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(54) Title: OPTIMIZED CROSS-SPECIES SPECIFIC BISPECIFIC SINGLE CHAIN ANTIBODY CONSTRUCTS

(57) Abstract: The present invention provides to a bispecific single chain antibody construct binding to a target cell surface antigen via a first binding domain and to the T cell surface antigen CD3 via a second binding domain, wherein serum albumin is fused to the C-terminus of the antibody construct. Moreover, the invention provides a polynucleotide encoding the antibody construct, a vector comprising said polynucleotide and a host cell transformed or transfected with said vector. Furthermore, the invention provides a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.

Optimized Cross-Species Specific Bispecific Single Chain Antibody Constructs

Field of the Invention

The present invention relates to a bispecific single chain antibody construct binding to a target cell surface antigen via a first binding domain and to the T cell surface antigen CD3 via a second binding domain, wherein serum albumin is fused to the C-terminus of the antibody construct. Moreover, the invention provides a polynucleotide encoding the antibody construct, a vector comprising said polynucleotide and a host cell transformed or transfected with said vector. Furthermore, the invention provides a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.

Background of the Invention

Bispecific molecules such as BiTE® (bispecific T cell engager) antibodies are recombinant protein constructs made from two flexibly linked antibody derived binding domains. One binding domain of BiTE® antibodies is specific for a selected tumor-associated surface antigen on target cells; the second binding domain is specific for CD3, a subunit of the T cell receptor complex on T cells. By their particular design BiTE® antibodies are uniquely suited to transiently connect T cells with target cells and, at the same time, potently activate the inherent cytolytic potential of T cells against target cells. An important further development of the first generation of BiTE® molecules (see WO 99/54440 and WO 2005/040220) developed into the clinic as AMG 103 and AMG 110 was the provision of bispecific antibody constructs binding to a context independent epitope at the N-terminus of the CD3ε chain (WO 2008/119567). BiTE® antibodies binding to this elected epitope did not only show cross-species specificity for human and *Callithrix jacchus, Saguinus oedipus* or *Saimiri sciureus* CD3ε chain, but also, due to using this epitope instead of previously described epitopes for CD3 binders in bispecific T cell engaging molecules, do not activate T cells to the same degree as observed for the previous generation of T cell engaging antibodies. This difference in T cell activation was connected with less or reduced T cell redistribution in patients, which was identified as a risk for side effects.

Definitions

It must be noted that as used herein, the singular forms “a”, “an”, and “the”, include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a

reagent" includes one or more of such different reagents and reference to "the method" includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

The term "and/or" wherever used herein includes the meaning of "and", "or" and "all or any other combination of the elements connected by said term".

The term "about" or "approximately" as used herein means within ±20%, preferably within ±15%, more preferably within ±10%, and most preferably within ±5% of a given value or range.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term "comprising" can be substituted with the term "containing" or "including" or sometimes when used herein with the term "having".

When used herein "consisting of" excludes any element, step, or ingredient not specified in the claim element. When used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

In each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms.

Detailed description of the Invention

For bispecific T cell engaging molecules comprising as their T cell binding entity a binding domain specific for the human and *Callithrix jacchus, Saguinus oedipus* or *Saimiri sciureus* CD3ε chain, wherein the epitope is part of an amino acid sequence comprised in the group consisting of SEQ ID NOs: 7, 8, 9, and 10 and comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu (SEQ ID NO: 1), it was observed that those molecules when used in

extremely high concentration showed T cell cytotoxicity, independent of the target specificity of the second binding domain and even in the absence of target cells. Although those high concentrations of bispeicific T cell engaging molecules are not relevant for every combination of disease and target in a treatment using the mode of action of T cell engaging molecules in case of a continuous i.v. administration, such high concentration issues may become relevant for specific administration routes or in combination with specific target settings and required compound concentrations.

Thus, the problem underlying the present invention was to provide bispecific single chain antibody constructs using a T cell binding domain of the latest generation, which avoid the T cell cytotoxicity even in high compound concentrations.

This problem was solved by providing a bispecific single chain antibody construct binding to a target cell surface antigen via a first binding domain and the T cell surface antigen CD3 via a second binding domain, wherein:

- the second binding domain binds to an epitope of human and *Callithrix jacchus, Saguinus oedipus* or *Saimiri sciureus* CD3ε chain, wherein the epitope is part of an amino acid sequence comprised in the group consisting of SEQ ID NO: 7 (human), SEQ ID NO: 8 (*Callithrix jacchus*), SEQ ID NO: 9 (*Saguinus oedipus*), and SEQ ID NO: 10 (*Saimiri sciureus*) and comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu (SEQ ID NO: **1**). and
- a serum albumin is fused to the C-terminus of the antibody construct;

wherein the bispecific single chain antibody construct does not have an amino acid sequence as depicted in SEQ ID NOs: **2 and 3**.

Without the intention to be bound by theory, the activation of T cells in the presence of a high concentration of the T cell engaging bispecific antibody constructs and in the absence of target cells is explained by dimerization or multimerization of the antibody constucts via the CD3 binding domain. Such di- or multimerization is sterically impaired by the fusion of an albumin or variant thereof to the C terminus of the antibody construct, while maintaining the characteristics of the antibody construct for its T cell engaging mode of action.
Those high concentrations of the T cell engaging bispecific antibody constructs in a patient are those concentrations in a specific compartment such as the serum. The fusion of the albumin to the C-terminus of the T cell engaging antibody construct prevents the activation of T cells in the absence of target cells up to a concentration of 2mg/ml, at least up to 1 mg/ml, more preferably up to 500 ng/ml.

Callithrix jacchus and Saguinus oedipus are both new world primate belonging to the family of *Callitrichidae*, while *Saimiri sciureus* is a new world primate belonging to the family of *Cebidae*.

Serum albumin is a protein physiologically produced by the liver; it occurs dissolved in blood plasma and is the most abundant blood protein in mammals. Albumin is essential for maintaining the oncotic pressure needed for proper distribution of body fluids between blood vessels and body tissues. It also acts as a plasma carrier by non-specifically binding several hydrophobic steroid hormones and as a transport protein for hemin and fatty acids. The term "serum albumin" respectively the human variant thereof ("human albumin") defines in the context of the invented proteins either the parental human serum albumin protein (sequence as described in SEQ ID NO: **4**) or any variant (e.g. such as albumin protein as depicted in SEQ ID NOs: 5-12 or 608 to 628) or fragment thereof preferably expressed as genetic fusion proteins and by chemical crosslinking etc. at least with one therapeutic protein. Variants comprising single or multiple mutations or fragments of albumin provide improved properties such as affinities to FcRn receptor and extended plasma half-life compared to its parent or reference. A preferred group of serum albumin sequences in connection with this invention is selected from a group consisting of SEQ ID NOs: 4, 6, 7, 8, 9, 10, 11, 12, 608, 609, 611, 612, 613, 614, 615, 616, 617, 618, 619, 621, 622, 623, 624, 625, 626, 627, and 628.

