	B C	C	160	I	2.8	153	162
3CQX	B C	C	164	L	1.1	164	187
3CQX	B C	C	167	Q	1.9	164	187
3CR3	A C	A	114	R	2.2	100	115
3CR3	A D	A	161	R	1.0	161	165
3CR3	A D	A	164	Y	1.3	161	165
3CR3	A D	D	97	Y	2.3	92	105
3CR3	B C	B	164	Y	2.4	161	165
3CR3	B C	C	97	Y	2.2	92	105
3CR3	B D	B	114	R	1.7	100	115
3CRP	A B	A	6	L	1.4	2	30
3CRP	A B	A	13	L	1.9	2	30
3CRP	A B	A	20	L	2.3	2	30
3CRP	A B	A	23	E	1.7	2	30
3CRP	A B	A	24	V	1.1	2	30
3CRP	A B	A	26	R	2.5	2	30

3CRP	A B	A	27	L	2.2	2	30
3CRP	A B	B	6	L	1.5	2	32
3CRP	A B	B	10	V	1.2	2	32
3CRP	A B	B	13	L	1.7	2	32
3CRP	A B	B	24	V	1.6	2	32
3CRP	A B	B	27	L	1.5	2	32
3CRP	A B	B	31	V	1.4	2	32
3CRP	D C	D	6	L	2.5	2	32
3CRP	D C	D	13	L	1.8	2	32
3CRP	D C	D	20	L	2.3	2	32
3CRP	D C	D	23	E	1.3	2	32
3CRP	D C	D	24	V	1.3	2	32
3CRP	D C	D	27	L	1.4	2	32
3CRP	D C	C	6	L	1.6	2	31
3CRP	D C	C	10	V	1.5	2	31
3CRP	D C	C	13	L	1.7	2	31
3CRP	D C	C	20	L	1.0	2	31
3CRP	D C	C	24	V	1.5	2	31
3CSL	A C	A	744	S	1.3	742	746
3CSL	B D	B	744	S	1.3	742	746
3CSY	C N	N	556	C	1.2	554	576
3CSY	I J	J	557	G	1.2	554	576
3CSY	I J	J	561	L	1.1	554	576
3CSY	I J	J	567	Q	1.8	554	576
3CSY	I J	J	569	L	1.5	554	576
3CSY	I J	J	573	L	1.2	554	576
3CSY	I J	J	584	I	5.8	584	596
3CSY	I J	J	588	K	1.2	584	596
3CSY	I N	N	594	L	1.1	584	596
3CSY	K J	J	594	L	1.3	584	596
3CSY	K L	L	561	L	1.1	554	576
3CSY	K L	L	569	L	1.3	554	576
3CSY	K L	L	573	L	1.3	554	576
3CSY	K L	L	584	I	1.3	584	596
3CSY	K L	L	585	L	1.6	584	596
3CSY	M L	L	594	L	1.4	584	596
3CSY	M N	N	554	L	1.3	554	576
3CSY	M N	N	559	R	1.8	554	576
3CSY	M N	N	561	L	4.4	554	576
3CSY	M N	N	563	N	3.3	554	576
3CSY	M N	N	566	T	3.6	554	576
3CSY	M N	N	567	Q	3.2	554	576
3CSY	M N	N	568	A	3.2	554	576
3CSY	M N	N	569	L	2.6	554	576
3CSY	M N	N	573	L	1.5	554	576
3CSY	M N	N	585	L	1.7	584	596
3CSY	O P	P	561	L	1.8	557	576
3CSY	O P	P	569	L	2.2	557	576
3CSY	O P	P	573	L	1.3	557	576
3CSY	O P	P	584	I	1.9	582	596
3CSY	O P	P	585	L	2.6	582	596
3CSY	O P	P	588	K	1.8	582	596
3CUE	A C	C	51	L	1.0	36	58
3CUE	A D	A	186	Y	1.2	169	192
3CUE	A F	A	34	L	1.2	30	50
3CUE	A F	A	41	H	1.1	30	50
3CUE	B D	B	64	F	1.7	59	77
3CUE	B D	B	65	L	2.4	59	77
3CUE	B D	B	72	Q	1.1	59	77
3CUE	B D	B	73	L	2.6	59	77

3CUE	B D	B	90	Y	1.4	80	102
3CUE	B D	B	94	I	1.0	80	102
3CUE	B D	B	97	R	1.1	80	102
3CUE	B D	D	18	W	1.3	9	19
3CUE	B D	D	29	L	1.2	27	45
3CUE	B D	D	30	F	2.3	27	45
3CUE	B D	D	32	L	1.0	27	45
3CUE	C E	C	111	Y	1.5	100	116
3CUE	C E	E	70	D	5.2	49	76
3CUE	C E	E	72	L	1.0	49	76
3CUE	C F	C	42	K	1.2	36	58
3CUE	C F	C	46	G	77.5	36	58
3CUE	G J	G	180	R	1.1	169	192
3CUE	G J	G	186	Y	2.0	169	192
3CUE	G L	G	41	H	1.2	30	50
3CUE	H J	H	64	F	1.7	59	77
3CUE	H J	H	65	L	2.4	59	77
3CUE	H J	H	72	Q	1.1	59	77
3CUE	H J	H	90	Y	1.4	80	102
3CUE	H J	H	94	I	1.0	80	102
3CUE	H J	H	97	R	1.0	80	102
3CUE	H J	J	18	W	1.2	9	19
3CUE	H J	J	29	L	1.2	27	45
3CUE	H J	J	30	F	2.3	27	45
3CUE	H J	J	32	L	1.0	27	45
3CUE	I K	I	111	Y	1.4	100	116
3CUE	I K	K	70	D	7.0	49	76
3CUE	I K	K	72	L	1.2	49	76
3CUE	I L	I	42	K	1.3	36	58
3CUE	I L	I	46	G	94.6	36	58
3CUE	M R	M	41	H	1.2	30	50
3CUE	N P	N	64	F	1.7	59	77
3CUE	N P	N	65	L	2.4	59	77
3CUE	N P	N	72	Q	1.1	59	77
3CUE	N P	N	90	Y	1.4	80	102
3CUE	N P	P	18	W	1.2	9	19
3CUE	O Q	O	111	Y	1.2	100	116
3CUE	O Q	Q	70	D	6.2	49	76
3CUE	O R	O	46	G	90.5	36	58
3CUE	O W	O	113	K	8.3	100	116
3CUE	O W	W	28	E	7.1	27	45
3CUE	O W	W	31	T	1.0	27	45
3CUE	O W	W	32	L	2.8	27	45
3CUE	O W	W	35	G	1.4	27	45
3CUE	Q R	R	21	K	1.1	21	29
3CUE	S V	S	186	Y	1.6	169	192
3CUE	S V	V	154	M	1.5	142	155
3CUE	S X	S	34	L	1.2	30	50
3CUE	S X	S	35	I	3.6	30	50
3CUE	S X	S	38	S	4.1	30	50
3CUE	S X	S	41	H	1.3	30	50
3CUE	T V	T	62	M	2.0	59	77
3CUE	T V	T	64	F	1.3	59	77
3CUE	T V	T	65	L	2.4	59	77
3CUE	T V	T	72	Q	1.1	59	77
3CUE	T V	T	73	L	2.6	59	77
3CUE	T V	T	90	Y	1.3	80	102
3CUE	T V	T	94	I	1.8	80	102
3CUE	T V	T	97	R	1.1	80	102
3CUE	T V	V	18	W	1.2	9	19

3CUE	T V	V	29	L	1.2	27	45
3CUE	T V	V	30	F	2.3	27	45
3CUE	T V	V	32	L	1.0	27	45
3CUE	U Q	U	113	K	1.1	100	116
3CUE	U W	U	111	Y	1.2	100	116
3CUE	U W	W	70	D	6.1	49	76
3CUE	U W	W	72	L	1.3	49	76
3CUE	U X	U	42	K	1.7	36	58
3CUE	U X	U	46	G	81.4	36	58
3CUE	W X	X	21	K	1.0	21	29
3CUP	A B	A	58	G	172.1	56	77
3CUP	A B	A	69	N	1.6	56	77
3CUP	A B	A	70	L	1.2	56	77
3CUP	A B	A	76	R	1.7	56	77
3CUQ	A B	A	36	M	1.6	35	53
3CUQ	A B	A	43	F	1.5	35	53
3CUQ	A B	A	50	F	1.2	35	53
3CUQ	A B	A	64	F	1.1	62	76
3CUQ	A B	A	75	I	1.3	62	76
3CUQ	A B	A	87	W	1.3	86	92
3CUQ	A B	A	95	D	1.8	93	115
3CUQ	A B	A	98	Y	2.3	93	115
3CUQ	A B	A	102	V	1.4	93	115
3CUQ	A B	A	106	E	1.5	93	115
3CUQ	A B	A	218	K	1.7	206	219
3CUQ	A B	B	184	L	2.6	174	194
3CUQ	A B	B	185	M	1.2	174	194
3CUQ	A B	B	191	M	1.2	174	194
3CUQ	A B	B	220	Y	2.3	215	225
3CUQ	A B	B	270	Y	1.9	266	276
3CUQ	A B	B	275	R	1.8	266	276
3CUQ	A B	B	286	D	1.1	284	293
3CUQ	A C	A	114	R	1.2	93	115
3CUQ	A C	C	25	T	1.1	23	44
3CUQ	B C	C	23	V	1.0	23	44
3CUQ	B C	C	27	Q	1.0	23	44
3CUQ	B D	D	25	T	2.2	23	41
3CVH	A L	A	154	E	4.5	152	162
3CVH	A L	A	155	R	1.1	152	162
3CVH	A L	A	158	A	3.4	152	162
3CVH	H L	L	123	Q	1.5	121	126
3CVH	M Q	M	146	K	1.0	138	151
3CW2	A C	C	193	V	1.6	192	205
3CW2	A C	C	197	K	1.0	192	205
3CW2	A C	C	200	I	1.2	192	205
3CW2	A K	A	163	Y	2.8	159	171
3CW2	A K	K	13	R	1.5	8	15
3CW2	A K	K	14	L	1.0	8	15
3CW2	B D	D	193	V	1.4	193	202
3CW2	B D	D	197	K	2.0	193	202
3CW2	B D	D	200	I	1.1	193	202
3CW2	B L	B	156	K	1.0	156	170
3CW2	B L	B	163	Y	2.1	156	170
3CW2	B L	L	7	Y	2.4	6	13
3CW2	B L	L	11	L	2.3	6	13
3CW2	E G	G	192	G	75.5	192	203
3CW2	E G	G	197	K	2.7	192	203
3CW2	E M	E	163	Y	2.9	156	170
3CW2	E M	M	14	L	2.2	11	15
3CW2	E M	M	22	G	7.9	20	24

3CW2	F H	H	193	V	1.6	192	202
3CW2	F H	H	197	K	1.8	192	202
3CW2	F H	H	200	I	1.2	192	202
3CW2	F N	F	163	Y	1.4	160	165
3CWB	A B	A	4	Y	2.1	4	9
3CWB	A C	A	435	N	2.8	434	440
3CWB	A C	A	436	R	1.9	434	440
3CWB	A D	A	434	Y	2.0	434	440
3CWB	A E	A	138	L	1.2	138	143
3CWB	A E	A	152	Y	1.2	145	158
3CWB	B S	B	83	F	1.7	82	92
3CWB	B S	B	135	W	1.3	134	139
3CWB	C D	C	73	N	1.3	63	74
3CWB	C D	C	78	W	2.6	77	105
3CWB	C D	C	224	Y	1.6	224	244
3CWB	C D	C	225	Y	1.0	224	244
3CWB	C D	C	227	F	1.7	224	244
3CWB	C D	C	231	L	2.0	224	244
3CWB	C D	D	201	R	1.0	199	233
3CWB	C D	D	205	G	151.8	199	233
3CWB	C D	D	208	M	1.1	199	233
3CWB	C D	D	227	W	3.0	199	233
3CWB	C E	C	51	L	1.4	32	54
3CWB	C E	C	79	L	1.8	77	105
3CWB	C F	C	320	P	1.2	320	342
3CWB	C F	F	69	S	1.2	53	72
3CWB	C G	C	327	W	1.8	320	342
3CWB	C G	C	335	I	1.0	320	342
3CWB	C G	C	338	W	1.5	320	342
3CWB	C G	C	351	I	1.2	349	377
3CWB	C G	G	58	L	1.4	47	69
3CWB	C G	G	59	Y	1.9	47	69
3CWB	C G	G	66	F	1.3	47	69
3CWB	C R	C	164	W	1.3	159	167
3CWB	D E	D	211	I	1.0	199	233
3CWB	D E	D	215	L	1.0	199	233
3CWB	D E	D	218	L	1.5	199	233
3CWB	D G	D	225	H	1.1	199	233
3CWB	D H	D	28	R	1.9	24	35
3CWB	D H	H	59	F	5.0	55	77
3CWB	D J	D	203	R	1.5	199	233
3CWB	D J	D	206	L	1.2	199	233
3CWB	D J	D	207	K	1.4	199	233
3CWB	D J	J	35	F	3.2	17	47
3CWB	D J	J	40	D	1.2	17	47
3CWB	D J	J	43	F	2.8	17	47
3CWB	D J	J	52	W	3.5	52	58
3CWB	E J	E	34	G	63.3	29	60
3CWB	E J	E	37	Y	1.1	29	60
3CWB	E J	E	38	L	1.0	29	60
3CWB	E J	E	49	Y	2.3	29	60
3CWB	E J	J	6	L	1.4	5	14
3CWB	E J	J	10	Y	2.0	5	14
3CWB	E J	J	20	F	1.7	17	47
3CWB	E J	J	24	V	1.5	17	47
3CWB	E J	J	31	F	1.7	17	47
3CWB	G H	H	56	E	1.3	55	77
3CWB	N O	N	4	Y	1.3	4	9
3CWB	N O	N	60	E	1.6	55	62
3CWB	N P	N	332	D	1.7	331	348

3CWB	N R	N	152	Y	1.1	145	158
3CWB	O F	O	83	F	2.5	82	92
3CWB	O F	O	84	R	1.0	82	92
3CWB	O F	O	135	W	1.5	134	152
3CWB	O F	F	96	E	1.4	89	108
3CWB	O F	F	100	E	1.0	89	108
3CWB	O F	F	104	R	1.2	89	108
3CWB	P E	P	164	W	1.3	159	167
3CWB	P Q	P	71	C	1.1	63	74
3CWB	P Q	P	72	R	2.0	63	74
3CWB	P Q	P	224	Y	2.9	224	244
3CWB	P Q	P	225	Y	1.1	224	244
3CWB	P Q	P	227	F	3.1	224	244
3CWB	P Q	P	231	L	2.9	224	244
3CWB	P Q	Q	200	Q	1.4	199	233
3CWB	P Q	Q	205	G	98.2	199	233
3CWB	P Q	Q	219	L	2.2	199	233
3CWB	P Q	Q	222	M	1.6	199	233
3CWB	P Q	Q	223	K	1.3	199	233
3CWB	P Q	Q	226	K	3.4	199	233
3CWB	P Q	Q	227	W	3.0	199	233
3CWB	P R	P	51	L	1.5	32	54
3CWB	P R	P	79	L	1.5	77	105
3CWB	P S	P	320	P	1.1	320	342
3CWB	P T	P	327	W	1.8	320	342
3CWB	P T	P	335	I	1.2	320	342
3CWB	P T	P	338	W	1.4	320	342
3CWB	Q R	Q	218	L	1.7	199	233
3CWB	Q R	Q	221	Y	1.7	199	233
3CWB	Q R	R	39	V	1.3	29	60
3CWB	Q T	Q	225	H	1.2	199	233
3CWB	Q U	U	59	F	3.5	55	77
3CWB	Q W	W	52	W	3.4	52	58
3CWB	R W	R	30	E	2.0	29	60
3CWB	R W	R	34	G	84.2	29	60
3CWB	R W	R	37	Y	1.0	29	60
3CWB	R W	R	38	L	2.8	29	60
3CWB	R W	R	49	Y	1.7	29	60
3CWB	R W	W	10	Y	3.1	5	12
3CWB	R W	W	20	F	1.7	17	47
3CWB	R W	W	24	V	1.6	17	47
3CWB	R W	W	31	F	1.6	17	47
3CWZ	A B	B	742	L	1.4	718	749
3CWZ	A B	B	746	M	1.1	718	749
3CX6	A B	A	98	V	3.2	84	106
3CX6	A B	A	230	R	1.7	227	232
3CXE	A B	B	75	G	55.9	73	84
3CXH	A B	A	365	R	1.0	360	379
3CXH	A B	A	369	L	1.5	360	379
3CXH	A B	A	372	L	2.2	360	379
3CXH	A B	A	375	G	169.8	360	379
3CXH	A B	A	407	F	1.9	403	413
3CXH	A B	B	65	L	1.0	64	75
3CXH	A B	B	68	V	1.4	64	75
3CXH	A B	B	72	E	1.3	64	75
3CXH	A B	B	129	Y	1.9	116	136
3CXH	A B	B	320	Y	1.1	318	327
3CXH	A B	B	323	L	2.5	318	327
3CXH	A C	A	341	D	1.1	340	357
3CXH	A C	A	342	D	1.7	340	357

3CXH	A C	A	447	R	1.4	445	451
3CXH	A C	C	5	K	1.0	3	7
3CXH	A E	A	163	H	2.0	156	169
3CXH	B R	B	65	L	1.3	64	75
3CXH	B R	B	69	R	1.5	64	75
3CXH	B R	B	121	E	1.4	116	136
3CXH	B R	R	120	L	1.4	102	122
3CXH	C D	C	224	Y	2.4	224	247
3CXH	C D	C	225	F	1.2	224	247
3CXH	C D	C	231	V	1.6	224	247
3CXH	C D	C	234	F	3.3	224	247
3CXH	C D	C	238	L	2.2	224	247
3CXH	C D	C	245	F	2.6	224	247
3CXH	C D	C	246	Y	2.5	224	247
3CXH	C D	D	270	G	51.6	262	297
3CXH	C D	D	274	V	1.9	262	297
3CXH	C D	D	277	L	2.2	262	297
3CXH	C D	D	281	Y	2.1	262	297
3CXH	C D	D	288	K	1.6	262	297
3CXH	C D	D	292	W	4.5	262	297
3CXH	C E	C	49	F	2.3	32	53
3CXH	C E	E	78	F	2.5	51	83
3CXH	C G	C	320	V	1.0	320	341
3CXH	C G	C	375	N	2.0	347	381
3CXH	C G	C	376	V	1.3	347	381
3CXH	C G	C	377	L	1.8	347	381
3CXH	C G	C	378	F	3.1	347	381
3CXH	C G	C	379	Y	3.8	347	381
3CXH	C G	C	380	I	2.9	347	381
3CXH	C G	G	5	F	1.0	5	18
3CXH	C G	G	8	I	1.4	5	18
3CXH	C G	G	12	G	35.0	5	18
3CXH	C G	G	13	D	1.0	5	18
3CXH	C G	G	16	L	1.7	5	18
3CXH	C G	G	32	F	5.7	19	37
3CXH	C G	G	33	I	1.5	19	37
3CXH	C G	G	45	F	2.4	45	49
3CXH	C G	G	48	L	1.2	45	49
3CXH	C G	G	79	H	1.7	65	84
3CXH	C H	C	324	F	2.7	320	341
3CXH	C H	C	327	F	1.9	320	341
3CXH	C H	C	328	I	1.1	320	341
3CXH	C H	C	331	F	2.6	320	341
3CXH	C H	C	335	L	1.3	320	341
3CXH	C H	C	347	P	1.3	347	381
3CXH	C H	C	348	Y	3.1	347	381
3CXH	C H	C	351	M	2.0	347	381
3CXH	C H	H	58	Y	1.2	53	81
3CXH	C H	H	62	P	1.1	53	81
3CXH	C H	H	66	Y	3.4	53	81
3CXH	C H	H	69	W	3.5	53	81
3CXH	C H	H	70	W	2.8	53	81
3CXH	C H	H	73	G	10.1	53	81
3CXH	C H	H	89	L	1.3	83	93
3CXH	C P	C	142	W	1.3	138	151
3CXH	C P	C	288	K	1.5	288	309
3CXH	D E	D	283	L	1.8	262	297
3CXH	D E	D	290	F	1.0	262	297
3CXH	D E	E	66	L	2.0	51	83
3CXH	D F	D	249	K	2.0	244	260

3CXH	D F	F	98	Y	1.1	89	111
3CXH	D F	F	124	V	4.7	124	140
3CXH	D F	F	127	F	1.8	124	140
3CXH	D F	F	128	F	4.0	124	140
3CXH	D F	F	135	D	1.3	124	140
3CXH	D F	F	143	F	7.1	141	145
3CXH	D H	D	290	F	2.2	262	297
3CXH	D I	D	87	H	1.2	87	105
3CXH	D I	D	268	R	1.7	262	297
3CXH	D I	D	271	L	2.1	262	297
3CXH	D I	D	272	K	3.0	262	297
3CXH	D I	D	276	I	1.0	262	297
3CXH	D I	I	32	F	5.1	18	44
3CXH	D I	I	33	D	1.7	18	44
3CXH	D I	I	36	I	1.5	18	44
3CXH	D I	I	39	W	1.4	18	44
3CXH	D I	I	40	Y	3.9	18	44
3CXH	D I	I	43	H	1.6	18	44
3CXH	D I	I	49	W	5.0	49	56
3CXH	E H	E	51	K	1.3	51	83
3CXH	E I	E	57	Y	1.4	51	83
3CXH	E I	E	65	L	1.6	51	83
3CXH	E I	I	7	Y	2.6	5	11
3CXH	E I	I	28	F	1.1	18	44
3CXH	F H	F	125	E	1.1	124	140
3CXH	G H	G	69	Y	1.8	65	84
3CXH	G H	G	73	Y	1.4	65	84
3CXH	L G	L	301	K	1.1	301	309
3CXH	L M	L	407	F	1.4	403	413
3CXH	L M	M	68	V	1.1	64	75
3CXH	L M	M	129	Y	2.5	116	137
3CXH	L M	M	320	Y	1.5	318	326
3CXH	L M	M	323	L	1.9	318	326
3CXH	L N	L	341	D	1.5	340	357
3CXH	L N	L	342	D	2.3	340	357
3CXH	L N	N	5	K	1.7	3	7
3CXH	L P	L	163	H	2.2	156	169
3CXH	L S	L	445	Y	1.2	445	451
3CXH	L T	T	18	V	1.5	18	44
3CXH	L T	T	19	G	1.1	18	44
3CXH	L T	T	22	F	1.5	18	44
3CXH	M G	M	65	L	1.4	64	75
3CXH	M G	M	69	R	1.3	64	75
3CXH	M G	M	117	H	1.1	116	137
3CXH	M G	G	62	R	1.8	54	63
3CXH	M G	G	120	L	1.4	102	122
3CXH	N E	N	164	W	1.8	158	167
3CXH	N E	N	174	P	1.5	173	205
3CXH	N E	N	288	K	1.5	288	309
3CXH	N O	N	76	Y	2.1	75	103
3CXH	N O	N	224	Y	2.2	224	247
3CXH	N O	N	225	F	1.1	224	247
3CXH	N O	N	231	V	1.7	224	247
3CXH	N O	N	234	F	1.3	224	247
3CXH	N O	N	235	L	1.0	224	247
3CXH	N O	N	238	L	2.1	224	247
3CXH	N O	N	245	F	2.4	224	247
3CXH	N O	N	246	Y	2.4	224	247
3CXH	N O	O	266	R	2.2	263	292
3CXH	N O	O	270	G	53.2	263	292

3CXH	N O	O	274	V	1.4	263	292
3CXH	N O	O	277	L	2.1	263	292
3CXH	N O	O	281	Y	2.4	263	292
3CXH	N O	O	288	K	1.5	263	292
3CXH	N O	O	295	I	1.1	293	297
3CXH	N P	N	49	F	1.9	32	53
3CXH	N P	N	67	H	1.0	61	72
3CXH	N P	P	78	F	1.6	51	82
3CXH	N R	N	375	N	1.8	346	381
3CXH	N R	N	376	V	1.2	346	381
3CXH	N R	N	377	L	1.4	346	381
3CXH	N R	N	378	F	2.7	346	381
3CXH	N R	N	379	Y	4.3	346	381
3CXH	N R	N	380	I	1.9	346	381
3CXH	N R	R	12	G	75.6	5	18
3CXH	N R	R	13	D	1.1	5	18
3CXH	N R	R	16	L	2.2	5	18
3CXH	N R	R	32	F	5.1	19	37
3CXH	N R	R	33	I	1.8	19	37
3CXH	N R	R	45	F	2.0	45	49
3CXH	N R	R	48	L	1.1	45	49
3CXH	N R	R	76	I	1.0	65	84
3CXH	N R	R	79	H	1.3	65	84
3CXH	N S	N	324	F	1.3	320	341
3CXH	N S	N	327	F	1.5	320	341
3CXH	N S	N	328	I	1.1	320	341
3CXH	N S	N	331	F	2.6	320	341
3CXH	N S	N	335	L	1.4	320	341
3CXH	N S	N	346	V	1.3	346	381
3CXH	N S	N	347	P	1.0	346	381
3CXH	N S	N	348	Y	1.2	346	381
3CXH	N S	N	351	M	5.6	346	381
3CXH	N S	S	62	P	1.4	54	81
3CXH	N S	S	66	Y	3.7	54	81
3CXH	N S	S	69	W	3.1	54	81
3CXH	N S	S	70	W	2.5	54	81
3CXH	N S	S	73	G	2.1	54	81
3CXH	O P	O	283	L	2.1	263	292
3CXH	O P	O	287	V	2.1	263	292
3CXH	O P	O	290	F	1.4	263	292
3CXH	O P	P	63	M	1.4	51	82
3CXH	O Q	O	249	K	2.1	244	260
3CXH	O Q	Q	77	Q	1.3	77	87
3CXH	O Q	Q	98	Y	1.4	89	111
3CXH	O Q	Q	124	V	1.0	124	140
3CXH	O Q	Q	127	F	1.7	124	140
3CXH	O Q	Q	128	F	4.1	124	140
3CXH	O Q	Q	143	F	6.7	141	145
3CXH	O R	R	73	Y	1.9	65	84
3CXH	O S	O	289	K	1.7	263	292
3CXH	O S	O	290	F	2.5	263	292
3CXH	O T	O	87	H	1.0	87	105
3CXH	O T	O	124	E	1.0	122	130
3CXH	O T	O	268	R	1.4	263	292
3CXH	O T	O	271	L	1.2	263	292
3CXH	O T	O	272	K	2.8	263	292
3CXH	O T	T	32	F	4.2	18	44
3CXH	O T	T	33	D	2.8	18	44
3CXH	O T	T	36	I	1.4	18	44
3CXH	O T	T	39	W	1.5	18	44

3CXH	O T	T	40	Y	2.7	18	44
3CXH	O T	T	43	H	1.4	18	44
3CXH	O T	T	49	W	4.1	49	56
3CXH	O T	T	52	V	1.0	49	56
3CXH	P T	P	65	L	1.7	51	82
3CXH	P T	T	7	Y	2.7	5	12
3CXH	P T	T	24	G	4.2	18	44
3CXH	P T	T	28	F	1.2	18	44
3CXH	P T	T	29	Q	1.0	18	44
3CXH	P U	P	127	Q	1.2	123	130
3CXH	Q S	Q	125	E	1.6	124	140
3CXH	R S	R	69	Y	3.0	65	84
3CXH	R S	R	73	Y	1.2	65	84
3CZU	A B	A	156	F	1.9	153	158
3D0L	A B	A	124	Q	1.3	122	128
3D1M	B C	B	156	R	1.3	156	170
3D24	A B	A	240	I	1.5	224	246
3D24	A B	A	258	M	1.8	254	264
3D24	A B	A	413	L	1.4	412	420
3D24	A B	B	210	L	2.6	208	215
3D24	A B	B	213	Y	2.1	208	215
3D24	A B	B	214	L	1.7	208	215
3D24	C D	C	240	I	2.6	225	246
3D24	C D	C	244	K	1.4	225	246
3D24	C D	C	254	L	2.3	254	264
3D24	C D	C	258	M	2.7	254	264
3D24	C D	C	413	L	1.3	412	421
3D24	C D	D	210	L	2.4	208	215
3D24	C D	D	213	Y	2.2	208	215
3D24	C D	D	214	L	1.4	208	215
3D2E	A B	A	572	N	1.1	559	587
3D2E	A B	A	579	Y	1.7	559	587
3D2E	A B	A	583	G	8.3	559	587
3D2E	A B	B	134	Y	1.7	129	136
3D2E	C D	C	572	N	1.3	559	587
3D2E	C D	C	575	E	1.4	559	587
3D2E	C D	C	579	Y	1.8	559	587
3D2E	C D	C	580	T	1.1	559	587
3D2E	C D	D	57	N	1.9	53	58
3D2E	C D	D	262	R	1.5	257	274
3D2E	C D	D	304	E	1.2	299	306
3D31	A C	A	95	F	2.4	89	100
3D31	A C	C	169	R	2.1	168	177
3D31	A C	C	170	L	1.0	168	177
3D31	A C	C	192	L	1.0	181	193
3D31	B D	B	95	F	1.3	89	100
3D31	B D	D	169	R	1.1	168	177
3D31	B D	D	192	L	2.2	181	193
3D32	A C	A	61	Q	2.7	59	70
3D32	A C	A	65	L	1.9	59	70
3D32	A C	A	69	R	1.2	59	70
3D32	B D	B	23	I	1.0	13	27
3D32	B D	B	61	Q	2.5	59	70
3D32	B D	B	65	L	1.7	59	70
3D32	B D	B	69	R	1.3	59	70
3D36	A C	A	224	G	351.0	211	230
3D36	A C	A	225	F	2.2	211	230
3D36	A C	A	228	L	2.7	211	230
3D36	A C	A	238	K	5.4	236	261
3D36	A C	A	242	Y	3.6	236	261

3D36	A C	C	8	L	2.4	6	19
3D36	A C	C	11	E	2.4	6	19
3D36	A C	C	25	F	3.8	23	36
3D3C	A J	A	15	Q	1.1	4	24
3D3C	A J	A	18	Y	4.2	4	24
3D3C	A J	A	22	L	2.2	4	24
3D3C	A J	A	114	F	2.5	100	115
3D3C	A J	J	15	H	1.2	15	32
3D3C	A J	J	16	R	1.0	15	32
3D3C	A J	J	19	D	1.7	15	32
3D3C	A J	J	26	V	1.0	15	32
3D3C	A K	A	32	Y	3.2	27	38
3D3C	A K	K	17	L	1.1	15	32
3D3C	B K	B	15	Q	1.7	4	24
3D3C	B K	B	18	Y	4.7	4	24
3D3C	B K	B	22	L	3.4	4	24
3D3C	B K	B	81	E	1.0	79	95
3D3C	B K	K	16	R	1.1	15	32
3D3C	C L	C	15	Q	1.3	4	24
3D3C	C L	C	18	Y	4.5	4	24
3D3C	C L	C	22	L	1.5	4	24
3D3C	C L	C	114	F	2.7	100	115
3D3C	C L	L	19	D	1.1	15	32
3D48	P R	P	51	I	1.0	50	55
3D48	P R	P	69	K	3.2	69	74
3D48	P R	P	177	R	4.6	161	194
3D48	P R	P	180	H	1.1	161	194
3D48	P R	P	181	K	1.5	161	194
3D4U	A B	A	120	W	2.5	113	123
3D4U	A B	A	121	K	1.5	113	123
3D4U	A B	B	4	V	1.5	2	6
3D4X	A B	A	31	R	2.1	21	36
3D4X	A B	A	122	H	4.8	119	137
3D4X	A B	B	30	R	3.9	20	35
3D4X	A B	B	34	V	1.7	20	35
3D4X	A D	A	97	N	1.1	95	113
3D4X	A D	D	37	W	3.0	36	41
3D4X	A D	D	101	E	4.0	101	119
3D4X	C B	B	37	W	3.4	36	42
3D4X	C D	C	31	R	2.9	21	36
3D4X	C D	C	122	H	2.2	119	137
3D4X	C D	D	30	R	3.3	20	35
3D4X	C D	D	34	V	1.6	20	35
3D4X	C D	D	124	P	1.2	124	142
3D54	A C	C	22	E	1.2	19	33
3D54	A D	A	124	D	1.3	116	129
3D54	C D	C	24	I	3.1	19	33
3D54	E H	E	124	D	1.4	116	129
3D54	G H	G	24	I	2.1	19	33
3D54	I L	I	124	D	1.7	116	129
3D54	I L	I	213	F	2.3	212	228
3D54	K L	K	24	I	2.6	19	33
3D5A	B H	B	178	R	1.5	171	179
3D5A	C N	C	12	L	1.9	12	16
3D5A	C N	C	29	Y	3.0	29	46
3D5A	C N	C	34	L	3.0	29	46
3D5A	C N	N	47	L	1.2	41	51
3D5A	C N	N	49	H	2.0	41	51
3D5A	D E	D	205	E	1.4	200	207
3D5A	E H	E	152	R	1.1	145	154

3D5A	G K	K	58	P	3.1	58	75
3D5A	G K	K	59	Y	2.3	58	75
3D5A	J N	N	41	R	4.3	41	51
3D5A	J N	N	45	R	1.1	41	51
3D5B	E T	T	8	K	1.1	4	12
3D5B	F P	F	34	W	2.8	30	41
3D5B	F P	F	184	Y	1.0	183	187
3D5B	O T	O	104	R	1.4	104	108
3D5B	O T	O	107	R	1.0	104	108
3D5B	Q Z	Q	51	R	2.0	44	58
3D5B	U V	U	40	F	2.5	32	73
3D5D	E T	T	8	K	1.1	4	12
3D5D	F P	F	31	H	1.4	30	41
3D5D	F P	F	34	W	3.6	30	41
3D5D	Q Z	Q	51	R	1.8	44	58
3D5D	U V	U	40	F	2.2	32	73
3D5O	A F	A	173	Y	2.5	166	174
3D5O	C F	C	171	S	3.5	166	175
3D5O	C F	C	173	Y	4.5	166	175
3D5O	C F	C	174	Q	3.6	166	175
3D69	A B	A	124	E	1.6	123	128
3D69	A B	A	125	E	1.4	123	128
3D69	L H	L	125	E	1.6	123	128
3D6N	A B	A	200	L	1.5	195	201
3D6N	A B	B	162	R	3.1	159	171
3D7U	A B	A	279	R	1.3	274	282
3D7U	A B	B	511	Y	2.1	509	518
3D7U	C D	C	280	S	2.1	274	282
3D7V	A B	A	230	G	1.4	225	236
3D7V	A B	A	231	M	1.8	225	236
3D7V	A B	A	245	S	1.0	244	254
3D7V	A B	A	248	R	1.3	244	254
3D7V	A B	A	249	V	1.9	244	254
3D7V	A B	A	253	V	1.2	244	254
3D7V	A B	A	262	G	84.1	261	282
3D7V	A B	A	263	R	3.5	261	282
3D7V	A B	A	318	F	1.0	312	319
3D7V	A B	B	55	E	2.7	54	75
3D7V	A B	B	57	W	1.0	54	75
3D7V	A B	B	58	I	3.3	54	75
3D7V	A B	B	63	R	2.7	54	75
3D7V	A B	B	65	I	2.4	54	75
3D7V	A B	B	66	G	130.7	54	75
3D7V	A B	B	67	D	2.9	54	75
3D7V	A B	B	73	Y	2.1	54	75
3D7W	A B	A	174	W	4.4	170	182
3D85	A B	A	124	Q	1.4	122	127
3D85	A C	C	136	P	1.2	136	167
3D85	C D	C	26	W	2.7	11	28
3D85	C D	C	60	P	1.6	60	66
3D85	C D	C	148	R	1.4	136	167
3D85	C D	C	159	R	1.5	136	167
3D85	C D	C	163	H	1.9	136	167
3D87	A B	A	60	P	2.7	60	66
3D87	A B	A	163	H	1.7	136	167
3D87	C D	C	26	W	1.1	11	28
3D87	C D	C	159	R	1.3	136	169
3D9A	C H	C	697	K	4.5	689	700
3D9A	L H	L	124	Q	1.1	122	127
3DA7	A D	D	36	D	1.3	35	43

3DA7	A D	D	40	D	5.8	35	43
3DA7	B C	C	18	H	1.0	14	25
3DA7	B C	C	36	D	2.5	35	43
3DA7	B C	C	40	D	4.2	35	43
3DA7	E F	F	36	D	1.7	35	44
3DA7	E F	F	40	D	6.7	35	44
3DA7	G H	G	73	K	1.6	73	79
3DA7	G H	H	35	L	1.6	35	46
3DA7	G H	H	36	D	1.5	35	46
3DA7	G H	H	40	D	6.7	35	46
3DA7	G H	H	41	C	1.0	35	46
3DA7	G H	H	44	G	14.3	35	46
3DA7	G H	H	45	W	2.9	35	46
3DAB	A B	A	53	M	1.0	49	63
3DAB	A B	A	57	G	166.1	49	63
3DAB	A B	B	19	F	2.8	19	26
3DAB	A B	B	23	W	4.2	19	26
3DAB	E F	E	57	G	82.4	49	63
3DAB	E F	E	60	I	1.2	49	63
3DAB	E F	F	19	F	3.3	19	26
3DAB	E F	F	23	W	3.6	19	26
3DAC	A B	A	54	G	130.7	46	60
3DAC	A B	A	57	I	1.3	46	60
3DAC	A B	A	96	Y	1.6	93	102
3DAC	A B	B	19	F	3.1	19	26
3DAC	A B	B	23	W	2.7	19	26
3DAC	M P	M	50	M	1.1	46	60
3DAC	M P	M	54	G	132.5	46	60
3DAC	M P	M	57	I	1.3	46	60
3DAC	M P	P	19	F	3.1	19	25
3DAC	M P	P	23	W	4.6	19	25
3DAW	A B	A	143	Y	1.7	137	145
3DAW	A B	A	291	K	1.0	287	296
3DAW	A B	A	345	I	1.7	338	347
3DAW	A B	B	267	R	1.2	266	275
3DAW	A B	B	269	R	4.7	266	275
3DAW	A B	B	270	M	1.4	266	275
3DBH	A B	A	12	K	1.0	8	13
3DBH	A B	A	44	E	1.4	40	48
3DBH	A B	A	51	L	1.5	49	53
3DBH	A B	A	339	Y	8.8	336	367
3DBH	A B	A	340	I	1.0	336	367
3DBH	A B	A	478	Y	1.0	476	486
3DBH	A B	A	484	R	2.3	476	486
3DBH	A B	A	499	G	104.5	491	511
3DBH	A B	B	18	N	1.1	18	22
3DBH	A B	B	114	R	2.7	103	115
3DBH	A B	B	279	R	1.1	278	286
3DBH	A B	B	294	S	1.1	293	313
3DBH	A B	B	298	V	1.1	293	313
3DBH	C D	C	22	D	1.7	22	30
3DBH	C D	C	51	L	1.5	40	53
3DBH	C D	C	67	G	181.9	67	71
3DBH	C D	C	68	E	1.2	67	71
3DBH	C D	C	340	I	1.2	336	369
3DBH	C D	C	478	Y	1.0	476	486
3DBH	C D	C	484	R	1.3	476	486
3DBH	C D	C	492	T	1.0	491	510
3DBH	C D	C	496	F	1.1	491	510
3DBH	C D	C	499	G	127.0	491	510