The term "antibody construct" refers to a molecule in which the structure and/or function is/are based on the structure and/or function of an antibody, e.g. of a full-length or whole immunoglobulin molecule. An antibody construct is hence capable of binding to its specific target or antigen. Furthermore, an antibody construct according to the invention comprises the minimum structural requirements of an antibody which allow for the target binding. This minimum requirement may e.g. be defined by the presence of at least the three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or the three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). The antibodies on which the constructs according to the invention are based include for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies.

Within the definition of "antibody constructs" according to the invention are full-length or whole antibodies including camelid antibodies and other immunoglobulin antibodies generated by biotechnological or protein engineering methods or processes. These full-length antibodies may be for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies. Also within the definition of "antibody constructs" are fragments of full-length antibodies, such as VH, VHH, VL, (s)dAb, Fv, Fd, Fab, Fab', F(ab')2

or "r IgG" ("half antibody"). Antibody constructs according to the invention may also be modified fragments of antibodies, also called antibody variants, such as scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab2, Fab3, diabodies, single chain diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies" exemplified by a structure which is as follows: (VH-VL-CH3)2, (scFv-CH3)2 or (scFv-CH3-scFv)2, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable domain, which might be VHH, VH or VL, that specifically bind an antigen or epitope independently of other V regions or domains.

Furthermore, the definition of the term "antibody constructs" includes monovalent, bivalent and polyvalent / multivalent constructs and, thus, monospecific constructs, specifically binding to only one antigenic structure, as well as bispecific and polyspecific / multispecific constructs, which specifically bind more than one antigenic structure, e.g. two, three or more, through distinct binding domains. Moreover, the definition of the term "antibody constructs" includes molecules consisting of only one polypeptide chain as well as molecules consisting of more than one polypeptide chain, which chains can be either identical (homodimers, homotrimers or homo oligomers) or different (heterodimer, heterotrimer or heterooligomer). Examples for the above identified antibodies and variants or derivatives thereof are described *inter alia* in Harlow and Lane, Antibodies a laboratory manual, CSHL Press (1988) and Using Antibodies: a laboratory manual, CSHL Press (1999), Kontermann and Dübel, Antibody Engineering, Springer, 2nd ed. 2010 and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009.

The antibody constructs of the present invention are preferably "*in vitro* generated antibody constructs". This term refers to an antibody construct according to the above definition where all or part of the variable region (e.g., at least one CDR) is generated in a non-immune cell selection, *e.g.*, an *in vitro* phage display, protein chip or any other method in which candidate sequences can be tested for their ability to bind to an antigen. This term thus preferably excludes sequences generated solely by genomic rearrangement in an immune cell in an animal. A "recombinant antibody" is an antibody made through the use of recombinant DNA technology or genetic engineering.

The present invention is directed to "single chain antibody constructs". Accordingly, those single chain antibody constructs only include those embodiments of the above described antibody constructs, which consist of a single peptide chain.

The term "monoclonal antibody" (mAb) or monoclonal antibody construct as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post-translation modifications (e.g., isomerizations, amidations) that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site or determinant on the antigen, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (or epitopes). In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, hence uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method.

For the preparation of monoclonal antibodies, any technique providing antibodies produced by continuous cell line cultures can be used. For example, monoclonal antibodies to be used may be made by the hybridoma method first described by Koehler *et al.*, Nature, 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567). Examples for further techniques to produce human monoclonal antibodies include the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96).

Hybridomas can then be screened using standard methods, such as enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance (BIACORE™) analysis, to identify one or more hybridomas that produce an antibody that specifically binds with a specified antigen. Any form of the relevant antigen may be used as the immunogen, *e.g.*, recombinant antigen, naturally occurring forms, any variants or fragments thereof, as well as an antigenic peptide thereof. Surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of a target antigen, such as the target cell surface antigen or CD3 epsilon (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13).

Another exemplary method of making monoclonal antibodies includes screening protein expression libraries, e.g., phage display or ribosome display libraries. Phage display is described, for example, in Ladner *et al.*, U.S. Patent No. 5,223,409; Smith (1985) Science

228:1315-1317, Clackson *et al.*, Nature, 352: 624-628 (1991) and Marks *et al.*, J. Mol. Biol., 222: 581-597 (1991).

In addition to the use of display libraries, the relevant antigen can be used to immunize a non-human animal, *e.g.*, a rodent (such as a mouse, hamster, rabbit or rat). In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig (immunoglobulin) loci. Using the hybridoma technology, antigen-specific monoclonal antibodies derived from the genes with the desired specificity may be produced and selected. See, e.g., XENOMOUSE™, Green *et al.* (1994) Nature Genetics 7:13-21, US 2003-0070185, WO 96/34096, and WO96/33735.

A monoclonal antibody can also be obtained from a non-human animal, and then modified, *e.g.*, humanized, deimmunized, rendered chimeric etc., using recombinant DNA techniques known in the art. Examples of modified antibody constructs include humanized variants of non-human antibodies, "affinity matured" antibodies (see, *e.g.* Hawkins et al. J. Mol. Biol. 254, 889-896 (1992) and Lowman *et al.*, Biochemistry 30, 10832- 10837 (1991)) and antibody mutants with altered effector function(s) (see, *e.g.*, US Patent 5,648,260, Kontermann and Dübel (2010), *loc. cit.* and Little (2009), *loc. cit.*).

In immunology, affinity maturation is the process by which B cells produce antibodies with increased affinity for antigen during the course of an immune response. With repeated exposures to the same antigen, a host will produce antibodies of successively greater affinities. Like the natural prototype, the *in vitro* affinity maturation is based on the principles of mutation and selection. The *in vitro* affinity maturation has successfully been used to optimize antibodies, antibody constructs, and antibody fragments. Random mutations inside the CDRs are introduced using radiation, chemical mutagens or error-prone PCR. In addition, the genetical diversity can be increased by chain shuffling. Two or three rounds of mutation and selection using display methods like phage display usually results in antibody fragments with affinities in the low nanomolar range.

A preferred type of an amino acid substitutional variation of the antibody constructs involves substituting one or more hypervariable region residues of a parent antibody (e. g. a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e.

g. 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e. g. binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the binding domain and, e.g., human the target cell surface antigen. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

The monoclonal antibodies and antibody constructs of the present invention specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816, 567; Morrison et al., Proc. Natl. Acad. Sci. USA, 81: 6851-6855 (1984)). Chimeric antibodies of interest herein include "primitized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (e.g., Old World Monkey, Ape etc.) and human constant region sequences. A variety of approaches for making chimeric antibodies have been described. See *e.g.*, Morrison *et al.*, Proc. Natl. Acad. ScL U.S.A. 81:6851 , 1985; Takeda *et al.*, Nature 314:452, 1985, Cabilly *et al.*, U.S. Patent No. 4,816,567; Boss *et al.*, U.S. Patent No. 4,816,397; Tanaguchi *et al.*, EP 0171496; EP 0173494; and GB 2177096.

An antibody, antibody construct or antibody fragment may also be modified by specific deletion of human T cell epitopes (a method called "deimmunization") by the methods disclosed in WO 98/52976 and WO 00/34317. Briefly, the heavy and light chain variable domains of an antibody can be analyzed for peptides that bind to MHC class II; these peptides represent potential T cell epitopes (as defined in WO 98/52976 and WO 00/34317). For detection of potential T cell epitopes, a computer modeling approach termed “peptide threading” can be applied, and in addition a database of human MHC class II binding

peptides can be searched for motifs present in the VH and VL sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable domains, or preferably, by single amino acid substitutions. Typically, conservative substitutions are made. Often, but not exclusively, an amino acid common to a position in human germline antibody sequences may be used. Human germline sequences are disclosed *e.g.* in Tomlinson, *et al.* (1992) J. Mol. Biol. 227:776-798; Cook, G.P. *et al.* (1995) Immunol. Today Vol. 16 (5): 237-242; and Tomlinson et al. (1995) EMBO J. 14: 14:4628-4638. The V BASE directory provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, LA. et al. MRC Centre for Protein Engineering, Cambridge, UK). These sequences can be used as a source of human sequence, *e.g.*, for framework regions and CDRs. Consensus human framework regions can also be used, for example as described in US Patent No. 6,300,064.

"Humanized" antibodies, antibody constructs or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) are antibodies or immunoglobulins of mostly human sequences, which contain (a) minimal sequence(s) derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region (also CDR) of the recipient are replaced by residues from a hypervariable region of a non-human (*e.g.*, rodent) species (donor antibody) such as mouse, rat, hamster or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, "humanized antibodies" as used herein may also comprise residues which are found neither in the recipient antibody nor the donor antibody. These modifications are made to further refine and optimize antibody performance. The humanized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al.*, Nature, 321: 522-525 (1986); Reichmann *et al.*, Nature, 332: 323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2: 593-596 (1992).

Humanized antibodies or fragments thereof can be generated by replacing sequences of the Fv variable domain that are not directly involved in antigen binding with equivalent sequences from human Fv variable domains. Exemplary methods for generating humanized antibodies or fragments thereof are provided by Morrison (1985) Science 229:1202-1207; by Oi *et al.* (1986) BioTechniques 4:214; and by US 5,585,089; US 5,693,761; US 5,693,762;

US 5,859,205; and US 6,407,213. Those methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin Fv variable domains from at least one of a heavy or light chain. Such nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, as well as from other sources. The recombinant DNA encoding the humanized antibody molecule can then be cloned into an appropriate expression vector.

Humanized antibodies may also be produced using transgenic animals such as mice that express human heavy and light chain genes, but are incapable of expressing the endogenous mouse immunoglobulin heavy and light chain genes. Winter describes an exemplary CDR grafting method that may be used to prepare the humanized antibodies described herein (U.S. Patent No. 5,225,539). All of the CDRs of a particular human antibody may be replaced with at least a portion of a non-human CDR, or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized antibody to a predetermined antigen.

A humanized antibody can be optimized by the introduction of conservative substitutions, consensus sequence substitutions, germline substitutions and/or back mutations. Such altered immunoglobulin molecules can be made by any of several techniques known in the art, (e.g., Teng *et al.*, Proc. Natl. Acad. Sci. U.S.A., 80: 7308-7312, 1983; Kozbor *et al.*, Immunology Today, 4: 7279, 1983; Olsson *et al.*, Meth. Enzymol., 92: 3-16, 1982, and EP 239 400.

The term "human antibody", "human antibody construct" and "human binding domain" includes antibodies, antibody constructs and binding domains having antibody regions such as variable and constant regions or domains which correspond substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat *et al.* (1991) (*loc. cit.*). The human antibodies, antibody constructs or binding domains of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs, and in particular, in CDR3. The human antibodies, antibody constructs or binding domains can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. The definition of human antibodies, antibody constructs and binding domains as used herein also contemplates fully human antibodies, which include only non-artificially and/or genetically altered human

sequences of antibodies as those can be derived by using technologies or systems such as the Xenomouse.

In some embodiments, the antibody constructs of the invention are "isolated" or "substantially pure" antibody constructs. "Isolated" or "substantially pure" when used to describe the antibody construct disclosed herein means an antibody construct that has been identified, separated and/or recovered from a component of its production environment. Preferably, the antibody construct is free or substantially free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. The antibody constructs may e.g. constitute at least about 5%, or at least about 50% by weight of the total protein in a given sample. It is understood that the isolated protein may constitute from 5% to 99.9% by weight of the total protein content, depending on the circumstances. The polypeptide may be made at a significantly higher concentration through the use of an inducible promoter or high expression promoter, such that it is made at increased concentration levels. The definition includes the production of an antibody construct in a wide variety of organisms and/or host cells that are known in the art. In preferred embodiments, the antibody construct will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Ordinarily, however, an isolated antibody construct will be prepared by at least one purification step.

The term "binding domain" characterizes in connection with the present invention a domain which (specifically) binds to / interacts with / recognizes a given target epitope or a given target site on the target molecules (antigens) and CD3, respectively. The structure and function of the first binding domain (recognizing the target cell surface antigen), and preferably also the structure and/or function of the second binding domain (CD3), is/are based on the structure and/or function of an antibody, e.g. of a full-length or whole immunoglobulin molecule. According to the invention, the first binding domain is characterized by the presence of three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). The second binding domain preferably also comprises the minimum structural requirements of an antibody which allow for the target binding. More preferably, the second binding domain comprises at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region)

and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). It is envisaged that the first and/or second binding domain is produced by or obtainable by phage-display or library screening methods rather than by grafting CDR sequences from a pre-existing (monoclonal) antibody into a scaffold.