3DBH	C D	D	62	E	1.0	59	69
3DBH	C D	D	114	R	2.6	103	115
3DBH	C D	D	279	R	1.7	278	286
3DBH	C D	D	283	G	1.4	278	286
3DBH	C D	D	304	A	1.6	293	313
3DBH	C D	D	309	K	1.0	293	313
3DBH	C H	C	448	Y	2.3	447	468
3DBH	C H	H	236	Q	1.2	225	239
3DBH	D J	D	148	I	1.2	148	162
3DBH	D J	D	151	R	1.0	148	162
3DBH	E F	E	44	E	5.7	40	48
3DBH	E F	E	47	K	1.9	40	48
3DBH	E F	E	67	G	227.0	67	72
3DBH	E F	E	71	G	117.6	67	72
3DBH	E F	E	336	S	1.0	336	368
3DBH	E F	E	447	N	1.4	447	468
3DBH	E F	E	484	R	2.3	476	486
3DBH	E F	E	492	T	1.3	491	511
3DBH	E F	E	496	F	1.2	491	511
3DBH	E F	E	499	G	129.3	491	511
3DBH	E F	F	19	H	2.0	18	26
3DBH	E F	F	23	F	1.9	18	26
3DBH	E F	F	62	E	1.3	59	70
3DBH	E F	F	114	R	2.8	103	115
3DBH	E F	F	305	T	1.0	293	313
3DBH	E K	K	128	E	1.2	123	135
3DBH	F K	F	151	R	1.5	148	160
3DBH	G H	G	51	L	1.2	40	53
3DBH	G H	G	67	G	111.5	67	72
3DBH	G H	G	68	E	1.0	67	72
3DBH	G H	G	71	G	135.5	67	72
3DBH	G H	G	339	Y	4.7	339	369
3DBH	G H	G	447	N	2.0	447	468
3DBH	G H	G	478	Y	1.1	476	486
3DBH	G H	G	499	G	50.6	491	511
3DBH	G H	H	110	F	1.8	103	115
3DBH	G H	H	114	R	2.1	103	115
3DBH	G H	H	283	G	1.2	278	286
3DBH	H L	H	148	I	9.2	148	160
3DBH	H L	H	151	R	9.9	148	160
3DBJ	A B	A	5	V	1.3	4	15
3DBJ	A B	A	9	I	2.7	4	15
3DBJ	A B	A	24	L	2.2	21	29
3DBJ	A B	A	28	K	1.4	21	29
3DBJ	A B	A	34	G	59.8	34	45
3DBJ	A B	A	38	L	2.4	34	45
3DBJ	A B	A	97	Y	1.6	78	102
3DBJ	A B	B	5	I	2.4	4	16
3DBJ	A B	B	31	F	2.4	21	33
3DBJ	A B	B	34	G	28.4	34	44
3DBJ	A B	B	93	R	2.1	78	102
3DBJ	A B	B	97	Y	3.4	78	102
3DBJ	C D	C	9	I	2.3	4	15
3DBJ	C D	C	24	L	2.1	21	29
3DBJ	C D	C	28	K	1.3	21	29
3DBJ	C D	C	34	G	58.9	34	45
3DBJ	C D	C	38	L	2.1	34	45
3DBJ	C D	C	97	Y	2.2	78	102
3DBJ	C D	D	5	I	1.8	4	16
3DBJ	C D	D	31	F	2.7	21	33

3DBJ	C D	D	34	G	28.3	34	44
3DBJ	C D	D	93	R	2.1	78	102
3DBJ	C D	D	97	Y	4.2	78	102
3DBJ	E F	E	9	I	1.6	4	15
3DBJ	E F	E	13	D	1.2	4	15
3DBJ	E F	E	24	L	2.2	21	29
3DBJ	E F	E	28	K	1.4	21	29
3DBJ	E F	E	34	G	60.1	34	45
3DBJ	E F	E	38	L	2.1	34	45
3DBJ	E F	E	97	Y	1.7	78	102
3DBJ	E F	F	5	I	5.7	4	16
3DBJ	E F	F	9	I	1.1	4	16
3DBJ	E F	F	31	F	2.7	21	33
3DBJ	E F	F	34	G	28.4	34	44
3DBJ	E F	F	93	R	2.4	78	102
3DBJ	E F	F	97	Y	3.5	78	102
3DBJ	G H	G	13	D	1.1	4	15
3DBJ	G H	G	24	L	2.2	21	29
3DBJ	G H	G	28	K	1.3	21	29
3DBJ	G H	G	34	G	59.9	34	45
3DBJ	G H	G	38	L	2.1	34	45
3DBJ	G H	G	97	Y	2.0	78	102
3DBJ	G H	H	5	I	1.8	4	16
3DBJ	G H	H	31	F	2.8	21	33
3DBJ	G H	H	34	G	28.5	34	44
3DBJ	G H	H	93	R	2.4	78	102
3DBJ	G H	H	97	Y	5.1	78	102
3DBO	A B	A	58	K	2.3	58	66
3DBO	A B	A	61	F	4.5	58	66
3DBO	A B	A	62	L	2.6	58	66
3DBO	A B	A	64	R	2.6	58	66
3DBO	A B	A	65	L	1.4	58	66
3DBO	A B	A	74	L	1.6	72	82
3DBO	A B	A	75	R	1.0	72	82
3DBO	A B	A	77	D	1.0	72	82
3DBO	A B	A	78	L	1.7	72	82
3DBO	A B	B	61	G	2.4	52	65
3DBO	A B	B	74	R	3.8	68	81
3DCG	A B	A	34	I	1.5	24	35
3DCG	A B	B	68	H	2.6	67	83
3DCG	A B	B	75	M	1.3	67	83
3DCG	B F	B	76	Y	4.0	67	83
3DCG	B F	B	104	L	1.1	100	110
3DCG	B F	B	108	N	1.1	100	110
3DCG	B F	F	145	L	3.2	145	155
3DCG	B F	F	146	Q	1.5	145	155
3DCG	B F	F	148	L	1.1	145	155
3DCG	B F	F	153	L	1.7	145	155
3DCG	C D	C	34	I	2.0	24	35
3DCG	C D	D	68	H	2.0	67	83
3DCG	C D	D	75	M	1.5	67	83
3DCG	D E	D	76	Y	4.1	67	83
3DCG	D E	D	104	L	2.1	100	111
3DCG	D E	E	145	L	2.9	145	155
3DCG	D E	E	146	Q	1.4	145	155
3DCG	D E	E	148	L	1.1	145	155
3DCG	D E	E	153	L	1.7	145	155
3DCO	A B	A	406	H	1.8	405	410
3DCO	A B	A	407	W	2.8	405	410
3DCO	N A	N	312	R	3.9	304	321

3DCO	N A	N	320	A	1.7	304	321
3DCO	N A	A	416	G	359.7	415	420
3DCO	N B	B	431	E	6.7	415	437
3DCO	N B	B	432	Y	1.4	415	437
3DCT	A B	A	299	V	1.6	280	304
3DCT	A B	A	317	I	1.7	313	338
3DCT	A B	A	321	K	1.2	313	338
3DCT	A B	A	464	L	1.1	463	469
3DCT	A B	B	749	L	1.4	747	755
3DCT	A B	B	752	L	1.0	747	755
3DCT	A B	B	753	L	1.5	747	755
3DD2	L H	L	14	E	1.4	14	14
3DD2	L H	L	14	E	2.4	14	14
3DD2	L H	L	14	L	1.8	14	14
3DD2	L H	L	14	Y	3.9	14	14
3DD7	A B	A	16	N	1.7	6	21
3DD7	A B	A	19	R	1.0	6	21
3DD7	A B	A	20	Y	4.8	6	21
3DD7	A B	A	78	N	1.0	72	87
3DD7	A B	B	56	F	2.8	55	63
3DD7	A B	B	60	F	4.3	55	63
3DD7	A B	B	64	D	1.3	64	69
3DD7	A B	B	67	N	2.3	64	69
3DD7	C B	B	56	F	1.0	55	63
3DD7	C D	C	8	E	1.1	6	21
3DD7	C D	C	12	L	1.0	6	21
3DD7	C D	C	19	R	1.5	6	21
3DD7	C D	C	20	Y	3.3	6	21
3DD7	C D	C	78	N	1.0	72	87
3DD7	C D	C	85	R	1.4	72	87
3DD7	C D	D	55	E	1.6	53	63
3DD7	C D	D	56	F	2.6	53	63
3DD7	C D	D	59	L	2.0	53	63
3DD7	C D	D	60	F	17.0	53	63
3DD7	C D	D	61	D	1.2	53	63
3DD7	C D	D	67	N	2.2	64	69
3DEG	C H	H	25	P	3.9	25	31
3DEP	A B	A	166	F	3.1	163	170
3DEP	A B	A	169	G	6.2	163	170
3DEP	A B	A	203	G	414.9	197	204
3DF0	A B	A	673	F	1.4	671	677
3DF0	A B	A	691	L	1.6	691	698
3DF0	A B	A	694	W	4.7	691	698
3DF0	A B	A	695	L	2.1	691	698
3DF0	A B	B	242	F	1.1	228	247
3DF0	A B	B	245	F	3.7	228	247
3DF0	A B	B	263	W	3.4	260	268
3DF0	A C	C	186	Y	1.1	184	191
3DF0	A C	C	190	L	1.1	184	191
3DF0	B C	B	129	V	1.1	119	133
3DF0	B C	B	170	W	3.1	163	183
3DF0	B C	C	216	L	1.6	214	221
3DF0	B C	C	220	F	4.5	214	221
3DGC	L R	L	57	F	1.3	50	67
3DGC	L R	L	172	M	1.7	167	178
3DGC	L S	L	51	Y	2.1	50	67
3DGC	L S	L	121	F	1.3	114	129
3DGC	L S	L	128	R	1.1	114	129
3DGC	M R	M	46	N	1.0	44	48
3DGC	M R	M	121	F	1.0	113	129

3DGC	M R	M	124	R	2.3	113	129
3DGC	M R	M	128	R	1.6	113	129
3DGE	A C	A	287	T	1.2	285	316
3DGE	A C	A	291	F	2.6	285	316
3DGE	A C	C	16	K	1.6	12	25
3DGE	A C	C	17	I	2.4	12	25
3DGE	A C	C	20	F	1.1	12	25
3DGE	A C	C	24	K	1.2	12	25
3DGE	A D	A	314	R	1.5	285	316
3DGE	A D	D	89	E	1.0	89	97
3DGE	B D	B	267	T	1.0	264	278
3DGE	B D	B	272	Y	1.6	264	278
3DGE	B D	B	275	T	1.3	264	278
3DGE	B D	B	291	F	1.2	285	316
3DGE	B D	D	17	I	3.0	12	24
3DGE	B D	D	20	F	2.2	12	24
3DGE	B D	D	21	N	1.3	12	24
3DGE	B D	D	109	P	2.5	109	121
3DGG	A B	A	127	Q	1.6	125	129
3DGG	C D	C	126	E	1.4	125	130
3DGG	C D	C	127	Q	2.0	125	130
3DGP	A B	B	16	I	1.2	14	28
3DHH	A B	A	12	L	3.7	10	14
3DHH	A B	A	28	L	1.1	25	29
3DHH	A B	A	33	M	1.9	31	35
3DHH	A B	A	45	E	1.9	41	47
3DHH	A B	A	55	Y	4.5	55	76
3DHH	A B	A	58	Y	1.1	55	76
3DHH	A B	A	59	V	1.9	55	76
3DHH	A B	A	63	R	2.1	55	76
3DHH	A B	A	105	Y	2.0	87	117
3DHH	A B	A	112	G	2.0	87	117
3DHH	A B	A	113	R	3.0	87	117
3DHH	A B	A	116	R	3.0	87	117
3DHH	A B	A	125	N	1.2	121	141
3DHH	A B	A	128	T	1.9	121	141
3DHH	A B	A	131	M	1.4	121	141
3DHH	A B	A	132	M	1.5	121	141
3DHH	A B	A	135	L	1.3	121	141
3DHH	A B	A	142	L	1.1	142	148
3DHH	A B	A	146	H	3.0	142	148
3DHH	A B	A	153	R	2.5	153	163
3DHH	A B	A	156	D	1.6	153	163
3DHH	A B	A	159	W	2.9	153	163
3DHH	A B	A	160	R	1.8	153	163
3DHH	A B	A	173	K	1.3	167	181
3DHH	A B	A	453	R	1.1	450	456
3DHH	A B	A	468	L	1.3	464	471
3DHH	A B	B	24	E	1.2	24	28
3DHH	A B	B	27	I	1.1	24	28
3DHH	A B	B	51	M	1.5	50	61
3DHH	A B	B	54	W	1.3	50	61
3DHH	A B	B	55	Y	3.4	50	61
3DHH	A B	B	80	Y	4.3	80	104
3DHH	A B	B	81	R	2.8	80	104
3DHH	A B	B	83	Y	2.8	80	104
3DHH	A B	B	85	L	1.1	80	104
3DHH	A B	B	88	D	1.9	80	104
3DHH	A B	B	91	E	2.4	80	104
3DHH	A B	B	126	R	1.4	125	143

3DHH	A B	B	127	Y	2.0	125	143
3DHH	A B	B	133	Q	2.3	125	143
3DHH	A B	B	153	I	2.3	146	177
3DHH	A B	B	154	L	1.4	146	177
3DHH	A B	B	158	D	1.2	146	177
3DHH	A B	B	160	L	1.3	146	177
3DHH	A B	B	161	R	3.0	146	177
3DHH	A B	B	171	H	2.0	146	177
3DHH	A B	B	187	R	2.6	186	193
3DHH	A B	B	191	E	1.4	186	193
3DHH	A B	B	200	R	1.8	194	208
3DHH	A B	B	204	E	3.5	194	208
3DHH	A C	A	334	G	2.9	317	338
3DHH	A C	A	337	Y	3.2	317	338
3DHH	A C	A	375	V	1.3	369	382
3DHH	A C	A	455	L	1.8	450	456
3DHH	A E	A	58	Y	1.1	55	76
3DHH	A E	A	61	I	1.4	55	76
3DHH	A E	A	206	L	1.4	185	215
3DHH	A E	A	233	R	1.2	218	236
3DHH	A E	A	295	Y	2.1	290	309
3DHH	A E	A	296	E	2.1	290	309
3DHH	A E	A	297	W	2.1	290	309
3DHH	A E	A	299	I	1.5	290	309
3DHH	A E	A	301	Q	4.0	290	309
3DHH	A E	A	304	R	3.3	290	309
3DHH	A E	A	308	D	3.6	290	309
3DHH	A E	E	9	L	1.2	3	10
3DHH	A E	E	78	E	2.1	74	80
3DHH	A E	E	79	I	1.1	74	80
3DHR	A B	A	31	R	3.1	21	36
3DHR	A B	A	34	I	1.0	21	36
3DHR	A B	A	103	H	1.5	95	113
3DHR	A B	A	107	V	1.2	95	113
3DHR	A B	A	122	H	2.2	119	137
3DHR	A B	B	30	R	4.4	20	35
3DHR	A B	B	34	V	1.2	20	35
3DHR	A B	B	112	I	1.9	100	119
3DHR	A D	A	95	P	1.2	95	113
3DHR	A D	D	37	W	3.2	36	42
3DHR	A D	D	102	N	1.6	100	119
3DHR	C B	C	95	P	1.3	95	113
3DHR	C B	B	37	W	3.2	36	42
3DHR	C B	B	102	N	1.5	100	119
3DHR	C D	C	31	R	2.6	20	36
3DHR	C D	C	103	H	1.6	95	113
3DHR	C D	C	107	V	1.3	95	113
3DHR	C D	C	119	P	1.5	119	137
3DHR	C D	C	122	H	2.5	119	137
3DHR	C D	D	34	V	1.7	20	35
3DHR	C D	D	112	I	2.2	100	119
3DHR	E F	E	31	R	3.4	21	36
3DHR	E F	E	103	H	1.6	95	113
3DHR	E F	E	107	V	1.1	95	113
3DHR	E F	E	122	H	2.4	119	137
3DHR	E F	F	30	R	2.4	20	35
3DHR	E F	F	34	V	1.7	20	35
3DHR	E F	F	112	I	2.4	100	119
3DHR	E H	E	95	P	1.3	95	113
3DHR	E H	H	37	W	3.2	36	42

3DHR	E H	H	102	N	1.5	100	119
3DHR	G F	G	95	P	1.2	95	113
3DHR	G F	F	37	W	3.4	36	42
3DHR	G F	F	102	N	1.4	100	119
3DHR	G H	G	31	R	3.5	21	36
3DHR	G H	G	103	H	1.9	95	113
3DHR	G H	G	107	V	1.1	95	113
3DHR	G H	G	122	H	2.5	119	136
3DHR	G H	H	30	R	2.6	20	35
3DHR	G H	H	33	I	1.2	20	35
3DHR	G H	H	34	V	1.5	20	35
3DHR	G H	H	112	I	2.0	100	119
3DHT	A B	A	31	R	4.0	20	36
3DHT	A B	A	122	H	2.4	119	137
3DHT	A B	B	30	R	1.9	20	35
3DHT	A B	B	34	V	1.2	20	35
3DHT	A B	B	116	H	1.8	100	118
3DHW	A C	A	126	M	1.0	122	127
3DHW	A C	A	141	E	1.4	138	164
3DHW	B D	B	119	L	5.0	118	127
3DHW	B D	B	126	M	2.0	118	127
3DHW	B D	B	141	E	1.9	131	166
3DHW	B D	D	153	R	1.3	143	155
3DHW	E G	E	126	M	1.2	119	127
3DHW	E G	E	141	E	1.6	138	142
3DHW	F H	F	141	E	1.9	138	156
3DI2	A B	A	10	K	3.2	9	26
3DI2	A B	A	15	V	1.8	9	26
3DI2	A B	A	16	L	3.3	9	26
3DI2	A B	A	18	V	1.4	9	26
3DI2	A B	A	77	L	1.5	74	89
3DI2	A B	A	85	G	1.0	74	89
3DI2	A B	A	88	I	2.3	74	89
3DI2	C D	C	15	V	2.1	10	26
3DI2	C D	C	18	V	1.6	10	26
3DI2	C D	C	74	D	1.0	74	123
3DI2	C D	C	77	L	1.4	74	123
3DI2	C D	C	80	L	4.0	74	123
3DIF	A B	A	124	Q	1.2	122	127
3DIF	C D	C	124	Q	1.4	122	127
3DIN	A C	A	329	V	1.3	329	345
3DIN	A C	A	798	F	1.6	788	813
3DIN	B F	B	774	E	39.0	766	776
3DIN	B F	B	798	F	1.5	788	813
3DIN	B F	F	410	E	1.2	392	413
3DIN	C D	C	32	I	2.3	18	33
3DIN	C D	C	224	L	1.0	214	231
3DIN	C D	C	228	F	1.2	214	231
3DIN	C D	D	50	I	2.1	30	61
3DIN	C D	D	55	V	1.6	30	61
3DIN	C E	C	30	M	1.1	18	33
3DIN	C E	C	121	R	1.7	110	141
3DIN	C E	C	162	M	1.5	157	163
3DIN	C E	C	170	F	1.3	164	179
3DIN	C E	C	177	R	1.2	164	179
3DIN	C E	E	12	I	5.3	10	32
3DIN	C E	E	18	Y	1.1	10	32
3DIN	C E	E	30	L	1.2	10	32
3DIN	C E	E	64	F	2.1	55	73
3DIN	F G	F	190	L	1.0	186	196

3DIN	F G	F	364	F	1.2	349	381
3DIN	F G	F	399	V	1.4	392	413
3DIN	F G	G	37	L	1.9	30	61
3DIN	F G	G	45	F	1.2	30	61
3DIN	F G	G	47	L	1.0	30	61
3DIN	F G	G	49	F	1.0	30	61
3DIN	F G	G	50	I	2.1	30	61
3DIN	F H	F	162	M	1.5	157	163
3DIN	F H	F	169	M	1.0	164	179
3DIN	F H	H	18	Y	1.5	10	32
3DIN	F H	H	26	K	1.0	10	32
3DIN	F H	H	30	L	1.4	10	32
3DIN	F H	H	64	F	2.3	55	73
3DKN	A B	A	220	F	1.2	209	227
3DKN	A B	A	224	V	1.0	209	227
3DKN	A B	A	377	V	1.4	377	394
3DKN	A B	B	14	F	1.4	3	22
3DKN	A B	B	43	G	37.3	30	56
3DKN	A B	B	51	G	359.9	30	56
3DKN	A C	A	29	W	1.5	23	43
3DKN	A C	A	36	L	1.4	23	43
3DKN	A C	A	157	L	1.0	137	163
3DKN	A C	A	160	I	1.7	137	163
3DKN	A C	C	33	V	1.5	30	49
3DKN	A C	C	34	I	1.5	30	49
3DL8	A G	A	284	V	1.4	284	300
3DL8	A G	A	287	N	3.9	284	300
3DL8	A G	A	288	H	1.4	284	300
3DL8	A G	A	584	R	42.1	574	620
3DL8	A G	A	587	G	59.3	574	620
3DL8	A G	A	588	N	41.3	574	620
3DL8	A G	A	590	F	41.7	574	620
3DL8	A G	A	592	S	40.6	574	620
3DL8	A G	A	594	K	41.9	574	620
3DL8	A G	A	735	R	2.7	705	743
3DL8	A G	A	751	E	1.2	750	777
3DL8	A G	A	757	F	1.7	750	777
3DL8	A G	G	107	Y	34.6	106	138
3DL8	B F	B	382	R	1.1	375	386
3DL8	B H	B	233	L	1.0	230	247
3DL8	B H	B	266	M	16.1	263	272
3DL8	B H	B	284	V	17.0	284	300
3DL8	B H	B	287	N	15.6	284	300
3DL8	B H	B	288	H	1.6	284	300
3DL8	B H	B	332	G	186.5	331	342
3DL8	B H	B	333	L	10.2	331	342
3DL8	B H	B	587	G	1094.8	574	620
3DL8	B H	B	758	A	1.3	750	777
3DL8	B H	H	106	D	17.1	106	138
3DL8	B H	H	337	A	15.6	330	339
3DL8	B H	H	356	T	15.7	354	386
3DL8	G C	C	59	L	17.9	29	62
3DL8	G E	G	110	Y	1.1	106	138
3DL8	G E	G	168	F	1.5	154	181
3DL8	G E	E	24	K	37.2	9	35
3DL8	G E	E	27	G	361.0	9	35
3DL8	G E	E	59	G	19.3	51	71
3DL8	H D	H	26	V	249.7	15	34
3DL8	H D	H	30	L	249.8	15	34
3DL8	H D	H	226	I	6.4	216	232

3DL8	H F	H	110	Y	1.9	106	138
3DL8	H F	H	168	F	1.5	154	181
3DL8	H F	F	24	K	34.5	9	35
3DL8	H F	F	27	G	372.6	9	35
3DL8	H F	F	33	F	1.3	9	35
3DL8	H F	F	63	L	1.6	51	71
3DMT	A C	A	51	R	1.0	43	52
3DMT	A C	C	51	R	1.0	43	52
3DMT	B C	B	12	R	1.1	12	24
3DMT	B C	B	45	Y	3.9	43	52
3DMT	B C	B	48	Y	1.4	43	52
3DMT	B C	B	49	Q	1.0	43	52
3DMT	B C	C	45	Y	3.4	43	52
3DMT	B C	C	48	Y	1.5	43	52
3DMT	B C	C	211	W	4.4	211	215
3DNL	A C	A	101	V	1.5	101	110
3DNL	A C	A	104	M	1.4	101	110
3DNL	A C	A	108	I	1.5	101	110
3DNL	A C	C	476	R	1.5	475	483
3DNL	A C	C	479	W	2.1	475	483
3DNL	B C	B	338	W	1.4	335	347
3DNL	B C	B	370	E	1.7	369	373
3DNL	B C	C	479	W	1.3	475	483
3DNL	B C	C	482	E	1.3	475	483
3DNL	D E	D	108	I	1.9	101	110
3DNL	D F	D	101	V	1.5	101	110
3DNL	D F	D	104	M	1.4	101	110
3DNL	D F	F	476	R	1.8	475	483
3DNL	D F	F	479	W	1.6	475	483
3DNL	E F	E	338	W	1.4	335	347
3DNL	E F	F	482	E	1.0	475	483
3DNL	G I	G	101	V	1.5	101	110
3DNL	G I	I	476	R	1.5	475	483
3DNL	G I	I	479	W	2.8	475	483
3DNL	H I	H	338	W	1.4	335	347
3DNL	H I	I	482	E	1.3	475	483
3DOE	A B	A	3	L	1.7	3	10
3DOE	A B	A	4	L	1.3	3	10
3DOE	A B	B	60	L	2.3	60	82
3DOE	A B	B	112	L	1.0	107	116
3DOE	A B	B	113	L	1.9	107	116
3DOE	A B	B	118	F	1.8	118	133
3DOM	A B	A	448	L	1.9	440	449
3DOM	A B	B	16	I	1.1	14	28
3DOM	C D	D	16	I	1.3	14	26
3DOM	C D	D	58	L	2.0	47	61
3DQV	A C	C	1720	I	1.5	1701	1722
3DQV	A D	D	1754	K	1.0	1754	1763
3DQV	B D	D	1710	L	1.2	1701	1722
3DQV	B D	D	1720	I	1.4	1701	1722
3DQV	C R	C	1551	L	1.7	1549	1564
3DQV	D Y	D	1551	L	1.6	1549	1566
3DQV	D Y	D	1604	F	1.9	1597	1608
3DQV	D Y	D	1607	N	2.2	1597	1608
3DRA	A B	A	32	Y	1.1	30	45
3DRA	A B	A	40	L	1.9	30	45
3DRA	A B	A	43	M	1.2	30	45
3DRA	A B	A	62	E	4.6	50	63
3DRA	A B	A	67	Y	1.7	67	79
3DRA	A B	A	71	I	2.7	67	79

3DRA	A B	A	75	N	1.0	67	79
3DRA	A B	A	148	S	1.6	144	157
3DRA	A B	A	181	S	1.2	180	191
3DRA	A B	A	259	F	1.9	258	271
3DRA	A B	A	266	K	1.3	258	271
3DRA	A B	A	295	F	1.4	293	302
3DRA	A B	A	296	W	2.1	293	302
3DRA	A B	A	298	Y	1.3	293	302
3DRA	A B	B	35	I	1.0	31	45
3DRA	A B	B	58	Y	1.0	52	67
3DRA	A B	B	245	E	1.8	241	249
3DS3	A C	A	211	L	1.9	211	218
3DS3	A C	C	3	F	3.6	3	11
3DS3	A C	C	6	L	2.1	3	11
3DS3	A C	C	9	Y	1.5	3	11
3DS3	A C	C	10	Y	2.2	3	11
3DS3	B D	B	162	R	1.0	161	174
3DS3	B D	B	183	N	10.9	179	193
3DS3	B D	B	211	L	2.6	211	218
3DS3	B D	B	215	M	1.1	211	218
3DS3	B D	D	3	F	1.3	3	11
3DS3	B D	D	6	L	2.4	3	11
3DS3	B D	D	9	Y	1.5	3	11
3DS3	B D	D	10	Y	2.0	3	11
3DTP	A B	A	749	G	316.5	749	759
3DTP	A B	A	856	R	2.4	855	860
3DTP	A B	A	867	F	1.1	861	970
3DTP	A B	A	874	L	1.4	861	970
3DTP	A B	A	881	R	2.0	861	970
3DTP	A B	A	884	L	1.4	861	970
3DTP	A B	A	888	M	1.1	861	970
3DTP	A B	A	891	L	1.6	861	970
3DTP	A B	A	895	K	1.3	861	970
3DTP	A B	A	898	L	1.6	861	970
3DTP	A B	A	902	V	1.2	861	970
3DTP	A B	A	909	L	1.3	861	970
3DTP	A B	A	915	R	1.1	861	970
3DTP	A B	A	919	L	1.8	861	970
3DTP	A B	A	926	L	1.2	861	970
3DTP	A B	A	930	V	1.1	861	970
3DTP	A B	A	933	M	1.4	861	970
3DTP	A B	A	936	R	1.3	861	970
3DTP	A B	A	937	L	2.3	861	970
3DTP	A B	A	940	E	1.9	861	970
3DTP	A B	A	941	E	2.5	861	970
3DTP	A B	A	947	L	1.1	861	970
3DTP	A B	A	950	K	1.8	861	970
3DTP	A B	A	951	K	1.7	861	970
3DTP	A B	A	961	L	1.4	861	970
3DTP	A B	A	962	K	1.0	861	970
3DTP	A B	A	965	I	1.6	861	970
3DTP	A B	B	399	T	2.4	395	404
3DTP	A B	B	864	K	2.1	857	876
3DTP	A B	B	874	L	1.1	857	876
3DTP	A B	B	880	R	2.4	877	973
3DTP	A B	B	884	L	2.0	877	973
3DTP	A B	B	891	L	2.2	877	973
3DTP	A B	B	909	L	1.3	877	973
3DTP	A B	B	913	E	1.2	877	973
3DTP	A B	B	919	L	1.7	877	973

3DTP	A B	B	923	K	1.2	877	973
3DTP	A B	B	926	L	3.2	877	973
3DTP	A B	B	930	V	1.4	877	973
3DTP	A B	B	933	M	1.8	877	973
3DTP	A B	B	937	L	2.5	877	973
3DTP	A B	B	950	K	1.2	877	973
3DTP	A B	B	951	K	2.1	877	973
3DTP	A B	B	954	L	2.0	877	973
3DTP	A B	B	957	E	1.2	877	973
3DTP	A B	B	961	L	2.3	877	973
3DTP	A B	B	965	I	1.2	877	973
3DTP	A C	A	799	F	4.4	797	809
3DTP	A C	A	800	Q	2.7	797	809
3DTP	A C	A	804	R	5.8	797	809
3DTP	A C	A	805	G	23.6	797	809
3DTP	A C	A	807	L	1.5	797	809
3DTP	A C	A	812	F	3.5	810	835
3DTP	A C	C	18	F	2.9	5	19
3DTP	A C	C	36	R	1.2	28	39
3DTP	A C	C	88	Y	2.2	85	95
3DTP	A C	C	92	L	1.5	85	95
3DTP	A C	C	94	V	1.4	85	95
3DTP	A C	C	123	E	1.5	121	129
3DTP	A C	C	127	L	1.9	121	129
3DTP	A C	C	147	V	1.0	140	149
3DTP	A E	A	824	V	1.3	810	835
3DTP	A E	A	829	C	1.1	810	835
3DTP	A E	A	833	L	2.6	810	835
3DTP	A E	E	65	L	1.3	63	67
3DTP	A E	E	86	L	1.5	76	87
3DTP	A E	E	115	F	1.3	108	118
3DTP	B D	B	731	R	14.6	727	732
3DTP	B D	B	797	I	1.2	794	798
3DTP	B D	B	799	F	2.5	799	811
3DTP	B D	B	802	Q	1.2	799	811
3DTP	B D	B	806	Y	1.9	799	811
3DTP	B D	B	807	L	1.4	799	811
3DTP	B D	D	17	L	1.2	5	18
3DTP	B D	D	106	A	13.9	105	115
3DTP	B D	D	109	R	21.1	105	115
3DTP	B D	D	110	H	14.5	105	115
3DTP	B D	D	123	E	1.0	122	129
3DTP	B D	D	140	Y	1.7	140	149
3DTP	B F	B	817	Q	5.5	817	831
3DTP	B F	B	822	M	1.0	817	831
3DTP	B F	B	825	I	1.7	817	831
3DTP	B F	B	826	Q	1.0	817	831
3DTP	B F	F	55	Q	4.2	55	62
3DTP	B F	F	115	F	1.4	114	119
3DTP	B F	F	132	F	1.8	131	136
3DTP	B F	F	135	F	2.0	131	136
3DTU	A B	A	92	G	35.4	92	109
3DTU	A B	A	178	L	1.8	178	182
3DTU	A B	A	345	Q	1.0	342	371
3DTU	A B	A	353	M	1.4	342	371
3DTU	A B	A	357	V	1.5	342	371
3DTU	A B	A	364	F	2.1	342	371
3DTU	A B	A	367	I	2.4	342	371
3DTU	A B	A	406	V	1.5	404	411
3DTU	A B	A	408	R	2.3	404	411

3DTU	A B	A	409	Y	2.4	404	411
3DTU	A B	A	410	Y	1.4	404	411
3DTU	A B	A	473	F	1.1	450	477
3DTU	A B	A	476	R	2.4	450	477
3DTU	A B	A	493	W	1.9	491	521
3DTU	A B	B	54	I	1.2	49	83
3DTU	A B	B	58	D	4.1	49	83
3DTU	A B	B	62	L	2.3	49	83
3DTU	A B	B	72	V	1.1	49	83
3DTU	A B	B	76	I	2.1	49	83
3DTU	A B	B	80	V	1.3	49	83
3DTU	A B	B	101	E	1.0	98	104
3DTU	A B	B	112	L	2.1	105	128
3DTU	A B	B	119	S	1.0	105	128
3DTU	A B	B	123	L	1.7	105	128
3DTU	A B	B	126	Q	1.8	105	128
3DTU	C B	B	175	E	1.3	174	183
3DTU	C D	C	92	G	69.2	92	109
3DTU	C D	C	99	I	1.5	92	109
3DTU	C D	C	178	L	1.8	178	182
3DTU	C D	C	342	L	3.5	342	371
3DTU	C D	C	345	Q	1.3	342	371
3DTU	C D	C	357	V	1.2	342	371
3DTU	C D	C	364	F	1.8	342	371
3DTU	C D	C	367	I	2.2	342	371
3DTU	C D	C	406	V	1.4	404	411
3DTU	C D	C	408	R	2.5	404	411
3DTU	C D	C	410	Y	1.8	404	411
3DTU	C D	C	476	R	2.9	450	477
3DTU	C D	C	493	W	1.7	491	521
3DTU	C D	D	54	I	1.1	49	83
3DTU	C D	D	58	D	3.6	49	83
3DTU	C D	D	62	L	2.4	49	83
3DTU	C D	D	65	I	1.3	49	83
3DTU	C D	D	72	V	1.1	49	83
3DTU	C D	D	76	I	2.0	49	83
3DTU	C D	D	112	L	1.9	105	128
3DTU	C D	D	119	S	1.1	105	128
3DTU	C D	D	123	L	1.8	105	128
3DTU	C D	D	124	F	1.6	105	128
3DTU	C D	D	126	Q	1.2	105	128
3DTU	C D	D	127	Q	1.2	105	128
3DTV	A C	C	113	R	1.0	104	115
3DTV	C D	D	95	E	1.2	83	98
3DUF	A B	A	153	G	61.9	146	162
3DUF	A B	A	156	L	1.1	146	162
3DUF	A B	A	157	G	19.0	146	162
3DUF	A B	A	160	M	1.3	146	162
3DUF	A B	A	161	R	1.8	146	162
3DUF	A B	A	187	F	4.3	179	191
3DUF	A B	A	353	F	1.3	353	365
3DUF	A B	B	61	G	53.1	59	72
3DUF	A B	B	64	G	330.5	59	72
3DUF	A B	B	65	L	2.3	59	72
3DUF	A B	B	68	G	241.3	59	72
3DUF	A B	B	69	L	1.4	59	72
3DUF	A B	B	71	L	1.2	59	72
3DUF	A B	B	101	R	1.5	100	104
3DUF	A B	B	102	Y	1.1	100	104
3DUF	A D	A	340	V	1.2	340	346

3DUF	A D	A	343	L	1.6	340	346
3DUF	A D	D	59	E	2.0	59	72
3DUF	C B	C	340	V	1.2	340	346
3DUF	C B	C	343	L	1.1	340	346
3DUF	C D	C	150	Q	1.1	146	161
3DUF	C D	C	153	G	58.2	146	161
3DUF	C D	C	156	L	2.9	146	161
3DUF	C D	C	157	G	71.1	146	161
3DUF	C D	C	160	M	1.2	146	161
3DUF	C D	C	187	F	4.8	179	191
3DUF	C D	C	353	F	1.3	353	366
3DUF	C D	C	357	E	1.4	353	366
3DUF	C D	D	61	G	26.8	59	72
3DUF	C D	D	64	G	203.8	59	72
3DUF	C D	D	65	L	2.0	59	72
3DUF	C D	D	68	G	280.0	59	72
3DUF	C D	D	69	L	2.2	59	72
3DUF	C D	D	71	L	1.0	59	72
3DUF	C D	D	101	R	1.3	100	104
3DUF	C D	D	102	Y	1.7	100	104
3DUF	C D	D	103	R	1.3	100	104
3DUF	D I	I	133	P	1.5	133	142
3DUF	D I	I	137	K	1.9	133	142
3DUF	E F	E	150	Q	1.9	148	161
3DUF	E F	E	153	G	59.6	148	161
3DUF	E F	E	157	G	124.4	148	161
3DUF	E F	E	191	F	2.0	179	192
3DUF	E F	E	353	F	1.5	353	362
3DUF	E F	F	61	G	22.2	59	72
3DUF	E F	F	64	G	453.6	59	72
3DUF	E F	F	68	G	114.5	59	72
3DUF	E F	F	96	Q	2.5	96	104
3DUF	E F	F	101	R	1.5	96	104
3DUF	E F	F	102	Y	1.2	96	104
3DUF	E H	E	340	V	1.2	340	346
3DUF	E H	E	343	L	1.1	340	346
3DUF	G F	G	340	V	1.0	340	346
3DUF	G F	G	358	Q	1.3	353	365
3DUF	G F	G	362	Y	2.8	353	365
3DUF	G H	G	153	G	84.8	146	161
3DUF	G H	G	156	L	1.2	146	161
3DUF	G H	G	157	G	27.9	146	161
3DUF	G H	G	160	M	1.1	146	161
3DUF	G H	G	180	D	1.1	179	191
3DUF	G H	G	187	F	3.9	179	191
3DUF	G H	G	353	F	1.3	353	365
3DUF	G H	H	60	S	1.3	59	72
3DUF	G H	H	61	G	114.4	59	72
3DUF	G H	H	64	G	291.0	59	72
3DUF	G H	H	65	L	2.0	59	72
3DUF	G H	H	68	G	204.2	59	72
3DUF	G H	H	69	L	1.3	59	72
3DUF	G H	H	71	L	1.3	59	72
3DUF	G H	H	101	R	1.6	100	104
3DUF	G H	H	102	Y	1.4	100	104
3DUF	H J	J	137	K	1.0	133	141
3DUF	H J	J	140	R	1.3	133	141
3DUH	A C	C	60	P	1.8	60	66
3DUH	A C	C	149	S	1.2	139	169
3DUH	A C	C	163	H	1.1	139	169

3DUH	B D	D	26	W	2.7	11	27
3DUH	B D	D	60	P	1.6	60	66
3DUH	B D	D	159	R	1.5	143	168
3DUH	B D	D	163	H	2.0	143	168
3DVE	A B	A	11	E	1.6	6	20
3DVE	A B	A	19	F	1.6	6	20
3DVE	A B	A	36	M	1.5	29	39
3DVE	A B	A	47	E	3.7	45	55
3DVE	A B	A	51	M	2.0	45	55
3DVE	A B	A	54	E	1.0	45	55
3DVE	A B	A	68	F	1.1	65	77
3DVE	A B	A	71	M	1.8	65	77
3DVE	A B	A	75	K	1.5	65	77
3DVE	A B	A	92	F	1.3	82	93
3DVE	A B	A	124	M	1.3	118	129
3DVE	A B	A	127	E	1.0	118	129
3DVE	A B	A	141	F	1.3	138	145
3DVE	A B	A	144	M	1.1	138	145
3DVE	A B	B	1854	M	1.5	1854	1870
3DVE	A B	B	1855	G	114.5	1854	1870
3DVE	A B	B	1856	K	1.6	1854	1870
3DVE	A B	B	1863	I	3.1	1854	1870
3DVE	A B	B	1864	F	1.9	1854	1870
3DVE	A B	B	1866	F	3.9	1854	1870
3DVE	A B	B	1867	Y	4.3	1854	1870
3DVE	A B	B	1868	K	1.8	1854	1870
3DVG	A B	A	126	Q	1.2	124	129
3DVU	A C	A	48	F	2.5	32	56
3DVU	A C	A	51	H	1.0	32	56
3DVU	A C	A	74	L	2.2	67	79
3DVU	A C	A	78	L	1.3	67	79
3DVU	A C	A	86	G	155.8	85	103
3DVU	A C	A	87	R	2.1	85	103
3DVU	A C	C	109	M	1.5	107	126
3DVU	A C	C	112	L	2.4	107	126
3DVU	A C	C	116	L	2.0	107	126
3DVU	A C	C	117	K	1.1	107	126
3DVU	A C	C	119	T	1.1	107	126
3DVU	A C	C	120	G	13.1	107	126
3DVU	A C	C	121	D	1.5	107	126
3DVU	A C	C	123	F	3.2	107	126
3DVU	B D	B	48	F	2.4	35	57
3DVU	B D	B	52	Y	1.2	35	57
3DVU	B D	B	74	L	1.7	67	79
3DVU	B D	B	78	L	1.2	67	79
3DVU	B D	B	86	G	81.3	85	101
3DVU	B D	B	87	R	1.0	85	101
3DVU	B D	D	112	L	1.9	108	125
3DVU	B D	D	116	L	1.6	108	125
3DVU	B D	D	120	G	7.7	108	125
3DVU	B D	D	121	D	1.2	108	125
3DVU	B D	D	123	F	3.2	108	125
3DW8	A B	A	10	L	1.3	10	21
3DW8	A B	A	17	I	1.5	10	21
3DW8	A B	A	54	F	3.0	50	55
3DW8	A B	A	63	D	1.1	63	75
3DW8	A B	A	179	P	1.9	179	194
3DW8	A B	A	183	R	1.6	179	194
3DW8	A C	A	456	Y	1.1	456	468
3DW8	A C	A	495	Y	2.7	495	511