According to the present invention, binding domains are preferably in the form of polypeptides. Such polypeptides may include proteinaceous parts and non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde). Proteins (including fragments thereof, preferably biologically active fragments, and peptides, usually having less than 30 amino acids) comprise two or more amino acids coupled to each other via a covalent peptide bond (resulting in a chain of amino acids). The term "polypeptide" as used herein describes a group of molecules, which usually consist of more than 30 amino acids. Polypeptides may further form multimers such as dimers, trimers and higher oligomers, i.e. consisting of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding higher order structures of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a hereteromultimer is an antibody molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms “peptide”, "polypeptide" and "protein" also refer to naturally modified peptides / polypeptides / proteins wherein the modification is effected e.g. by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A “peptide”, "polypeptide" or "protein" when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art and described herein below.

As mentioned above, a binding domain may typically comprise an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both. Fd fragments, for example, have two VH regions and often retain some antigen-binding function of the intact antigen-binding domain. Examples of (modified) antigen-binding antibody fragments include (1) a Fab fragment, a monovalent fragment having the VL, VH, CL and CH1 domains; (2) a F(ab')2 fragment, a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; (3) an Fd fragment having the two VH and CH1 domains; (4) an Fv fragment having the VL and VH domains of a single arm of an antibody, (5) a dAb fragment (Ward et al., (1989) Nature 341 :544-546), which has a VH domain; (6) an isolated complementarity determining region (CDR), and (7) a single chain Fv (scFv) , the latter being preferred (for example, derived from an scFv-library).

Antibodies and antibody constructs comprising at least one human binding domain avoid some of the problems associated with antibodies or antibody constructs that possess non-human such as rodent (*e.g.* murine, rat, hamster or rabbit) variable and/or constant regions. The presence of such rodent derived proteins can lead to the rapid clearance of the antibodies or antibody constructs or can lead to the generation of an immune response against the antibody or antibody construct by a patient. In order to avoid the use of rodent derived antibodies or antibody constructs, human or fully human antibodies / antibody constructs can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful models of human disease. Furthermore, the use of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

An important practical application of such a strategy is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated offers the opportunity to study the mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs) – an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies or antibody constructs are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies / antibody constructs. The use of fully human antibodies or antibody constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which require repeated compound administrations.

One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for

antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be readily produced and selected. This general strategy was demonstrated in connection with the generation of the first XenoMouse mouse strains (see Green et al. Nature Genetics 7:13-21 (1994)). The XenoMouse strains were engineered with yeast artificial chromosomes (YACs) containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was recently extended to the introduction of greater than approximately 80% of the human antibody repertoire through introduction of megabase sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez *et al.* Nature Genetics 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620.

The production of the XenoMouse mice is further discussed and delineated in U.S. patent applications Ser. No. 07/466,008, Ser. No. 07/610,515, Ser. No. 07/919,297, Ser. No. 07/922,649, Ser. No. 08/031,801, Ser. No. 08/112,848, Ser. No. 08/234,145, Ser. No. 08/376,279, Ser. No. 08/430,938, Ser. No. 08/464,584, Ser. No. 08/464,582, Ser. No. 08/463,191, Ser. No. 08/462,837, Ser. No. 08/486,853, Ser. No. 08/486,857, Ser. No. 08/486,859, Ser. No. 08/462,513, Ser. No. 08/724,752, and Ser. No. 08/759,620; and U.S. Pat. Nos. 6,162,963, 6,150,584, 6,114,598, 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez *et al.* Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998), EP 0 463 151 B1, WO 94/02602, WO 96/34096, WO 98/24893, WO 00/76310, and WO 03/47336.

In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through

the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more VH genes, one or more DH genes, one or more JH genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani *et al.* and U.S. Pat. Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877,397, 5,874,299, and 6,255,458 each to Lonberg and Kay, U.S. Pat. Nos. 5,591,669 and 6,023.010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205, 5,721,367, and 5,789,215 to Berns *et al.*, and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, Ser. No. 07/575,962, Ser. No. 07/810,279, Ser. No. 07/853,408, Ser. No. 07/904,068, Ser. No. 07/990,860, Ser. No. 08/053,131, Ser. No. 08/096,762, Ser. No. 08/155,301, Ser. No. 08/161,739, Ser. No. 08/165,699, Ser. No. 08/209,741. See also EP 0 546 073 B1, WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175. See further Taylor *et al.* (1992), Chen *et al.* (1993), Tuaillon *et al.* (1993), Choi *et al.* (1993), Lonberg *et al.* (1994), Taylor *et al.* (1994), and Tuaillon *et al.* (1995), Fishwild *et al.* (1996).

Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961. Xenerex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996; 5,698,767; and 5,958,765.

Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. It is however expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or multi-dose utilizations of the antibody. Thus, it would be desirable to provide antibody constructs comprising a fully human binding domain against the target cell surface antigen and a fully human binding domain against CD3 in order to vitiate concerns and/or effects of HAMA or HACA response.

The terms “(specifically) binds to”, (specifically) recognizes", “is (specifically) directed to”, and “(specifically) reacts with” mean in accordance with this invention that a binding domain interacts or specifically interacts with one or more, preferably at least two, more preferably at least three and most preferably at least four amino acids of an epitope located on the target protein or antigen (the target cell surface antigen / CD3).

The term "epitope" refers to a site on an antigen to which a binding domain, such as an antibody or immunoglobulin or derivative or fragment of an antibody or of an immunoglobulin, specifically binds. An “epitope” is antigenic and thus the term epitope is sometimes also referred to herein as “antigenic structure” or “antigenic determinant”. Thus, the binding domain is an “antigen interaction site”. Said binding/interaction is also understood to define a “specific recognition”.

“Epitopes” can be formed both by contiguous amino acids or non-contiguous amino acids juxtaposed by tertiary folding of a protein. A “linear epitope” is an epitope where an amino acid primary sequence comprises the recognized epitope. A linear epitope typically includes at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

A "conformational epitope", in contrast to a linear epitope, is an epitope wherein the primary sequence of the amino acids comprising the epitope is not the sole defining component of the epitope recognized (e.g., an epitope wherein the primary sequence of amino acids is not necessarily recognized by the binding domain). Typically a conformational epitope comprises an increased number of amino acids relative to a linear epitope. With regard to recognition of conformational epitopes, the binding domain recognizes a three-dimensional structure of the antigen, preferably a peptide or protein or fragment thereof (in the context of the present invention, the antigen for one of the binding domains is comprised within the the target cell surface antigen protein). For example, when a protein molecule folds to form a three-dimensional structure, certain amino acids and/or the polypeptide backbone forming the conformational epitope become juxtaposed enabling the antibody to recognize the epitope. Methods of determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy.

The interaction between the binding domain and the epitope or epitope cluster implies that a binding domain exhibits appreciable affinity for the epitope or epitope cluster on a particular protein or antigen (here: the target cell surface antigen and CD3, respectively) and, generally, does not exhibit significant reactivity with proteins or antigens other than the target cell surface antigen or CD3. “Appreciable affinity” includes binding with an affinity of about 10^{-6} M (KD) or stronger. Preferably, binding is considered specific when the binding affinity is about 10^{-12} to 10^{-8} M, 10^{-12} to 10^{-9} M, 10^{-12} to 10^{-10} M, 10^{-11} to 10^{-8} M, preferably of about 10^{-11} to 10^{-9} M. Whether a binding domain specifically reacts with or binds to a target can be tested

readily by, *inter alia*, comparing the reaction of said binding domain with a target protein or antigen with the reaction of said binding domain with proteins or antigens other than the target cell surface antigen or CD3. Preferably, a binding domain of the invention does not essentially or substantially bind to proteins or antigens other than the target cell surface antigen or CD3 (*i.e.*, the first binding domain is not capable of binding to proteins other than the target cell surface antigen and the second binding domain is not capable of binding to proteins other than CD3).

The term "does not essentially / substantially bind" or "is not capable of binding" means that a binding domain of the present invention does not bind a protein or antigen other than the target cell surface antigen or CD3, *i.e.*, does not show reactivity of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% with proteins or antigens other than the target cell surface antigen or CD3, whereby binding to the target cell surface antigen or CD3, respectively, is set to be 100%.

Specific binding is believed to be effected by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of secondary modifications of said structures. The specific interaction of the antigen-interaction-site with its specific antigen may result in a simple binding of said site to the antigen. Moreover, the specific interaction of the antigen-interaction-site with its specific antigen may alternatively or additionally result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

The term "variable" refers to the portions of the antibody or immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody (i.e., the "variable domain(s)"). The pairing of a variable heavy chain (VH) and a variable light chain (VL) together forms a single antigen-binding site. The CH domain most proximal to VH is designated as CH1. Each light (L) chain is linked to a heavy (H) chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype.

Variability is not evenly distributed throughout the variable domains of antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-domains are called "hypervariable regions" or "complementarity determining regions" (CDRs). The more conserved (i.e., non-hypervariable) portions of the variable domains are

called the "framework" regions (FRM) and provide a scaffold for the six CDRs in three dimensional space to form an antigen-binding surface. The variable domains of naturally occurring heavy and light chains each comprise four FRM regions (FR1, FR2, FR3, and FR4), largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site (see Kabat *et al.*, *loc. cit.*). The constant domains are not directly involved in antigen binding, but exhibit various effector functions, such as, for example, antibody-dependent, cell-mediated cytotoxicity and complement activation.

The terms "CDR", and its plural "CDRs", refer to the complementarity determining region of which three make up the binding character of a light chain variable region (CDR-L1, CDR-L2 and CDR-L3) and three make up the binding character of a heavy chain variable region (CDR-H1, CDR-H2 and CDR-H3). CDRs contain most of the residues responsible for specific interactions of the antibody with the antigen and hence contribute to the functional activity of an antibody molecule: they are the main determinants of antigen specificity.

The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat (an approach based on cross-species sequence variability), Chothia (an approach based on crystallographic studies of antigen-antibody complexes), and/or MacCallum (Kabat *et al.*, *loc. cit.*; Chothia *et al.*, J. Mol. Biol, 1987, 196: 901-917; and MacCallum *et al.*, J. Mol. Biol, 1996, 262: 732). Still another standard for characterizing the antigen binding site is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, *e.g.*, Protein Sequence and Structure Analysis of Antibody Variable Domains. In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg). To the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, the numbering in accordance with the so-called Kabat system is preferred.

Typically, CDRs form a loop structure that can be classified as a canonical structure. The term "canonical structure" refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia *et al.*, Nature, 1989, 342: 877; Martin and Thornton, J. Mol. Biol, 1996, 263: 800). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (*i.e.*, outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues.

The term "canonical structure" may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat *et al.*, loc. cit.). The Kabat numbering scheme (system) is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner and is the preferred scheme applied in the present invention as also mentioned elsewhere herein. Additional structural considerations can also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering can be described by the numbering system of Chothia et al and/or revealed by other techniques, for example, crystallography and two- or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (e.g., based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia *et al.*, loc. cit. and their implications for construing canonical aspects of antibody structure, are described in the literature. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, eds. Harlow *et al.*, 1988.

The CDR3 of the light chain and, particularly, the CDR3 of the heavy chain may constitute the most important determinants in antigen binding within the light and heavy chain variable regions. In some antibody constructs, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. *In vitro* selection schemes in which

CDR3 alone is varied can be used to vary the binding properties of an antibody or determine which residues contribute to the binding of an antigen. Hence, CDR3 is typically the greatest source of molecular diversity within the antibody-binding site. H3, for example, can be as short as two amino acid residues or greater than 26 amino acids.

The sequence of antibody genes after assembly and somatic mutation is highly varied, and these varied genes are estimated to encode 10^{10} different antibody molecules (Immunoglobulin Genes, 2nd ed., eds. Jonio et al., Academic Press, San Diego, CA, 1995). Accordingly, the immune system provides a repertoire of immunoglobulins. The term "repertoire" refers to at least one nucleotide sequence derived wholly or partially from at least one sequence encoding at least one immunoglobulin. The sequence(s) may be generated by rearrangement in vivo of the V, D, and J segments of heavy chains, and the V and J segments of light chains. Alternatively, the sequence(s) can be generated from a cell in response to which rearrangement occurs, e.g., *in vitro* stimulation. Alternatively, part or all of the sequence(s) may be obtained by DNA splicing, nucleotide synthesis, mutagenesis, and other methods, see, e.g., U.S. Patent 5,565,332. A repertoire may include only one sequence or may include a plurality of sequences, including ones in a genetically diverse collection.

The term “bispecific” as used herein refers to an antibody construct which is “at least bispecific”, i.e., it comprises at least a first binding domain and a second binding domain, wherein the first binding domain binds to one antigen or target, and the second binding domain binds to another antigen or target (here: CD3). Accordingly, antibody constructs according to the invention comprise specificities for at least two different antigens or targets. The term “bispecific antibody construct” of the invention also encompasses multispecific antibody constructs such as trispecific antibody constructs, the latter ones including three binding domains, or constructs having more than three (e.g. four, five…) specificities.

Given that the antibody constructs according to the invention are (at least) bispecific, they do not occur naturally and they are markedly different from naturally occurring products. A "bispecific" antibody construct or immunoglobulin is hence an artificial hybrid antibody or immunoglobulin having at least two distinct binding sites with different specificities. Bispecific antibodies can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai & Lachmann, Clin. Exp. Immunol. 79:315-321 (1990).