3DW8	A C	A	498	R	1.0	495	511
3DW8	A C	A	499	M	1.1	495	511
3DW8	A C	A	503	F	1.0	495	511
3DW8	A C	C	71	I	1.0	62	73
3DW8	A C	C	72	G	4.1	62	73
3DW8	A F	A	360	N	1.0	358	363
3DW8	D E	D	11	Y	1.1	10	21
3DW8	D E	D	17	I	1.4	10	21
3DW8	D E	D	18	D	1.8	10	21
3DW8	D E	D	54	F	1.4	50	55
3DW8	D E	D	63	D	1.2	63	75
3DW8	D E	D	179	P	2.0	179	187
3DW8	D E	D	183	R	2.3	179	187
3DW8	D E	D	218	D	1.9	218	233
3DW8	D E	D	219	S	2.9	218	233
3DW8	D E	D	221	R	1.3	218	233
3DW8	D F	D	495	Y	1.1	495	506
3DWL	A D	A	114	F	3.3	103	118
3DWL	A D	A	144	E	1.8	136	148
3DWL	A D	D	266	R	2.1	265	283
3DWL	A D	D	271	F	3.5	265	283
3DWL	A D	D	275	A	1.0	265	283
3DWL	A D	D	277	K	2.1	265	283
3DWL	A H	A	214	R	2.5	213	224
3DWL	B C	B	82	K	1.1	78	83
3DWL	B I	B	114	F	2.4	103	118
3DWL	B I	B	144	E	1.9	136	148
3DWL	B I	I	271	F	1.4	265	283
3DWL	B I	I	274	K	1.6	265	283
3DWL	B I	I	277	K	1.1	265	283
3DWL	C G	G	140	G	42.9	139	148
3DWL	D F	D	191	I	1.5	188	202
3DWL	D F	D	192	F	1.3	188	202
3DWL	D F	D	196	F	1.4	188	202
3DWL	D F	D	200	F	2.9	188	202
3DWL	D F	D	280	M	2.2	265	283
3DWL	D F	D	287	R	2.2	284	299
3DWL	D F	D	288	V	1.3	284	299
3DWL	D F	D	291	F	3.1	284	299
3DWL	D F	D	295	L	3.1	284	299
3DWL	D F	F	81	E	1.1	81	88
3DWL	D F	F	82	I	1.0	81	88
3DWL	D F	F	90	F	1.1	89	96
3DWL	D F	F	93	F	1.3	89	96
3DWL	D F	F	131	L	1.4	128	151
3DWL	D F	F	134	F	2.2	128	151
3DWL	D F	F	138	F	1.3	128	151
3DWL	D F	F	149	M	1.7	128	151
3DWL	D F	F	153	L	2.0	153	166
3DWL	D F	F	164	Y	3.5	153	166
3DWL	D F	F	165	L	1.9	153	166
3DWL	F G	G	127	L	1.8	125	133
3DWL	F G	G	130	H	1.0	125	133
3DWL	F G	G	142	I	1.3	139	148
3DWL	F G	G	146	L	1.7	139	148
3DWL	H L	L	140	G	57.0	139	148
3DWL	I K	I	191	I	2.6	188	202
3DWL	I K	I	192	F	1.2	188	202
3DWL	I K	I	194	K	1.3	188	202
3DWL	I K	I	196	F	1.7	188	202

3DWL	I K	I	200	F	2.9	188	202
3DWL	I K	I	258	C	1.7	255	260
3DWL	I K	I	280	M	1.5	265	283
3DWL	I K	I	284	M	1.1	284	299
3DWL	I K	I	291	F	4.5	284	299
3DWL	I K	I	292	Q	1.2	284	299
3DWL	I K	I	294	V	1.0	284	299
3DWL	I K	I	295	L	2.2	284	299
3DWL	I K	K	81	E	1.5	81	88
3DWL	I K	K	93	F	1.6	89	96
3DWL	I K	K	134	F	2.6	128	151
3DWL	I K	K	153	L	1.7	153	166
3DWL	I K	K	160	V	1.1	153	166
3DWL	I K	K	164	Y	2.6	153	166
3DWL	I K	K	165	L	1.8	153	166
3DWL	K L	L	127	L	1.6	125	133
3DWL	K L	L	130	H	1.0	125	133
3DWL	K L	L	142	I	1.4	139	148
3DWL	K L	L	146	L	1.6	139	148
3DXA	A D	A	69	T	1.0	57	85
3DXA	A E	A	72	Q	1.5	57	85
3DXA	A J	A	84	Y	1.6	57	85
3DXA	D E	E	145	E	1.0	145	151
3DXA	D E	E	147	E	1.7	145	151
3DXA	D E	E	150	H	1.2	145	151
3DXA	F J	F	72	Q	1.6	57	85
3DXA	I J	J	150	H	1.1	145	151
3DXA	K N	K	66	I	1.4	57	85
3DXA	K O	K	72	Q	1.4	57	85
3DXA	N O	O	147	E	1.0	145	151
3DXC	A B	A	658	Y	2.0	644	666
3DXC	A B	B	674	L	2.4	669	681
3DXC	A B	B	677	M	1.0	669	681
3DXC	A B	B	678	Q	1.6	669	681
3DXC	A B	B	685	P	1.0	685	693
3DXC	A B	B	687	Y	3.0	685	693
3DXC	A B	B	689	F	2.2	685	693
3DXC	A B	B	690	F	1.5	685	693
3DXC	C D	C	658	Y	1.9	644	664
3DXC	C D	D	678	Q	1.9	669	681
3DXC	C D	D	687	Y	1.0	685	690
3DXC	C D	D	689	F	1.2	685	690
3DXR	A B	A	19	K	1.2	13	40
3DXR	A B	A	58	K	1.5	50	80
3DXR	A B	A	62	K	2.5	50	80
3DXR	A B	A	65	K	1.7	50	80
3DXR	A B	A	66	H	1.4	50	80
3DXR	A B	A	74	F	2.4	50	80
3DXR	A B	B	33	F	1.1	16	45
3DXR	A B	B	37	V	1.3	16	45
3DXR	A B	B	41	Y	1.6	16	45
3DXR	A B	B	58	E	1.3	56	83
3DXR	A B	B	59	S	1.4	56	83
3DXR	A B	B	66	V	1.2	56	83
3DXR	A B	B	70	F	1.7	56	83
3DZU	A D	A	193	Q	1.6	188	198
3DZU	A D	A	196	L	3.9	188	198
3DZU	A D	A	356	K	1.1	353	359
3DZU	A D	A	394	E	1.1	386	408
3DZU	A D	A	397	Y	1.6	386	408

3DZU	A D	A	417	K	1.4	414	420
3DZU	A D	A	423	P	3.7	421	431
3DZU	A D	D	237	L	2.1	230	238
3DZU	A D	D	351	E	1.5	350	354
3DZU	A D	D	407	E	2.0	403	425
3DZU	A D	D	434	K	1.6	431	459
3DZU	A D	D	436	L	1.3	431	459
3E 20	A B	B	288	F	1.2	275	290
3E 20	A B	B	404	G	9.2	396	405
3E 20	D C	C	288	F	3.2	275	290
3E 20	D C	C	404	G	8.3	396	405
3E 20	E H	H	288	F	1.2	275	290
3E 95	A C	A	122	K	1.3	121	130
3E 95	B C	C	28	F	5.1	26	40
3E 95	B C	C	31	L	1.3	26	40
3E 95	B C	C	32	D	1.6	26	40
3E 95	B C	C	34	L	2.2	26	40
3E 95	B C	C	38	Q	1.0	26	40
3E0J	A B	A	213	L	1.3	209	224
3E0J	A B	A	217	L	1.2	209	224
3E0J	A B	A	231	E	1.6	229	237
3E0J	A B	B	35	N	1.6	34	53
3E0J	A B	B	42	Y	3.1	34	53
3E0J	A B	B	115	F	1.9	112	125
3E0J	C D	C	213	L	1.1	209	224
3E0J	C D	C	217	L	1.1	209	224
3E0J	C D	C	220	D	1.0	209	224
3E0J	C D	C	231	E	1.7	229	237
3E0J	C D	D	42	Y	3.1	34	53
3E0J	C D	D	115	F	2.2	112	125
3E0J	C D	D	118	D	1.1	112	125
3E0J	E F	E	213	L	1.0	209	224
3E0J	E F	E	217	L	1.1	209	224
3E0J	E F	E	220	D	1.4	209	224
3E0J	E F	E	231	E	1.5	229	237
3E0J	E F	E	274	E	1.2	264	290
3E0J	E F	F	23	Y	1.1	23	30
3E0J	E F	F	39	Q	1.1	34	53
3E0J	E F	F	115	F	2.4	112	125
3E0J	E F	F	118	D	1.4	112	125
3E0J	G H	G	213	L	1.0	209	224
3E0J	G H	G	217	L	1.1	209	224
3E0J	G H	G	220	D	2.9	209	224
3E0J	G H	G	229	E	1.2	229	237
3E0J	G H	G	231	E	1.4	229	237
3E0J	G H	G	278	M	3.0	265	290
3E0J	G H	G	281	E	2.3	265	290
3E0J	G H	G	284	L	3.3	265	290
3E0J	G H	G	289	S	1.0	265	290
3E0J	G H	H	24	K	2.4	23	30
3E0J	G H	H	28	Y	2.6	23	30
3E0J	G H	H	35	N	1.2	34	53
3E0J	G H	H	39	Q	1.5	34	53
3E0J	G H	H	42	Y	2.8	34	53
3E0J	G H	H	115	F	2.5	112	125
3E0J	G H	H	119	Y	2.0	112	125
3E0J	G H	H	123	K	2.8	112	125
3E1K	G H	G	377	V	1.1	376	393
3E1K	G H	H	856	V	1.2	853	860
3E1K	I J	J	859	Y	1.0	853	860

3E1K	M N	N	853	M	1.1	853	860
3E1R	A C	A	180	K	1.7	166	210
3E1R	A C	A	184	W	4.9	166	210
3E1R	A C	A	187	Y	4.6	166	210
3E1R	A C	A	190	Q	1.1	166	210
3E1R	A C	A	194	Y	1.4	166	210
3E1Y	A F	A	291	F	1.0	277	292
3E1Y	A F	A	401	Q	4.3	397	405
3E1Y	B E	B	291	F	1.1	277	292
3E1Y	B E	B	401	Q	3.0	397	405
3E2K	A D	A	108	I	1.0	107	112
3E2K	A D	A	110	E	1.3	107	112
3E2K	B C	B	108	I	1.0	107	112
3E2K	B C	B	110	E	1.7	107	112
3E2K	B C	B	111	K	1.2	107	112
3E2Z	A B	A	83	K	2.3	80	91
3E2Z	A B	A	86	L	1.4	80	91
3E2Z	A B	A	136	Y	2.4	135	146
3E2Z	A B	A	137	G	17.6	135	146
3E2Z	A B	A	140	F	1.8	135	146
3E2Z	A B	A	317	P	1.0	316	331
3E2Z	A B	B	83	K	1.1	80	91
3E2Z	A B	B	136	Y	1.7	135	146
3E2Z	A B	B	140	F	1.3	135	146
3E2Z	A B	B	305	T	1.9	297	309
3E2Z	A B	B	317	P	1.1	316	331
3E2Z	A B	B	318	L	1.0	316	331
3E3Q	A D	A	155	Y	1.8	152	175
3E3Q	B C	B	155	Y	1.9	152	175
3E3Q	B C	B	163	E	1.3	152	175
3E3Q	c d	c	155	Y	1.8	152	175
3E3Q	c d	c	159	Y	1.7	152	175
3E3Q	H I	H	155	Y	2.1	152	175
3E3Q	H I	H	163	E	2.0	152	175
3E3Q	L M	L	155	Y	2.0	152	175
3E3Q	L M	L	163	E	1.6	152	175
3E3Q	L N	L	77	N	1.1	57	85
3E3Q	P R	P	155	Y	2.0	152	175
3E3Q	P R	P	157	R	2.2	152	175
3E3Q	P R	P	159	Y	1.4	152	175
3E3Q	U V	U	155	Y	1.8	152	175
3E3Q	Y Z	Y	155	Y	2.2	152	175
3E6P	L H	L	414	E	2.4	414	414
3E6P	L H	L	414	E	1.8	414	414
3E6P	L H	L	414	L	1.6	414	414
3E6P	L H	L	414	L	1.1	414	414
3E6P	L H	L	414	Y	3.5	414	414
3E7S	A B	A	395	D	4.0	393	412
3E7S	A B	A	399	V	1.6	393	412
3E7S	A B	A	406	L	1.0	393	412
3E7S	A B	A	419	H	5.0	419	437
3E7S	A B	A	420	H	4.5	419	437
3E7S	A B	A	444	W	1.6	444	448
3E7S	A B	B	395	D	2.4	393	412
3E7S	A B	B	399	V	1.4	393	412
3E7S	A B	B	419	H	2.6	419	437
3E7S	A B	B	420	H	2.9	419	437
3E7S	A B	B	444	W	1.9	444	448
3E8C	A G	A	133	R	3.2	128	136
3E8C	A G	A	230	E	2.9	217	234

3E8C	A G	G	10	F	3.1	6	13
3E8C	B H	B	129	F	2.3	128	136
3E8C	B H	B	230	E	2.7	217	234
3E8C	B H	H	10	F	2.5	6	13
3E8C	C I	C	129	F	1.7	128	136
3E8C	C I	I	10	F	3.0	7	13
3E8C	D J	D	129	F	1.7	128	136
3E8C	D J	D	230	E	1.4	217	234
3E8C	D J	J	10	F	2.5	6	13
3E8C	E K	E	129	F	2.2	128	136
3E8C	E K	E	230	E	1.4	217	234
3E8C	E K	K	7	Y	2.1	6	13
3E8C	E K	K	10	F	3.0	6	13
3E8C	F L	F	230	E	1.7	217	234
3E8C	F L	L	10	F	3.0	9	13
3E8U	H L	L	124	Q	1.8	122	128
3E9J	B C	B	174	F	1.1	171	187
3EA5	A B	A	77	D	2.1	77	81
3EA5	A B	A	79	Y	1.3	77	81
3EA5	A B	A	107	D	1.0	101	112
3EA5	A B	A	110	R	1.0	101	112
3EA5	A B	A	111	V	1.1	101	112
3EA5	A B	A	157	F	1.0	157	170
3EA5	A B	A	163	W	1.0	157	170
3EA5	A B	A	167	K	1.0	157	170
3EA5	A B	B	14	I	1.1	3	16
3EA5	A B	B	26	E	1.5	19	36
3EA5	A B	B	60	L	1.4	55	67
3EA5	A B	B	63	L	1.2	55	67
3EA5	A B	B	66	K	1.3	55	67
3EA5	A B	B	76	K	1.2	74	88
3EA5	A B	B	567	Q	1.2	563	587
3EA5	A B	B	570	Q	1.4	563	587
3EA5	C D	C	77	D	2.3	77	81
3EA5	C D	C	167	K	1.5	159	170
3EA5	C D	D	60	L	1.3	55	67
3EA5	C D	D	63	L	1.6	55	67
3EA5	C D	D	66	K	1.3	55	67
3EA5	C D	D	161	Y	1.1	149	164
3EA5	C D	D	207	D	1.2	195	208
3EA5	C D	D	288	E	1.8	280	307
3EA5	C D	D	291	S	1.0	280	307
3EA5	C D	D	350	S	1.2	347	362
3EA5	C D	D	616	D	1.3	615	630
3EAB	A G	A	120	H	2.1	110	137
3EAB	A G	A	124	F	2.5	110	137
3EAB	A G	A	127	I	1.1	110	137
3EAB	A G	A	177	L	1.6	169	196
3EAB	A G	A	180	K	1.9	169	196
3EAB	A G	G	159	E	1.7	151	160
3EAB	A G	G	177	G	1.5	175	196
3EAB	A G	G	185	Q	2.0	175	196
3EAB	A G	G	186	D	1.5	175	196
3EAB	A G	G	187	E	1.2	175	196
3EAB	B H	B	117	R	1.5	110	137
3EAB	B H	B	120	H	2.1	110	137
3EAB	B H	B	124	F	4.7	110	137
3EAB	B H	B	177	L	1.7	169	193
3EAB	B H	B	180	K	2.0	169	193
3EAB	B H	H	178	T	1.0	175	196

3EAB	B H	H	184	E	1.7	175	196
3EAB	B H	H	186	D	1.4	175	196
3EAB	B H	H	188	L	1.6	175	196
3EAB	B H	H	191	R	1.0	175	196
3EAB	C I	C	117	R	1.3	110	137
3EAB	C I	C	124	F	3.0	110	137
3EAB	C I	C	177	L	1.5	169	196
3EAB	C I	C	180	K	2.4	169	196
3EAB	C I	I	177	G	1.3	175	196
3EAB	C I	I	178	T	1.2	175	196
3EAB	C I	I	184	E	1.9	175	196
3EAB	C I	I	186	D	1.6	175	196
3EAB	C I	I	188	L	2.5	175	196
3EAB	C I	I	191	R	1.4	175	196
3EAB	C I	I	192	L	2.1	175	196
3EAB	D J	D	117	R	1.3	110	137
3EAB	D J	D	120	H	3.7	110	137
3EAB	D J	D	124	F	3.8	110	137
3EAB	D J	D	131	L	1.7	110	137
3EAB	D J	D	134	D	1.0	110	137
3EAB	D J	D	177	L	1.4	169	194
3EAB	D J	D	180	K	1.6	169	194
3EAB	D J	D	191	R	1.4	169	194
3EAB	D J	J	177	G	5.1	174	192
3EAB	D J	J	184	E	2.9	174	192
3EAB	D J	J	185	Q	3.7	174	192
3EAB	D J	J	186	D	1.1	174	192
3EAB	D J	J	188	L	1.9	174	192
3EAB	D J	J	191	R	1.0	174	192
3EAB	E K	E	117	R	1.7	112	137
3EAB	E K	E	120	H	2.8	112	137
3EAB	E K	E	124	F	3.9	112	137
3EAB	E K	E	131	L	1.9	112	137
3EAB	E K	E	177	L	1.5	169	196
3EAB	E K	E	180	K	1.9	169	196
3EAB	E K	E	187	M	1.4	169	196
3EAB	E K	K	177	G	1.0	174	193
3EAB	E K	K	184	E	3.2	174	193
3EAB	E K	K	186	D	1.0	174	193
3EAB	E K	K	187	E	1.0	174	193
3EAB	E K	K	188	L	2.4	174	193
3EAB	E K	K	191	R	1.2	174	193
3EAB	E K	K	192	L	2.8	174	193
3EAB	F L	F	117	R	1.6	110	137
3EAB	F L	F	120	H	4.5	110	137
3EAB	F L	F	124	F	4.2	110	137
3EAB	F L	F	131	L	8.0	110	137
3EAB	F L	F	177	L	1.5	169	193
3EAB	F L	F	180	K	2.1	169	193
3EAB	F L	L	177	G	1.5	175	194
3EAB	F L	L	184	E	1.7	175	194
3EAB	F L	L	185	Q	3.9	175	194
3EAB	F L	L	186	D	1.4	175	194
3EAB	F L	L	187	E	1.0	175	194
3EAB	F L	L	191	R	1.6	175	194
3EAB	F L	L	192	L	2.5	175	194
3EB6	A B	B	5	R	1.5	1	16
3EBA	A B	B	91	D	2.0	90	100
3EBA	A B	B	95	C	5.2	90	100
3ECH	A C	A	17	F	3.4	7	31

3ECH	A C	A	24	I	2.1	7	31
3ECH	A C	A	41	H	1.2	37	49
3ECH	A C	A	105	H	2.0	99	122
3ECH	A C	A	109	E	1.8	99	122
3ECH	A C	A	112	M	1.8	99	122
3ECH	A C	A	116	H	1.0	99	122
3ECH	A C	C	32	Y	1.1	32	43
3ECH	A C	C	45	W	7.0	44	50
3ECH	A C	C	48	Y	4.3	44	50
3ECH	B C	B	14	M	1.4	9	31
3ECH	B C	B	21	R	2.2	9	31
3ECH	B C	B	24	I	1.2	9	31
3ECH	B C	B	37	P	1.2	37	49
3ECH	B C	B	41	H	1.1	37	49
3ECH	B C	C	37	R	2.1	32	43
3EDL	A B	A	210	Y	1.9	209	216
3EDL	A B	A	406	H	1.8	405	410
3EDL	A B	A	407	W	2.8	405	410
3EDL	D F	F	434	E	1.1	415	436
3EDL	G D	G	419	T	19.1	417	430
3EDL	G D	G	420	E	2.7	417	430
3EDL	G D	G	423	S	30.1	417	430
3EDL	G F	G	253	R	3.2	253	260
3EDL	G F	G	254	K	2.6	253	260
3EDL	G F	G	257	V	1.8	253	260
3EDL	G F	F	406	H	2.1	405	412
3EDL	G F	F	407	W	4.5	405	412
3EDL	G F	F	411	E	1.9	405	412
3EDQ	A B	A	70	D	1.2	67	81
3EDQ	A B	A	74	L	1.4	67	81
3EDQ	A B	B	216	I	2.4	214	226
3EDQ	A B	B	223	L	1.0	214	226
3EDQ	B D	B	240	N	1.0	232	246
3EDQ	B D	D	234	H	2.2	232	246
3EDQ	B D	D	240	N	1.1	232	246
3EDQ	C D	C	74	L	1.4	67	81
3EDQ	C D	D	216	I	2.3	214	228
3EDX	A B	A	14	E	1.4	14	14
3EDX	A B	A	14	E	1.7	14	14
3EDX	A B	A	14	L	1.8	14	14
3EDX	A B	A	14	L	2.0	14	14
3EDX	A B	B	242	I	1.4	235	245
3EDX	C D	C	1	F	1.8	1	1
3EDX	C D	C	14	L	1.6	14	14
3EDX	C D	D	242	I	1.3	235	245
3EDX	E F	E	1	F	1.5	1	1
3EDX	E F	E	14	E	1.5	14	14
3EDX	E F	E	14	L	2.0	14	14
3EFD	H K	K	145	H	1.0	132	156
3EFF	B M	M	146	E	1.4	140	155
3EFF	B M	M	153	R	2.2	140	155
3EFF	D K	K	146	E	2.3	140	155
3EG5	A B	A	66	R	4.7	65	73
3EG5	A B	A	67	L	1.3	65	73
3EG5	A B	A	70	L	1.8	65	73
3EG5	A B	A	103	H	2.4	87	105
3EG5	A B	A	104	H	1.4	87	105
3EG5	A B	B	100	K	1.1	98	107
3EG5	A B	B	115	M	1.2	109	123
3EG5	A B	B	210	R	1.3	202	216

3EG5	A B	B	213	K	1.1	202	216
3EG5	C D	C	66	R	3.7	65	73
3EG5	C D	C	67	L	1.3	65	73
3EG5	C D	C	70	L	4.1	65	73
3EG5	C D	C	103	H	2.4	87	105
3EG5	C D	D	100	K	1.1	98	107
3EG5	C D	D	115	M	1.2	109	123
3EG5	C D	D	210	R	1.1	202	216
3EH3	A B	A	66	Y	25.4	65	89
3EH3	A B	A	303	L	1.6	292	327
3EH3	A B	A	310	L	1.1	292	327
3EH3	A B	A	314	F	2.8	292	327
3EH3	A B	A	373	Y	1.7	370	376
3EH3	A B	B	18	W	1.5	10	39
3EH3	A B	B	26	L	2.0	10	39
3EH3	A B	B	33	I	1.7	10	39
3EH3	A C	A	314	F	1.4	292	327
3EH3	A C	A	371	L	2.7	370	376
3EH3	A C	A	374	V	1.0	370	376
3EH3	A C	C	7	G	28.3	6	19
3EH3	A C	C	12	I	1.3	6	19
3EH3	A C	C	22	F	2.8	20	33
3EH3	A C	C	30	F	1.3	20	33
3EH3	B C	B	14	Y	1.0	10	39
3EH3	B C	B	18	W	2.2	10	39
3EH3	B C	B	29	F	1.8	10	39
3EH3	B C	B	33	I	1.1	10	39
3EH3	B C	C	12	I	1.4	6	19
3EHU	A C	C	38	M	1.3	27	41
3EHU	A C	C	39	E	1.7	27	41
3EHU	B D	D	38	M	1.3	27	41
3EI2	A B	B	105	I	1.0	105	114
3EI2	A B	B	106	L	2.6	105	114
3EI2	A B	B	107	H	1.6	105	114
3EI2	A B	B	109	I	1.0	105	114
3EI4	A B	B	70	V	1.5	69	79
3EI4	A B	B	71	R	1.3	69	79
3EI4	A B	B	73	L	1.2	69	79
3EI4	A B	B	90	L	3.0	83	100
3EI4	C D	D	70	V	1.2	69	79
3EI4	C D	D	71	R	1.2	69	79
3EI4	C D	D	73	L	1.1	69	79
3EI4	C D	D	90	L	1.4	83	100
3EI4	C D	D	93	S	1.0	83	100
3EI4	C D	D	96	H	1.0	83	100
3EI4	E F	F	71	R	1.2	69	79
3EI4	E F	F	73	L	1.1	69	79
3EI4	E F	F	76	H	1.0	69	79
3EI4	E F	F	84	P	1.2	83	100
3EI4	E F	F	87	Q	1.8	83	100
3EI4	E F	F	90	L	1.5	83	100
3EIQ	A C	A	111	E	1.5	110	124
3EIQ	A C	A	160	G	172.6	159	164
3EIQ	A C	A	283	R	1.8	282	291
3EIQ	A C	A	354	E	1.6	353	361
3EIQ	A C	A	357	I	2.3	353	361
3EIQ	A C	A	390	F	4.6	381	391
3EIQ	A C	C	183	E	1.1	181	190
3EIQ	A C	C	186	E	1.3	181	190
3EIQ	A C	C	361	H	2.1	360	374

3EIQ	D C	D	160	G	149.7	159	164
3EIQ	D C	C	300	V	1.4	289	303
3EIQ	D C	C	337	E	1.3	326	342
3EIQ	D C	C	346	E	1.0	344	355
3EJB	A B	A	57	L	1.3	57	70
3EJB	A B	A	60	V	2.0	57	70
3EJB	A B	A	61	E	1.5	57	70
3EJB	A B	A	67	E	1.1	57	70
3EJB	A B	A	76	D	1.2	76	82
3EJB	C D	C	57	L	1.0	57	70
3EJB	C D	C	60	V	1.0	57	70
3EJB	C D	C	61	E	1.7	57	70
3EJB	C D	C	67	E	1.0	57	70
3EJB	E F	E	57	L	1.5	57	70
3EJB	E F	E	60	V	2.3	57	70
3EJB	E F	E	61	E	1.2	57	70
3EJB	E F	E	67	E	1.0	57	70
3EJB	E F	E	68	E	1.0	57	70
3EJB	E F	E	76	D	1.1	76	82
3EJB	E F	F	174	R	1.4	174	201
3EJB	G H	G	57	L	3.4	57	70
3EJB	G H	G	58	D	1.9	57	70
3EJB	G H	G	60	V	1.3	57	70
3EJB	G H	G	61	E	2.7	57	70
3EJB	G H	G	76	D	3.1	76	82
3EJJ	A X	A	6	H	1.7	5	9
3EJJ	A X	A	14	G	161.3	13	24
3EJJ	A X	A	15	H	1.4	13	24
3EJJ	A X	A	82	E	1.6	72	89
3EN1	A B	A	356	E	1.2	352	366
3EN1	A B	A	359	R	2.9	352	366
3EN1	A B	A	363	L	2.0	352	366
3EN1	A B	A	364	R	1.3	352	366
3EN1	A B	A	375	D	3.1	372	387
3EN1	A B	A	377	G	2.9	372	387
3EN1	A B	A	378	E	1.6	372	387
3EN1	A B	B	87	M	1.4	85	95
3EN1	A B	B	90	G	3.7	85	95
3EN1	A B	B	94	K	2.3	85	95
3ENO	A C	A	49	E	2.2	40	50
3ENO	A C	A	97	L	1.2	81	99
3ENO	A C	C	79	V	1.5	59	81
3ENO	B D	D	79	V	1.0	59	80
3ENO	B F	B	49	E	4.5	40	63
3ENO	B F	B	92	R	2.0	81	99
3ENO	B F	B	97	L	1.5	81	99
3ENO	B F	F	75	A	3.6	59	81
3ENS	A B	B	127	W	3.6	125	131
3ENS	C D	D	127	W	3.9	125	132
3EO1	B F	F	61	V	2.5	57	68
3EO1	H L	L	60	T	3.3	57	68
3EO1	H L	L	61	V	2.4	57	68
3EOA	A B	A	124	Q	1.6	122	126
3EOA	B J	J	147	F	1.2	144	161
3EOA	H I	I	147	F	2.5	144	161
3EQS	A B	A	54	L	1.3	50	64
3EQS	A B	A	58	G	65.1	50	64
3EQS	A B	A	61	I	1.4	50	64
3EQS	A B	A	99	I	1.5	96	106
3EQS	A B	B	3	F	4.0	3	11

3EQS	A B	B	6	Y	2.3	3	11
3EQS	A B	B	7	W	4.3	3	11
3EQS	A B	B	10	L	1.4	3	11
3EQY	A C	A	53	M	1.6	49	63
3EQY	A C	A	57	G	58.2	49	63
3EQY	A C	A	60	I	1.4	49	63
3EQY	A C	A	99	Y	3.0	96	105
3EQY	A C	C	3	F	4.1	3	10
3EQY	A C	C	6	Y	2.8	3	10
3EQY	A C	C	7	W	4.5	3	10
3EQY	B D	B	53	M	1.6	49	63
3EQY	B D	B	57	G	62.5	49	63
3EQY	B D	B	60	I	1.5	49	63
3EQY	B D	B	99	Y	3.1	96	105
3EQY	B D	D	3	F	4.1	3	10
3EQY	B D	D	6	Y	2.8	3	10
3EQY	B D	D	7	W	4.7	3	10
3ERC	A D	D	371	L	1.5	363	373
3ERC	B C	B	55	R	1.1	40	56
3ERC	B C	C	371	L	1.3	363	373
3ESW	A B	A	12	F	2.9	12	18
3ESW	A B	A	15	I	1.8	12	18
3ESW	A B	A	20	L	1.8	20	31
3ESW	A B	A	321	I	1.6	306	325
3ESW	A B	A	324	I	1.0	306	325
3ESW	A B	B	263	L	1.0	259	269
3ESW	A B	B	276	L	1.7	276	287
3ESW	A B	B	280	L	1.2	276	287
3ET6	A B	A	502	L	1.5	501	513
3ET6	A B	A	506	Y	1.2	501	513
3ET6	A B	B	506	Y	1.2	501	515
3ETB	H J	J	637	K	1.8	633	639
3ETR	A B	A	123	S	1.7	115	131
3ETR	A B	B	341	Q	2.4	340	346
3ETR	A C	A	31	R	3.2	26	32
3ETR	A C	A	115	F	3.4	115	131
3ETR	A C	A	157	L	1.1	154	164
3ETR	A C	C	1197	G	164.3	1188	1209
3ETR	A C	C	1204	G	3.6	1188	1209
3ETR	B C	B	269	K	2.5	263	271
3ETR	B C	B	507	F	2.8	505	528
3ETR	B C	C	1306	R	1.1	1302	1309
3ETR	L M	L	141	D	1.1	136	143
3ETR	L M	M	341	Q	2.6	340	346
3ETR	L N	L	31	R	1.8	26	35
3ETR	L N	L	115	F	3.5	115	131
3ETR	L N	L	154	R	1.8	154	162
3ETR	L N	L	157	L	1.1	154	162
3ETR	L N	N	1196	E	1.3	1188	1209
3ETR	L N	N	1197	G	107.8	1188	1209
3ETR	L N	N	1204	G	3.9	1188	1209
3ETR	M N	M	269	K	1.2	263	271
3ETR	M N	M	270	F	1.3	263	271
3ETR	M N	M	507	F	2.1	505	528
3ETR	M N	M	514	S	1.4	505	528
3ETR	M N	M	517	F	2.0	505	528
3ETR	M N	N	1306	R	1.2	1302	1309
3EU7	A X	X	31	W	1.6	31	36
3EU7	A X	X	32	F	2.2	31	36
3EUB	A B	A	141	D	1.0	136	142

3EUB	A B	B	341	Q	1.9	340	346
3EUB	A B	B	345	V	1.8	340	346
3EUB	A C	A	31	R	2.5	26	35
3EUB	A C	A	115	F	3.9	115	131
3EUB	A C	A	154	R	1.3	154	162
3EUB	A C	A	157	L	1.3	154	162
3EUB	A C	C	585	Q	1.7	582	588
3EUB	A C	C	1197	G	53.5	1188	1207
3EUB	A C	C	1204	G	1.6	1188	1207
3EUB	B C	B	507	F	2.6	505	527
3EUB	B C	B	514	S	1.0	505	527
3EUB	B C	C	680	R	1.0	675	684
3EUB	B C	C	1306	R	1.5	1302	1309
3EUB	J K	K	341	Q	1.6	340	346
3EUB	J L	J	31	R	2.6	26	35
3EUB	J L	J	115	F	4.3	115	131
3EUB	J L	J	154	R	1.3	154	162
3EUB	J L	J	157	L	1.1	154	162
3EUB	J L	L	585	Q	1.3	582	588
3EUB	J L	L	1197	G	53.1	1188	1207
3EUB	J L	L	1204	G	3.0	1188	1207
3EUB	K L	K	507	F	3.2	505	527
3EUB	K L	K	517	F	1.2	505	527
3EUB	K L	L	1303	E	1.6	1302	1309
3EUB	S T	T	270	F	1.6	263	271
3EUB	S T	T	341	Q	2.4	340	346
3EUB	S U	S	31	R	1.6	26	35
3EUB	S U	S	157	L	1.0	154	160
3EUB	S U	U	1197	G	59.0	1188	1209
3EUB	S U	U	1204	G	2.2	1188	1209
3EUB	T U	T	507	F	2.9	505	528
3EUB	T U	T	517	F	2.4	505	528
3EUB	T U	U	1303	E	1.0	1302	1309
3EUH	A C	A	277	Y	1.0	252	291
3EUH	A C	A	284	F	1.9	252	291
3EUH	A C	A	301	L	2.2	296	307
3EUH	A C	A	305	V	1.0	296	307
3EUH	A C	C	102	M	2.1	99	113
3EUH	A C	C	118	L	1.1	117	121
3EUH	A C	C	136	L	1.0	126	137
3EUH	A D	D	102	M	1.2	99	114
3EUH	B E	B	277	Y	1.1	247	286
3EUH	B E	B	281	V	1.6	247	286
3EUH	B E	B	284	F	2.8	247	286
3EUH	B E	B	300	R	1.0	296	307
3EUH	B E	B	302	R	1.2	296	307
3EUH	B E	B	305	V	1.6	296	307
3EUH	B E	E	102	M	1.6	99	113
3EUH	B E	E	103	M	1.5	99	113
3EUH	B E	E	106	K	1.1	99	113
3EUH	B E	E	195	R	1.1	191	196
3EUH	B F	F	102	M	1.4	99	112
3EUK	C E	E	395	H	1.1	395	408
3EUK	C E	E	396	F	2.2	395	408
3EUK	C E	E	400	R	1.3	395	408
3EUK	H L	H	1313	I	1.1	1309	1318
3EVS	B C	C	66	F	2.8	64	68
3EX7	A B	A	55	S	1.1	54	68
3EX7	A B	A	56	V	1.2	54	68
3EX7	A B	A	124	Y	2.1	116	142

3EX7	A B	A	128	D	1.7	116	142
3EX7	A B	A	135	S	2.4	116	142
3EX7	A B	A	139	L	1.9	116	142
3EX7	A B	A	140	H	4.0	116	142
3EX7	A C	C	358	R	2.9	358	366
3EX7	A C	C	387	R	2.0	385	396
3EX7	A C	C	390	R	4.5	385	396
3EX7	A C	C	391	D	2.2	385	396
3EX7	A C	C	394	Q	1.9	385	396
3EX7	C D	C	155	Y	1.2	146	156
3EX7	C D	C	202	Y	2.8	197	207
3EX7	C D	C	205	Y	3.2	197	207
3EX7	C D	C	261	E	1.8	261	276
3EX7	C D	C	292	W	1.8	287	300
3EX7	C D	C	391	D	1.5	385	396
3EX7	E G	E	140	H	2.8	116	142
3EX7	E H	E	134	F	1.6	116	142
3EX7	E H	H	358	R	3.2	358	366
3EX7	E H	H	359	E	1.1	358	366
3EX7	E H	H	390	R	1.8	386	396
3EX7	E H	H	391	D	1.1	386	396
3EX7	H I	H	202	Y	2.4	197	207
3EX7	H I	H	205	Y	2.8	197	207
3EX7	H I	H	206	R	1.6	197	207
3EX7	H I	H	288	R	1.1	287	300
3EX7	H I	H	292	W	1.5	287	300
3EXG	A B	A	143	P	4.5	140	155
3EXG	A B	A	144	L	1.1	140	155
3EXG	A B	A	147	G	176.2	140	155
3EXG	A B	A	154	Y	3.6	140	155
3EXG	A B	A	177	E	1.7	173	185
3EXG	A B	A	181	M	2.6	173	185
3EXG	A B	B	61	G	88.8	59	73
3EXG	A B	B	64	G	99.4	59	73
3EXG	A B	B	65	I	2.0	59	73
3EXG	A B	B	68	G	54.3	59	73
3EXG	A B	B	101	Y	3.4	100	104
3EXG	A B	B	102	Y	2.4	100	104
3EXG	A D	D	308	L	2.7	306	311
3EXG	A P	A	44	R	2.0	29	56
3EXG	A P	A	314	R	1.8	303	327
3EXG	C B	B	85	F	1.1	83	89
3EXG	C B	B	308	L	1.9	306	311
3EXG	C B	B	309	E	1.4	306	311
3EXG	C B	B	310	D	1.2	306	311
3EXG	C D	C	143	P	2.3	140	156
3EXG	C D	C	146	A	2.3	140	156
3EXG	C D	C	147	G	169.0	140	156
3EXG	C D	C	150	L	1.1	140	156
3EXG	C D	C	154	Y	2.7	140	156
3EXG	C D	C	181	M	1.6	173	185
3EXG	C D	D	60	M	2.0	59	72
3EXG	C D	D	61	G	29.7	59	72
3EXG	C D	D	64	G	7.0	59	72
3EXG	C D	D	65	I	1.9	59	72
3EXG	C D	D	68	G	241.8	59	72
3EXG	C D	D	71	M	2.4	59	72
3EXG	C D	D	102	Y	2.7	100	104
3EXG	E D	E	273	R	1.4	269	285
3EXG	E F	E	147	G	94.1	140	155