The at least two binding domains and the variable domains of the antibody construct of the present invention may or may not comprise peptide linkers (spacer peptides). The term "peptide linker" defines in accordance with the present invention an amino acid sequence by which the amino acid sequences of one (variable and/or binding) domain and another (variable and/or binding) domain of the antibody construct of the invention are linked with each other. An essential technical feature of such peptide linker is that said peptide linker does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344.

In the event that a linker is used, this linker is preferably of a length and sequence sufficient to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. For peptide linkers which connect the at least two binding domains in the antibody construct of the invention (or two variable domains), those peptide linkers are preferred which comprise only a few number of amino acid residues, e.g. 12 amino acid residues or less. Thus, peptide linker of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s) wherein Gly-rich linkers are preferred. A particularly preferred "single" amino acid in context of said "peptide linker" is Gly. Accordingly, said peptide linker may consist of the single amino acid Gly. Another preferred embodiment of a peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly_4Ser, or polymers thereof, i.e. $(Gly_4Ser)x$, where x is an integer of 1 or greater. The characteristics of said peptide linker, which comprise the absence of the promotion of secondary structures are known in the art and are described *e.g.* in Dall'Acqua et al. (Biochem. (1998) 37, 9266-9273), Cheadle et al. (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which also do not promote any secondary structures are preferred. The linkage of said domains to each other can be provided by, e.g. genetic engineering, as described in the examples. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (*e.g.* WO 99/54440 or Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001).

Bispecific single chain molecules are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56. Techniques described for the production of single chain antibodies (see, *inter alia*, US Patent

4,946,778, Kontermann and Dübel (2010), *loc. cit.* and Little (2009), *loc. cit.*) can be adapted to produce single chain antibody constructs specifically recognizing (an) elected target(s).

Bivalent (also called divalent) or bispecific single-chain variable fragments (bi-scFvs or di-scFvs having the format $(scFv)_2$) can be engineered by linking two scFv molecules. If these two scFv molecules have the same binding specificity, the resulting $(scFv)_2$ molecule will preferably be called bivalent (*i.e.* it has two valences for the same target epitope). If the two scFv molecules have different binding specificities, the resulting $(scFv)_2$ molecule will preferably be called bispecific. The linking can be done by producing a single peptide chain with two VH regions and two VL regions, yielding tandem scFvs (see *e.g.* Kufer P. *et al.*, (2004) Trends in Biotechnology 22(5):238-244). Another possibility is the creation of scFv molecules with linker peptides that are too short for the two variable regions to fold together (*e.g.* about five amino acids), forcing the scFvs to dimerize. This type is known as diabodies (see *e.g.* Hollinger, Philipp *et al.*, (July 1993) Proceedings of the National Academy of Sciences of the United States of America 90 (14): 6444-8.).

Single domain antibodies comprise merely one (monomeric) antibody variable domain which is able to bind selectively to a specific antigen, independently of other V regions or domains. The first single domain antibodies were engineered from havy chain antibodies found in camelids, and these are called V_HH fragments. Cartilaginous fishes also have heavy chain antibodies (IgNAR) from which single domain antibodies called V_{NAR} fragments can be obtained. An alternative approach is to split the dimeric variable domains from common immunoglobulins e.g. from humans or rodents into monomers, hence obtaining VH or VL as a single domain Ab. Although most research into single domain antibodies is currently based on heavy chain variable domains, nanobodies derived from light chains have also been shown to bind specifically to target epitopes. Examples of single domain antibodies are called sdAb, nanobodies or single variable domain antibodies.

A $(\text{single domain mAb})_2$ is hence a monoclonal antibody construct composed of (at least) two single domain monoclonal antibodies, which are individually selected from the group comprising VH, VL, V_HH and V_{NAR}. The linker is preferably in the form of a peptide linker. Similarly, an "scFv-single domain mAb" is a monoclonal antibody construct composed of at least one single domain antibody as described above and one scFv molecule as described above. Again, the linker is preferably in the form of a peptide linker.

Bispecific single chain molecules are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer,

Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56. Techniques described for the production of single chain antibodies (see, *inter alia*, US Patent 4,946,778, Kontermann and Dübel (2010), *loc. cit.* and Little (2009), *loc. cit.*) can be adapted to produce single chain antibody constructs specifically recognizing (an) elected target(s).

Bivalent (also called divalent) or bispecific single-chain variable fragments (bi-scFvs or di-scFvs having the format $(scFv)_2$) can be engineered by linking two scFv molecules. If these two scFv molecules have the same binding specificity, the resulting $(scFv)_2$ molecule will preferably be called bivalent (*i.e.* it has two valences for the same target epitope). If the two scFv molecules have different binding specificities, the resulting $(scFv)_2$ molecule will preferably be called bispecific. The linking can be done by producing a single peptide chain with two VH regions and two VL regions, yielding tandem scFvs (see *e.g.* Kufer P. *et al.*, (2004) Trends in Biotechnology 22(5):238-244). Another possibility is the creation of scFv molecules with linker peptides that are too short for the two variable regions to fold together (*e.g.* about five amino acids), forcing the scFvs to dimerize. This type is known as diabodies (see *e.g.* Hollinger, Philipp *et al.*, (July 1993) Proceedings of the National Academy of Sciences of the United States of America 90 (14): 6444-8.).

Single domain antibodies comprise merely one (monomeric) antibody variable domain which is able to bind selectively to a specific antigen, independently of other V regions or domains. The first single domain antibodies were engineered from havy chain antibodies found in camelids, and these are called V_HH fragments. Cartilaginous fishes also have heavy chain antibodies (IgNAR) from which single domain antibodies called V_{NAR} fragments can be obtained. An alternative approach is to split the dimeric variable domains from common immunoglobulins e.g. from humans or rodents into monomers, hence obtaining VH or VL as a single domain Ab. Although most research into single domain antibodies is currently based on heavy chain variable domains, nanobodies derived from light chains have also been shown to bind specifically to target epitopes. Examples of single domain antibodies are called sdAb, nanobodies or single variable domain antibodies.

A $(single\ domain\ mAb)_2$ is hence a monoclonal antibody construct composed of (at least) two single domain monoclonal antibodies, which are individually selected from the group comprising VH, VL, V_HH and V_{NAR}. The linker is preferably in the form of a peptide linker. Similarly, an "scFv-single domain mAb" is a monoclonal antibody construct composed of at least one single domain antibody as described above and one scFv molecule as described above. Again, the linker is preferably in the form of a peptide linker.

It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target antigen and CD3, a further function. In this format, the antibody construct is a trifunctional or multifunctional antibody construct by targeting target cells through binding to the target antigen, mediating cytotoxic T cell activity through CD3 binding and providing a further function such as a label (fluorescent etc.), a therapeutic agent such as a toxin or radionuclide, etc.

Covalent modifications of the antibody constructs are also included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antibody construct are introduced into the molecule by reacting specific amino acid residues of the antibody construct with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0. Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Derivatization with bifunctional agents is useful for crosslinking the antibody constructs of the present invention to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the antibody constructs included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (*e.g.*, the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the antibody construct is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the amino acid sequence of an antibody construct is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the antibody construct is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330, and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the starting antibody construct may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin *et al.*, 1987, *Arch. Biochem. Biophys.* 259:52 and by Edge *et al.*, 1981, *Anal. Biochem.* 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, 1987, Meth. Enzymol. 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin *et al.*, 1982, J. Biol. Chem. 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

Other modifications of the antibody construct are contemplated herein. For example, another type of covalent modification of the antibody construct comprises linking the antibody construct to various non-proteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody construct, e.g. in order to facilitate the addition of polymers such as PEG.

In some embodiments, the covalent modification of the antibody constructs of the invention comprises the addition of one or more labels. The labelling group may be coupled to the antibody construct *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and can be used in performing the present invention. The term "label" or "labelling group" refers to any detectable label. In general, labels fall into a variety of classes, depending on the assay in which they are to be detected – the following examples include, but are not limited to:

a) isotopic labels, which may be radioactive or heavy isotopes, such as radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{89}Zr, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I)
b) magnetic labels (*e.g.,* magnetic particles)
c) redox active moieties
d) optical dye (including, but not limited to, chromophores, phosphors and fluorophores) such as fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors),

chemiluminescent groups, and fluorophores which can be either "small molecule" fluores or proteinaceous fluores

e) enzymatic groups (*e.g.* horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase)
f) biotinylated groups
g) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.)

By "fluorescent label" is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland.

Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5292658, 5418155, 5683888, 5741668, 5777079, 5804387, 5874304, 5876995, 5925558).

Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz *et al.*, 1988, *Science* 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and

derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe *et al.*, 1994, *FEBS Letters* 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow *et al.*, 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising the target antigen antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric target antigen antibody fragments or derivatives that form are recovered from the culture supernatant.

The antibody construct of the invention may also comprise additional domains, which are *e.g.* helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of the molecule. Domains helpful for the isolation of an antibody construct may be selected from peptide motives or secondarily introduced moieties, which can be captured in an isolation method, e.g. an isolation column. Non-limiting embodiments of such additional domains comprise peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants thereof (e.g. StrepII-tag) and His-tag. All herein disclosed antibody constructs characterized by the identified CDRs are preferred to comprise a His-tag domain, which is generally known as a repeat of consecutive His residues in the amino acid sequence of a molecule, preferably of six His residues.

T cells or T lymphocytes are a type of lymphocyte (itself a type of white blood cell) that play a central role in cell-mediated immunity. There are several subsets of T cells, each with a distinct function. T cells can be distinguished from other lymphocytes, such as B cells and NK cells, by the presence of a T cell receptor (TCR) on the cell surface. The TCR is responsible for recognizing antigens bound to major histocompatibility complex (MHC) molecules and is composed of two different protein chains. In 95% of the T cells, the TCR consists of an alpha (α) and beta (β) chain. When the TCR engages with antigenic peptide and MHC (peptide / MHC complex), the T lymphocyte is activated through a series of biochemical events mediated by associated enzymes, co-receptors, specialized adaptor molecules, and activated or released transcription factors

The CD3 receptor complex is a protein complex and is composed of four chains. In mammals, the complex contains a CD3γ (gamma) chain, a CD3δ (delta) chain, and two CD3ε (epsilon) chains. These chains associate with the T cell receptor (TCR) and the so-called ζ (zeta) chain to form the T cell receptor CD3 complex and to generate an activation

signal in T lymphocytes. The CD3γ (gamma), CD3δ (delta), and CD3ε (epsilon) chains are highly related cell-surface proteins of the immunoglobulin superfamily containing a single extracellular immunoglobulin domain. The intracellular tails of the CD3 molecules contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif or ITAM for short, which is essential for the signaling capacity of the TCR. The CD3 epsilon molecule is a polypeptide which in humans is encoded by the *CD3E* gene which resides on chromosome 11. The sequence of a preferred human CD3 epsilon extracellular domain is shown in SEQ ID NO: 605, and the most preferred CD3 binding epitope corresponding to amino acid residues 1-27 of the human CD3 epsilon extracellular domain is represented in SEQ ID NO: 604.

The redirected lysis of target cells via the recruitment of T cells by a multispecific, at least bispecific, antibody construct involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis, and are not affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see, for example, WO 2007/042261.

Cytotoxicity mediated by bispecific antibody constructs can be measured in various ways. Effector cells can be e.g. stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). If the target cells are of macaque origin or express or are transfected with macaque target cell antigen, the effector cells should also be of macaque origin such as a macaque T cell line, e.g. 4119LnPx. The target cells should express (at least the extracellular domain of) target cell antigen, e.g. human or macaque target cell antigen. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with target cell antigen, e.g. human or macaque target cell antigen. Alternatively, the target cells can be a target cell antigen positive natural expresser cell line, such as a human cancer cell line. Usually EC50 values are expected to be lower with target cell lines expressing higher levels of target cell antigen on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of bispecific antibody constructs can be measured in a ^{51}chromium release assay (incubation time of about 18 hours) or in a in a FACS-based cytotoxicity assay (incubation time of about 48 hours). Modifications of the assay incubation time (cytotoxic reaction) are also possible. Other methods of measuring cytotoxicity are well-known to the skilled person and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

The cytotoxic activity mediated by bispecific antibody constructs of the present invention is preferably measured in a cell-based cytotoxicity assay. It is represented by the EC_{50} value, which corresponds to the half maximal effective concentration (concentration of the antibody construct which induces a cytotoxic response halfway between the baseline and maximum). Preferably, the EC_{50} value of the bispecific antibody constructs is ≤20.000 pg/ml, more preferably ≤5000 pg/ml, even more preferably ≤1000 pg/ml, even more preferably ≤500 pg/ml, even more preferably ≤350 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml.