3EXG	E F	E	150	L	3.6	140	155
3EXG	E F	E	154	Y	3.9	140	155
3EXG	E F	E	181	M	1.2	173	185
3EXG	E F	F	61	G	23.1	59	73
3EXG	E F	F	64	G	32.6	59	73
3EXG	E F	F	65	I	4.0	59	73
3EXG	E F	F	68	G	200.0	59	73
3EXG	E F	F	101	Y	2.8	100	104
3EXG	E F	F	102	Y	2.7	100	104
3EXG	E H	H	308	L	2.1	306	311
3EXG	E H	H	321	F	2.1	316	327
3EXG	G F	F	308	L	2.2	306	310
3EXG	G H	G	147	G	123.0	147	156
3EXG	G H	G	150	L	1.2	147	156
3EXG	G H	G	154	Y	3.6	147	156
3EXG	G H	G	181	M	1.6	173	185
3EXG	G H	H	61	G	62.9	59	72
3EXG	G H	H	64	G	87.2	59	72
3EXG	G H	H	65	I	4.3	59	72
3EXG	G H	H	68	G	149.2	59	72
3EXG	G H	H	101	Y	3.4	100	104
3EXG	G H	H	102	Y	2.9	100	104
3EXG	I J	I	147	G	160.4	140	155
3EXG	I J	I	154	Y	2.8	140	155
3EXG	I J	J	61	G	23.1	59	72
3EXG	I J	J	64	G	96.9	59	72
3EXG	I J	J	68	G	124.5	59	72
3EXG	I J	J	101	Y	3.7	90	104
3EXG	I J	J	102	Y	2.7	90	104
3EXG	I L	L	308	L	1.4	306	311
3EXG	K J	J	308	L	1.8	306	311
3EXG	K J	J	310	D	1.3	306	311
3EXG	K L	K	147	G	217.1	140	155
3EXG	K L	K	150	L	1.0	140	155
3EXG	K L	K	154	Y	3.3	140	155
3EXG	K L	L	61	G	44.2	59	72
3EXG	K L	L	64	G	26.2	59	72
3EXG	K L	L	65	I	1.4	59	72
3EXG	K L	L	68	G	252.7	59	72
3EXG	K L	L	101	Y	1.2	90	104
3EXG	K L	L	102	Y	2.3	90	104
3EXG	M N	M	143	P	11.0	142	156
3EXG	M N	M	147	G	117.3	142	156
3EXG	M N	M	150	L	1.1	142	156
3EXG	M N	M	154	Y	4.1	142	156
3EXG	M N	M	181	M	1.5	173	185
3EXG	M N	N	61	G	45.2	59	72
3EXG	M N	N	64	G	20.4	59	72
3EXG	M N	N	65	I	1.2	59	72
3EXG	M N	N	68	G	175.3	59	72
3EXG	M N	N	101	Y	2.8	90	104
3EXG	M N	N	102	Y	2.4	90	104
3EXG	M P	P	307	I	1.2	306	311
3EXG	O N	N	85	F	1.6	83	89
3EXG	O N	N	88	Q	1.1	83	89
3EXG	O N	N	308	L	1.6	306	311
3EXG	O N	N	310	D	1.2	306	311
3EXG	O P	O	144	L	1.1	140	155
3EXG	O P	O	147	G	107.3	140	155
3EXG	O P	O	150	L	2.7	140	155

3EXG	O P	O	154	Y	2.4	140	155
3EXG	O P	P	61	G	31.9	59	72
3EXG	O P	P	64	G	192.7	59	72
3EXG	O P	P	68	G	189.7	59	72
3EXG	O P	P	101	Y	2.9	90	104
3EXG	O P	P	102	Y	2.9	90	104
3EXG	Q R	Q	147	G	187.9	140	155
3EXG	Q R	Q	154	Y	3.0	140	155
3EXG	Q R	R	61	G	91.2	59	72
3EXG	Q R	R	64	G	35.3	59	72
3EXG	Q R	R	68	G	113.2	59	72
3EXG	Q R	R	101	Y	4.6	100	104
3EXG	Q R	R	102	Y	2.7	100	104
3EXG	Q T	T	308	L	2.4	306	311
3EXG	Q T	T	321	F	1.0	316	327
3EXG	Q T	T	325	K	1.1	316	327
3EXG	S R	R	85	F	1.5	83	89
3EXG	S R	R	308	L	2.4	306	311
3EXG	S T	S	143	P	1.7	140	156
3EXG	S T	S	147	G	139.2	140	156
3EXG	S T	S	150	L	1.1	140	156
3EXG	S T	S	154	Y	2.5	140	156
3EXG	S T	S	181	M	1.4	173	185
3EXG	S T	T	60	M	1.1	59	72
3EXG	S T	T	61	G	8.3	59	72
3EXG	S T	T	64	G	9.4	59	72
3EXG	S T	T	65	I	1.5	59	72
3EXG	S T	T	68	G	220.0	59	72
3EXG	S T	T	71	M	2.5	59	72
3EXG	S T	T	100	T	2.2	90	104
3EXG	S T	T	101	Y	2.7	90	104
3EXG	S T	T	102	Y	2.8	90	104
3EXG	S T	T	103	M	2.2	90	104
3EXG	U V	U	147	G	182.9	140	155
3EXG	U V	U	150	L	2.8	140	155
3EXG	U V	U	154	Y	3.1	140	155
3EXG	U V	V	61	G	8.7	59	72
3EXG	U V	V	64	G	63.8	59	72
3EXG	U V	V	68	G	151.3	59	72
3EXG	U V	V	101	Y	2.3	90	104
3EXG	U V	V	102	Y	2.7	90	104
3EXG	U X	X	308	L	1.2	306	311
3EXG	U X	X	310	D	1.1	306	311
3EXG	W B	B	46	K	1.3	43	48
3EXG	W V	V	308	L	2.1	306	311
3EXG	W V	V	321	F	1.9	316	327
3EXG	W X	W	144	L	1.3	140	156
3EXG	W X	W	147	G	96.0	140	156
3EXG	W X	W	154	Y	3.4	140	156
3EXG	W X	X	60	M	1.1	59	72
3EXG	W X	X	61	G	29.2	59	72
3EXG	W X	X	64	G	129.3	59	72
3EXG	W X	X	65	I	1.7	59	72
3EXG	W X	X	68	G	142.1	59	72
3EXG	W X	X	101	Y	1.6	100	104
3EXG	W X	X	102	Y	3.2	100	104
3EXG	Y Z	Y	143	P	1.0	140	155
3EXG	Y Z	Y	147	G	120.8	140	155
3EXG	Y Z	Y	150	L	2.3	140	155
3EXG	Y Z	Y	154	Y	2.3	140	155

3EXG	Y Z	Z	61	G	48.7	59	72
3EXG	Y Z	Z	64	G	17.4	59	72
3EXG	Y Z	Z	65	I	1.9	59	72
3EXG	Y Z	Z	68	G	164.0	59	72
3EXG	Y Z	Z	101	Y	3.4	90	104
3EXG	Y Z	Z	102	Y	2.1	90	104
3EXH	A B	A	147	G	237.5	140	156
3EXH	A B	A	150	L	1.2	140	156
3EXH	A B	A	154	Y	3.6	140	156
3EXH	A B	A	181	M	1.1	173	185
3EXH	A B	B	61	G	58.9	59	72
3EXH	A B	B	64	G	57.5	59	72
3EXH	A B	B	65	I	1.6	59	72
3EXH	A B	B	68	G	127.8	59	72
3EXH	A B	B	101	Y	3.2	90	104
3EXH	A B	B	102	Y	2.6	90	104
3EXH	A C	A	173	G	80.7	173	185
3EXH	A C	A	176	F	2.1	173	185
3EXH	A C	A	177	E	1.0	173	185
3EXH	A C	A	180	N	1.8	173	185
3EXH	A C	C	173	G	84.4	173	185
3EXH	A C	C	176	F	1.6	173	185
3EXH	A C	C	180	N	2.4	173	185
3EXH	A D	D	33	Y	1.6	30	34
3EXH	A D	D	85	F	1.8	83	89
3EXH	A D	D	308	L	2.2	306	311
3EXH	A D	D	310	D	1.1	306	311
3EXH	A D	D	321	F	1.0	316	327
3EXH	A D	D	325	K	1.0	316	327
3EXH	A G	A	153	K	2.0	140	156
3EXH	A G	G	280	E	1.9	275	285
3EXH	A G	G	284	K	1.4	275	285
3EXH	B C	B	33	Y	1.2	30	34
3EXH	B C	B	308	L	2.1	306	311
3EXH	B C	B	309	E	3.5	306	311
3EXH	B C	B	321	F	1.1	316	327
3EXH	B C	B	325	K	1.3	316	327
3EXH	B C	C	168	G	5.0	167	171
3EXH	D C	D	61	G	62.9	59	72
3EXH	D C	D	64	G	44.5	59	72
3EXH	D C	D	65	I	4.0	59	72
3EXH	D C	D	68	G	129.7	59	72
3EXH	D C	D	101	Y	3.8	90	104
3EXH	D C	D	102	Y	2.3	90	104
3EXH	D C	C	147	G	216.6	140	156
3EXH	D C	C	150	L	1.0	140	156
3EXH	D C	C	154	Y	4.4	140	156
3EXH	E C	E	153	K	1.5	140	156
3EXH	E C	C	280	E	1.8	275	285
3EXH	E C	C	284	K	1.6	275	285
3EXH	E F	E	147	G	231.5	140	156
3EXH	E F	E	150	L	1.0	140	156
3EXH	E F	E	154	Y	4.5	140	156
3EXH	E F	E	181	M	1.4	173	185
3EXH	E F	F	61	G	66.6	59	72
3EXH	E F	F	64	G	32.1	59	72
3EXH	E F	F	65	I	3.5	59	72
3EXH	E F	F	68	G	151.1	59	72
3EXH	E F	F	101	Y	3.5	100	104
3EXH	E F	F	102	Y	2.8	100	104

3EXH	E G	E	173	G	95.2	173	185
3EXH	E G	E	176	F	1.3	173	185
3EXH	E G	E	180	N	2.1	173	185
3EXH	E G	E	184	L	1.8	173	185
3EXH	E G	G	173	G	157.7	173	185
3EXH	E G	G	176	F	1.8	173	185
3EXH	E G	G	177	E	1.3	173	185
3EXH	E G	G	180	N	2.3	173	185
3EXH	E H	H	321	F	1.3	316	327
3EXH	E H	H	325	K	1.2	316	327
3EXH	F C	C	276	E	1.1	275	285
3EXH	F G	F	308	L	2.1	306	311
3EXH	F G	F	309	E	3.1	306	311
3EXH	F G	F	325	K	1.3	316	327
3EXH	H G	H	61	G	18.3	59	72
3EXH	H G	H	64	G	27.8	59	72
3EXH	H G	H	65	I	5.4	59	72
3EXH	H G	H	68	G	137.0	59	72
3EXH	H G	H	101	Y	3.2	100	104
3EXH	H G	H	102	Y	1.1	100	104
3EXH	H G	G	144	L	1.0	140	155
3EXH	H G	G	147	G	176.7	140	155
3EXH	H G	G	154	Y	3.3	140	155
3EXH	H G	G	177	E	1.0	173	185
3EYF	A B	A	124	E	1.0	123	128
3EYF	A B	A	125	Q	1.6	123	128
3EYF	C D	C	125	Q	1.4	123	129
3EYJ	A B	B	48	I	1.0	38	57
3EYJ	A B	B	97	E	1.1	76	103
3EYJ	A B	B	104	N	2.5	104	127
3EYJ	A B	B	115	M	1.3	104	127
3EYJ	A B	B	152	I	1.1	146	154
3EYM	A B	B	48	I	1.1	38	56
3EYM	A B	B	89	I	1.8	76	127
3EYM	A B	B	92	W	2.4	76	127
3EYM	A B	B	97	E	1.4	76	127
3EYM	A B	B	100	V	1.5	76	127
3EYM	A B	B	103	E	1.5	76	127
3EYM	A B	B	104	N	1.1	76	127
3EYM	A B	B	105	Q	1.5	76	127
3EYM	A B	B	108	I	1.6	76	127
3EYM	A B	B	115	M	1.4	76	127
3EYM	A D	D	50	G	150.9	38	56
3EYM	C B	B	79	D	1.1	76	127
3EYM	C D	D	48	I	1.2	38	56
3EYM	C D	D	89	I	1.9	76	127
3EYM	C D	D	92	W	2.2	76	127
3EYM	C D	D	97	E	1.2	76	127
3EYM	C D	D	100	V	1.8	76	127
3EYM	C D	D	103	E	2.4	76	127
3EYM	C D	D	104	N	2.7	76	127
3EYM	C D	D	105	Q	2.3	76	127
3EYM	C D	D	108	I	1.3	76	127
3EYM	C D	D	115	M	1.0	76	127
3EYM	C F	F	50	G	183.8	38	56
3EYM	C F	F	54	R	3.4	38	56
3EYM	C F	F	106	H	2.3	76	127
3EYM	C F	F	110	L	2.8	76	127
3EYM	E B	B	50	G	144.9	38	56
3EYM	E F	E	110	S	2.2	105	116

3EYM	E F	F	48	I	1.0	38	56
3EYM	E F	F	52	L	1.2	38	56
3EYM	E F	F	89	I	3.1	76	127
3EYM	E F	F	92	W	2.4	76	127
3EYM	E F	F	97	E	1.1	76	127
3EYM	E F	F	100	V	1.4	76	127
3EYM	E F	F	104	N	2.6	76	127
3EYM	E F	F	108	I	1.5	76	127
3EYM	E F	F	115	M	1.5	76	127
3EYQ	C D	C	124	E	5.1	124	128
3EZB	A B	A	72	I	1.0	67	81
3EZB	A B	A	74	E	1.0	67	81
3EZB	A B	A	75	G	188.5	67	81
3EZB	A B	A	115	L	2.2	100	118
3EZB	A B	B	317	R	1.1	316	329
3EZB	A B	B	324	K	1.3	316	329
3EZB	A B	B	327	K	1.3	316	329
3EZB	A B	B	347	L	13.1	347	353
3EZB	A B	B	348	F	1.9	347	353
3EZJ	A B	A	50	R	1.3	49	63
3EZJ	A B	A	53	Y	1.5	49	63
3EZJ	A B	A	57	L	1.3	49	63
3EZJ	A B	A	61	E	1.6	49	63
3EZJ	A B	A	116	R	1.0	115	130
3EZJ	A B	A	123	R	1.5	115	130
3EZJ	A B	A	124	Q	1.7	115	130
3EZJ	A B	A	127	D	1.4	115	130
3EZJ	C D	C	50	R	1.2	49	63
3EZJ	C D	C	51	Q	3.9	49	63
3EZJ	C D	C	53	Y	4.0	49	63
3EZJ	C D	C	54	Q	3.1	49	63
3EZJ	C D	C	57	L	4.4	49	63
3EZJ	C D	C	116	R	1.8	115	130
3EZJ	C D	C	123	R	1.4	115	130
3EZJ	C D	C	124	Q	1.8	115	130
3EZJ	C D	C	127	D	1.4	115	130
3EZJ	E F	E	53	Y	1.4	49	63
3EZJ	E F	E	57	L	1.4	49	63
3EZJ	E F	E	61	E	2.1	49	63
3EZJ	E F	E	123	R	2.9	119	128
3EZJ	E F	E	124	Q	1.3	119	128
3EZJ	G H	G	53	Y	1.5	49	63
3EZJ	G H	G	57	L	1.4	49	63
3EZJ	G H	G	61	E	4.6	49	63
3EZJ	G H	G	124	Q	1.9	119	130
3EZQ	A B	A	232	Y	1.6	225	239
3EZQ	A B	A	295	I	1.8	287	319
3EZQ	A B	A	305	T	2.0	287	319
3EZQ	A B	B	176	L	1.7	171	186
3EZQ	A B	B	180	V	1.0	171	186
3EZQ	A B	B	184	R	1.2	171	186
3EZQ	C D	C	232	Y	1.7	225	239
3EZQ	C D	C	291	Y	1.9	287	319
3EZQ	C D	C	295	I	2.1	287	319
3EZQ	C D	D	103	V	1.0	94	106
3EZQ	C D	D	172	L	1.1	171	186
3EZQ	C D	D	176	L	2.0	171	186
3EZQ	C D	D	179	E	1.1	171	186
3EZQ	C D	D	180	V	1.0	171	186
3EZQ	C D	D	184	R	1.1	171	186

3EZQ	E F	E	228	D	1.0	225	239
3EZQ	E F	E	232	Y	1.8	225	239
3EZQ	E F	E	235	T	1.7	225	239
3EZQ	E F	E	291	Y	1.9	287	319
3EZQ	E F	E	295	I	2.0	287	319
3EZQ	E F	F	102	N	2.1	94	106
3EZQ	E F	F	142	R	1.2	137	152
3EZQ	E F	F	172	L	1.1	171	186
3EZQ	E F	F	176	L	1.7	171	186
3EZQ	E F	F	180	V	1.0	171	186
3EZQ	G H	G	232	Y	1.6	225	239
3EZQ	G H	G	291	Y	2.0	287	319
3EZQ	G H	G	295	I	2.1	287	319
3EZQ	G H	H	103	V	1.0	94	106
3EZQ	G H	H	172	L	1.2	171	186
3EZQ	G H	H	176	L	2.0	171	186
3EZQ	G H	H	180	V	1.0	171	186
3EZQ	G H	H	189	R	1.4	187	191
3EZQ	I J	I	232	Y	1.6	225	239
3EZQ	I J	I	291	Y	2.3	287	319
3EZQ	I J	I	295	I	2.0	287	319
3EZQ	I J	J	172	L	1.2	171	186
3EZQ	I J	J	176	L	1.7	171	186
3EZQ	I J	J	180	V	1.0	171	186
3EZQ	K L	K	232	Y	1.5	225	239
3EZQ	K L	K	291	Y	2.2	287	318
3EZQ	K L	K	295	I	4.5	287	318
3EZQ	K L	K	305	T	1.0	287	318
3EZQ	K L	L	172	L	1.1	171	186
3EZQ	K L	L	176	L	1.9	171	186
3EZQ	K L	L	184	R	1.2	171	186
3EZQ	M N	M	232	Y	2.0	225	239
3EZQ	M N	M	291	Y	1.8	287	318
3EZQ	M N	M	295	I	2.1	287	318
3EZQ	M N	M	305	T	1.5	287	318
3EZQ	M N	M	306	L	1.3	287	318
3EZQ	M N	M	309	K	1.5	287	318
3EZQ	M N	N	103	V	1.0	94	106
3EZQ	M N	N	172	L	1.2	171	186
3EZQ	M N	N	176	L	2.0	171	186
3EZQ	M N	N	180	V	1.0	171	186
3EZQ	M N	N	182	Q	1.1	171	186
3EZQ	M N	N	184	R	1.2	171	186
3EZQ	M N	N	189	R	1.3	187	191
3EZQ	O P	O	232	Y	1.2	225	239
3EZQ	O P	O	291	Y	1.1	287	319
3EZQ	O P	O	294	L	1.4	287	319
3EZQ	O P	O	295	I	2.7	287	319
3EZQ	O P	O	305	T	2.6	287	319
3EZQ	O P	P	173	V	1.0	171	186
3EZQ	O P	P	175	D	1.4	171	186
3EZQ	O P	P	176	L	2.7	171	186
3EZQ	O P	P	179	E	1.6	171	186
3EZQ	O P	P	180	V	1.0	171	186
3F02	A C	A	34	Y	2.5	25	40
3F02	A C	A	50	P	1.4	50	64
3F02	A C	A	264	L	2.3	264	271
3F02	A C	A	268	E	1.4	264	271
3F02	B D	B	34	Y	2.1	25	40
3F02	B D	B	50	P	1.4	50	64

3F02	B D	B	264	L	2.0	264	271
3F02	B D	B	268	E	1.0	264	271
3F1E	C N	C	9	G	71.1	7	11
3F1E	C N	C	29	Y	1.6	27	45
3F1E	C N	C	30	R	1.0	27	45
3F1E	C N	N	49	H	2.2	41	51
3F1E	D E	D	205	E	1.7	200	207
3F1E	D E	E	107	R	2.0	104	112
3F1E	F R	R	65	I	1.0	60	76
3F1E	G K	K	59	Y	2.1	58	75
3F1E	J N	N	41	R	1.1	41	51
3F1E	J N	N	45	R	1.7	41	51
3F1F	E T	T	8	K	1.3	4	12
3F1F	F P	F	117	R	1.8	103	121
3F1F	N U	U	61	W	1.8	32	73
3F1F	N U	U	63	V	1.5	32	73
3F1F	O T	O	107	R	1.2	104	110
3F1F	O T	T	103	R	1.2	100	104
3F1F	Q Z	Q	51	R	1.7	44	58
3F1F	Q Z	Z	48	F	1.4	41	52
3F1F	Q Z	Z	180	V	1.4	180	189
3F1F	Q Z	Z	183	L	1.4	180	189
3F1F	U V	U	43	G	39.9	32	73
3F1I	H S	H	409	L	1.1	405	430
3F1I	H S	H	416	V	1.1	405	430
3F1I	H S	H	419	F	2.1	405	430
3F1I	H S	H	423	M	1.7	405	430
3F1I	H S	H	443	F	2.9	437	500
3F1I	H S	H	446	I	1.0	437	500
3F1I	H S	H	450	H	1.7	437	500
3F1I	H S	H	453	L	2.3	437	500
3F1I	H S	H	457	L	2.0	437	500
3F1I	H S	H	460	L	1.9	437	500
3F1I	H S	H	467	Y	3.1	437	500
3F1I	H S	H	473	K	1.5	437	500
3F1I	H S	H	474	L	1.7	437	500
3F1I	H S	H	477	I	2.2	437	500
3F1I	H S	H	481	R	2.4	437	500
3F1I	H S	H	484	L	2.4	437	500
3F1I	H S	H	488	R	2.1	437	500
3F1I	H S	H	491	H	1.2	437	500
3F1I	H S	S	307	M	1.7	304	316
3F1I	H S	S	311	L	2.0	304	316
3F1I	H S	S	314	L	2.0	304	316
3F1I	H S	S	343	I	1.2	327	376
3F1I	H S	S	347	L	1.7	327	376
3F1I	H S	S	354	H	2.0	327	376
3F1I	H S	S	357	L	2.3	327	376
3F1I	H S	S	360	L	2.8	327	376
3F1I	H S	S	361	N	1.0	327	376
3F1I	H S	S	364	V	1.5	327	376
3F1I	H S	S	368	L	1.8	327	376
3F1I	H S	S	371	Y	2.8	327	376
3F1I	H S	S	374	L	1.7	327	376
3F1S	A B	A	293	D	2.1	288	294
3F1S	A B	B	246	D	1.7	245	249
3F1S	A B	B	251	L	1.1	250	256
3F1S	A B	B	353	L	1.9	352	360
3F2O	A C	C	196	E	1.9	195	200
3F3P	A D	D	318	G	13.2	300	319

3F3P	A D	D	373	E	1.5	371	376
3F3P	B C	C	318	G	21.5	300	319
3F3P	B D	D	471	F	1.1	467	475
3F3P	B D	D	534	I	1.3	532	545
3F3P	B D	D	537	E	1.9	532	545
3F3P	E G	G	471	F	1.2	467	475
3F3P	E G	G	507	L	1.1	504	510
3F3P	E G	G	537	E	1.1	532	545
3F3P	E G	G	540	T	1.1	532	545
3F3P	E H	H	318	G	42.4	300	319
3F3P	E H	H	373	E	1.2	371	376
3F3P	F G	G	318	G	21.9	300	319
3F3P	F H	H	471	F	1.3	467	475
3F3P	F H	H	506	E	2.6	504	510
3F3P	F H	H	507	L	1.1	504	510
3F3P	I K	K	471	F	1.1	467	475
3F3P	I L	L	311	L	1.0	300	319
3F3P	I L	L	318	G	50.5	300	319
3F3P	J K	K	318	G	6.7	300	319
3F3P	J K	K	373	E	1.0	371	376
3F3P	J L	L	471	F	1.0	467	475
3F3P	J L	L	506	E	1.1	504	510
3F5C	A B	A	550	L	1.0	550	560
3F5C	A B	B	275	P	2.9	275	279
3F5C	A B	B	400	K	1.2	399	421
3F5C	A C	A	537	Y	1.0	525	542
3F5C	A C	A	538	Y	2.0	525	542
3F5C	A C	C	401	Y	1.8	399	421
3F6Q	A B	A	43	R	2.5	37	44
3F6Q	A B	A	106	Y	1.9	103	110
3F6Q	A B	A	109	F	3.2	103	110
3F6Q	A B	B	61	H	2.4	60	68
3F6Q	A B	B	62	D	2.0	60	68
3F6Q	A B	B	65	M	1.0	60	68
3F6Q	A B	B	67	F	1.2	60	68
3F6Z	A B	A	35	E	1.7	25	36
3F6Z	A B	A	109	V	1.1	109	116
3F6Z	A B	A	112	R	1.1	109	116
3F6Z	C D	C	35	E	1.2	25	37
3F6Z	C D	C	62	W	3.2	60	64
3F6Z	C D	C	63	W	2.3	60	64
3F6Z	C D	C	112	R	1.1	109	116
3F75	A P	A	147	M	1.0	147	151
3F75	A P	A	150	Q	1.8	147	151
3F75	A P	P	147	Y	1.7	131	153
3F75	A P	P	148	I	1.1	131	153
3F75	A P	P	170	R	2.6	170	177
3F75	A P	P	173	F	2.5	170	177
3F7P	A C	A	157	P	1.6	157	175
3F7P	A C	A	159	L	1.1	157	175
3F7P	B D	B	123	R	1.3	123	140
3F8U	A B	A	59	H	1.3	58	73
3F8U	A B	A	410	K	1.8	407	423
3F8U	C B	C	173	K	2.0	166	178
3F8U	C D	C	59	H	2.1	58	73
3F8U	C D	C	407	G	6.3	407	423
3F9K	A C	A	6	E	1.8	5	16
3F9K	A C	A	10	E	1.4	5	16
3F9K	A C	A	13	E	1.3	5	16
3F9K	A C	A	174	T	1.3	172	186

3F9K	A C	C	360	K	1.0	348	362
3F9K	A C	C	401	K	1.7	394	403
3F9K	B C	B	95	R	1.2	94	106
3F9K	B C	B	128	M	1.3	124	134
3F9K	B C	B	131	W	2.6	124	134
3F9K	B K	B	2	L	2.1	2	16
3F9K	B K	K	420	Y	1.0	410	430
3F9K	c e	c	6	E	1.0	5	16
3F9K	c e	e	401	K	1.2	394	403
3F9K	d e	d	95	R	1.2	94	106
3F9K	d e	d	128	M	1.0	124	134
3F9K	d e	d	131	W	1.7	124	134
3F9K	d e	d	132	W	1.2	124	134
3F9K	d O	d	35	Q	1.0	30	39
3F9K	E G	E	6	E	1.0	5	16
3F9K	E G	E	10	E	1.3	5	16
3F9K	E G	G	401	K	1.4	394	403
3F9K	F G	F	131	W	2.2	124	134
3F9K	F K	K	413	M	1.1	410	430
3F9K	g i	g	6	E	2.1	5	16
3F9K	g i	g	10	E	1.7	5	16
3F9K	g i	g	13	E	1.8	5	16
3F9K	g i	g	14	K	1.2	5	16
3F9K	g i	i	398	T	1.0	394	403
3F9K	g i	i	401	K	3.2	394	403
3F9K	g i	i	402	K	1.9	394	403
3F9K	I K	I	6	E	1.5	5	16
3F9K	I K	I	10	E	1.1	5	16
3F9K	I K	I	13	E	1.5	5	16
3F9K	I K	K	360	K	1.6	348	362
3F9K	I K	K	401	K	1.3	394	403
3F9K	I K	K	402	K	1.0	394	403
3F9K	J a	J	35	Q	1.2	30	39
3F9K	J K	J	95	R	1.1	94	106
3F9K	J K	J	128	M	1.2	124	134
3F9K	J K	J	131	W	2.1	124	134
3F9K	M O	M	6	E	1.7	5	16
3F9K	M O	M	10	E	1.2	5	16
3F9K	M O	M	13	E	1.5	5	16
3F9K	M O	O	401	K	1.8	394	403
3F9K	N O	N	95	R	1.2	94	106
3F9K	N O	N	128	M	2.1	124	134
3F9K	N O	N	131	W	2.0	124	134
3F9K	Q S	Q	6	E	1.8	5	16
3F9K	Q S	Q	10	E	1.3	5	16
3F9K	Q S	S	401	K	1.4	394	403
3F9K	R C	C	413	M	1.2	410	430
3F9K	R e	R	2	L	2.5	2	16
3F9K	R e	e	394	T	1.3	394	403
3F9K	R S	R	128	M	1.7	124	134
3F9K	R S	R	131	W	2.4	124	134
3F9K	U W	U	6	E	1.2	5	16
3F9K	U W	W	401	K	2.0	394	403
3F9K	U W	W	402	K	1.0	394	403
3F9K	V i	V	35	Q	1.0	30	39
3F9K	V i	i	436	L	1.1	435	440
3F9K	V O	O	413	M	1.0	410	430
3F9K	V W	V	95	R	1.2	94	106
3F9K	V W	V	131	W	1.8	124	134
3F9K	Y a	Y	6	E	1.9	5	16

3F9K	Y a	Y	10	E	1.4	5	16
3F9K	Y a	a	360	K	1.4	348	362
3F9K	Y a	a	361	N	1.0	348	362
3F9K	Y a	a	401	K	1.7	394	403
3F9K	Y a	a	402	K	1.1	394	403
3F9K	Z a	Z	95	R	1.1	94	106
3F9K	Z a	Z	131	W	1.9	124	134
3FAL	A B	A	348	R	2.1	343	360
3FAL	A B	A	352	E	1.3	343	360
3FAL	A B	A	397	Y	2.5	386	408
3FAL	A B	A	419	L	1.0	414	420
3FAL	A B	A	423	P	2.4	421	432
3FAL	A B	A	424	A	1.7	421	432
3FAL	A B	A	426	R	2.1	421	432
3FAL	A B	A	427	S	1.5	421	432
3FAL	A B	B	400	L	1.4	399	424
3FAL	A B	B	406	L	1.2	399	424
3FAL	A B	B	410	V	1.3	399	424
3FAL	A B	B	413	R	2.6	399	424
3FAL	A D	A	276	L	1.0	264	277
3FAL	A D	A	305	W	1.8	294	317
3FAL	A D	A	451	F	1.5	451	458
3FAL	A D	A	455	M	1.3	451	458
3FAL	A D	A	456	L	2.1	451	458
3FAL	A D	A	457	E	1.0	451	458
3FAL	A D	D	281	R	1.1	281	303
3FAL	A D	D	436	L	1.6	435	443
3FAL	A D	D	439	E	2.5	435	443
3FAL	C B	C	276	L	1.1	276	286
3FAL	C B	C	305	W	2.3	294	317
3FAL	C B	C	451	F	1.0	451	458
3FAL	C B	C	453	M	1.5	451	458
3FAL	C B	B	285	I	1.1	281	303
3FAL	C B	B	435	P	1.3	435	443
3FAL	C D	C	397	Y	1.8	386	408
3FAL	C D	C	427	S	1.2	421	433
3FAL	C D	C	430	L	1.2	421	433
3FAL	C D	D	400	L	1.4	399	428
3FAL	C D	D	413	R	2.5	399	428
3FBI	A B	B	26	F	2.7	25	36
3FBI	A B	B	32	F	1.8	25	36
3FBI	A B	B	41	Y	2.3	39	47
3FBI	A B	B	57	F	1.0	56	65
3FBI	A B	B	60	Y	3.2	56	65
3FBI	A B	B	63	Y	3.3	56	65
3FBI	C D	C	21	V	1.6	19	23
3FBI	C D	C	65	Y	1.6	62	66
3FBI	C D	D	26	F	2.2	25	36
3FBI	C D	D	32	F	2.9	25	36
3FBI	C D	D	60	Y	3.1	56	64
3FBI	C D	D	63	Y	4.3	56	64
3FCS	A B	B	261	R	1.0	259	263
3FCS	A B	B	262	L	2.6	259	263
3FCS	A B	B	293	G	1.4	292	302
3FCS	A B	B	297	E	1.7	292	302
3FCS	A B	B	324	L	1.2	315	325
3FCS	C D	D	261	R	1.0	259	263
3FCS	C D	D	262	L	1.9	259	263
3FCS	C D	D	297	E	1.9	292	302
3FCS	C D	D	324	L	1.0	315	325

3FCU	A B	B	261	R	1.2	259	263
3FCU	A B	B	262	L	2.2	259	263
3FCU	A B	B	321	Y	1.5	315	325
3FCU	A B	B	324	L	1.3	315	325
3FCU	C D	D	262	L	1.3	259	263
3FCU	C D	D	293	G	1.7	292	302
3FCU	C D	D	321	Y	1.1	315	324
3FCU	E F	F	262	L	2.2	259	263
3FCU	E F	F	293	G	1.1	292	302
3FCU	E F	F	321	Y	1.2	315	325
3FCU	E F	F	324	L	1.4	315	325
3FDL	A B	A	97	F	2.3	26	101
3FDL	A B	A	108	L	2.1	102	111
3FDL	A B	A	126	V	1.3	119	131
3FDL	A B	A	129	E	1.2	119	131
3FDL	A B	A	130	L	1.0	119	131
3FDL	A B	A	138	G	188.0	137	157
3FDL	A B	A	139	R	2.7	137	157
3FDL	A B	B	90	I	2.4	87	106
3FDL	A B	B	93	E	1.1	87	106
3FDL	A B	B	94	L	3.7	87	106
3FDL	A B	B	95	R	2.5	87	106
3FDL	A B	B	96	R	1.4	87	106
3FDL	A B	B	97	I	2.6	87	106
3FDL	A B	B	98	G	8.8	87	106
3FDL	A B	B	99	D	3.1	87	106
3FDL	A B	B	101	F	4.2	87	106
3FDO	A B	A	53	M	1.4	49	64
3FDO	A B	A	57	G	115.0	49	64
3FDO	A B	B	19	F	4.0	19	26
3FDO	A B	B	22	Y	2.2	19	26
3FDO	A B	B	23	W	3.9	19	26
3FDS	C D	C	145	V	1.2	140	154
3FDS	C D	C	149	D	1.0	140	154
3FDS	C D	C	152	L	1.7	140	154
3FDZ	A B	A	59	K	1.2	59	72
3FDZ	A B	A	62	I	1.3	59	72
3FDZ	A B	A	63	R	2.2	59	72
3FDZ	A B	A	66	W	5.4	59	72
3FDZ	A B	A	69	Q	1.2	59	72
3FDZ	A B	A	70	D	3.3	59	72
3FDZ	A B	B	62	I	1.3	59	72
3FDZ	A B	B	63	R	3.0	59	72
3FDZ	A B	B	66	W	4.8	59	72
3FDZ	A B	B	70	D	1.7	59	72
3FFC	A D	A	162	G	1.7	152	175
3FFC	A D	A	167	W	3.2	152	175
3FFC	A G	A	75	R	1.6	57	85
3FFC	F B	F	79	R	1.2	57	85
3FFC	F I	F	162	G	2.8	152	175
3FFC	F I	F	167	W	3.2	152	175
3FFD	A B	B	132	E	1.2	131	135
3FFD	A B	B	133	E	2.2	131	135
3FFD	A P	P	26	H	1.4	15	30
3FFD	A P	P	27	L	1.9	15	30
3FFD	B P	P	16	Q	1.2	15	30
3FFD	B P	P	23	F	2.3	15	30
3FGC	A B	A	17	Q	1.6	17	34
3FGC	A B	A	18	T	1.6	17	34
3FGC	A B	A	21	M	2.9	17	34

3FGC	A B	A	22	K	1.3	17	34
3FGC	A B	A	57	V	1.7	55	65
3FGC	A B	A	61	H	2.0	55	65
3FGC	A B	A	64	G	100.1	55	65
3FGC	A B	A	92	L	2.5	83	97
3FGC	A B	A	96	M	2.2	83	97
3FGC	A B	A	115	R	2.0	111	117
3FGC	A B	A	116	V	3.9	111	117
3FGC	A B	B	17	S	1.3	17	31
3FGC	A B	B	21	I	1.4	17	31
3FGC	A B	B	57	T	2.4	55	65
3FGC	A B	B	60	G	4.6	55	65
3FGC	A B	B	61	F	4.0	55	65
3FGC	A B	B	64	G	79.7	55	65
3FGC	A B	B	85	R	2.9	83	97
3FGC	A B	B	92	L	2.3	83	97
3FGC	A B	B	95	Q	1.4	83	97
3FGC	A B	B	96	M	2.0	83	97
3FGC	A B	B	116	F	3.4	111	117
3FGC	A D	A	249	H	1.1	236	259
3FGC	A D	D	202	K	1.6	198	215
3FGC	A D	D	270	E	1.0	260	271
3FGC	C D	C	18	T	1.3	17	33
3FGC	C D	C	22	K	1.5	17	33
3FGC	C D	C	57	V	1.9	55	65
3FGC	C D	C	61	H	1.9	55	65
3FGC	C D	C	64	G	36.2	55	65
3FGC	C D	C	85	R	1.1	83	97
3FGC	C D	C	92	L	2.3	83	97
3FGC	C D	C	96	M	2.2	83	97
3FGC	C D	C	116	V	2.4	111	117
3FGC	C D	D	17	S	1.1	17	31
3FGC	C D	D	21	I	1.7	17	31
3FGC	C D	D	25	L	1.0	17	31
3FGC	C D	D	60	G	1.6	55	65
3FGC	C D	D	61	F	4.1	55	65
3FGC	C D	D	64	G	97.9	55	65
3FGC	C D	D	85	R	1.9	83	97
3FGC	C D	D	92	L	1.7	83	97
3FGC	C D	D	96	M	1.8	83	97
3FGC	C D	D	116	F	4.1	111	117
3FH6	F B	F	417	I	1.3	410	420
3FH6	F B	B	98	F	2.0	98	104
3FH6	F B	B	102	L	1.1	98	104
3FH6	F G	F	78	F	1.4	68	90
3FH6	F G	F	82	P	4.6	68	90
3FH6	F G	F	83	L	1.5	68	90
3FH6	F G	F	317	Y	1.5	314	327
3FH6	F G	F	331	I	1.1	329	340
3FH6	F G	F	334	L	8.8	329	340
3FH6	F G	F	336	F	7.6	329	340
3FH6	F G	F	338	G	356.7	329	340
3FH6	F G	F	446	L	1.0	441	448
3FH6	F G	F	501	L	6.6	487	508
3FH6	F G	G	13	L	1.0	9	27
3FH6	F G	G	20	L	2.0	9	27
3FH6	F G	G	31	L	1.2	28	36
3FH6	F G	G	143	L	1.3	136	151
3FH6	G A	A	98	F	2.4	92	102
3FH6	H D	D	47	R	1.1	42	51

3FH6	H I	H	78	F	1.4	68	90
3FH6	H I	H	82	P	4.6	68	90
3FH6	H I	H	83	L	1.5	68	90
3FH6	H I	H	317	Y	1.5	314	327
3FH6	H I	H	331	I	1.0	329	340
3FH6	H I	H	334	L	1.6	329	340
3FH6	H I	H	337	K	1.7	329	340
3FH6	H I	H	338	G	353.0	329	340
3FH6	H I	H	446	L	1.0	441	448
3FH6	H I	H	501	L	6.5	487	508
3FH6	H I	I	12	R	1.4	9	27
3FH6	H I	I	13	L	1.1	9	27
3FH6	H I	I	20	L	2.0	9	27
3FH6	H I	I	31	L	1.2	28	36
3FH6	H I	I	143	L	1.3	136	151
3FH6	H I	I	260	W	1.0	259	285
3FH6	I C	C	98	F	2.5	92	102
3FH9	A B	A	31	R	3.0	21	36
3FH9	A B	A	34	L	1.1	21	36
3FH9	A B	A	107	V	1.0	95	113
3FH9	A B	A	122	H	3.6	119	137
3FH9	A B	B	30	R	3.5	22	35
3FH9	A B	B	34	V	1.2	22	35
3FH9	A B	B	116	R	1.4	100	119
3FHI	A B	A	129	F	2.7	128	136
3FHI	A B	A	230	E	1.5	217	234
3FHI	A B	A	244	I	1.1	243	253
3FHI	A B	A	247	Y	2.0	243	253
3FHI	A B	B	201	L	1.4	200	205
3FHI	A B	B	234	M	1.2	226	239
3FIC	C N	C	9	G	134.0	7	12
3FIC	C N	N	49	H	1.1	41	51
3FIC	K G	K	59	Y	1.9	58	75
3FIE	A C	A	113	Y	1.5	102	114
3FIE	A C	A	322	W	2.0	313	324
3FIH	D E	D	197	H	1.1	196	204
3FIH	D E	D	201	E	1.0	196	204
3FIH	K G	K	60	F	1.5	59	73
3FIH	M S	M	82	L	1.0	66	83
3FIH	N C	C	39	R	1.3	25	45
3FIK	Q R	Q	39	I	1.0	31	42
3FIK	Q R	Q	46	Y	1.2	43	48
3FIN	F P	F	34	W	2.0	30	41
3FIN	F P	F	187	V	1.0	183	189
3FIN	U V	U	39	L	1.1	32	55
3FIN	U V	U	40	F	1.6	32	55
3FIN	U V	U	43	G	1.0	32	55
3FKS	A D	A	285	L	1.4	273	287
3FKS	A D	A	286	L	1.1	273	287
3FKS	A D	A	360	Y	2.2	356	362
3FKS	A D	D	290	G	58.8	285	291
3FKS	A E	A	302	Y	2.1	300	309
3FKS	A E	E	192	R	1.5	191	205
3FKS	B E	B	285	L	1.2	273	287
3FKS	B E	E	290	G	8.1	285	295
3FKS	B F	B	301	F	1.4	300	306
3FKS	B F	B	302	Y	2.5	300	306
3FKS	B F	F	196	D	1.4	194	203
3FKS	B F	F	424	F	1.7	419	426
3FKS	C D	C	302	Y	2.7	300	311

3FKS	C D	C	400	R	1.4	392	403
3FKS	C D	D	193	E	1.4	191	205
3FKS	C F	C	212	R	2.0	212	223
3FKS	C F	C	285	L	1.3	273	287
3FKS	C F	C	360	Y	1.0	356	362
3FKS	C F	F	326	F	1.4	320	327
3FKS	D G	D	387	I	1.3	385	392
3FKS	D G	D	390	I	1.4	385	392
3FKS	D G	D	391	L	1.2	385	392
3FKS	D G	G	19	I	1.6	13	30
3FKS	E G	E	386	D	1.2	365	392
3FKS	E G	G	271	I	1.0	247	273
3FKS	F G	F	390	I	1.5	385	392
3FKS	F G	G	9	R	1.2	3	12
3FKS	G H	G	44	M	1.3	36	56
3FKS	G H	G	50	L	1.5	36	56
3FKS	G H	G	209	L	1.1	205	226
3FKS	G H	G	212	Y	2.1	205	226
3FKS	G I	G	212	Y	1.5	205	226
3FKS	G I	I	10	Y	1.8	10	21
3FKS	J M	J	212	R	2.2	212	225
3FKS	J M	J	214	T	1.3	212	225
3FKS	J M	J	286	L	1.2	273	287
3FKS	J M	J	360	Y	1.2	356	362
3FKS	J M	M	290	G	127.0	285	291
3FKS	J N	J	302	Y	2.4	300	311
3FKS	J N	J	309	E	1.7	300	311
3FKS	J N	N	193	E	2.6	191	205
3FKS	J N	N	271	L	1.3	258	273
3FKS	K N	K	285	L	1.1	273	287
3FKS	K N	N	290	G	66.3	285	291
3FKS	K O	K	302	Y	4.1	300	306
3FKS	K O	K	309	E	2.1	307	311
3FKS	K O	O	194	G	8.6	194	205
3FKS	K O	O	198	Y	1.3	194	205
3FKS	K O	O	226	P	1.2	226	248
3FKS	K O	O	267	E	1.2	258	273
3FKS	K O	O	337	R	1.1	337	343
3FKS	K O	O	423	V	1.0	422	426
3FKS	K P	P	257	R	2.2	247	275
3FKS	K X	X	464	E	3.2	463	473
3FKS	L M	L	302	Y	2.9	300	311
3FKS	L M	L	306	R	1.4	300	311
3FKS	L M	M	193	E	2.7	191	205
3FKS	L M	M	194	G	1.5	191	205
3FKS	L M	M	196	D	2.5	191	205
3FKS	L M	M	424	F	1.2	422	426
3FKS	L O	L	212	R	1.4	212	225
3FKS	L O	L	285	L	1.3	273	287
3FKS	L O	O	290	G	156.2	285	291
3FKS	M P	P	273	G	125.7	247	275
3FKS	N P	P	25	I	1.0	24	28
3FKS	N P	P	259	R	2.5	247	275
3FKS	N P	P	271	I	1.0	247	275
3FKS	O P	P	247	M	1.0	247	275
3FKS	P R	P	151	L	1.4	140	153
3FKS	P R	P	211	E	1.7	206	222
3FKS	S V	S	212	R	2.0	212	225
3FKS	S V	S	214	T	2.3	212	225
3FKS	S V	S	285	L	1.3	273	287

3FKS	S V	S	286	L	1.1	273	287
3FKS	S V	S	360	Y	1.8	356	362
3FKS	S V	V	290	G	6.5	285	296
3FKS	S V	V	328	H	1.4	320	329
3FKS	S W	S	305	S	4.7	305	311
3FKS	S W	S	306	R	1.2	305	311
3FKS	S W	W	191	T	1.9	191	205
3FKS	S W	W	226	P	1.3	226	230
3FKS	T W	T	285	L	1.0	273	286
3FKS	T W	W	290	G	4.8	285	294
3FKS	T W	W	328	H	1.1	320	329
3FKS	T X	T	339	Y	1.1	339	348
3FKS	T X	X	194	G	5.9	191	205
3FKS	T X	X	199	R	2.3	191	205
3FKS	T X	X	266	S	1.0	258	272
3FKS	T X	X	337	R	1.2	337	343
3FKS	T X	X	423	V	1.0	422	426
3FKS	T X	X	424	F	1.4	422	426
3FKS	U V	U	302	Y	3.4	300	304
3FKS	U V	V	193	E	1.9	191	202
3FKS	U X	U	213	S	1.6	212	225
3FKS	U X	U	214	T	1.4	212	225
3FKS	U X	U	285	L	1.4	273	287
3FKS	U X	U	360	Y	2.4	356	361
3FKS	U X	X	290	G	204.5	285	291
3FKS	U X	X	326	F	1.3	320	329
3FKS	V Y	Y	19	I	1.4	3	30
3FKS	V Y	Y	273	G	1.9	214	275
3FKS	W Y	Y	259	R	1.8	214	275
3FKS	W Y	Y	264	T	1.1	214	275
3FKS	X Y	X	390	I	4.4	385	391
3FKU	A B	B	93	T	1.0	75	109
3FKU	A B	B	101	L	1.0	75	109
3FKU	A B	B	104	N	1.7	75	109
3FKU	A B	B	108	L	1.8	75	109
3FKU	A B	B	111	H	3.0	110	126
3FKU	A B	B	115	V	1.0	110	126
3FKU	A D	A	107	H	1.2	102	111
3FKU	B Y	B	41	T	1.0	38	59
3FKU	C B	B	50	N	1.1	38	59
3FKU	C D	C	107	H	1.4	102	111
3FKU	C D	D	89	L	1.4	77	126
3FKU	C D	D	101	L	1.2	77	126
3FKU	C D	D	104	N	1.6	77	126
3FKU	C D	D	108	L	2.0	77	126
3FKU	C D	D	111	H	1.9	77	126
3FKU	C F	C	104	E	1.2	102	111
3FKU	C F	C	107	H	2.9	102	111
3FKU	C F	C	108	L	1.1	102	111
3FKU	D Z	D	42	Q	1.0	38	59
3FKU	D Z	D	49	T	1.4	38	59
3FKU	E B	E	107	H	1.6	102	111
3FKU	E B	B	76	R	2.5	75	109
3FKU	E D	D	110	F	1.0	77	126
3FKU	E F	E	106	K	1.1	102	111
3FKU	E F	F	52	V	3.0	38	59
3FKU	E F	F	89	L	1.5	78	103
3FKU	E F	F	100	V	1.3	78	103
3FKU	E F	F	101	L	1.1	78	103
3FKU	E F	F	104	N	1.9	104	117

3FKU	E F	F	108	L	2.4	104	117
3FKU	F X	F	42	Q	1.0	38	59
3FKU	G H	H	93	T	1.1	87	108
3FKU	G H	H	104	N	1.5	87	108
3FKU	G H	H	111	H	1.5	109	126
3FKU	G J	G	107	H	2.1	102	112
3FKU	G J	J	76	R	1.0	75	86
3FKU	I J	I	103	E	1.0	102	111
3FKU	I J	J	93	T	1.0	87	126
3FKU	I J	J	101	L	1.9	87	126
3FKU	I J	J	104	N	2.1	87	126
3FKU	I J	J	108	L	1.5	87	126
3FKU	I J	J	111	H	5.2	87	126
3FKU	I L	I	104	E	1.1	102	111
3FKU	I L	I	107	H	2.0	102	111
3FKU	I L	I	108	L	1.2	102	111
3FKU	K H	K	107	H	1.6	102	111
3FKU	K J	J	110	F	2.0	87	126
3FKU	K L	L	93	T	1.1	78	126
3FKU	K L	L	108	L	5.2	78	126
3FKU	K L	L	111	H	1.8	78	126
3FLO	A B	A	254	L	2.4	254	276
3FLO	A B	A	265	I	1.5	254	276
3FLO	A B	A	461	L	1.4	461	475
3FLO	A B	B	1324	L	1.4	1323	1342
3FLO	A B	B	1325	Q	2.0	1323	1342
3FLO	A B	B	1329	Q	1.0	1323	1342
3FLO	A B	B	1332	H	1.4	1323	1342
3FLO	A B	B	1335	R	2.3	1323	1342
3FLO	A B	B	1338	I	1.0	1323	1342
3FLO	A B	B	1339	S	1.6	1323	1342
3FLO	A B	B	1448	Y	1.0	1435	1451
3FLO	C D	C	254	L	2.2	254	276
3FLO	C D	C	461	L	1.6	461	475
3FLO	C D	D	1324	L	2.5	1323	1342
3FLO	C D	D	1325	Q	1.3	1323	1342
3FLO	C D	D	1327	T	1.0	1323	1342
3FLO	C D	D	1332	H	1.3	1323	1342
3FLO	C D	D	1335	R	2.1	1323	1342
3FLO	C D	D	1448	Y	1.4	1435	1452
3FLO	E F	E	254	L	3.2	254	276
3FLO	E F	F	1324	L	1.7	1323	1342
3FLO	E F	F	1335	R	2.1	1323	1342
3FLO	G H	G	254	L	2.4	254	276
3FLO	G H	G	461	L	1.3	461	475
3FLO	G H	H	1324	L	2.1	1323	1342
3FLO	G H	H	1325	Q	1.7	1323	1342
3FLO	G H	H	1332	H	1.3	1323	1342
3FLO	G H	H	1335	R	1.7	1323	1342
3FLO	G H	H	1448	Y	1.1	1435	1452
3FMO	A B	B	219	G	14.7	218	225
3FMO	A B	B	223	D	1.4	218	225
3FMO	A B	B	253	H	1.3	253	263
3FMO	A B	B	256	Q	1.4	253	263
3FMO	A B	B	259	R	2.8	253	263
3FMP	A B	B	219	G	3.7	218	229
3FMP	A B	B	223	D	2.5	218	229
3FMP	A B	B	255	D	1.7	253	263
3FMP	A B	B	256	Q	1.2	253	263
3FMP	A B	B	259	R	3.3	253	263

3FMP	C D	D	219	G	2.7	218	229
3FMP	C D	D	220	T	1.0	218	229
3FMP	C D	D	223	D	2.5	218	229
3FMP	C D	D	259	R	2.6	253	263
3FN1	A B	A	400	I	2.3	398	404
3FOE	A C	C	513	H	1.2	509	522
3FOE	A C	C	515	Q	205.1	509	522
3FOE	A C	C	519	L	17.4	509	522
3FOE	A C	C	530	V	4.4	527	533
3FOE	B D	B	12	I	47.0	12	16
3FOE	B D	B	19	R	3.4	17	26
3FOE	B D	B	20	Y	9.5	17	26
3FOE	B D	B	25	I	3.6	17	26
3FOE	B D	D	513	H	1.1	509	522
3FOE	B D	D	516	T	17.1	509	522
3FOE	B D	D	519	L	38.9	509	522
3FOE	B D	D	530	V	10.3	527	533
3FOE	B D	D	616	R	27.7	613	617
3FOE	B D	D	621	L	18.2	619	623
3FPN	A B	A	219	D	1.3	214	228
3FPN	A B	B	170	N	3.4	169	179
3FS4	A B	A	30	E	1.2	21	36
3FS4	A B	A	31	R	3.3	21	36
3FS4	A B	A	34	I	1.5	21	36
3FS4	A B	A	111	I	1.0	95	113
3FS4	A B	A	119	P	1.3	119	137
3FS4	A B	A	122	H	1.8	119	137
3FS4	A B	B	30	R	1.7	20	35
3FS4	A B	B	34	V	1.4	20	35
3FS4	A B	B	112	I	1.0	100	119
3FS4	A B	B	124	P	1.7	124	142
3FS4	A D	A	95	P	1.4	95	113
3FS4	A D	D	37	W	2.3	36	41
3FS4	C B	C	95	P	1.2	95	113
3FS4	C B	B	37	W	3.5	36	41
3FS4	C B	B	102	N	1.4	100	119
3FS4	C D	C	31	R	2.5	21	36
3FS4	C D	C	34	I	1.8	21	36
3FS4	C D	C	122	H	1.3	119	137
3FS4	C D	D	124	P	1.1	124	142
3FSG	B D	B	225	L	1.0	221	230
3FSG	B D	B	252	E	2.9	251	266
3FSG	B D	B	256	F	3.5	251	266
3FSG	B D	D	225	L	1.2	221	230
3FSG	B D	D	252	E	2.9	251	266
3FSG	B D	D	253	A	2.9	251	266
3FSG	B D	D	256	F	3.5	251	266
3FSG	B D	D	264	E	1.9	251	266
3FSH	B C	C	582	L	1.5	582	598
3FSH	B C	C	589	L	2.1	582	598
3FSH	B C	C	594	R	1.7	582	598
3FSH	B C	C	597	F	1.3	582	598
3FUB	A B	A	155	L	1.2	153	163
3FUB	A B	A	171	R	4.7	165	179
3FUB	C D	C	155	L	1.1	153	163
3FUB	C D	C	159	K	1.0	153	163
3FUB	C D	C	171	R	2.5	165	179
3FUB	C D	C	175	I	1.7	165	179
3FWB	A B	A	50	K	2.3	42	52
3FWB	A B	A	104	L	1.1	94	106

3FWB	A B	A	105	F	2.6	94	106
3FWB	A B	A	118	L	3.2	115	125
3FWB	A B	A	120	R	1.7	115	125
3FWB	A B	A	121	V	1.1	115	125
3FWB	A B	A	122	A	1.5	115	125
3FWB	A B	A	124	E	2.2	115	125
3FWB	A B	A	137	M	2.9	131	141
3FWB	A B	A	154	F	1.0	151	161
3FWB	A B	A	157	I	1.7	151	161
3FWB	A B	B	789	K	1.7	753	804
3FWB	A B	B	794	L	1.0	753	804
3FWB	A B	B	795	K	3.5	753	804
3FWB	A B	B	798	F	1.3	753	804
3FWB	A B	B	799	F	4.1	753	804
3FWB	A B	B	802	W	8.3	753	804
3FWB	B C	B	757	R	1.9	753	804
3FWB	B C	B	761	I	1.2	753	804
3FWB	B C	B	767	E	1.2	753	804
3FWB	B C	B	768	L	1.7	753	804
3FWB	B C	B	769	Y	3.2	753	804
3FWB	B C	B	772	F	3.1	753	804
3FWB	B C	B	773	L	2.4	753	804
3FWB	B C	B	777	L	2.4	753	804
3FWB	B C	B	780	I	2.0	753	804
3FWB	B C	B	781	Y	3.6	753	804
3FWB	B C	B	788	L	1.2	753	804
3FWB	B C	C	29	L	1.5	21	36
3FWB	B C	C	38	W	1.9	38	52
3FWB	B C	C	42	V	1.1	38	52
3FWB	B C	C	43	K	1.6	38	52
3FWB	B C	C	58	F	2.1	58	72
3FWB	B C	C	62	L	1.6	58	72
3FWB	B C	C	70	L	1.1	58	72
3FWB	B C	C	82	L	1.8	75	93
3FWB	B C	C	85	I	2.2	75	93
3FWC	A B	A	27	E	2.1	19	32
3FWC	A B	A	31	L	1.0	19	32
3FWC	A B	A	50	K	1.2	42	52
3FWC	A B	A	97	E	1.9	94	106
3FWC	A B	A	105	F	2.2	94	106
3FWC	A B	A	121	V	1.1	115	125
3FWC	A B	A	154	F	1.8	151	159
3FWC	A B	A	157	I	1.8	151	159
3FWC	A B	B	779	L	1.1	725	804
3FWC	A B	B	789	K	2.5	725	804
3FWC	A B	B	790	R	1.5	725	804
3FWC	A B	B	796	K	1.1	725	804
3FWC	A B	B	797	K	1.2	725	804
3FWC	A B	B	798	F	1.3	725	804
3FWC	A B	B	799	F	2.4	725	804
3FWC	A B	B	802	W	4.4	725	804
3FWC	B C	B	761	I	2.0	725	804
3FWC	B C	B	768	L	1.3	725	804
3FWC	B C	B	769	Y	4.1	725	804
3FWC	B C	B	772	F	5.0	725	804
3FWC	B C	B	773	L	1.8	725	804
3FWC	B C	B	777	L	1.4	725	804
3FWC	B C	B	780	I	1.8	725	804
3FWC	B C	B	781	Y	2.7	725	804
3FWC	B C	B	787	E	1.2	725	804

3FWC	B C	C	16	L	1.0	8	18
3FWC	B C	C	22	Y	1.4	21	36
3FWC	B C	C	29	L	1.6	21	36
3FWC	B C	C	38	W	1.0	38	51
3FWC	B C	C	43	K	1.4	38	51
3FWC	B C	C	47	K	1.7	38	51
3FWC	B C	C	58	F	3.5	58	68
3FWC	B C	C	62	L	1.4	58	68
3FWC	B C	C	82	L	1.2	75	91
3FWC	B C	C	85	I	2.5	75	91
3FWC	B C	C	89	L	1.4	75	91
3FWC	B D	B	726	I	1.4	725	804
3FWC	B D	B	730	I	2.8	725	804
3FWC	B D	B	734	L	2.7	725	804
3FWC	B D	B	735	V	1.6	725	804
3FWC	B D	B	738	V	1.5	725	804
3FWC	B D	B	739	V	1.8	725	804
3FWC	B D	B	743	V	1.7	725	804
3FWC	B D	B	746	I	1.8	725	804
3FWC	B D	B	747	V	1.0	725	804
3FWC	B D	B	751	F	1.0	725	804
3FWC	B D	D	13	Q	1.6	9	19
3FWC	B D	D	29	L	1.7	21	36
3FWC	B D	D	30	K	1.0	21	36
3FWC	B D	D	38	W	1.6	38	53
3FWC	B D	D	42	V	1.2	38	53
3FWC	B D	D	43	K	1.3	38	53
3FWC	B D	D	58	F	1.2	58	73
3FWC	B D	D	62	L	1.8	58	73
3FWC	B D	D	70	L	1.3	58	73
3FWC	B D	D	81	V	1.2	75	90
3FWC	B D	D	85	I	1.1	75	90
3FWC	E F	E	97	E	2.0	94	106
3FWC	E F	E	105	F	2.6	94	106
3FWC	E F	E	125	L	2.2	115	126
3FWC	E F	E	137	M	1.0	131	141
3FWC	E F	E	138	I	1.1	131	141
3FWC	E F	E	157	I	1.7	151	160
3FWC	E F	F	789	K	1.5	723	798
3FWC	E F	F	794	L	1.1	723	798
3FWC	E F	F	797	K	1.6	723	798
3FWC	E F	F	799	F	2.0	799	804
3FWC	E F	F	802	W	6.1	799	804
3FWC	F G	F	761	I	1.8	723	798
3FWC	F G	F	768	L	1.5	723	798
3FWC	F G	F	769	Y	1.0	723	798
3FWC	F G	F	772	F	3.7	723	798
3FWC	F G	F	773	L	1.4	723	798
3FWC	F G	F	780	I	2.3	723	798
3FWC	F G	F	783	D	1.4	723	798
3FWC	F G	G	22	Y	1.2	21	28
3FWC	F G	G	43	K	1.4	38	50
3FWC	F G	G	46	T	1.4	38	50
3FWC	F G	G	47	K	1.3	38	50
3FWC	F G	G	85	I	2.3	78	93
3FWC	F H	F	726	I	1.4	723	798
3FWC	F H	F	730	I	2.3	723	798
3FWC	F H	F	735	V	1.3	723	798
3FWC	F H	F	738	V	1.6	723	798
3FWC	F H	F	739	V	2.0	723	798

3FWC	F H	F	743	V	1.7	723	798
3FWC	F H	F	746	I	1.8	723	798
3FWC	F H	F	750	E	1.0	723	798
3FWC	F H	F	751	F	3.0	723	798
3FWC	F H	H	9	K	1.4	5	20
3FWC	F H	H	13	Q	1.7	5	20
3FWC	F H	H	16	L	1.5	5	20
3FWC	F H	H	22	Y	1.7	21	36
3FWC	F H	H	25	I	1.4	21	36
3FWC	F H	H	29	L	1.1	21	36
3FWC	F H	H	30	K	1.2	21	36
3FWC	F H	H	38	W	2.9	38	53
3FWC	F H	H	39	V	1.3	38	53
3FWC	F H	H	43	K	1.8	38	53
3FWC	F H	H	47	K	1.0	38	53
3FWC	F H	H	58	F	1.2	58	73
3FWC	F H	H	62	L	1.4	58	73
3FWC	F H	H	65	V	1.3	58	73
3FWC	F H	H	70	L	1.6	58	73
3FWC	F H	H	85	I	1.0	75	92
3FWC	F H	H	86	R	1.2	75	92
3FWC	I J	I	27	E	1.6	19	32
3FWC	I J	I	31	L	1.8	19	32
3FWC	I J	I	50	K	1.9	42	52
3FWC	I J	I	97	E	1.1	94	106
3FWC	I J	I	105	F	2.2	94	106
3FWC	I J	I	118	L	1.0	115	125
3FWC	I J	I	137	M	2.0	131	141
3FWC	I J	I	154	F	2.6	151	159
3FWC	I J	J	782	M	1.6	729	805
3FWC	I J	J	789	K	1.7	729	805
3FWC	I J	J	795	K	2.0	729	805
3FWC	I J	J	796	K	1.5	729	805
3FWC	I J	J	797	K	1.2	729	805
3FWC	I J	J	798	F	1.1	729	805
3FWC	I J	J	799	F	3.1	729	805
3FWC	I J	J	802	W	4.5	729	805
3FWC	J K	J	769	Y	1.9	729	805
3FWC	J K	J	772	F	4.9	729	805
3FWC	J K	J	773	L	1.4	729	805
3FWC	J K	J	777	L	2.0	729	805
3FWC	J K	J	778	Y	1.2	729	805
3FWC	J K	J	781	Y	2.6	729	805
3FWC	J K	J	787	E	1.1	729	805
3FWC	J K	K	22	Y	1.3	21	36
3FWC	J K	K	29	L	1.5	21	36
3FWC	J K	K	38	W	2.3	38	51
3FWC	J K	K	43	K	1.6	38	51
3FWC	J K	K	47	K	2.0	38	51
3FWC	J K	K	58	F	3.9	58	73
3FWC	J K	K	78	R	1.0	75	91
3FWC	J K	K	82	L	1.4	75	91
3FWC	J K	K	85	I	2.0	75	91
3FWC	J L	J	730	I	1.2	729	805
3FWC	J L	J	735	V	1.2	729	805
3FWC	J L	J	738	V	1.8	729	805
3FWC	J L	J	743	V	1.4	729	805
3FWC	J L	J	746	I	2.4	729	805
3FWC	J L	J	751	F	2.9	729	805
3FWC	J L	L	29	L	1.5	21	36

3FWC	J L	L	30	K	1.2	21	36
3FWC	J L	L	43	K	1.0	38	50
3FWC	J L	L	58	F	1.3	58	73
3FWC	J L	L	62	L	1.5	58	73
3FWC	J L	L	70	L	1.0	58	73
3FWC	M N	M	20	E	1.0	19	32
3FWC	M N	M	27	E	1.3	19	32
3FWC	M N	M	50	K	1.6	42	53
3FWC	M N	M	105	F	2.8	94	106
3FWC	M N	M	118	L	2.6	115	125
3FWC	M N	M	121	V	1.0	115	125
3FWC	M N	M	137	M	3.9	132	141
3FWC	M N	M	154	F	1.4	151	160
3FWC	M N	M	157	I	1.5	151	160
3FWC	M N	N	787	E	1.0	723	804
3FWC	M N	N	789	K	1.6	723	804
3FWC	M N	N	795	K	3.2	723	804
3FWC	M N	N	796	K	1.2	723	804
3FWC	M N	N	797	K	1.3	723	804
3FWC	M N	N	798	F	1.5	723	804
3FWC	M N	N	799	F	3.0	723	804
3FWC	M N	N	802	W	7.2	723	804
3FWC	M N	N	803	Q	1.6	723	804
3FWC	N O	N	760	F	1.9	723	804
3FWC	N O	N	761	I	1.5	723	804
3FWC	N O	N	764	M	1.7	723	804
3FWC	N O	N	768	L	1.0	723	804
3FWC	N O	N	769	Y	2.4	723	804
3FWC	N O	N	772	F	3.4	723	804
3FWC	N O	N	774	H	1.0	723	804
3FWC	N O	N	777	L	1.6	723	804
3FWC	N O	N	781	Y	2.3	723	804
3FWC	N O	N	787	E	1.2	723	804
3FWC	N O	O	9	K	1.3	7	19
3FWC	N O	O	47	K	1.0	38	51
3FWC	N O	O	58	F	3.5	58	65
3FWC	N O	O	82	L	1.3	75	94
3FWC	N O	O	85	I	2.0	75	94
3FWC	N O	O	89	L	1.8	75	94
3FWC	N P	N	726	I	1.6	723	804
3FWC	N P	N	730	I	1.7	723	804
3FWC	N P	N	734	L	2.4	723	804
3FWC	N P	N	735	V	1.6	723	804
3FWC	N P	N	738	V	1.5	723	804
3FWC	N P	N	739	V	1.2	723	804
3FWC	N P	N	743	V	1.4	723	804
3FWC	N P	N	746	I	2.9	723	804
3FWC	N P	N	748	K	1.1	723	804
3FWC	N P	P	9	K	1.3	5	19
3FWC	N P	P	29	L	1.4	21	36
3FWC	N P	P	30	K	1.2	21	36
3FWC	N P	P	38	W	1.6	38	53
3FWC	N P	P	47	K	1.0	38	53
3FWC	N P	P	50	M	1.8	38	53
3FWC	N P	P	62	L	1.2	58	73
3FWC	N P	P	70	L	1.7	58	73
3FWC	N P	P	81	V	1.2	75	94
3FWC	N P	P	85	I	1.7	75	94
3FXD	A B	A	13	I	2.3	7	24
3FXD	A B	A	17	L	1.2	7	24

3FXD	A B	A	31	F	1.6	30	52
3FXD	A B	A	35	I	1.6	30	52
3FXD	A B	A	42	I	1.9	30	52
3FXD	A B	A	45	R	1.1	30	52
3FXD	A B	B	41	I	1.4	41	59
3FXD	A B	B	52	V	1.0	41	59
3FXD	A B	B	71	V	1.1	63	84
3FXD	A B	B	75	L	1.9	63	84
3FXD	A B	B	79	V	1.1	63	84
3FXD	C D	C	9	Q	1.2	7	24
3FXD	C D	C	13	I	1.9	7	24
3FXD	C D	C	17	L	1.2	7	24
3FXD	C D	C	31	F	2.2	30	50
3FXD	C D	C	35	I	1.6	30	50
3FXD	C D	D	52	V	1.4	41	55
3FXD	C D	D	71	V	1.2	63	84
3FXD	C D	D	72	L	1.6	63	84
3FXD	C D	D	75	L	1.9	63	84
3FXD	C D	D	78	K	1.5	63	84
3FXD	C D	D	79	V	1.0	63	84
3G03	A B	A	58	G	129.4	50	64
3G03	A B	A	99	I	1.0	96	106
3G03	A B	B	19	F	3.7	19	27
3G03	A B	B	22	Y	2.0	19	27
3G03	A B	B	23	W	3.7	19	27
3G03	A B	B	26	L	1.6	19	27
3G04	A B	A	123	E	1.3	122	127
3G04	A B	A	124	E	1.2	122	127
3G33	A D	A	59	V	1.4	56	72
3G33	A D	A	66	R	2.0	56	72
3G33	A D	A	71	F	1.1	56	72
3G33	A D	D	34	L	1.2	24	38
3G33	A D	D	37	R	1.6	24	38
3G33	C B	C	60	R	2.5	56	72
3G33	C B	C	66	R	1.7	56	72
3G33	C B	C	67	R	1.0	56	72
3G33	C B	C	71	F	1.8	56	72
3G33	C B	B	34	L	2.1	24	38
3G33	C B	B	37	R	1.4	24	38
3G33	C B	B	113	L	1.0	99	114
3G3A	A B	B	112	R	3.4	109	116
3G3A	A H	H	123	W	1.9	120	124
3G3A	C D	D	102	G	8.6	89	104
3G3A	C D	D	109	V	2.1	109	116
3G3A	C D	D	112	R	2.8	109	116
3G3A	C F	F	123	W	2.2	120	124
3G3A	E D	D	123	W	2.1	120	124
3G3A	E F	F	112	R	2.6	109	116
3G3B	A B	B	112	R	2.8	109	116
3G3B	C D	D	112	R	2.0	109	116
3G3B	E F	F	112	R	1.0	109	116
3G3B	G F	F	5	R	1.4	5	15
3G43	B E	B	12	F	1.8	6	20
3G43	B E	B	19	F	2.5	6	20
3G43	B E	B	68	F	1.8	65	78
3G43	B E	B	72	M	1.3	65	78
3G43	B E	B	92	F	1.5	83	93
3G43	B E	B	124	M	1.0	118	129
3G43	B E	B	145	M	1.0	138	146
3G43	B E	E	1666	F	4.0	1666	1681

3G43	B E	E	1667	Y	2.9	1666	1681
3G43	B E	E	1670	F	2.1	1666	1681
3G43	B E	E	1671	L	1.0	1666	1681
3G43	B E	E	1672	I	2.6	1666	1681
3G43	B E	E	1675	Y	2.5	1666	1681
3G43	B E	E	1676	F	7.1	1666	1681
3G43	B E	E	1677	R	1.0	1666	1681
3G43	B E	E	1679	F	3.4	1666	1681
3G43	C E	C	105	L	1.1	102	112
3G43	C E	C	124	M	1.7	118	129
3G43	C E	C	127	E	1.2	118	129
3G43	C E	E	1637	I	2.1	1609	1652
3G43	C E	E	1640	I	1.9	1609	1652
3G43	C E	E	1641	W	6.3	1609	1652
3G43	C E	E	1642	K	1.1	1609	1652
3G43	C E	E	1646	M	1.2	1609	1652
3G43	C F	C	19	F	1.2	6	20
3G43	C F	C	54	E	1.3	45	55
3G43	C F	C	71	M	1.8	65	76
3G43	C F	F	1610	L	1.7	1609	1650
3G43	C F	F	1611	F	2.9	1609	1650
3G43	C F	F	1616	T	1.2	1609	1650
3G43	C F	F	1618	L	1.9	1609	1650
3G43	C F	F	1619	R	1.0	1609	1650
3G43	D E	D	19	F	2.1	6	20
3G43	D E	D	51	M	1.4	45	55
3G43	D E	D	71	M	1.3	65	76
3G43	D E	E	1610	L	2.0	1609	1652
3G43	D E	E	1611	F	3.0	1609	1652
3G43	D E	E	1613	L	2.1	1609	1652
3G43	D E	E	1614	V	1.1	1609	1652
3G43	D E	E	1618	L	1.0	1609	1652
3G43	D E	E	1620	I	1.0	1609	1652
3G43	D F	D	11	E	1.4	6	20
3G43	D F	D	92	F	1.8	82	93
3G43	D F	D	105	L	1.2	102	109
3G43	D F	D	108	V	1.5	102	109
3G43	D F	D	124	M	1.6	118	129
3G43	D F	F	1637	I	1.8	1609	1650
3G43	D F	F	1639	K	1.3	1609	1650
3G43	D F	F	1641	W	5.6	1609	1650
3G43	D F	F	1643	R	1.2	1609	1650
3G43	D F	F	1644	T	1.1	1609	1650
3G43	D F	F	1646	M	1.2	1609	1650
3G43	D F	F	1647	K	1.3	1609	1650
3G43	D F	F	1648	L	2.3	1609	1650
3G43	D F	F	1649	L	1.9	1609	1650
3G4S	A Z	Z	103	V	1.0	102	106
3G4S	F M	F	37	T	1.0	33	43
3G4S	F M	F	38	K	1.0	33	43
3G4S	F M	F	41	E	1.0	33	43
3G4S	F M	F	62	H	1.9	62	69
3G4S	F M	M	8	I	1.1	8	12
3G4S	S V	V	24	K	1.3	14	29
3G5O	A B	A	53	E	2.9	49	63
3G5O	A B	A	57	E	1.2	49	63
3G5O	A B	A	58	T	1.5	49	63
3G5O	A B	A	61	W	4.1	49	63
3G5O	A B	A	62	L	1.5	49	63
3G5O	A B	A	68	R	1.0	67	80

3G5O	A B	A	75	D	1.4	67	80
3G5O	A B	A	77	D	1.2	67	80
3G5O	A B	A	78	I	1.1	67	80
3G5O	A B	A	86	E	1.1	86	93
3G5O	A B	A	89	I	2.1	86	93
3G5O	A B	A	90	R	3.3	86	93
3G5O	A B	A	92	E	1.4	86	93
3G5O	A B	B	25	T	1.4	24	32
3G5O	A B	B	27	R	1.9	24	32
3G5O	A B	B	31	H	1.6	24	32
3G5O	A B	B	38	L	1.6	35	46
3G5O	A B	B	42	V	1.1	35	46
3G5O	A B	B	43	E	2.3	35	46
3G5O	D C	D	58	T	1.5	49	64
3G5O	D C	D	61	W	6.6	49	64
3G5O	D C	D	62	L	1.1	49	64
3G5O	D C	D	67	I	1.0	67	80
3G5O	D C	D	71	I	1.2	67	80
3G5O	D C	D	75	D	2.0	67	80
3G5O	D C	D	86	E	1.2	86	93
3G5O	D C	D	89	I	2.2	86	93
3G5O	D C	D	90	R	2.9	86	93
3G5O	D C	C	27	R	1.8	24	33
3G5O	D C	C	30	L	1.4	24	33
3G5O	D C	C	38	L	1.7	35	46
3G5O	D C	C	42	V	1.2	35	46
3G5O	D C	C	43	E	2.0	35	46
3G65	B C	C	169	V	1.3	163	175
3G6A	L H	L	125	E	1.1	123	128
3G6D	H A	A	14	I	1.4	8	24
3G6D	L A	A	97	K	1.1	92	107
3G6D	L H	L	124	E	1.4	123	128
3G6D	L H	L	125	E	1.4	123	128
3G6J	A B	A	578	K	1.6	578	584
3G6J	A B	A	594	I	1.1	591	601
3G6J	A B	B	1410	Y	2.2	1409	1413
3G6J	C D	C	578	K	1.0	578	584
3G6J	C D	C	594	I	1.0	591	601
3G6J	C D	D	1018	E	1.0	1017	1037
3G6J	G H	G	124	Q	1.2	122	127
3G9K	D F	D	79	V	1.0	72	87
3G9K	D F	D	179	R	2.0	173	181
3G9K	D F	D	209	T	1.0	204	217
3G9K	D F	D	270	G	29.2	270	275
3G9K	D F	D	273	L	2.0	270	275
3G9K	D F	F	434	P	1.1	433	446
3G9K	D F	F	435	Q	1.4	433	446
3G9K	D F	F	442	D	1.3	433	446
3G9K	L S	L	79	V	1.0	72	87
3G9K	L S	L	180	I	1.6	173	181
3G9K	L S	L	221	F	1.0	218	222
3G9K	L S	L	270	G	9.4	270	275
3G9K	L S	L	273	L	1.9	270	275
3G9K	L S	S	442	D	1.3	432	446
3G9V	A B	A	123	W	1.3	122	126
3G9V	A B	A	125	E	4.1	122	126
3G9V	A B	B	57	F	1.4	50	66
3G9V	C D	D	50	P	1.4	50	66
3G9V	C D	D	57	F	2.9	50	66
3G9V	C D	D	168	D	1.2	167	178

3G9V	C D	D	171	F	1.1	167	178
3G9V	C D	D	172	M	1.0	167	178
3G9V	C D	D	176	N	1.0	167	178
3GBM	A B	A	110	H	1.1	105	114
3GBM	A B	B	93	T	1.1	75	127
3GBM	A B	B	100	V	1.8	75	127
3GBM	A B	B	101	L	1.1	75	127
3GBM	A B	B	104	N	2.4	75	127
3GBM	A B	B	108	L	4.0	75	127
3GBM	A B	B	111	H	1.6	75	127
3GBM	A B	B	115	V	1.0	75	127
3GBM	B H	B	42	Q	1.1	38	59
3GBM	B H	B	45	I	1.4	38	59
3GBM	B H	B	56	I	1.1	38	59
3GBM	C D	C	110	H	1.2	105	113
3GBM	C D	D	55	I	1.3	38	59
3GBM	C D	D	93	T	1.3	75	127
3GBM	C D	D	101	L	1.4	75	127
3GBM	C D	D	104	N	3.4	75	127
3GBM	C D	D	107	T	1.6	75	127
3GBM	C D	D	108	L	1.8	75	127
3GBM	D I	D	45	I	4.1	38	59
3GBM	D I	D	53	N	1.9	38	59
3GBM	D I	D	56	I	1.0	38	59
3GBM	H L	L	124	E	1.6	122	127
3GBN	A B	B	89	L	1.9	75	127
3GBN	A B	B	93	T	1.3	75	127
3GBN	A B	B	97	E	1.0	75	127
3GBN	A B	B	100	V	1.7	75	127
3GBN	A B	B	101	L	1.0	75	127
3GBN	A B	B	104	N	3.1	75	127
3GBN	A B	B	108	L	2.0	75	127
3GBN	A B	B	111	H	2.9	75	127
3GBN	A B	B	115	V	1.0	75	127
3GBN	B H	B	42	Q	1.9	38	59
3GBN	B H	B	45	I	2.1	38	59
3GBN	B H	B	53	N	2.4	38	59
3GBN	B H	B	56	I	1.2	38	59
3GCG	A B	A	66	R	1.5	65	73
3GCG	A B	A	67	L	1.5	65	73
3GCG	A B	A	70	L	1.0	65	73
3GCG	A B	B	65	Q	1.0	51	66
3GCG	A B	B	78	E	1.4	72	99
3GCG	A B	B	89	R	1.2	72	99
3GCG	A B	B	133	H	1.7	130	137
3GCG	A B	B	156	I	1.3	155	178
3GCG	A B	B	159	F	3.1	155	178
3GE8	A B	A	12	L	3.3	10	14
3GE8	A B	A	28	L	1.0	25	29
3GE8	A B	A	33	M	1.9	31	35
3GE8	A B	A	55	Y	3.2	55	76
3GE8	A B	A	58	Y	1.1	55	76
3GE8	A B	A	59	V	1.0	55	76
3GE8	A B	A	62	Q	1.1	55	76
3GE8	A B	A	105	Y	1.5	87	117
3GE8	A B	A	113	R	2.7	87	117
3GE8	A B	A	116	R	2.8	87	117
3GE8	A B	A	125	N	1.1	121	141
3GE8	A B	A	128	T	2.0	121	141
3GE8	A B	A	131	M	1.1	121	141

3GE8	A B	A	132	M	1.5	121	141
3GE8	A B	A	135	L	1.5	121	141
3GE8	A B	A	139	Q	1.4	121	141
3GE8	A B	A	142	L	1.2	142	148
3GE8	A B	A	153	R	2.5	153	163
3GE8	A B	A	156	D	1.9	153	163
3GE8	A B	A	159	W	2.9	153	163
3GE8	A B	A	173	K	1.5	167	182
3GE8	A B	A	453	R	1.2	450	456
3GE8	A B	A	469	K	1.6	464	471
3GE8	A B	B	24	E	1.3	24	28
3GE8	A B	B	27	I	1.3	24	28
3GE8	A B	B	51	M	1.3	50	61
3GE8	A B	B	54	W	1.8	50	61
3GE8	A B	B	55	Y	3.4	50	61
3GE8	A B	B	80	Y	3.4	80	104
3GE8	A B	B	81	R	2.0	80	104
3GE8	A B	B	83	Y	2.0	80	104
3GE8	A B	B	91	E	1.7	80	104
3GE8	A B	B	126	R	1.5	125	143
3GE8	A B	B	127	Y	1.7	125	143
3GE8	A B	B	133	Q	2.3	125	143
3GE8	A B	B	138	Y	1.0	125	143
3GE8	A B	B	153	I	2.5	146	177
3GE8	A B	B	160	L	1.3	146	177
3GE8	A B	B	161	R	1.1	146	177
3GE8	A B	B	168	Y	3.3	146	177
3GE8	A B	B	171	H	1.8	146	177
3GE8	A B	B	172	E	1.0	146	177
3GE8	A B	B	187	R	1.0	186	193
3GE8	A B	B	191	E	1.3	186	193
3GE8	A B	B	197	Q	2.9	197	207
3GE8	A B	B	200	R	1.7	197	207
3GE8	A B	B	201	E	1.1	197	207
3GE8	A B	B	204	E	6.3	197	207
3GE8	A C	A	334	G	3.3	317	338
3GE8	A C	A	375	V	1.4	369	382
3GE8	A C	A	455	L	1.7	450	456
3GE8	A E	A	61	I	1.7	55	76
3GE8	A E	A	206	L	1.4	200	215
3GE8	A E	A	214	E	1.3	200	215
3GE8	A E	A	295	Y	1.9	290	309
3GE8	A E	A	296	E	2.5	290	309
3GE8	A E	A	297	W	1.1	290	309
3GE8	A E	A	299	I	1.5	290	309
3GE8	A E	A	301	Q	2.5	290	309
3GE8	A E	A	304	R	1.8	290	309
3GE8	A E	A	307	I	1.6	290	309
3GE8	A E	A	308	D	2.4	290	309
3GE8	A E	A	317	W	1.1	317	338
3GE8	A E	E	9	L	2.9	3	10
3GE8	A E	E	75	Q	1.2	74	78
3GE8	B H	H	29	E	1.5	24	34
3GE8	D F	D	12	L	1.5	10	14
3GE8	D F	D	28	L	1.1	25	29
3GE8	D F	D	33	M	2.0	31	35
3GE8	D F	D	55	Y	5.4	55	76
3GE8	D F	D	58	Y	1.9	55	76
3GE8	D F	D	59	V	2.1	55	76
3GE8	D F	D	63	R	3.4	55	76

3GE8	D F	D	105	Y	2.6	87	117
3GE8	D F	D	113	R	2.3	87	117
3GE8	D F	D	116	R	2.9	87	117
3GE8	D F	D	125	N	1.2	121	141
3GE8	D F	D	128	T	2.1	121	141
3GE8	D F	D	131	M	1.6	121	141
3GE8	D F	D	132	M	1.5	121	141
3GE8	D F	D	135	L	1.4	121	141
3GE8	D F	D	139	Q	1.2	121	141
3GE8	D F	D	142	L	1.0	142	148
3GE8	D F	D	153	R	2.2	153	157
3GE8	D F	D	156	D	1.2	153	157
3GE8	D F	D	159	W	3.1	158	163
3GE8	D F	D	173	K	1.5	167	182
3GE8	D F	D	177	D	1.0	167	182
3GE8	D F	D	453	R	1.5	450	456
3GE8	D F	F	51	M	1.6	50	61
3GE8	D F	F	54	W	1.8	50	61
3GE8	D F	F	55	Y	3.4	50	61
3GE8	D F	F	80	Y	4.3	80	104
3GE8	D F	F	81	R	2.5	80	104
3GE8	D F	F	83	Y	2.6	80	104
3GE8	D F	F	84	N	1.1	80	104
3GE8	D F	F	85	L	1.4	80	104
3GE8	D F	F	87	Q	1.0	80	104
3GE8	D F	F	88	D	2.5	80	104
3GE8	D F	F	91	E	2.5	80	104
3GE8	D F	F	126	R	1.5	125	143
3GE8	D F	F	127	Y	1.9	125	143
3GE8	D F	F	133	Q	2.4	125	143
3GE8	D F	F	134	M	5.8	125	143
3GE8	D F	F	138	Y	1.0	125	143
3GE8	D F	F	158	D	1.1	146	177
3GE8	D F	F	160	L	1.3	146	177
3GE8	D F	F	161	R	2.2	146	177
3GE8	D F	F	163	L	1.0	146	177
3GE8	D F	F	168	Y	3.9	146	177
3GE8	D F	F	171	H	1.9	146	177
3GE8	D F	F	187	R	1.2	186	193
3GE8	D F	F	200	R	1.8	194	208
3GE8	D F	F	204	E	3.2	194	208
3GE8	D G	D	334	G	3.1	326	338
3GE8	D G	D	337	Y	2.5	326	338
3GE8	D G	D	375	V	1.0	369	382
3GE8	D G	D	455	L	1.6	450	456
3GE8	D H	D	57	E	1.2	55	76
3GE8	D H	D	61	I	1.5	55	76
3GE8	D H	D	206	L	1.3	200	215
3GE8	D H	D	233	R	1.1	218	236
3GE8	D H	D	295	Y	2.0	290	309
3GE8	D H	D	296	E	1.8	290	309
3GE8	D H	D	299	I	1.4	290	309
3GE8	D H	D	301	Q	2.8	290	309
3GE8	D H	D	304	R	3.7	290	309
3GE8	D H	D	308	D	2.1	290	309
3GE8	D H	H	9	L	2.2	4	10
3GE8	D H	H	78	E	2.1	74	81
3GE8	D H	H	79	I	1.1	74	81
3GE8	F E	E	29	E	1.7	24	34
3GFK	A B	A	43	K	1.7	39	49

3GFK	A B	A	76	L	2.6	76	86
3GFK	A B	A	80	Y	1.9	76	86
3GFK	A B	B	260	V	2.1	260	269
3GFK	A B	B	261	R	1.2	260	269
3GFK	A B	B	263	Y	2.3	260	269
3GFK	A B	B	264	N	2.3	260	269
3GFK	A B	B	267	K	2.1	260	269
3GFK	A B	B	268	R	1.6	260	269
3GGR	A C	C	165	E	1.5	160	167
3GGR	B C	C	88	V	1.0	86	93
3GHG	A B	A	48	G	17.8	48	76
3GHG	A B	A	53	G	137.8	48	76
3GHG	A B	A	73	L	1.2	48	76
3GHG	A B	A	140	V	1.1	99	161
3GHG	A B	A	147	M	1.7	99	161
3GHG	A B	A	149	R	1.1	99	161
3GHG	A B	A	156	I	1.1	99	161
3GHG	A B	A	158	I	1.7	99	161
3GHG	A B	B	100	L	1.3	89	102
3GHG	A B	B	104	V	1.1	103	108
3GHG	A B	B	125	W	1.2	117	126
3GHG	A B	B	175	L	1.1	159	187
3GHG	A B	B	178	K	2.0	159	187
3GHG	A B	B	192	Y	2.8	188	195
3GHG	A C	A	62	F	2.5	48	76
3GHG	A C	A	69	L	1.5	48	76
3GHG	A C	A	104	R	1.1	99	161
3GHG	A C	A	115	L	1.8	99	161
3GHG	A C	A	150	L	1.1	99	161
3GHG	A C	C	25	I	2.4	22	40
3GHG	A C	C	29	L	1.4	22	40
3GHG	A C	C	36	V	1.1	22	40
3GHG	A C	C	68	Y	1.1	47	69
3GHG	A C	C	83	T	1.0	79	97
3GHG	B C	B	79	G	74.6	79	88
3GHG	B C	B	165	L	1.0	159	187
3GHG	B C	B	179	I	1.6	159	187
3GHG	B C	B	183	E	1.3	159	187
3GHG	B C	B	186	V	2.1	159	187
3GHG	B C	C	25	I	1.3	22	40
3GHG	B C	C	43	L	2.0	41	46
3GHG	B C	C	103	H	1.3	98	105
3GHG	B C	C	124	L	2.1	113	133
3GHG	B C	C	131	L	1.5	113	133
3GHG	D E	D	48	G	56.9	48	64
3GHG	D E	D	52	K	1.2	48	64
3GHG	D E	D	53	G	167.1	48	64
3GHG	D E	D	126	V	1.3	115	157
3GHG	D E	D	154	I	1.1	115	157
3GHG	D E	D	156	I	1.3	115	157
3GHG	D E	D	177	D	1.1	175	188
3GHG	D E	E	82	L	1.0	79	87
3GHG	D E	E	86	L	1.0	79	87
3GHG	D E	E	93	I	1.0	88	103
3GHG	D E	E	125	W	1.8	118	139
3GHG	D E	E	157	V	1.2	151	158
3GHG	D E	E	171	I	1.3	166	189
3GHG	D E	E	175	L	1.0	166	189
3GHG	D E	E	178	K	2.2	166	189
3GHG	D F	D	51	M	1.5	48	64

3GHG	D F	D	62	F	1.8	48	64
3GHG	D F	D	108	Y	2.3	98	114
3GHG	D F	D	136	L	1.4	115	157
3GHG	D F	F	87	R	7.6	86	106
3GHG	E F	E	79	G	31.0	79	87
3GHG	E F	E	86	L	1.0	79	87
3GHG	E F	E	115	F	1.4	104	117
3GHG	E F	E	183	E	1.1	166	189
3GHG	E F	F	25	I	1.2	22	28
3GHG	E F	F	32	Y	1.0	29	33
3GHG	E F	F	120	K	1.0	111	134
3GHG	E F	F	124	L	1.9	111	134
3GHG	E F	F	131	L	1.0	111	134
3GHG	E F	F	132	E	1.1	111	134
3GHG	G H	G	48	G	39.6	48	76
3GHG	G H	G	53	G	176.8	48	76
3GHG	G H	G	66	I	1.1	48	76
3GHG	G H	G	116	R	1.4	77	161
3GHG	G H	G	126	V	1.0	77	161
3GHG	G H	G	147	M	1.2	77	161
3GHG	G H	G	149	R	1.0	77	161
3GHG	G H	G	150	L	1.1	77	161
3GHG	G H	G	155	D	1.2	77	161
3GHG	G H	G	159	R	1.6	77	161
3GHG	G H	G	178	Y	1.6	175	190
3GHG	G H	H	82	L	2.0	79	89
3GHG	G H	H	93	I	1.3	90	100
3GHG	G H	H	156	T	1.8	154	189
3GHG	G H	H	168	L	1.0	154	189
3GHG	G H	H	178	K	2.1	154	189
3GHG	G I	G	62	F	3.2	48	76
3GHG	G I	G	65	R	1.1	48	76
3GHG	G I	G	122	L	1.2	77	161
3GHG	G I	G	136	L	1.7	77	161
3GHG	G I	G	139	N	4.4	77	161
3GHG	G I	G	150	L	2.4	77	161
3GHG	G I	G	154	I	1.0	77	161
3GHG	G I	I	33	Q	1.1	22	35
3GHG	G I	I	114	Y	1.3	78	121
3GHG	G I	I	125	K	1.6	122	134
3GHG	G I	I	128	V	1.1	122	134
3GHG	H I	H	79	G	126.8	79	89
3GHG	H I	H	147	E	1.0	141	149
3GHG	H I	H	165	L	1.5	154	189
3GHG	H I	H	183	E	1.0	154	189
3GHG	H I	H	186	V	1.7	154	189
3GHG	H I	I	25	I	1.3	22	35
3GHG	H I	I	43	L	1.6	39	67
3GHG	H I	I	53	K	1.0	39	67
3GHG	H I	I	57	V	2.6	39	67
3GHG	H I	I	96	Y	1.2	78	121
3GHG	H I	I	103	H	1.1	78	121
3GHG	H I	I	110	L	2.1	78	121
3GHG	H I	I	124	L	1.7	122	134
3GHG	H I	I	131	L	1.7	122	134
3GHG	J K	J	48	G	13.5	48	160
3GHG	J K	J	53	G	2.5	48	160
3GHG	J K	J	55	I	1.5	48	160
3GHG	J K	J	148	K	1.7	48	160
3GHG	J K	K	82	L	1.8	79	89

3GHG	J K	K	149	H	1.3	138	158
3GHG	J K	K	171	I	1.0	166	192
3GHG	J K	K	178	K	2.2	166	192
3GHG	J L	J	51	M	1.1	48	160
3GHG	J L	J	62	F	1.7	48	160
3GHG	J L	J	76	Y	1.1	48	160
3GHG	J L	J	129	K	1.8	48	160
3GHG	J L	J	150	L	1.0	48	160
3GHG	J L	J	157	K	1.6	48	160
3GHG	J L	L	29	L	1.2	22	46
3GHG	J L	L	37	D	1.5	22	46
3GHG	J L	L	61	I	1.1	47	69
3GHG	J L	L	128	V	1.2	107	135
3GHG	J L	L	132	E	1.0	107	135
3GHG	K L	K	79	G	135.6	79	89
3GHG	K L	K	125	W	1.5	118	137
3GHG	K L	K	129	Q	1.1	118	137
3GHG	K L	K	183	E	1.2	166	192
3GHG	K L	K	186	V	1.0	166	192
3GHG	K L	L	25	I	1.2	22	46
3GHG	K L	L	43	L	1.3	22	46
3GHG	K L	L	50	V	1.0	47	69
3GHG	K L	L	60	L	1.6	47	69
3GHG	K L	L	67	T	1.1	47	69
3GHG	K L	L	68	Y	1.4	47	69
3GHG	K L	L	103	H	1.3	93	106
3GHG	K L	L	110	L	1.0	107	135
3GHG	K L	L	124	L	1.3	107	135
3GHG	K L	L	131	L	1.5	107	135
3GIZ	L H	L	124	Q	1.7	122	128
3GJ5	A B	A	78	G	6.9	77	81
3GJ5	C D	C	78	G	11.6	77	81
3GJ7	A B	A	78	G	9.5	77	81
3GJ8	A B	A	78	G	9.9	77	81
3GJ8	C D	C	78	G	6.1	77	81
3GJF	A H	A	65	R	1.5	57	85
3GJF	A L	A	65	R	1.9	57	85
3GJF	D K	D	65	R	1.0	57	85
3GJF	K M	K	127	E	1.3	125	130
3GJF	L H	L	126	E	1.3	125	130
3GJF	L H	L	127	E	1.1	125	130
3GJX	B A	B	1	M	1.5	0	10
3GJX	B A	B	2	E	1.1	0	10
3GJX	B A	B	4	L	2.9	0	10
3GJX	B A	B	8	L	2.8	0	10
3GJX	B A	A	518	V	1.1	510	531
3GJX	B A	A	525	L	2.7	510	531
3GJX	B A	A	561	F	2.4	559	572
3GJX	B A	A	568	K	2.9	559	572
3GJX	B A	A	716	D	1.4	714	735
3GJX	C A	C	139	H	1.4	137	142
3GJX	C A	C	140	R	1.9	137	142
3GJX	C A	C	141	K	1.1	137	142
3GJX	C A	A	124	K	1.2	124	141
3GJX	C A	A	129	K	1.0	124	141
3GJX	C A	A	316	Q	1.6	314	333
3GJX	C A	A	324	L	1.3	314	333
3GJX	C A	A	371	E	1.5	363	384
3GJX	C A	A	843	E	1.1	842	858
3GJX	E D	E	1	M	1.5	0	10

3GJX	E D	E	4	L	2.5	0	10
3GJX	E D	E	8	L	2.6	0	10
3GJX	E D	D	518	V	1.2	510	531
3GJX	E D	D	525	L	2.7	510	531
3GJX	E D	D	561	F	2.1	559	572
3GJX	E D	D	568	K	2.7	559	572
3GJX	F D	F	77	D	1.1	77	81
3GJX	F D	F	78	G	2.2	77	81
3GJX	F D	F	140	R	1.6	137	142
3GJX	F D	F	141	K	1.4	137	142
3GJX	F D	D	124	K	1.1	124	141
3GJX	F D	D	129	K	1.3	124	141
3GJX	F D	D	270	E	1.3	261	274
3GJX	F D	D	324	L	1.4	314	333
3GJX	F D	D	371	E	1.3	363	384
3GKW	H L	L	124	Q	1.4	122	127
3GLH	A B	A	187	R	1.5	178	192
3GLH	A B	A	191	L	1.7	178	192
3GLH	A B	B	23	H	1.9	22	34
3GLH	A B	B	30	N	1.2	22	34
3GLH	A B	B	164	V	1.0	164	169
3GLH	A E	A	299	R	1.5	295	313
3GLH	A E	A	302	V	1.0	295	313
3GLH	A E	E	310	L	2.2	308	324
3GLH	A E	E	317	L	1.4	308	324
3GLH	D E	D	220	L	1.4	214	223
3GLH	D E	D	347	M	1.6	345	359
3GLH	D E	D	354	L	1.0	345	359
3GLH	D E	D	357	L	1.9	345	359
3GLH	D E	E	253	M	1.7	241	260
3GLH	D E	E	257	K	1.2	241	260
3GLH	D E	E	283	P	1.2	283	303
3GLH	D E	E	287	Q	1.3	283	303
3GLH	D E	E	295	H	1.4	283	303
3GLH	F G	F	187	R	1.0	178	192
3GLH	F G	F	190	L	1.0	178	192
3GLH	F G	G	326	Q	1.2	322	342
3GLH	F J	F	299	R	1.1	295	313
3GLH	F N	F	270	R	1.0	269	276
3GLH	I J	I	347	M	1.6	345	359
3GLH	I J	J	91	D	1.2	90	101
3GLH	I J	J	253	M	1.6	241	260
3GLH	I J	J	257	K	1.1	241	260
3GLH	I J	J	283	P	1.1	283	303
3GLH	I J	J	295	H	1.3	283	303
3GLH	K L	K	28	P	1.3	28	46
3GLH	K L	K	187	R	1.6	178	192
3GLH	K L	K	190	L	1.2	178	192
3GLH	K L	K	191	L	1.1	178	192
3GLH	K L	K	329	L	1.1	320	331
3GLH	K L	L	23	H	1.0	22	34
3GLH	K O	K	258	V	1.3	249	263
3GLH	K O	K	299	R	2.0	295	313
3GLH	K O	K	302	V	1.4	295	313
3GLH	K O	K	310	L	1.0	295	313
3GLH	K O	O	310	L	2.4	308	324
3GLH	N O	N	334	I	1.2	322	338
3GLH	N O	N	345	R	2.0	345	359
3GLH	N O	N	347	M	1.0	345	359
3GLH	N O	O	253	M	1.0	241	260

3GLH	N O	O	287	Q	14.7	283	303
3GLI	A B	A	179	L	1.1	178	192
3GLI	A B	A	230	L	1.3	226	239
3GLI	A E	A	262	R	1.4	243	267
3GLI	A E	A	299	R	2.2	295	313
3GLI	A E	A	302	V	1.1	295	313
3GLI	A E	A	310	L	1.5	295	313
3GLI	A E	E	310	L	2.4	308	324
3GLI	A E	E	311	L	1.0	308	324
3GLI	A E	E	317	L	1.7	308	324
3GLI	A E	E	318	R	1.0	308	324
3GLI	B O	B	355	R	1.2	345	359
3GLI	C O	O	9	L	1.1	4	12
3GLI	D E	D	261	G	222.9	261	274
3GLI	D E	D	334	I	1.4	322	338
3GLI	D E	D	345	R	1.0	345	358
3GLI	D E	D	354	L	1.2	345	358
3GLI	D E	E	94	R	1.0	90	102
3GLI	D O	D	326	Q	3.5	322	338
3GLI	D O	D	330	Q	2.7	322	338
3GLI	D O	O	7	W	2.7	4	12
3GLI	F G	F	186	E	1.5	178	192
3GLI	F G	F	187	R	2.1	178	192
3GLI	F G	F	191	L	1.0	178	192
3GLI	F G	F	230	L	1.1	226	239
3GLI	F G	F	329	L	1.1	321	331
3GLI	F G	G	30	N	1.1	22	34
3GLI	F J	F	262	R	1.3	243	267
3GLI	F J	F	299	R	1.6	295	313
3GLI	F J	F	302	V	1.2	295	313
3GLI	F J	F	310	L	1.3	295	313
3GLI	F J	J	310	L	2.7	308	324
3GLI	F J	J	317	L	1.0	308	324
3GLI	G P	G	355	R	1.3	345	359
3GLI	I E	E	272	G	47.6	272	280
3GLI	I J	I	261	G	150.5	261	274
3GLI	I J	I	345	R	1.3	345	358
3GLI	I J	I	354	L	1.6	345	358
3GLI	I J	J	130	K	1.0	129	134
3GLI	I P	I	327	L	2.7	322	338
3GM1	A E	A	881	Y	1.1	879	896
3GM1	A E	A	988	K	1.8	969	1001
3GM1	A E	E	267	D	1.2	266	274
3GM1	A E	E	270	M	1.1	266	274
3GM1	A E	E	273	L	1.6	266	274
3GM1	A F	A	907	V	2.3	903	930
3GM1	A F	A	917	L	1.5	903	930
3GM1	A F	A	918	R	2.0	903	930
3GM1	A F	A	921	I	1.4	903	930
3GM1	A F	A	925	D	1.0	903	930
3GM1	A F	A	947	N	1.3	933	963
3GM1	A F	A	954	I	1.4	933	963
3GM1	A F	F	269	L	2.2	268	273
3GM1	A F	F	270	M	1.3	268	273
3GM1	B C	B	888	V	1.1	879	895
3GM1	B C	C	266	L	1.8	265	274
3GM1	B C	C	270	M	1.9	265	274
3GM1	B C	C	273	L	1.7	265	274
3GM1	B D	B	915	L	2.2	903	926
3GM1	B D	B	918	R	3.3	903	926

3GM1	B D	B	922	G	2.1	903	926
3GM1	B D	B	925	D	2.2	903	926
3GM1	B D	B	954	I	1.0	933	963
3GM1	B D	D	266	L	1.6	264	273
3GM1	B D	D	269	L	2.4	264	273
3GM1	B D	D	270	M	1.0	264	273
3GMW	A B	A	110	E	1.1	107	111
3GMW	A B	A	132	N	1.3	132	142
3GMW	C D	C	107	P	1.4	107	111
3GMW	C D	C	110	E	1.7	107	111
3GMW	C D	C	132	N	1.3	132	142
3GNI	A B	A	92	F	1.8	92	107
3GNI	A B	A	93	E	1.0	92	107
3GNI	A B	A	141	L	1.2	140	151
3GNI	A B	A	178	F	2.0	178	195
3GNI	A B	A	223	Y	1.6	223	238
3GNI	A B	A	227	R	1.3	223	238
3GNI	A B	A	301	K	1.6	299	308
3GNI	A B	A	305	F	1.0	299	308
3GNI	A B	B	-9	H	1.2	-9	-5
3GNI	A B	B	124	L	1.0	109	125
3GRW	L H	L	123	E	1.0	122	127
3GTM	A B	A	329	L	1.0	325	330
3GTM	A B	A	370	I	1.1	368	374
3GTM	A B	A	658	L	1.5	639	661
3GTM	A B	A	810	P	4.1	810	826
3GTM	A B	A	813	F	2.7	810	826
3GTM	A B	A	814	F	3.3	810	826
3GTM	A B	A	818	M	2.3	810	826
3GTM	A B	A	820	G	14.7	810	826
3GTM	A B	A	825	I	5.0	810	826
3GTM	A B	A	1413	G	5.7	1405	1415
3GTM	A B	A	1428	V	1.0	1424	1430
3GTM	A B	B	1026	L	1.4	1023	1039
3GTM	A B	B	1132	E	1.0	1132	1142
3GTM	A B	B	1135	R	1.9	1132	1142
3GTM	A B	B	1203	L	1.6	1198	1209
3GTM	A B	B	1204	F	1.9	1198	1209
3GTM	A B	B	1207	L	2.6	1198	1209
3GTM	A E	A	1006	I	2.1	1005	1009
3GTM	A E	A	1007	I	1.8	1005	1009
3GTM	A E	A	1017	L	3.8	1010	1026
3GTM	A E	A	1317	M	1.8	1313	1318
3GTM	A E	E	164	L	3.4	158	168
3GTM	A E	E	183	P	1.0	183	189
3GTM	A F	A	495	E	1.1	495	500
3GTM	A F	F	88	Y	1.4	87	96
3GTM	A F	F	89	E	1.0	87	96
3GTM	A F	F	92	R	2.4	87	96
3GTM	A F	F	99	L	1.3	97	103
3GTM	A F	F	102	S	1.1	97	103
3GTM	A I	A	714	F	1.0	714	720
3GTM	A K	A	548	N	1.3	543	553
3GTM	A K	A	551	Y	3.0	543	553
3GTM	A K	A	552	W	2.4	543	553
3GTM	A K	K	47	R	1.7	40	48
3GTM	A S	A	734	E	1.0	729	737
3GTM	A S	A	755	F	1.4	755	764
3GTM	A S	A	823	G	2.2	810	826
3GTM	A S	A	1172	L	1.1	1166	1173

3GTM	A S	S	200	R	2.8	194	203
3GTM	A S	S	248	I	1.0	241	257
3GTM	B C	B	847	D	1.4	843	849
3GTM	B C	B	848	R	1.6	843	849
3GTM	B C	C	35	R	1.0	27	39
3GTM	B C	C	38	I	1.4	27	39
3GTM	B C	C	62	F	4.0	60	70
3GTM	B C	C	65	H	1.4	60	70
3GTM	B C	C	69	L	1.4	60	70
3GTM	B I	B	311	L	1.5	308	321
3GTM	B J	B	190	Y	3.4	188	192
3GTM	B J	J	33	G	53.1	32	38
3GTM	B J	J	45	C	1.0	44	52
3GTM	B J	J	47	R	1.7	44	52
3GTM	B J	J	51	L	1.5	44	52
3GTM	B J	J	59	K	1.2	56	61
3GTM	C J	J	19	E	1.1	17	24
3GTM	C K	C	29	M	1.4	27	39
3GTM	C K	C	35	R	1.7	27	39
3GTM	C K	C	251	L	1.6	245	264
3GTM	C K	C	255	V	1.5	245	264
3GTM	C K	C	258	I	3.0	245	264
3GTM	C K	C	262	L	1.6	245	264
3GTM	C K	K	42	L	1.2	40	48
3GTM	C K	K	45	L	1.4	40	48
3GTM	C K	K	84	K	1.1	83	112
3GTM	C K	K	95	I	1.0	83	112
3GTM	C K	K	97	K	1.1	83	112
3GTM	C K	K	98	L	2.2	83	112
3GTM	C K	K	105	F	3.2	83	112
3GTM	C K	K	108	E	1.1	83	112
3GTM	C K	K	109	W	2.4	83	112
3GTM	C L	C	60	D	1.5	60	70
3GTM	C L	C	68	G	19.2	60	70
3GTU	A B	A	81	R	1.8	72	83
3GTU	A B	A	98	I	1.2	90	116
3GTU	A B	B	98	I	1.6	94	120
3GTU	A B	B	101	D	1.4	94	120
3GTU	A B	B	102	I	1.5	94	120
3GTU	C D	C	73	N	1.2	72	83
3GTU	C D	C	81	R	1.7	72	83
3GTU	C D	C	94	I	1.3	90	116
3GTU	C D	C	98	I	1.8	90	116
3GTU	C D	C	99	L	1.4	90	116
3GTU	C D	C	102	Q	1.4	90	116
3GTU	C D	D	82	Y	1.0	76	87
3GTU	C D	D	101	D	2.2	94	120
3GTU	C D	D	102	I	7.1	94	120
3GTU	C D	D	105	N	1.3	94	120
3GZ1	B P	B	40	Y	1.2	33	49
3GZ1	B P	B	44	Y	2.2	33	49
3GZ1	B P	B	47	Y	3.0	33	49
3GZ1	B P	B	82	I	1.1	70	83
3GZ1	B P	B	108	F	1.4	105	117
3GZD	B C	B	407	F	1.1	407	412
3GZD	D C	D	47	I	2.2	44	57
3GZD	D C	D	55	W	1.8	44	57
3GZD	D C	D	101	E	1.0	99	120
3GZD	D C	D	104	N	2.7	99	120
3GZD	D C	C	47	I	1.2	44	57

3GZD	D C	C	55	W	1.9	44	57
3GZD	D C	C	101	E	1.0	99	133
3GZD	D C	C	104	N	2.9	99	133
3GZU	A G	A	474	F	1.7	466	477
3GZU	B J	B	507	M	10.7	505	514
3GZU	B O	O	28	S	1.0	28	42
3H0L	A B	A	313	N	1.6	304	314
3H0L	A B	A	332	I	1.7	332	344
3H0L	A B	A	333	F	1.2	332	344
3H0L	A B	A	336	Y	2.0	332	344
3H0L	A B	A	340	R	1.5	332	344
3H0L	A B	A	359	L	1.8	346	360
3H0L	A B	A	368	Y	1.1	368	386
3H0L	A C	A	333	F	1.6	332	344
3H0L	A C	A	336	Y	2.0	332	344
3H0L	A C	A	338	R	1.6	332	344
3H0L	A C	A	340	R	2.3	332	344
3H0L	A C	A	342	E	1.1	332	344
3H0L	A C	A	349	K	2.3	346	360
3H0L	A C	A	353	M	2.4	346	360
3H0L	A C	A	370	K	2.4	368	386
3H0L	A C	A	373	K	1.3	368	386
3H0L	A C	A	374	V	2.2	368	386
3H0L	A C	A	375	R	1.7	368	386
3H0L	A C	A	376	R	2.2	368	386
3H0L	A C	A	377	L	2.3	368	386
3H0L	A C	A	412	I	2.7	411	416
3H0L	A C	A	415	Y	1.1	411	416
3H0L	A C	C	6	W	2.0	4	14
3H0L	A C	C	26	F	4.0	20	37
3H0L	A C	C	30	L	1.5	20	37
3H0L	A C	C	33	I	1.5	20	37
3H0L	A C	C	34	L	1.0	20	37
3H0L	A C	C	36	F	3.4	20	37
3H0L	A C	C	40	L	3.6	39	43
3H0L	A E	E	387	K	1.2	386	400
3H0L	B C	C	71	R	1.5	71	77
3H0L	D E	D	313	N	1.4	304	314
3H0L	D E	D	332	I	1.8	332	344
3H0L	D E	D	336	Y	2.0	332	344
3H0L	D E	D	359	L	1.9	346	360
3H0L	D E	D	368	Y	1.6	368	386
3H0L	D F	D	333	F	1.0	332	344
3H0L	D F	D	349	K	2.3	346	360
3H0L	D F	D	350	R	1.2	346	360
3H0L	D F	D	353	M	2.8	346	360
3H0L	D F	D	354	L	1.1	346	360
3H0L	D F	D	357	F	1.2	346	360
3H0L	D F	D	370	K	2.2	368	386
3H0L	D F	D	373	K	1.5	368	386
3H0L	D F	D	374	V	2.0	368	386
3H0L	D F	D	377	L	1.6	368	386
3H0L	D F	D	412	I	3.2	411	416
3H0L	D F	D	415	Y	1.1	411	416
3H0L	D F	F	6	W	2.3	4	14
3H0L	D F	F	10	I	1.2	4	14
3H0L	D F	F	26	F	2.1	20	37
3H0L	D F	F	30	L	2.1	20	37
3H0L	D F	F	33	I	1.5	20	37
3H0L	D F	F	36	F	3.2	20	37

3H0L	D H	H	292	K	1.0	285	294
3H0L	E F	F	13	L	1.7	4	14
3H0L	E F	F	71	R	2.5	71	77
3H0L	G E	E	292	K	1.3	285	294
3H0L	G H	G	313	N	1.2	304	314
3H0L	G H	G	336	Y	1.4	332	344
3H0L	G H	G	359	L	1.6	346	360
3H0L	G I	G	333	F	1.1	332	344
3H0L	G I	G	340	R	1.9	332	344
3H0L	G I	G	349	K	2.5	346	360
3H0L	G I	G	350	R	1.6	346	360
3H0L	G I	G	353	M	2.4	346	360
3H0L	G I	G	373	K	1.4	368	386
3H0L	G I	G	374	V	2.3	368	386
3H0L	G I	G	377	L	1.7	368	386
3H0L	G I	G	412	I	2.6	411	416
3H0L	G I	G	415	Y	1.0	411	416
3H0L	G I	I	6	W	2.2	4	14
3H0L	G I	I	10	I	1.8	4	14
3H0L	G I	I	22	E	1.2	20	37
3H0L	G I	I	26	F	2.4	20	37
3H0L	G I	I	30	L	2.2	20	37
3H0L	G I	I	33	I	1.5	20	37
3H0L	G I	I	34	L	1.0	20	37
3H0L	G I	I	36	F	3.0	20	37
3H0L	G K	G	22	K	1.0	21	40
3H0L	H I	I	71	R	1.4	71	77
3H0L	J K	J	336	Y	2.0	332	344
3H0L	J K	J	359	L	2.1	346	360
3H0L	J K	J	368	Y	1.2	368	386
3H0L	J L	J	304	I	1.0	304	314
3H0L	J L	J	333	F	1.0	332	344
3H0L	J L	J	340	R	2.2	332	344
3H0L	J L	J	349	K	2.1	346	360
3H0L	J L	J	350	R	1.4	346	360
3H0L	J L	J	353	M	2.9	346	360
3H0L	J L	J	354	L	1.1	346	360
3H0L	J L	J	357	F	1.4	346	360
3H0L	J L	J	370	K	2.6	368	386
3H0L	J L	J	373	K	1.6	368	386
3H0L	J L	J	374	V	1.2	368	386
3H0L	J L	J	375	R	1.4	368	386
3H0L	J L	J	377	L	1.6	368	386
3H0L	J L	J	412	I	2.6	411	416
3H0L	J L	J	415	Y	1.1	411	416
3H0L	J L	L	6	W	2.4	4	14
3H0L	J L	L	10	I	1.3	4	14
3H0L	J L	L	22	E	1.6	20	37
3H0L	J L	L	26	F	1.6	20	37
3H0L	J L	L	30	L	2.3	20	37
3H0L	J L	L	33	I	1.5	20	37
3H0L	J L	L	36	F	3.1	20	37
3H0L	K L	K	55	K	3.4	55	68
3H0L	K L	K	58	V	2.7	55	68
3H0L	K L	L	71	R	2.1	71	77
3H0L	M N	M	313	N	1.3	304	314
3H0L	M N	M	336	Y	2.2	332	344
3H0L	M N	M	359	L	1.7	346	360
3H0L	M N	M	368	Y	1.0	363	386
3H0L	M O	M	332	I	1.1	332	344

3H0L	M O	M	340	R	2.1	332	344
3H0L	M O	M	349	K	2.0	346	360
3H0L	M O	M	350	R	1.1	346	360
3H0L	M O	M	353	M	2.7	346	360
3H0L	M O	M	354	L	1.1	346	360
3H0L	M O	M	357	F	1.1	346	360
3H0L	M O	M	373	K	1.7	363	386
3H0L	M O	M	374	V	1.2	363	386
3H0L	M O	M	377	L	1.6	363	386
3H0L	M O	M	412	I	2.6	411	418
3H0L	M O	O	6	W	1.9	4	14
3H0L	M O	O	10	I	1.3	4	14
3H0L	M O	O	26	F	1.9	20	37
3H0L	M O	O	30	L	2.0	20	37
3H0L	M O	O	33	I	1.9	20	37
3H0L	M O	O	34	L	1.0	20	37
3H0L	M O	O	36	F	2.9	20	37
3H0L	N O	O	71	R	1.9	71	77
3H0L	P N	N	387	K	1.1	386	400
3H0L	P N	N	390	K	1.1	386	400
3H0L	P N	N	394	K	1.2	386	400
3H0L	P Q	P	359	L	1.9	346	360
3H0L	P Q	P	368	Y	1.2	368	386
3H0L	P R	P	332	I	1.2	332	344
3H0L	P R	P	340	R	2.4	332	344
3H0L	P R	P	349	K	2.4	346	360
3H0L	P R	P	353	M	2.8	346	360
3H0L	P R	P	370	K	1.0	368	386
3H0L	P R	P	373	K	1.4	368	386
3H0L	P R	P	374	V	1.9	368	386
3H0L	P R	P	375	R	1.0	368	386
3H0L	P R	P	376	R	1.1	368	386
3H0L	P R	P	377	L	1.4	368	386
3H0L	P R	P	412	I	2.6	411	416
3H0L	P R	R	6	W	2.2	4	14
3H0L	P R	R	10	I	1.3	4	14
3H0L	P R	R	26	F	1.8	20	37
3H0L	P R	R	30	L	2.1	20	37
3H0L	P R	R	33	I	1.5	20	37
3H0L	P R	R	34	L	1.0	20	37
3H0L	P R	R	36	F	2.9	20	37
3H0L	P R	R	40	L	3.6	39	43
3H0L	P R	R	42	E	1.0	39	43
3H0L	P U	P	271	E	1.1	267	283
3H0L	Q R	R	71	R	2.2	71	77
3H0L	S T	S	313	N	1.2	304	314
3H0L	S T	S	359	L	1.9	346	360
3H0L	S U	S	299	I	1.4	298	303
3H0L	S U	S	332	I	1.1	332	344
3H0L	S U	S	333	F	1.1	332	344
3H0L	S U	S	336	Y	1.2	332	344
3H0L	S U	S	340	R	2.1	332	344
3H0L	S U	S	349	K	1.5	346	360
3H0L	S U	S	350	R	1.0	346	360
3H0L	S U	S	353	M	2.4	346	360
3H0L	S U	S	357	F	1.8	346	360
3H0L	S U	S	373	K	1.6	368	386
3H0L	S U	S	374	V	2.1	368	386
3H0L	S U	S	375	R	1.5	368	386
3H0L	S U	S	377	L	1.6	368	386

3H0L	S U	S	412	I	3.2	411	418
3H0L	S U	S	415	Y	1.0	411	418
3H0L	S U	U	6	W	2.3	4	14
3H0L	S U	U	10	I	1.5	4	14
3H0L	S U	U	26	F	4.5	20	37
3H0L	S U	U	30	L	2.1	20	37
3H0L	S U	U	33	I	1.4	20	37
3H0L	S U	U	36	F	3.3	20	37
3H0L	T U	U	71	R	2.5	71	77
3H0L	V T	T	387	K	1.1	386	400
3H0L	V W	V	313	N	1.3	304	314
3H0L	V W	V	332	I	1.3	332	344
3H0L	V W	V	336	Y	1.9	332	344
3H0L	V W	V	359	L	1.6	346	360
3H0L	V W	V	368	Y	1.2	368	386
3H0L	V X	V	332	I	1.5	332	344
3H0L	V X	V	340	R	2.1	332	344
3H0L	V X	V	349	K	1.7	346	360
3H0L	V X	V	353	M	2.1	346	360
3H0L	V X	V	354	L	1.2	346	360
3H0L	V X	V	357	F	1.7	346	360
3H0L	V X	V	373	K	1.5	368	386
3H0L	V X	V	374	V	1.0	368	386
3H0L	V X	V	375	R	1.1	368	386
3H0L	V X	V	377	L	1.5	368	386
3H0L	V X	V	412	I	3.2	411	416
3H0L	V X	X	6	W	1.6	4	14
3H0L	V X	X	10	I	2.5	4	14
3H0L	V X	X	26	F	1.5	20	37
3H0L	V X	X	30	L	1.5	20	37
3H0L	V X	X	33	I	1.7	20	37
3H0L	V X	X	34	L	1.1	20	37
3H0L	V X	X	36	F	3.2	20	37
3H0L	W X	X	71	R	1.5	71	77
3H0T	A B	A	128	E	2.7	126	131
3H11	A B	A	440	L	1.2	439	455
3H11	A B	A	444	I	1.7	439	455
3H11	A B	A	447	N	1.1	439	455
3H11	A B	A	448	G	3.9	439	455
3H11	A B	A	451	Y	1.2	439	455
3H11	A B	B	417	R	2.5	405	420
3H11	A B	B	425	L	1.3	424	437
3H11	A B	B	429	T	1.0	424	437
3H11	A B	B	433	Y	1.3	424	437
3H1C	T U	T	528	G	1.1	516	541
3H1C	T U	T	536	V	1.0	516	541
3H2U	A B	A	928	L	1.2	918	938
3H2U	A B	A	932	E	3.9	918	938
3H2U	A B	A	953	D	2.1	943	971
3H2U	C D	C	932	E	4.0	918	938
3H2U	C D	C	953	D	1.0	943	971
3H2V	A E	A	925	R	1.6	918	937
3H2V	A E	A	928	L	1.0	918	937
3H2V	A E	A	953	D	1.2	943	972
3H2V	B F	B	928	L	1.4	918	937
3H2V	C G	C	928	L	1.1	918	937
3H2V	C G	C	950	C	1.6	943	972
3H2V	C G	C	953	D	1.1	943	972
3H2V	D G	D	1013	D	1.4	1013	1021
3H2V	D H	D	950	C	1.2	943	972

3H2V	D H	D	953	D	1.0	943	972
3H32	A B	A	133	I	1.2	120	163
3H32	A B	A	145	V	1.3	120	163
3H32	A B	A	148	K	1.2	120	163
3H32	A B	A	149	R	1.5	120	163
3H32	A B	A	157	K	2.8	120	163
3H32	A B	A	158	I	1.1	120	163
3H32	A B	A	177	D	1.2	175	188
3H32	A B	B	168	L	1.2	154	193
3H32	A B	B	171	I	1.0	154	193
3H32	A B	B	175	L	1.2	154	193
3H32	A B	B	178	K	1.9	154	193
3H32	A B	B	192	Y	1.3	154	193
3H32	A C	A	150	L	1.5	120	163
3H32	B C	B	169	R	1.0	154	193
3H32	B C	B	172	L	1.3	154	193
3H32	B C	B	179	I	1.8	154	193
3H32	B C	B	183	E	1.2	154	193
3H32	B C	C	110	L	1.5	102	135
3H32	B C	C	120	K	1.9	102	135
3H32	B C	C	127	K	1.0	102	135
3H32	B C	C	131	L	1.4	102	135
3H32	D E	D	133	I	1.1	121	161
3H32	D E	D	144	L	1.2	121	161
3H32	D E	D	145	V	1.0	121	161
3H32	D E	D	147	M	2.3	121	161
3H32	D E	D	149	R	1.2	121	161
3H32	D E	D	153	D	2.8	121	161
3H32	D E	D	156	I	1.9	121	161
3H32	D E	D	175	L	1.3	175	188
3H32	D E	D	177	D	2.8	175	188
3H32	D E	D	179	E	1.3	175	188
3H32	D E	D	181	Q	1.5	175	188
3H32	D E	E	168	L	1.7	154	193
3H32	D E	E	175	L	2.2	154	193
3H32	D E	E	178	K	3.4	154	193
3H32	D E	E	182	L	1.0	154	193
3H32	D F	D	136	L	1.4	121	161
3H32	E F	E	165	L	1.1	154	193
3H32	E F	E	168	L	1.1	154	193
3H32	E F	E	169	R	1.1	154	193
3H32	E F	E	172	L	2.0	154	193
3H32	E F	E	179	I	1.7	154	193
3H32	E F	E	183	E	1.4	154	193
3H32	E F	E	186	V	1.2	154	193
3H32	E F	F	109	Y	1.0	106	135
3H32	E F	F	110	L	2.0	106	135
3H32	E F	F	113	I	1.9	106	135
3H32	E F	F	120	K	1.8	106	135
3H32	E F	F	124	L	2.1	106	135
3H32	E F	F	127	K	1.2	106	135
3H32	E F	F	131	L	1.1	106	135
3H32	E F	F	209	I	1.3	208	213
3H42	A B	B	266	I	2.2	261	277
3H42	A B	B	269	E	2.4	261	277
3H42	A B	B	295	R	1.5	295	307
3H42	A B	B	303	R	1.0	295	307
3H42	L H	L	129	E	1.3	127	132
3H4P	A a	a	71	L	1.7	71	76
3H4P	A a	a	73	K	1.2	71	76

3H4P	A b	b	72	Y	1.4	71	76
3H4P	B b	b	67	A	1.0	65	70
3H4P	B b	b	71	L	2.2	71	76
3H4P	E e	E	94	R	2.3	92	103
3H4P	E e	E	102	L	1.5	92	103
3H4P	E e	e	71	L	1.0	71	76
3H4P	F f	f	71	L	1.3	71	76
3H4P	G a	a	88	L	1.5	88	96
3H4P	G a	a	91	N	1.2	88	96
3H4P	H i	i	72	Y	1.2	71	76
3H4P	I i	i	71	L	1.0	71	76
3H4P	J j	j	71	L	2.3	71	76
3H4P	J j	j	73	K	1.2	71	76
3H4P	J j	j	75	R	1.3	71	76
3H4P	K k	k	71	L	2.8	71	76
3H4P	L l	l	71	L	1.3	71	76
3H4P	L l	l	74	M	1.6	71	76
3H4P	L m	m	72	Y	2.0	71	76
3H4P	M m	M	94	R	1.7	92	103
3H4P	M m	m	71	L	1.3	71	76
3H4P	M n	n	88	L	1.2	84	94
3H4P	N n	n	66	I	1.0	65	70
3H4P	N n	n	71	L	1.2	71	76
3H4S	A E	A	1151	G	17.9	1133	1155
3H4S	A E	A	1154	S	1.3	1133	1155
3H4S	A E	A	1229	L	1.3	1222	1242
3H4S	A E	A	1230	V	1.2	1222	1242
3H4S	A E	A	1232	Y	2.8	1222	1242
3H4S	A E	E	45	G	7.2	35	50
3H4S	A E	E	62	L	1.1	59	65
3H4S	A E	E	103	M	1.3	96	114
3H4S	A E	E	106	L	1.2	96	114
3H4S	A E	E	110	M	1.0	96	114
3H6P	A C	A	18	F	1.4	18	75
3H6P	A C	A	21	K	1.8	18	75
3H6P	A C	A	25	M	1.9	18	75
3H6P	A C	C	21	Y	3.0	21	39
3H6P	A C	C	25	L	1.2	21	39
3H6P	A C	C	32	I	2.2	21	39
3H6P	A C	C	69	Y	1.1	51	74
3H6P	A D	A	51	F	1.4	18	75
3H6P	A D	A	57	R	1.5	18	75
3H6P	A D	A	58	F	1.6	18	75
3H6P	A D	A	68	L	2.3	18	75
3H6P	A D	A	71	I	1.7	18	75
3H6P	A D	D	54	W	1.7	51	73
3H6P	A D	D	58	W	1.5	51	73
3H6P	A D	D	64	D	1.6	51	73
3H6P	A D	D	65	L	1.5	51	73
3H6P	A D	D	72	M	2.0	51	73
3H6P	B C	B	51	F	1.2	15	77
3H6P	B C	B	58	F	2.6	15	77
3H6P	B C	B	68	L	2.2	15	77
3H6P	B C	B	69	L	1.5	15	77
3H6P	B C	B	76	L	1.6	15	77
3H6P	B C	C	54	W	1.2	51	74
3H6P	B C	C	58	W	1.8	51	74
3H6P	B C	C	65	L	2.0	51	74
3H6P	B C	C	72	M	1.8	51	74
3H6P	B D	B	21	K	1.5	15	77

3H6P	B D	B	25	M	1.8	15	77
3H6P	B D	D	21	Y	3.1	21	40
3H6P	B D	D	25	L	1.3	21	40
3H6P	B D	D	32	I	2.3	21	40
3H6P	B D	D	35	E	1.0	21	40
3H6P	B D	D	39	L	1.0	21	40
3H6P	B D	D	69	Y	1.4	51	73
3H87	A C	A	112	I	1.3	112	124
3H87	A C	A	113	P	1.5	112	124
3H87	A D	A	28	L	3.1	25	29
3H87	A D	A	45	E	2.7	37	46
3H87	A D	A	72	E	3.0	66	74
3H87	A D	D	49	A	2.3	49	59
3H87	A D	D	51	D	3.1	49	59
3H87	A D	D	52	L	3.8	49	59
3H87	A D	D	54	R	4.6	49	59
3H87	A D	D	55	L	1.7	49	59
3H87	A D	D	56	R	1.2	49	59
3H87	B C	B	28	L	1.8	25	30
3H87	B C	B	29	V	1.5	25	30
3H87	B C	B	58	E	1.3	53	63
3H87	B C	B	61	F	3.0	53	63
3H87	B C	B	72	E	4.4	66	74
3H87	B C	B	113	P	1.1	112	124
3H87	B C	C	38	Q	2.3	28	41
3H87	B C	C	52	L	1.2	49	59
3H87	B C	C	54	R	5.9	49	59
3H87	B C	C	55	L	1.7	49	59
3H87	B C	C	67	L	1.5	65	72
3H9R	A B	A	198	F	1.0	198	206
3H9R	A B	A	199	L	1.6	198	206
3H9R	A B	A	245	W	2.1	242	255
3H9R	A B	A	246	F	1.8	242	255
3HAE	G I	G	127	E	1.0	125	130
3HAE	L H	L	127	E	1.3	125	130
3HAE	P S	P	72	Q	1.2	57	85
3HAE	P S	P	75	R	1.0	57	85
3HAE	P T	P	65	R	1.4	57	85
3HAE	S T	S	126	E	1.0	125	130
3HAE	S T	S	127	E	1.4	125	130
3HAX	A C	A	68	W	2.7	62	73
3HAX	A C	A	72	I	1.2	62	73
3HAX	A C	A	221	H	2.8	220	234
3HAX	A C	A	225	D	4.4	220	234
3HAX	A C	A	229	F	1.9	220	234
3HAX	A C	A	238	Y	1.2	236	243
3HAX	A C	C	42	G	2.2	42	54
3HAX	A C	C	45	R	4.5	42	54
3HAX	A C	C	46	R	3.3	42	54
3HAX	A C	C	49	K	2.0	42	54
3HAX	A C	C	53	L	1.2	42	54
3HAX	C D	C	44	Y	1.9	42	54
3HAX	C D	C	48	W	2.8	42	54
3HAX	C D	D	66	H	1.4	65	74
3HAY	A B	A	134	E	1.7	125	135
3HAY	A C	A	68	W	3.2	62	73
3HAY	A C	A	221	H	2.3	220	234
3HAY	A C	A	225	D	2.2	220	234
3HAY	A C	A	229	F	1.5	220	234
3HAY	A C	C	45	R	2.4	42	54

3HAY	A C	C	46	R	1.4	42	54
3HAY	C D	C	44	Y	2.6	42	54
3HAY	C D	C	45	R	1.6	42	54
3HAY	C D	C	48	W	2.2	42	54
3HAY	C D	D	61	E	1.0	61	74
3HAY	C D	D	66	H	2.0	61	74
3HAY	C D	D	70	L	1.2	61	74
3HC0	A B	B	124	Q	1.2	122	127
3HC0	H L	L	124	Q	1.0	122	127
3HD7	A B	A	32	L	2.2	29	69
3HD7	A B	A	39	V	1.3	29	69
3HD7	A B	A	43	V	1.5	29	69
3HD7	A B	A	60	L	1.0	29	69
3HD7	A B	A	85	K	1.8	70	113
3HD7	A B	A	99	L	1.2	70	113
3HD7	A B	A	106	I	1.0	70	113
3HD7	A B	B	205	L	1.4	190	284
3HD7	A B	B	257	Y	2.5	190	284
3HD7	A B	B	260	K	1.2	190	284
3HD7	A B	B	264	K	1.0	190	284
3HD7	A B	B	268	I	2.1	190	284
3HD7	A B	B	275	L	1.4	190	284
3HD7	A D	A	45	I	1.3	29	69
3HD7	A D	A	63	L	1.5	29	69
3HD7	A D	A	77	F	1.9	70	113
3HD7	B C	B	192	L	1.4	190	284
3HD7	B C	B	199	H	2.2	190	284
3HD7	B C	B	209	I	1.9	190	284
3HD7	B C	B	213	H	1.8	190	284
3HD7	B C	B	217	M	1.4	190	284
3HD7	B C	B	224	E	1.3	190	284
3HD7	B C	B	234	E	2.8	190	284
3HD7	B C	B	244	V	1.1	190	284
3HD7	B C	B	251	T	1.1	190	284
3HD7	B C	B	255	V	1.3	190	284
3HD7	B C	C	21	L	1.2	18	78
3HD7	B C	C	32	M	1.9	18	78
3HD7	B C	C	43	G	3.8	18	78
3HD7	B C	C	45	R	1.6	18	78
3HD7	B C	C	49	M	1.5	18	78
3HD7	B C	C	50	L	1.6	18	78
3HD7	B C	C	59	R	2.1	18	78
3HD7	B C	C	60	V	1.4	18	78
3HD7	B C	C	63	G	3.9	18	78
3HD7	C D	C	33	L	1.1	18	78
3HD7	C D	C	36	V	1.0	18	78
3HD7	C D	C	57	L	1.3	18	78
3HD7	C D	C	61	E	1.4	18	78
3HD7	C D	C	71	M	1.4	18	78
3HD7	C D	D	153	V	1.1	139	185
3HD7	C D	D	160	L	1.2	139	185
3HD7	C D	D	163	M	1.1	139	185
3HD7	C D	D	181	I	1.8	139	185
3HD7	E F	E	32	L	1.6	29	69
3HD7	E F	E	39	V	1.3	29	69
3HD7	E F	E	46	M	3.0	29	69
3HD7	E F	E	47	R	1.6	29	69
3HD7	E F	E	53	V	1.6	29	69
3HD7	E F	E	60	L	1.6	29	69
3HD7	E F	E	78	E	1.5	70	110

3HD7	E F	E	85	K	2.3	70	110
3HD7	E F	E	89	W	1.4	70	110
3HD7	E F	E	91	K	1.7	70	110
3HD7	E F	E	95	M	1.5	70	110
3HD7	E F	E	96	M	1.3	70	110
3HD7	E F	E	99	L	1.7	70	110
3HD7	E F	E	102	I	1.5	70	110
3HD7	E F	E	106	I	1.9	70	110
3HD7	E F	F	205	L	1.9	189	284
3HD7	E F	F	211	E	1.1	189	284
3HD7	E F	F	216	F	1.8	189	284
3HD7	E F	F	243	Y	1.6	189	284
3HD7	E F	F	246	R	1.0	189	284
3HD7	E F	F	250	D	1.5	189	284
3HD7	E F	F	257	Y	3.3	189	284
3HD7	E F	F	265	K	1.2	189	284
3HD7	E F	F	267	M	1.5	189	284
3HD7	E F	F	268	I	3.6	189	284
3HD7	E F	F	275	L	1.0	189	284
3HD7	E F	F	278	I	1.0	189	284
3HD7	E H	E	59	K	1.0	29	69
3HD7	E H	E	63	L	1.6	29	69
3HD7	E H	E	70	L	1.2	70	110
3HD7	E H	E	77	F	1.3	70	110
3HD7	E H	H	178	I	1.7	147	200
3HD7	E H	H	189	K	1.0	147	200
3HD7	F G	F	199	H	1.3	189	284
3HD7	F G	F	213	H	1.7	189	284
3HD7	F G	F	216	F	1.0	189	284
3HD7	F G	F	227	G	3.5	189	284
3HD7	F G	F	234	E	1.7	189	284
3HD7	F G	F	237	V	1.0	189	284
3HD7	F G	F	244	V	1.3	189	284
3HD7	F G	G	35	L	1.1	29	80
3HD7	F G	G	43	G	1.4	29	80
3HD7	F G	G	59	R	2.0	29	80
3HD7	F G	G	63	G	11.3	29	80
3HD7	F H	F	216	F	1.2	189	284
3HD7	G H	G	19	D	1.3	18	28
3HD7	G H	G	29	T	2.6	29	80
3HD7	G H	G	57	L	1.3	29	80
3HD7	G H	G	61	E	2.2	29	80
3HD7	G H	H	145	E	1.3	140	146
3HD7	G H	H	180	R	1.5	147	200
3HD7	G H	H	181	I	2.1	147	200
3HD7	G H	H	184	K	1.2	147	200
3HE6	A C	A	79	R	1.7	60	88
3HE6	A C	A	149	V	1.4	141	152
3HE6	A D	A	83	E	5.0	60	88
3HE6	A D	A	86	K	4.8	60	88
3HE7	A C	A	79	R	1.1	60	87
3HE7	C D	D	140	H	1.6	135	142
3HEI	A B	A	129	F	2.1	126	131
3HEI	E F	E	129	F	2.2	126	131
3HEI	G H	G	129	F	2.1	126	132
3HEI	K L	K	129	F	1.7	126	132
3HEI	M N	M	129	F	2.0	126	131
3HEI	O P	O	129	F	1.0	126	131
3HFM	H Y	Y	97	K	1.9	89	99
3HG1	A D	A	62	G	13.3	57	85

3HG1	A D	A	167	W	1.1	152	175
3HG1	A E	A	65	R	1.3	57	85
3HGK	A F	A	213	F	2.3	210	216
3HGK	A H	A	215	K	1.1	210	216
3HGK	B E	B	213	F	2.0	210	216
3HGK	B E	E	179	H	1.3	176	180
3HGK	C G	C	213	F	4.1	210	216
3HGK	C G	G	176	M	1.1	176	180
3HGK	C G	G	179	H	1.3	176	180
3HGK	D F	D	215	K	1.6	210	216
3HGK	D H	D	213	F	1.8	210	216
3HH2	A C	C	48	K	2.5	43	52
3HH2	A D	D	47	F	1.4	43	52
3HH2	A D	D	51	I	1.3	43	52
3HH2	A D	D	192	R	4.3	188	199
3HH2	B C	B	59	H	1.3	56	65
3HH2	B C	C	47	F	1.6	43	52
3HH2	B C	C	192	R	2.8	188	199
3HH2	B D	D	48	K	2.2	43	52
3HHL	A B	A	14	Q	1.5	9	18
3HHL	A D	A	11	V	1.4	9	18
3HHL	A D	A	15	F	1.3	9	18
3HHL	A D	D	11	V	1.1	9	18
3HHL	A D	D	15	F	1.2	9	18
3HHL	B C	B	11	V	1.2	9	18
3HHL	B C	B	15	F	1.4	9	18
3HHL	B C	C	11	V	1.2	9	18
3HHL	B C	C	15	F	1.1	9	18
3HHR	A B	A	25	F	2.1	6	33
3HHR	A B	A	42	Y	1.9	38	47
3HHR	A B	A	64	R	3.8	64	69
3HHR	A B	A	171	D	1.3	155	185
3HHR	A B	A	179	I	1.3	155	185
3HHR	A C	A	8	R	2.3	6	33
3HHR	A C	A	11	D	2.1	6	33
3HHR	A C	A	12	N	2.0	6	33
3HHR	A C	A	16	R	1.9	6	33
3HHR	A C	A	120	G	10.6	107	128
3HHZ	A K	K	377	E	1.5	375	384
3HHZ	A K	K	380	G	2.1	375	384
3HHZ	B L	L	380	G	7.3	375	385
3HHZ	B L	L	384	D	1.7	375	385
3HHZ	C M	C	258	Q	1.4	256	261
3HHZ	C M	M	376	V	1.2	375	385
3HHZ	C M	M	377	E	1.9	375	385
3HHZ	C M	M	380	G	2.8	375	385
3HHZ	D N	N	380	G	15.4	375	385
3HHZ	D N	N	384	D	1.5	375	385
3HHZ	E O	O	377	E	1.1	375	385
3HJW	A B	A	68	W	3.2	62	73
3HJW	A B	A	221	H	2.7	220	234
3HJW	A B	A	222	D	1.7	220	234
3HJW	A B	A	225	D	4.3	220	234
3HJW	A B	A	229	F	2.4	220	234
3HJW	A B	B	42	G	3.4	42	53
3HJW	A B	B	45	R	2.8	42	53
3HJW	A B	B	46	R	2.3	42	53
3HJW	A B	B	49	K	1.7	42	53
3HJW	A B	B	50	R	1.5	42	53
3HJW	B C	B	44	Y	2.0	42	53

3HJW	B C	B	47	R	2.2	42	53
3HJW	B C	B	48	W	5.9	42	53
3HJW	B C	B	51	E	1.1	42	53
3HJW	B C	C	66	H	2.0	65	74
3HJW	B C	C	69	P	3.4	65	74
3HJW	B C	C	70	L	2.1	65	74
3HJW	B C	C	73	E	1.2	65	74
3HJY	A B	A	229	F	1.2	220	234
3HJY	A B	B	50	R	1.2	42	52
3HKI	A B	A	14	E	1.9	14	14
3HKI	D E	D	1	F	1.6	1	1
3HKI	D E	D	14	E	1.4	14	14
3HKI	D E	D	14	E	2.2	14	14
3HKI	D E	D	14	L	2.0	14	14
3HKI	D E	D	14	Y	1.6	14	14
3HKJ	A B	A	14	E	2.4	14	14
3HKJ	A B	A	14	E	2.3	14	14
3HKJ	A B	A	14	L	1.1	14	14
3HKJ	A B	A	14	Y	3.8	14	14
3HKJ	D E	D	14	E	1.2	14	14
3HKJ	D E	D	14	E	1.5	14	14
3HKJ	D E	D	14	Y	4.2	14	14
3HKZ	A B	A	277	F	1.3	272	278
3HKZ	A B	A	501	D	3.4	499	507
3HKZ	A B	A	648	L	2.2	648	652
3HKZ	A B	A	728	M	5.8	724	729
3HKZ	A B	A	792	P	1.1	792	802
3HKZ	A B	A	795	L	1.0	792	802
3HKZ	A B	A	821	R	1.4	818	826
3HKZ	A B	B	1048	R	1.2	1048	1052
3HKZ	A B	B	1097	F	1.4	1095	1107
3HKZ	A C	A	89	H	1.1	87	96
3HKZ	A C	A	819	M	1.2	818	826
3HKZ	A C	A	874	R	1.6	867	875
3HKZ	A C	C	70	I	1.2	70	75
3HKZ	A C	C	71	G	62.6	70	75
3HKZ	A C	C	73	V	1.0	70	75
3HKZ	A C	C	79	G	16.2	76	81
3HKZ	A C	C	80	E	1.1	76	81
3HKZ	A C	C	315	L	2.1	310	318
3HKZ	A C	C	342	L	1.3	341	346
3HKZ	A C	C	374	I	1.2	369	376
3HKZ	A G	A	549	K	4.9	548	556
3HKZ	A K	A	479	I	1.0	470	480
3HKZ	A Y	A	125	W	1.7	123	132
3HKZ	B D	D	57	I	1.1	55	64
3HKZ	B L	L	22	H	1.5	22	34
3HKZ	B N	N	32	G	217.2	31	38
3HKZ	B N	N	58	E	1.7	56	61
3HKZ	C B	B	1097	F	1.9	1095	1107
3HKZ	C E	E	22	L	1.0	22	29
3HKZ	C H	C	292	I	1.2	286	296
3HKZ	C K	K	18	V	3.0	14	23
3HKZ	C K	K	34	R	7.9	29	42
3HKZ	C K	K	35	V	6.8	29	42
3HKZ	C K	K	38	A	6.8	29	42
3HKZ	D L	D	28	I	2.3	28	34
3HKZ	D L	D	30	R	1.9	28	34
3HKZ	D L	D	243	L	1.3	238	261
3HKZ	D L	D	246	G	31.3	238	261

3HKZ	D L	D	249	I	1.2	238	261
3HKZ	D L	D	250	I	1.0	238	261
3HKZ	D L	D	252	K	1.6	238	261
3HKZ	D L	D	253	I	1.3	238	261
3HKZ	D L	D	257	E	1.1	238	261
3HKZ	D L	D	260	L	1.7	238	261
3HKZ	D L	L	27	L	2.0	22	34
3HKZ	D L	L	30	G	24.4	22	34
3HKZ	D L	L	66	K	1.0	65	85
3HKZ	D L	L	73	I	1.3	65	85
3HKZ	D L	L	79	M	2.2	65	85
3HKZ	D L	L	83	Y	3.1	65	85
3HKZ	D L	L	84	I	1.5	65	85
3HKZ	D L	L	87	I	1.5	86	90
3HKZ	D N	N	56	I	6.5	56	61
3HKZ	D N	N	60	I	1.1	56	61
3HKZ	E F	F	40	Y	2.0	37	42
3HKZ	H K	K	15	F	1.6	14	23
3HKZ	I J	I	475	E	4.9	470	480
3HKZ	I J	I	476	A	4.2	470	480
3HKZ	I J	I	479	I	5.2	470	480
3HKZ	I J	I	500	Q	4.8	500	507
3HKZ	I J	I	501	D	4.3	500	507
3HKZ	I J	I	504	S	4.8	500	507
3HKZ	I J	I	637	R	2.5	622	640
3HKZ	I J	I	724	F	4.1	724	729
3HKZ	I J	I	795	L	1.1	792	802
3HKZ	I J	I	821	R	1.1	818	825
3HKZ	I J	J	668	Y	1.4	664	670
3HKZ	I J	J	1035	C	2.3	1031	1036
3HKZ	I J	J	1048	R	1.5	1048	1052
3HKZ	I M	I	89	H	1.2	87	96
3HKZ	I M	I	614	W	1.0	611	618
3HKZ	I M	I	819	M	1.1	818	825
3HKZ	I M	I	820	Q	4.4	818	825
3HKZ	I M	I	821	R	4.8	818	825
3HKZ	I M	I	822	R	5.2	818	825
3HKZ	I M	I	871	I	1.2	867	876
3HKZ	I M	I	875	V	2.4	867	876
3HKZ	I M	M	50	K	1.7	49	62
3HKZ	I M	M	54	L	1.9	49	62
3HKZ	I M	M	58	E	1.3	49	62
3HKZ	I M	M	70	I	1.2	70	83
3HKZ	I M	M	71	G	45.1	70	83
3HKZ	I M	M	78	V	4.9	70	83
3HKZ	I M	M	79	G	48.4	70	83
3HKZ	I M	M	80	E	2.3	70	83
3HKZ	I M	M	81	P	5.3	70	83
3HKZ	I M	M	82	G	4.6	70	83
3HKZ	I M	M	312	H	1.4	310	321
3HKZ	I M	M	319	V	2.1	310	321
3HKZ	I M	M	356	D	1.2	350	357
3HKZ	I M	M	374	I	1.1	369	376
3HKZ	I U	I	479	I	2.4	470	480
3HKZ	I U	U	29	R	1.1	29	44
3HKZ	I U	U	30	Y	2.2	29	44
3HKZ	I V	I	519	E	1.1	518	524
3HKZ	I V	I	522	Q	2.0	518	524
3HKZ	J O	J	958	L	1.1	950	961
3HKZ	J O	O	208	E	1.0	208	213

3HKZ	J V	V	22	H	1.2	22	32
3HKZ	J W	W	32	G	150.6	31	38
3HKZ	J W	W	58	E	1.9	56	61
3HKZ	J W	W	59	V	1.5	56	61
3HKZ	M J	M	374	I	1.4	369	376
3HKZ	M J	J	1097	F	2.0	1095	1107
3HKZ	M T	M	287	E	1.0	286	296
3HKZ	M U	U	31	E	1.0	29	44
3HKZ	O V	O	28	I	1.5	28	34
3HKZ	O V	O	246	G	45.1	238	261
3HKZ	O V	O	250	I	1.5	238	261
3HKZ	O V	O	253	I	2.1	238	261
3HKZ	O V	O	254	E	1.2	238	261
3HKZ	O V	O	256	L	1.1	238	261
3HKZ	O V	O	257	E	10.9	238	261
3HKZ	O V	O	260	L	2.1	238	261
3HKZ	O V	V	24	L	1.8	22	32
3HKZ	O V	V	27	L	2.1	22	32
3HKZ	O V	V	30	G	108.8	22	32
3HKZ	O V	V	77	R	1.4	65	85
3HKZ	O V	V	79	M	2.6	65	85
3HKZ	O V	V	84	I	1.5	65	85
3HKZ	O W	W	56	I	7.4	56	61
3HKZ	O W	W	60	I	1.1	56	61
3HKZ	Q R	R	21	L	1.3	20	25
3HKZ	Q R	R	24	V	1.3	20	25
3HKZ	Q R	R	34	L	1.4	34	42
3HKZ	Q R	R	40	Y	3.1	34	42
3HKZ	Q R	R	71	I	1.5	66	73
3HKZ	T Z	T	25	I	1.1	25	29
3HKZ	T Z	Z	51	W	1.7	45	54
3HNS	H L	L	123	E	1.2	122	127
3HNS	H L	L	124	Q	2.0	122	127
3HO5	B H	B	377	D	1.0	376	381
3HO5	B H	B	380	E	1.2	376	381
3HOU	A B	A	370	I	1.1	368	372
3HOU	A B	A	501	L	1.1	495	505
3HOU	A B	A	527	T	3.7	526	536
3HOU	A B	A	654	N	3.8	639	661
3HOU	A B	A	658	L	1.1	639	661
3HOU	A B	A	746	M	1.3	742	750
3HOU	A B	A	761	M	1.2	755	764
3HOU	A B	A	810	P	3.3	810	844
3HOU	A B	A	813	F	2.4	810	844
3HOU	A B	A	814	F	3.0	810	844
3HOU	A B	A	820	G	3.0	810	844
3HOU	A B	A	821	R	1.3	810	844
3HOU	A B	A	824	L	1.1	810	844
3HOU	A B	A	825	I	1.5	810	844
3HOU	A B	A	1413	G	134.7	1405	1415
3HOU	A B	B	1023	V	1.3	1023	1039
3HOU	A B	B	1052	V	1.1	1052	1061
3HOU	A B	B	1134	E	1.1	1132	1142
3HOU	A B	B	1139	I	1.7	1132	1142
3HOU	A B	B	1203	L	1.2	1198	1210
3HOU	A B	B	1206	E	1.9	1198	1210
3HOU	A B	B	1207	L	1.3	1198	1210
3HOU	A E	A	942	F	1.1	923	947
3HOU	A E	A	1006	I	2.0	1005	1015
3HOU	A E	A	1017	L	1.5	1016	1026

3HOU	A E	E	163	E	3.1	158	168
3HOU	A E	E	167	R	2.9	158	168
3HOU	A F	A	495	E	1.0	495	505
3HOU	A F	A	504	L	1.4	495	505
3HOU	A F	F	88	Y	2.3	87	103
3HOU	A F	F	92	R	2.2	87	103
3HOU	A F	F	95	G	21.7	87	103
3HOU	A K	A	551	Y	3.5	543	553
3HOU	A K	A	552	W	2.4	543	553
3HOU	A P	P	204	D	1.5	204	218
3HOU	A P	P	208	E	1.4	204	218
3HOU	A P	P	209	R	1.7	204	218
3HOU	A P	P	212	K	1.5	204	218
3HOU	B C	B	847	D	1.9	843	848
3HOU	B C	C	35	R	1.8	27	40
3HOU	B C	C	38	I	2.2	27	40
3HOU	B C	C	62	F	2.8	60	70
3HOU	B C	C	65	H	2.1	60	70
3HOU	B I	B	318	V	1.4	308	321
3HOU	B I	B	319	E	1.1	308	321
3HOU	B I	B	593	P	1.4	593	602
3HOU	B I	B	594	A	1.4	593	602
3HOU	B J	B	190	Y	2.6	187	193
3HOU	B J	J	33	G	41.2	32	39
3HOU	B J	J	36	L	1.6	32	39
3HOU	B J	J	51	L	2.0	44	53
3HOU	B J	J	59	K	1.5	56	62
3HOU	B K	K	40	H	2.1	40	51
3HOU	C J	J	15	G	11.6	15	24
3HOU	C J	J	61	L	10.1	56	62
3HOU	C K	C	244	V	1.3	244	265
3HOU	C K	C	248	I	1.6	244	265
3HOU	C K	C	255	V	2.3	244	265
3HOU	C K	C	258	I	1.5	244	265
3HOU	C K	C	259	L	1.2	244	265
3HOU	C K	C	262	L	1.5	244	265
3HOU	C K	K	94	I	1.5	83	111
3HOU	C K	K	95	I	1.8	83	111
3HOU	C K	K	97	K	1.0	83	111
3HOU	C K	K	98	L	1.4	83	111
3HOU	C K	K	101	L	1.2	83	111
3HOU	C K	K	102	K	1.0	83	111
3HOU	C K	K	105	F	4.3	83	111
3HOU	C K	K	109	W	1.0	83	111
3HOU	C L	C	68	G	13.0	60	70
3HOU	D G	D	66	R	1.6	54	70
3HOU	D G	D	141	L	1.0	139	151
3HOU	D G	D	147	Y	3.0	139	151
3HOU	D G	D	175	F	2.8	174	182
3HOU	D G	D	190	E	1.3	188	195
3HOU	D G	D	194	L	1.0	188	195
3HOU	M D	M	28	R	1.6	24	31
3HOU	M D	D	204	D	1.8	204	218
3HOU	M D	D	205	D	1.3	204	218
3HOU	M N	M	95	F	2.6	93	104
3HOU	M N	M	325	I	1.0	325	330
3HOU	M N	M	370	I	1.1	368	372
3HOU	M N	M	654	N	3.9	639	661
3HOU	M N	M	761	M	1.3	755	764
3HOU	M N	M	813	F	2.8	810	844

3HOU	M N	M	814	F	2.8	810	844
3HOU	M N	M	820	G	4.6	810	844
3HOU	M N	M	821	R	1.4	810	844
3HOU	M N	M	824	L	1.1	810	844
3HOU	M N	M	839	R	2.1	810	844
3HOU	M N	M	843	K	1.2	810	844
3HOU	M N	M	1066	V	1.0	1064	1078
3HOU	M N	M	1413	G	157.8	1405	1415
3HOU	M N	M	1424	V	3.6	1424	1430
3HOU	M N	M	1425	S	1.4	1424	1430
3HOU	M N	M	1428	V	1.0	1424	1430
3HOU	M N	N	1026	L	1.0	1023	1039
3HOU	M N	N	1132	E	2.1	1132	1142
3HOU	M N	N	1133	M	2.0	1132	1142
3HOU	M N	N	1134	E	1.0	1132	1142
3HOU	M N	N	1135	R	1.6	1132	1142
3HOU	M N	N	1139	I	1.8	1132	1142
3HOU	M N	N	1148	K	1.3	1144	1151
3HOU	M N	N	1203	L	1.1	1198	1210
3HOU	M N	N	1206	E	1.1	1198	1210
3HOU	M N	N	1207	L	1.1	1198	1210
3HOU	M Q	M	942	F	1.0	923	944
3HOU	M Q	M	1017	L	1.5	1016	1026
3HOU	M R	M	504	L	1.8	495	505
3HOU	M R	R	88	Y	3.0	87	103
3HOU	M R	R	92	R	2.3	87	103
3HOU	M R	R	95	G	17.8	87	103
3HOU	M W	M	551	Y	1.0	543	553
3HOU	M W	M	552	W	1.9	543	553
3HOU	N O	N	847	D	1.5	843	848
3HOU	N O	O	35	R	1.3	27	40
3HOU	N O	O	38	I	1.1	27	40
3HOU	N O	O	62	F	2.5	60	70
3HOU	N O	O	65	H	2.2	60	70
3HOU	N O	O	69	L	1.1	60	70
3HOU	N U	N	308	W	1.0	308	321
3HOU	N U	N	318	V	1.1	308	321
3HOU	N U	N	593	P	1.3	593	602
3HOU	N U	N	594	A	1.4	593	602
3HOU	N V	N	190	Y	2.5	187	193
3HOU	N V	V	33	G	42.0	32	39
3HOU	N V	V	44	Y	2.0	44	53
3HOU	N V	V	59	K	1.2	56	62
3HOU	N W	W	40	H	2.2	40	51
3HOU	O V	V	15	G	11.1	15	24
3HOU	O V	V	57	I	2.0	56	62
3HOU	O W	O	255	V	2.4	244	265
3HOU	O W	O	258	I	2.4	244	265
3HOU	O W	O	259	L	1.3	244	265
3HOU	O W	W	42	L	1.3	40	51
3HOU	O W	W	45	L	1.2	40	51
3HOU	O W	W	95	I	1.9	83	111
3HOU	O W	W	105	F	3.8	83	111
3HOU	O X	O	68	G	11.9	60	70
3HOU	P S	P	59	I	1.0	54	70
3HOU	P S	P	147	Y	4.7	139	151
3HOU	P S	P	150	N	6.9	139	151
3HOU	P S	P	175	F	1.5	174	182
3HOU	P S	P	190	E	1.5	188	194
3HOU	R S	R	100	Q	1.0	87	103

3HOY	A B	A	30	I	1.4	24	31
3HOY	A B	A	304	M	2.7	288	305
3HOY	A B	A	325	I	1.9	325	330
3HOY	A B	A	329	L	6.3	325	330
3HOY	A B	A	340	L	1.9	336	342
3HOY	A B	A	370	I	1.0	368	372
3HOY	A B	A	497	T	1.2	495	505
3HOY	A B	A	501	L	1.3	495	505
3HOY	A B	A	810	P	1.3	810	828
3HOY	A B	A	813	F	2.9	810	828
3HOY	A B	A	814	F	2.9	810	828
3HOY	A B	A	820	G	14.0	810	828
3HOY	A B	A	824	L	1.2	810	828
3HOY	A B	A	825	I	1.0	810	828
3HOY	A B	A	1066	V	1.0	1064	1075
3HOY	A B	A	1406	V	2.4	1406	1415
3HOY	A B	A	1409	L	2.9	1406	1415
3HOY	A B	A	1413	G	78.0	1406	1415
3HOY	A B	B	1023	V	1.5	1023	1038
3HOY	A B	B	1026	L	1.2	1023	1038
3HOY	A B	B	1135	R	2.4	1132	1142
3HOY	A B	B	1138	M	1.2	1132	1142
3HOY	A B	B	1141	H	1.9	1132	1142
3HOY	A B	B	1149	E	1.2	1144	1154
3HOY	A B	B	1200	A	3.8	1198	1210
3HOY	A B	B	1203	L	5.9	1198	1210
3HOY	A B	B	1206	E	1.9	1198	1210
3HOY	A B	B	1207	L	3.4	1198	1210
3HOY	A E	A	942	F	1.4	927	947
3HOY	A E	A	1006	I	1.1	1005	1015
3HOY	A E	A	1378	Q	1.1	1365	1379
3HOY	A F	A	503	Q	1.4	495	505
3HOY	A F	A	504	L	1.8	495	505
3HOY	A F	F	88	Y	3.0	87	103
3HOY	A F	F	92	R	1.4	87	103
3HOY	A F	F	95	G	25.1	87	103
3HOY	A G	G	22	M	1.0	22	35
3HOY	A K	A	551	Y	4.2	544	553
3HOY	A K	A	552	W	2.0	544	553
3HOY	B C	C	35	R	2.7	27	39
3HOY	B C	C	38	I	1.6	27	39
3HOY	B C	C	62	F	1.9	60	70
3HOY	B C	C	65	H	26.1	60	70
3HOY	B C	C	66	R	24.2	60	70
3HOY	B C	C	69	L	25.2	60	70
3HOY	B I	B	308	W	1.3	308	321
3HOY	B I	B	315	K	1.1	308	321
3HOY	B I	B	318	V	1.4	308	321
3HOY	B J	B	190	Y	2.7	186	192
3HOY	B J	J	33	G	52.9	32	39
3HOY	B J	J	44	Y	1.5	44	53
3HOY	B J	J	59	K	1.1	56	62
3HOY	B K	K	40	H	1.2	40	51
3HOY	C J	J	15	G	38.4	15	24
3HOY	C J	J	57	I	1.2	56	62
3HOY	C J	J	61	L	1.7	56	62
3HOY	C K	C	29	M	1.9	27	39
3HOY	C K	C	33	L	1.3	27	39
3HOY	C K	C	35	R	1.7	27	39
3HOY	C K	C	245	V	1.1	240	262

3HOY	C K	C	248	I	2.6	240	262
3HOY	C K	C	251	L	1.7	240	262
3HOY	C K	C	258	I	2.1	240	262
3HOY	C K	C	265	M	1.0	263	268
3HOY	C K	K	42	L	1.6	40	51
3HOY	C K	K	95	I	1.6	83	111
3HOY	C K	K	97	K	1.6	83	111
3HOY	C K	K	98	L	2.0	83	111
3HOY	C K	K	101	L	1.9	83	111
3HOY	C K	K	102	K	1.3	83	111
3HOY	C K	K	105	F	5.4	83	111
3HOY	C K	K	109	W	1.5	83	111
3HOY	C L	C	68	G	5.9	60	70
3HOY	D G	D	141	L	1.0	139	151
3HOY	D G	D	147	Y	2.9	139	151
3HOY	D G	D	175	F	10.3	174	182
3HOY	D G	D	179	Q	2.6	174	182
3HOY	F G	F	100	Q	1.1	87	103
3HPG	A H	A	100	R	1.6	96	110
3HPG	A H	A	134	Y	1.4	126	136
3HPG	B G	B	130	L	2.5	126	135
3HPG	B G	B	134	Y	1.6	126	135
3HPG	C J	C	130	L	1.2	126	136
3HPG	C J	C	134	Y	1.3	126	136
3HPG	C J	J	370	V	1.2	370	379
3HPG	D I	D	130	L	1.1	126	136
3HPG	D I	D	134	Y	1.5	126	136
3HPG	E L	E	100	R	1.2	96	110
3HPG	E L	E	127	S	1.0	126	136
3HPG	E L	E	134	Y	1.3	126	136
3HPG	F K	F	100	R	1.5	96	110
3HPG	F K	F	130	L	1.6	126	135
3HPG	F K	F	134	Y	1.7	126	135
3HPG	F K	K	370	V	3.5	370	379
3HQR	A S	A	251	I	1.0	248	252
3HQR	A S	A	396	R	1.3	393	405
3HQR	A S	A	403	Y	2.8	393	405
3HRD	A B	A	211	H	1.7	210	221
3HRD	A B	A	272	T	1.4	268	275
3HRD	A B	A	319	R	1.9	313	324
3HRD	A B	A	322	V	1.1	313	324
3HRD	A B	A	323	H	1.8	313	324
3HRD	A B	A	364	G	12.2	355	373
3HRD	A B	A	377	P	2.5	377	384
3HRD	A B	A	381	R	1.1	377	384
3HRD	A B	A	404	L	1.2	404	419
3HRD	A B	A	407	T	2.1	404	419
3HRD	A B	A	414	K	2.6	404	419
3HRD	A B	A	418	V	2.0	404	419
3HRD	A B	B	59	E	3.1	49	62
3HRD	A B	B	234	F	2.3	217	238
3HRD	A B	B	289	E	2.3	288	308
3HRD	A B	B	293	I	1.5	288	308
3HRD	A B	B	304	E	1.0	288	308
3HRD	A D	A	21	V	1.4	17	23
3HRD	A D	A	268	R	2.7	268	275
3HRD	A D	D	30	R	1.9	25	33
3HRD	A D	D	94	L	1.2	88	96
3HRD	A D	D	103	Y	3.4	103	119
3HRD	B C	C	270	Y	1.7	268	291

3HRD	B C	C	277	G	76.4	268	291
3HRD	B D	B	221	E	1.3	217	238
3HRD	B D	B	226	G	184.1	217	238
3HRD	B D	D	143	K	1.9	142	158
3HRD	C D	C	38	I	1.0	34	42
3HRD	C D	C	104	Q	1.7	103	109
3HRD	C D	C	107	N	1.4	103	109
3HRD	C D	C	108	L	2.1	103	109
3HRD	E F	E	211	H	2.3	210	221
3HRD	E F	E	272	T	1.4	268	275
3HRD	E F	E	323	H	1.4	313	325
3HRD	E F	E	356	P	6.7	355	372
3HRD	E F	E	360	V	1.0	355	372
3HRD	E F	E	377	P	1.1	377	384
3HRD	E F	E	404	L	1.2	404	419
3HRD	E F	E	414	K	2.0	404	419
3HRD	E F	F	51	T	1.1	49	62
3HRD	E F	F	55	Q	1.0	49	62
3HRD	E F	F	59	E	8.3	49	62
3HRD	E F	F	234	F	1.8	217	238
3HRD	E F	F	289	E	2.1	287	297
3HRD	E F	F	293	I	1.3	287	297
3HRD	E H	E	18	L	1.1	17	23
3HRD	E H	E	21	V	1.5	17	23
3HRD	E H	E	22	M	1.1	17	23
3HRD	E H	E	268	R	2.7	268	275
3HRD	E H	H	94	L	1.1	88	97
3HRD	E H	H	103	Y	3.4	103	117
3HRD	F G	G	277	G	144.3	266	291
3HRD	F H	F	221	E	1.2	217	238
3HRD	F H	F	226	G	104.8	217	238
3HRD	F H	H	143	K	1.8	142	157
3HRD	G H	G	38	I	1.0	35	42
3HRD	G H	G	104	Q	1.9	103	109
3HRD	G H	G	107	N	1.5	103	109
3HRD	G H	G	108	L	2.2	103	109
3HRW	A B	A	122	H	1.4	119	137
3HRW	A B	B	30	R	1.6	23	32
3HRW	A B	B	112	I	1.2	100	117
3HRW	A B	B	124	P	1.0	124	140
3HRW	C B	C	95	P	1.8	95	110
3HRW	C D	C	103	H	1.1	95	110
3HRW	C D	C	107	V	1.1	95	110
3HRW	C D	C	119	P	2.5	119	137
3HRW	C D	C	122	H	2.1	119	137
3HRW	C D	D	30	R	2.3	21	35
3HRW	C D	D	112	I	1.7	100	115
3HRW	C D	D	124	P	3.0	124	139
3HRZ	A B	A	573	Q	1.3	573	583
3HRZ	A B	A	576	I	1.0	573	583
3HRZ	B C	B	910	P	1.4	910	914
3HRZ	C D	C	1491	E	2.0	1486	1494
3HRZ	C D	C	1616	F	1.3	1597	1617
3HS0	A B	A	560	K	2.2	560	565
3HS0	A B	A	563	Y	2.0	560	565
3HS0	C I	I	629	G	1.6	628	634
3HS0	F G	F	576	I	1.1	573	583
3HS0	H D	D	629	G	3.6	628	634
3HS0	H D	D	633	R	1.4	628	634
3HUJ	A G	A	80	D	1.6	60	88

3HUJ	A G	A	84	F	1.5	60	88
3HUJ	A G	A	147	V	3.6	139	149
3HUJ	C E	C	84	F	1.1	60	88
3HUJ	G H	H	135	E	2.4	135	139
3HUJ	G H	H	137	E	1.3	135	139
3I1H	A B	A	77	K	1.1	64	79
3I1H	A B	A	87	G	240.4	86	107
3I1H	A B	A	88	R	3.8	86	107
3I1H	A B	A	91	T	1.0	86	107
3I1H	A B	A	95	F	1.0	86	107
3I1H	A B	B	75	G	71.5	74	87
3I1H	A B	B	78	L	1.9	74	87
3I1H	A B	B	81	I	1.0	74	87
3I1H	A B	B	82	G	33.8	74	87
3I1H	A B	B	83	D	2.5	74	87
3I2C	L H	L	128	Q	1.2	126	131
3I3T	A B	A	304	E	2.1	302	317
3I3T	E D	E	289	K	1.2	281	290
3I3T	E F	E	304	E	2.0	302	317
3I3T	G H	G	304	E	2.0	302	317
3KIN	A B	B	262	L	2.7	257	272
3KIN	A B	B	283	K	1.7	283	288
3KIN	A B	B	287	I	2.2	283	288
3KIN	A B	B	313	E	1.7	311	326
3KIN	A B	B	318	L	2.6	311	326
3KIN	A B	B	320	F	1.3	311	326
3KIN	A B	B	321	G	7.5	311	326
3KIN	A B	B	324	A	1.6	311	326
3KIN	A B	B	325	K	1.1	311	326
3KIN	C D	C	73	D	1.0	68	75
3KIN	C D	D	259	L	1.0	257	272
3KIN	C D	D	287	I	2.1	283	288
3KIN	C D	D	313	E	1.0	311	327
3KIN	C D	D	318	L	1.6	311	327
3KIN	C D	D	320	F	2.8	311	327
3KIN	C D	D	321	G	97.2	311	327
3MON	A B	B	15	L	1.8	11	26
3MON	A B	B	18	F	2.6	11	26
3MON	C D	D	15	L	2.7	10	27
3MON	C D	D	18	F	2.1	10	27
3MON	C D	D	22	E	2.8	10	27
3MON	C D	D	23	E	1.0	10	27
3MON	E F	F	15	L	1.7	10	27
3MON	E F	F	16	G	5.1	10	27
3MON	E F	F	18	F	3.3	10	27
3MON	G H	H	15	L	2.1	10	26
3MON	G H	H	18	F	1.7	10	26
3PRO	A C	C	8	L	1.1	7	16
3PRO	A C	C	14	R	1.3	7	16
3PRO	A C	C	15	D	2.1	7	16
3PRO	A C	C	34	R	1.0	20	36
3PRO	A C	C	99	D	2.0	88	104
3PRO	B D	D	8	L	1.8	6	16
3PRO	B D	D	26	Y	1.5	20	36
3PRO	B D	D	99	D	1.8	88	103
3UBP	A C	A	10	K	1.4	5	26
3UBP	A C	A	34	E	1.5	32	50
3UBP	A C	A	76	M	1.4	73	77
3UBP	B C	C	5	R	2.7	5	12
3UBP	B C	C	8	Y	1.1	5	12

3UBP	B C	C	9	A	1.0	5	12
3YGS	C P	P	15	L	1.1	14	21
3YGS	C P	P	61	I	1.1	52	65
4RUB	A S	A	159	R	1.1	155	162
4RUB	A S	A	429	K	1.3	413	433
4RUB	A T	A	186	G	60.6	182	196
4RUB	A T	A	190	Y	1.4	182	196
4RUB	A T	A	191	E	1.1	182	196
4RUB	A T	A	219	L	1.4	214	233
4RUB	A T	A	223	E	3.3	214	233
4RUB	A T	A	226	Y	1.2	214	233
4RUB	A T	A	256	F	1.2	247	261
4RUB	B T	B	156	Q	1.5	155	163
4RUB	B T	B	229	Q	1.0	214	233
4RUB	B T	B	429	K	1.6	413	433
4RUB	C U	C	229	Q	1.6	214	233
4RUB	C U	C	232	T	1.8	214	233
4RUB	C U	C	428	V	1.7	413	434
4RUB	C U	C	429	K	1.1	413	434
4RUB	C U	C	431	R	1.5	413	434
4RUB	C U	C	432	N	1.4	413	434
4RUB	C U	U	28	S	1.1	23	37
4RUB	C U	U	32	Y	2.1	23	37
4RUB	C V	C	186	G	38.3	182	196
4RUB	C V	C	187	R	1.7	182	196
4RUB	C V	C	190	Y	1.0	182	196
4RUB	C V	C	219	L	1.4	214	233
4RUB	C V	C	222	A	1.4	214	233
4RUB	C V	C	223	E	2.0	214	233
4RUB	C V	C	227	K	1.9	214	233
4RUB	C V	C	256	F	1.4	247	261
4RUB	C V	C	260	L	1.8	247	261
4RUB	D V	D	156	Q	1.5	155	162
4RUB	D V	D	421	R	2.6	413	433
4RUB	D V	V	25	Q	1.0	23	37
4SGB	E I	E	57	H	1.2	56	59
5CSC	A B	A	21	I	16.5	7	30
5CSC	A B	A	24	F	3.7	7	30
5CSC	A B	A	243	V	1.5	243	254
5CSC	A B	A	246	H	1.0	243	254
5CSC	A B	A	250	L	1.8	243	254
5CSC	A B	A	267	N	7.4	264	270
5CSC	A B	A	427	T	1.0	427	433
5CSC	A B	A	431	I	3.6	427	433
5CSC	A B	B	24	F	4.0	7	28
5CSC	A B	B	25	R	1.4	7	28
5CSC	A B	B	39	D	1.0	38	42
5CSC	A B	B	246	H	1.5	243	252
5CSC	A B	B	250	L	1.0	243	252
5CSC	A B	B	251	V	1.0	243	252
5CSC	A B	B	427	T	1.3	427	433
6RLX	A B	A	13	K	2.3	13	19
6RLX	A B	B	11	L	1.1	9	22
6RLX	A B	B	18	I	2.9	9	22
6RLX	A D	D	12	V	1.2	9	22
6RLX	C B	B	9	R	1.0	9	22
6RLX	C B	B	12	V	1.2	9	22
6RLX	C D	C	13	K	2.9	13	19
6RLX	C D	D	11	L	1.5	9	22
6RLX	C D	D	18	I	2.0	9	22

7CEI	A B	A	52	D	1.4	51	56
7CEI	A B	A	55	Y	1.2	51	56
7CEI	A B	B	520	R	1.6	515	523
7FAB	L H	L	120	E	1.5	118	123
7INS	A B	A	16	L	1.1	13	19
7INS	A B	B	11	L	1.5	2	20
7INS	A B	B	15	L	1.4	2	20
7INS	A D	D	2	V	1.1	2	20
7INS	C D	C	16	L	1.2	13	19
7INS	C D	D	11	L	1.7	2	20
7INS	C D	D	15	L	1.5	2	20
7INS	C D	D	18	V	1.3	2	20
7INS	E F	F	11	L	1.6	2	20
7INS	E F	F	18	V	1.3	2	20
9PAI	A B	A	31	S	1.0	22	43
9PAI	A B	A	38	F	3.0	22	43
9PAI	A B	A	100	L	1.3	89	101
9PAI	A B	A	265	L	1.7	265	271
9PAI	A B	A	277	I	1.2	274	283

[0092] As noted *supra*, HIPP interactions can be categorized according to their identified function as defined in the PDB (Figure 5B). Some HIPP interactions could fall into more than one function category. A subset of HIPP interactions were categorized by function and each HIPP interaction was limited to one category (*see* Tables 3–16). Helical interfaces are involved in a wide distribution of functions ranging from enzymatic activity to protein associations. The largest category, energy metabolism and various enzymes, accounts for 34% of HIPP interactions. This category contains many hydrolases, oxidoreductases, and transferases, among other enzymes (Table 5). The protein synthesis and turnover category contains chaperones, proteosomes, ribosomes, and other proteins involved in protein synthesis (Table 10). The transcription category contains proteins that are either part of transcription regulation, such as activators or repressors, or are part of the transcription machinery, such as those that bind to DNA (Table 15). The DNA binding category contains proteins that target DNA but are not involved in transcription (Table 4).

[0093] The length of each helix participating in the interface of the identified complexes was also examined (*see* Table 2). Helix length was calculated as the total length of polypeptide chain that contained any interface residues. Thus, the full length of the helix, including residues that may not be part of the interface, were included. This analysis indicates that helices involved in protein interactions range from five residues to 113 residues. The number of helix residues directly engaged in binding has been assessed previously by examining 122 homodimers and 204 protein–protein heterocomplexes (Guharoy et al., "Secondary Structure Based Analysis and Classification of Biological Interfaces: Identification of Binding Motifs in Protein–Protein Interactions," *Bioinformatics* 23:1909-1918 (2007), which is hereby incorporated by reference in its entirety). This study implicated an average helix length of seven residues in binding (Guharoy et al., "Secondary Structure Based Analysis and Classification of Biological Interfaces: Identification of Binding Motifs in Protein–Protein Interactions," *Bioinformatics* 23:1909-1918 (2007), which is hereby incorporated by reference in its entirety). Together, these studies emphasize the short length of the helical domain involved in protein interactions.

[0094] This study reveals new classes of previously unidentified targets for helix mimetics. Some of the identified targets will potentially aid in drug discovery

efforts. In this regard, it is interesting to note that this query identified a number of kinases that may be regulated by helix mimetics (*see* Table 6 above). In this collection, the secondary structures are helical structures. The specific amino acid interface residues comprising the helical structures at the interface of the two-chain inter-protein interactions are shown in Table 6.

[0095] Kinases are an important class of potential drug targets. Typical kinase inhibitors mimic ATP or substrate conformations. New types of scaffolds that can specifically regulate the function of therapeutically important kinases will fill an important gap in a medicinal chemist's repertoire (Fedorov et al., "Insights for the Development of Specific Kinase Inhibitors by Targeted Structural Genomics," *Drug Discov. Today* 12:365-372 (2007), which is hereby incorporated by reference in its entirety). These scaffolds can be generated using the data provided in Tables 2, 6, and 17.

[0096] In summary, a collection of helical interfaces in protein–protein interactions have been identified and analyzed using various computer executable codes and scripts. This study was undertaken to address the significant chasm in the elegant design of helix mimetics and their sporadic use in biology. This study provides an extensive list of potential targets for the emerging classes of helix mimetics.

[0097] Although preferred embodiments have been depicted and described in detail herein, it will be apparent to those skilled in the relevant art that various modifications, additions, substitutions, and the like can be made without departing from the spirit of the invention and these are therefore considered to be within the scope of the invention as defined in the claims which follow.

WHAT IS CLAIMED:

1. A method of generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction said method comprising:

retrieving, from a protein database, multi-entity protein structures having one or more inter-chain interactions;

extracting, from the retrieved multi-entity protein structures, two-chain protein structures;

distinguishing the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions;

identifying the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface; and

storing in a memory storage device the protein secondary structures at an interface of the identified two-chain inter-protein interactions.

2. The method according to claim 1, further comprising:

classifying the identified two-chain inter-protein interactions by biological function.

3. The method according to claim 1, further comprising:

removing, prior to storing, any redundant two-chain inter-protein interactions from the identified two-chain inter-protein interactions that comprise a protein secondary structure at their interface.

4. The method according to claim 1, further comprising:

querying the protein data base at various time intervals to identify one or more additional multi-entity protein structures;

repeating the retrieving, extracting, distinguishing, and identifying steps;

identifying any non-redundant secondary structures at an interface of a two-chain inter-protein interaction; and

storing the identified non-redundant secondary structures in the memory storage device.

5. The method according to claim 1, wherein the protein secondary structure comprises a helical structure.

6. The method according to claim 1, wherein the protein secondary structures comprise a β-strand structure.

7. The method according to claim 1, wherein the protein secondary structures comprise a β-turn structure.

8. The method according to claim 1, wherein said identifying comprises:

measuring ϕ and φ angles of at least four contiguous amino acid residues of each chain of the two-chain inter-protein interactions; and

identifying secondary structures present at an interface of the two-chain inter-protein interactions based on said measuring.

9. The method according to claim 1, wherein said identifying comprises:

identifying interface amino acid residues of at least one of the identified two-chain inter-protein interactions.

10. The method according to claim 9, wherein said identifying interface amino acid residues comprises:

identifying an amino acid residue in one chain of an identified two-chain inter-protein interaction having at least one atom within a 5 Å radius of an atom in the other chain of the identified two-chain inter-protein interaction.

11. The method according to claim 9, wherein said identifying interface amino acid residues comprises:

measuring density of C_β atoms surrounding a C_β atom of an amino acid residue in one chain of an identified two-chain inter-protein interaction; and

identifying interface amino acid residues based on said measuring.

12. The method according to claim 9 further comprising:

determining which of the identified interface amino acid residues are hot spot amino acid residues.

13. The method according to claim 12, wherein said determining is carried out using an amino acid mutagenesis analysis.

14. A computer readable medium having stored thereon instructions that when executed by a processor generate a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction, the computer readable medium having residing thereon machine executable code that when executed by at least one processor, causes the processor to perform steps comprising:

retrieving, from a protein database, multi-entity protein structures having one or more inter-chain interactions;

extracting, from the retrieved multi-entity protein structures, two-chain protein structures;

distinguishing the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions;

identifying the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface; and

storing in a memory storage device the protein secondary structures at an interface of the identified two-chain inter-protein interactions.

15. The medium according to claim 14, wherein the machine executable code further contains instructions for:

classifying the identified two-chain inter-protein interactions by biological function.

16. The medium according to claim 14, wherein the machine executable code further contains instructions for:

removing, prior to storing, any redundant two-chain inter-protein interactions from the identified two-chain inter-protein interactions that comprise a protein secondary structure at their interface.

17. The medium according to claim 14, wherein the machine executable code further contains instructions for:

querying the protein data base at various time intervals to identify one or more additional multi-entity protein structures;

repeating the retrieving, extracting, distinguishing, and identifying steps;

identifying any non-redundant secondary structures at an interface of a two-chain inter-protein interactions; and

storing the identified non-redundant secondary structures in the memory storage device.

18. The medium according to claim 14, wherein the protein secondary structure comprises a helical structure.

19. The medium according to claim 14, wherein the protein secondary structures comprise a β-strand structure.

20. The medium according to claim 14, wherein the protein secondary structures comprise a β-turn structure.

21. The medium according to claim 14, wherein said identifying comprises:

measuring ϕ and φ angles of at least four contiguous amino acid residues of each chain of the two-chain inter-protein interactions; and

identifying secondary structures present at an interface of the two-chain inter-protein interactions based on said measuring.

22. The medium according to claim 14, wherein said identifying comprises:

identifying interface amino acid residues of at least one of the identified two-chain inter-protein interactions.

23. The medium according to claim 22, wherein said identifying interface amino acid residues comprises:

identifying an amino acid residue in one chain of an identified two-chain inter-protein interaction having at least one atom within a 5 Å radius of an atom in the other chain of the identified two-chain inter-protein interaction.

24. The medium according to claim 22, wherein said identifying interface amino acid residues comprises:

measuring density of C_β atoms surrounding a C_β atom of an amino acid residue in one chain of an identified two-chain inter-protein interaction; and

identifying interface amino acid residues based on said measuring.

25. The medium according to claim 22 further comprising:

determining which of the identified interface amino acid residues are hot spot amino acid residues.

26. The medium according to claim 25, wherein said determining is carried out using an amino acid mutagenesis analysis.

27. A system for generating a database of protein secondary structures that are at an interface of a two-chain inter-protein interaction, the system comprising:

a retrieval module that retrieves, from a protein database stored on a memory storage device, multi-entity protein structures having one or more inter-chain interactions;

an extraction module that extracts, from the retrieved multi-entity protein structures, two-chain protein structures;

a distinguishing module that distinguishes the extracted two-chain protein structures having inter-protein interactions from the extracted two-chain protein structures having only intra-protein interactions;

an identification module that identifies the distinguished two-chain inter-protein interactions that comprise a protein secondary structure at their interface; and

a storage module for storing to a memory storage device the protein secondary structures at an interface of the identified two-chain inter-protein interactions.

28. The system according to claim 27, further comprising:

a classification module that classifies the identified two-chain inter-protein interactions by biological function.

29. The system according to claim 27, further comprising:

a removal module that removes, prior to storing, any redundant two-chain inter-protein interactions from the identified two-chain inter-protein interactions that comprise a protein secondary structure at their interface.

30. The system according to claim 27, wherein the secondary structures comprise a helical structure.

31. The system according to claim 27, wherein the secondary structures comprise a β-strand structure.

32. The system according to claim 27, wherein the secondary structures comprise a β-turn.

33. The system according to claim 27, wherein the identification module is configured to measure ϕ and φ angles of at least four contiguous amino acid residues of each chain of the two-chain inter-protein interactions and identify secondary structures present at an interface of the two-chain inter-protein interactions based on the measured angles.

34. The system according to claim 27, wherein the identification module is configured to identify interface amino acid residues of at least one of the identified two-chain inter-protein interactions.

35. The system according to claim 34, wherein the identification system is configured to identify an amino acid residue in one chain of an identified two-chain inter-protein interaction having at least one atom within a 5 Å radius of an atom in the other chain of the identified two-chain inter-protein interaction.

36. The system according to claim 34, wherein the identification system is configured to measure density of C_β atoms surrounding a C_β atom of an amino acid residue in one chain of an identified two-chain inter-protein interaction and identify interface amino acid residues based on the measured density.

37. The system according to claim 34 further comprising:

a module for determining which of the identified interface amino acid residues are hot spot amino acid residues.

38. The system according to claim 37, wherein the system for determining which of the identified interface amino acid residues are hot spot amino acid residues is configured to carry out an amino acid mutagenesis analysis.

39. The system according to claim 27, further comprising:

a query module that queries the protein data base at various time intervals to identify one or more additional multi-entity protein structures, and

a comparison module that compares the identified secondary structures at an interface of a two-chain inter-protein interaction to identify non-redundant secondary structures.

40. A collection of isolated protein secondary structures that are at an interface of a two-chain inter-protein interaction, wherein the collection contains about 1%, about 5%, about 10%, about 20%, about 40%, about 60%, about 80%, or about 100% of the isolated protein secondary structures of Table 2.

41. The collection according to claim 40, wherein the collection contains *m* through *n* secondary structures, where *m* and *n* are integers and *n* is greater than *m*.

42. The collection according to claim 41, wherein *m* is an integer selected from the group consisting of 2, 4, 8, 10, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, and 5000; and *n* is an integer selected from the group consisting of 10, 15, 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, and 10000.

43. The collection according to claim 40, wherein the collection is a collection of helical protein secondary structures.

44. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating cell cycle.

45. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating DNA binding.

46. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating energy metabolism and/or enzymatic activity.

47. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating immune system function.

48. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating cell membrane proteins and/or receptor interactions.

49. The collection according to claim 40, wherein the collection is a collection of helical protein secondary structures potentially involved in modulating protein binding or have an unknown function.

50. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating protein synthesis and/or turnover.

51. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating RNA binding.

52. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating cell signaling.

53. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating cellular structure and/or cellular adhesion.

54. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating gene transcription.

55. The collection according to claim 40, wherein the collection is a collection of protein secondary structures potentially involved in modulating cellular transport.

56. The collection according to claim 40, wherein the collection is a collection of protein secondary structures that are from toxins, viruses, or bacteria.

57. A method of identifying a therapeutic drug candidate potentially effective in modulating a two-chain inter-protein interaction having a secondary structure at its interface, said method comprising:

providing a therapeutic drug candidate;

selecting a protein secondary structure from the collection according to claim 40;

providing an agent, wherein the agent mimics the protein secondary structure;

contacting the therapeutic drug candidate with the agent under conditions effective for the therapeutic drug candidate to bind to the agent; and

detecting whether any binding occurs between the therapeutic drug candidate and the agent, wherein binding between the therapeutic drug candidate and the agent indicates that the therapeutic drug candidate is potentially effective in modulating a two-chain inter-protein interaction having the protein secondary structure at its interface.

58. A method of identifying a therapeutic drug candidate potentially effective in modulating a two-chain inter-protein interaction having a secondary structure at its interface, said method comprising:

selecting a protein secondary structure from the collection according to claim 40;

providing a therapeutic drug candidate, wherein the drug candidate mimics the protein secondary structure;

providing at least one protein of a two-chain inter-protein interaction having the protein secondary structure at its interface;

contacting the therapeutic drug candidate with the at least one protein under conditions effective for the therapeutic drug candidate to bind to the at least one protein; and

detecting whether any binding occurs between the therapeutic drug candidate and the at least one protein, wherein binding between the therapeutic drug candidate and the at least one protein indicates that the therapeutic drug candidate is potentially effective in modulating the two-chain inter-protein interaction.

59. The method according to claim 57, wherein said contacting is carried out *in vitro*.

60. The method according to claim 57, wherein said contacting is carried out *ex vivo*.

61. The method according to claim 57, wherein said contacting is carried out *in vivo*.

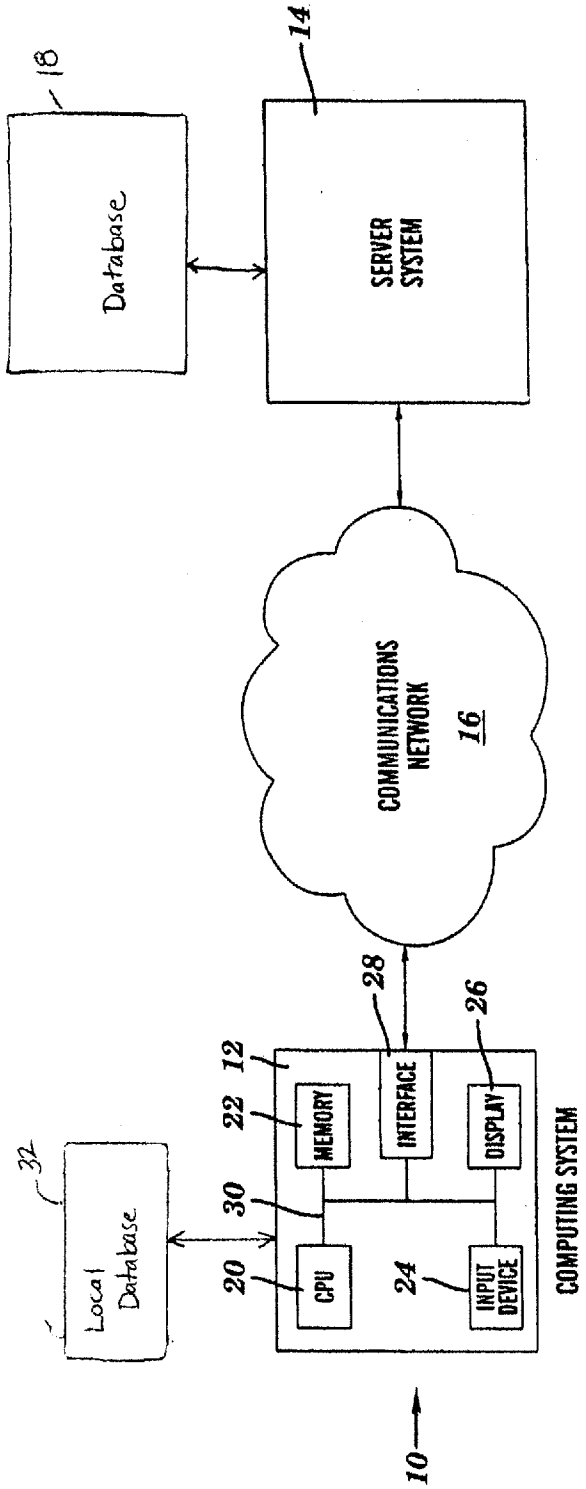

18
Database
14
SERVER SYSTEM
COMMUNICATIONS NETWORK 16
28
26
12
22
MEMORY
INTERFACE
DISPLAY
32
Local Database
30
20
CPU
24
INPUT DEVICE
COMPUTING SYSTEM
10

Figure 1A

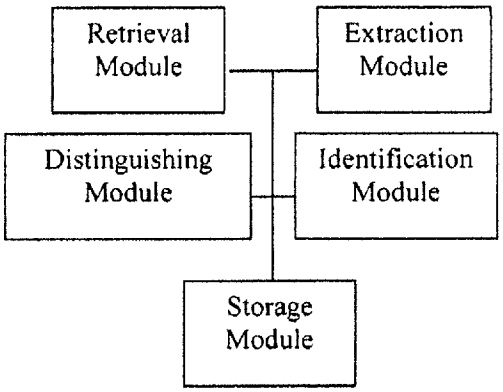

Retrieval Module
Extraction Module
Distinguishing Module
Identification Module
Storage Module

Figure 1B

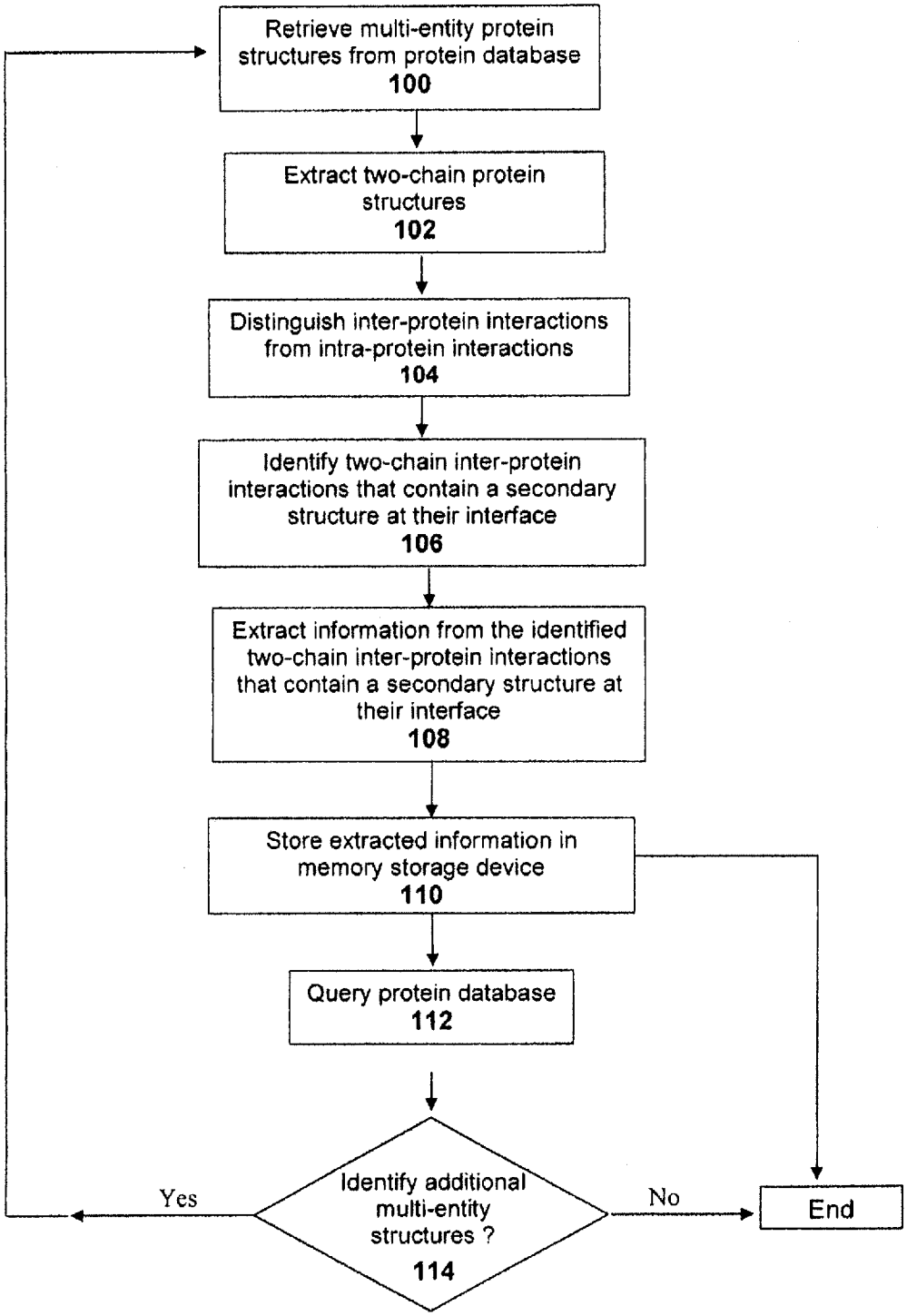

Retrieve multi-entity protein structures from protein database
100
Extract two-chain protein structures
102
Distinguish inter-protein interactions from intra-protein interactions
104
Identify two-chain inter-protein interactions that contain a secondary structure at their interface
106
Extract information from the identified two-chain inter-protein interactions that contain a secondary structure at their interface
108
Store extracted information in memory storage device
110
Query protein database
112
Identify additional multi-entity structures ?
114
Yes
No
End

Figure 2

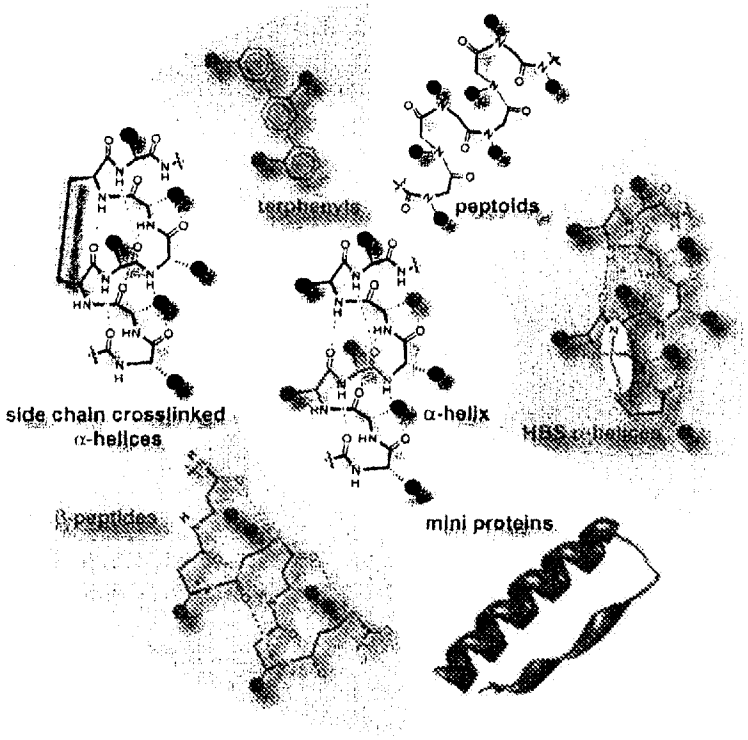

terphenyls
peptoids
side chain crosslinked
α-helices
α-helix
β-peptides
mini proteins

Figure 3

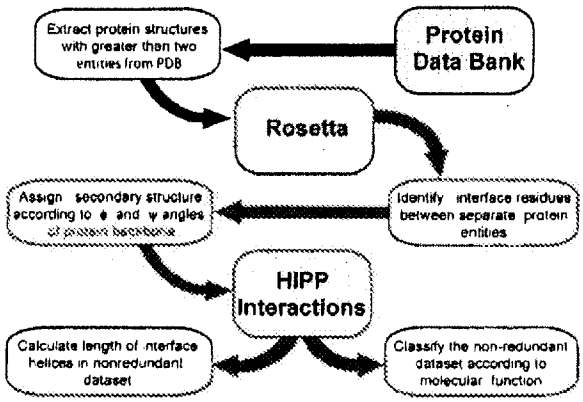
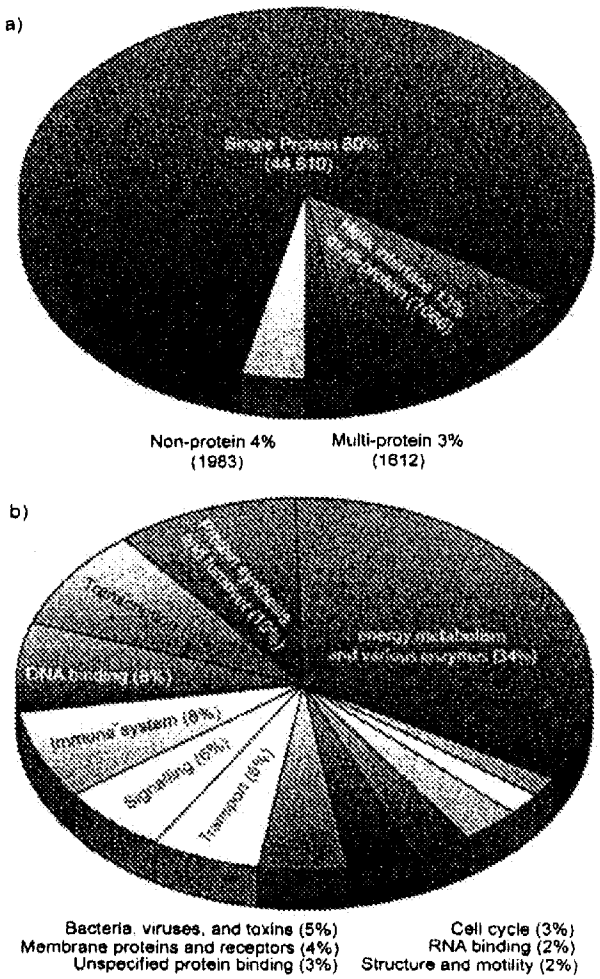

Protein Data Bank
Extract protein structures with greater than two entities from PDB
Rosetta
Identify interface residues between separate protein entities
Assign secondary structure according to φ and ψ angles
HIPP Interactions
Classify the non-redundant dataset according to molecular function
Calculate length of interface helices in nonredundant dataset

Figure 4


a)
Non-protein 4%
(1983)
Multi-protein 3%
(1612)
b)
DNA binding (8%)
Immune system (6%)
Signaling (6%)
Transport (6%)
Bacteria, viruses, and toxins (5%)
Membrane proteins and receptors (4%)
Unspecified protein binding (3%)
Cell cycle (3%)
RNA binding (2%)
Structure and motility (2%)

Figures 5A–B