Any of the above given EC_{50} values can be combined with any one of the indicated scenarios of a cell-based cytotoxicity assay, *e.g.* in line with the methods described in the appended example. For example, when (human) CD8 positive T cells or a macaque T cell line are used as effector cells, the EC_{50} value of the bispecific antibody construct of the invention (*e.g.* a target cell antigen/CD3 bispecific construct) is preferably ≤1000 pg/ml, more preferably ≤500 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml. If in this assay the target cells are (human or macaque) cells transfected with the target antigen (*e.g.* target cell antigen), such as CHO cells, the EC_{50} value of the bispecific antibody construct is preferably ≤150 pg/ml, more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤30 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml. If the target cells are a positive natural expresser cell line (*e.g.* of target cell antigen), then the EC_{50} value is preferably ≤350 pg/ml, more preferably ≤250 pg/ml, even more preferably ≤200 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤150 pg/ml, even more preferably ≤100 pg/ml, and most preferably ≤50 pg/ml, or lower. When (human) PBMCs are used as effector cells, the EC_{50} value of the bispecific antibody construct is preferably ≤1000 pg/ml, more preferably ≤750 pg/ml, more preferably ≤500 pg/ml, even more preferably ≤350 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, and most preferably ≤50 pg/ml, or lower.

Preferably, the bispecific antibody constructs of the present invention do not induce / mediate lysis or do not essentially induce / mediate lysis of target cell antigen negative cells such as CHO cells. The term “do not induce lysis”, “do not essentially induce lysis”, “do not mediate lysis” or “do not essentially mediate lysis” means that an antibody constructs of the present invention does not induce or mediate lysis of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% of target cell antigen negative cells, whereby lysis of a target cell antigen positive cell line

is set to be 100%. This usually applies for concentrations of the antibody construct of up to 500 nM. The skilled person knows how to measure cell lysis without further ado. Moreover, the present specification teaches specific instructions how to measure cell lysis.

The difference in cytotoxic activity between the monomeric and the dimeric isoform of individual bispecific antibody constructs is referred to as "potency gap". This potency gap can e.g. be calculated as ratio between EC_{50} values of the molecule's monomeric and dimeric form. Potency gaps of the bispecific antibody constructs of the present invention are preferably ≤ 5, more preferably ≤ 4, even more preferably ≤ 3, even more preferably ≤ 2 and most preferably ≤ 1.

As well as the second binding domain the first (or any further) binding domain(s) of the antibody construct of the invention is/are preferably cross-species specific for members of the mammalian order of primates. Cross-species specific CD3 binding domains are, for example, described in WO 2008/119567. According to one embodiment, the first and second binding domain, in addition to binding to human target cell antigen and human CD3, respectively, will also bind to the target cell antigen / CD3 of primates including (but not limited to) new world primates (such as *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus*), old world primates (such baboons and macaques), gibbons, and non-human *hominidae*.

In one aspect of the invention, the first binding domain binds to human CDH19 (SEQ ID NO: 606) and further binds to macaque CDH19, such as CDH19 of *Macaca fascicularis* (SEQ ID NO: 607). The affinity of the first binding domain for macaque CDH19 is preferably ≤15 nM, more preferably ≤10 nM, even more preferably ≤5 nM, even more preferably ≤1 nM, even more preferably ≤0.5 nM, even more preferably ≤0.1 nM, and most preferably ≤0.05 nM or even ≤0.01 nM.

Preferably the affinity gap of the antibody constructs according to the invention for binding to its macaque vs human target antigen, e.g. macaque CDH19 versus human CDH19 [maCDH19:huCDH19] is between 0.1 and 10, more preferably between 0.2 and 5, even more preferably between 0.3 and 2.5, even more preferably between 0.4 and 2, and most preferably between 0.5 and 1.

In one embodiment the invention provides a bispecific single chain antibody construct, wherein serum albumin is a human serum albumin or an FcRn binding optimized variant thereof. Variants of human albumin are described e.g. in WO 2014/072481.

In one embodiment of the antibody construct of the invention, the serum albumin comprises an amino acid sequence selected from the group consting of SEQ ID NOs: 4 to 12 and 608 to 628.

Also in one embodiment of the antibody construct of the invention, the serum albumin is linked to the antibody construct via a peptide linker. It is preferred that the peptide linker has the amino acid sequence $(GGGGS)_n$ (SEQ ID NO: 13)$_n$, $(PGGGGS)_n$ (SEQ ID NO: 2707)$_n$, or $(PGGDGS)_n$ (SEQ ID NO: 2708)$_n$, wherein "n" is an integer in the range of 1 to 5. Further preferred is that "n" is an integer in the range of 1 to 3, and most preferably "n" is 1 or 2.

In one embodiment of the antibody construct of the invention the second binding domain comprises a VL region having CDR-L1-L3 and a VH region having CDR-H1 -H3 selected from the group consisting of:

(a) CDR-L1-L3 as depicted in SEQ ID NOs:14-16 and CDR-H1-H3 as depicted in SEQ ID NOs:17-19;
(b) CDR-L1-L3 as depicted in SEQ ID NOs:26-28 and CDR-H1-H3 as depicted in SEQ ID NOs:29-31;
(c) CDR-L1-L3 as depicted in SEQ ID NOs:38-40 and CDR-H1-H3 as depicted in SEQ ID NOs:41-43;
(d) CDR-L1-L3 as depicted in SEQ ID NOs:50-52 and CDR-H1-H3 as depicted in SEQ ID NOs:53-55;
(e) CDR-L1-L3 as depicted in SEQ ID NOs:62-64 and CDR-H1-H3 as depicted in SEQ ID NOs:65-67;
(f) CDR-L1-L3 as depicted in SEQ ID NOs:74-76 and CDR-H1-H3 as depicted in SEQ ID NOs:77-79;
(g) CDR-L1-L3 as depicted in SEQ ID NOs:86-88 and CDR-H1-H3 as depicted in SEQ ID NOs:89-91;
(h) CDR-L1-L3 as depicted in SEQ ID NOs:98-100 and CDR-H1-H3 as depicted in SEQ ID NOs:101-103;
(i) CDR-L1-L3 as depicted in SEQ ID NOs:110-112 and CDR-H1-H3 as depicted in SEQ ID NOs:113-115; and
(j) CDR-L1-L3 as depicted in SEQ ID NOs:122-124 and CDR-H1-H3 as depicted in SEQ ID NOs:125-127.

In one embodiment of the antibody construct of the invention the second binding domain comprises pairs of VH and VL chains selected from the group consisting of:

(a) a VH-chain as depicted in SEQ ID NO: 20 and a VL-chain as depicted in SEQ ID NO: 22;
(b) a VH-chain as depicted in SEQ ID NO: 32 and a VL-chain as depicted in SEQ ID NO: 34;
(c) a VH-chain as depicted in SEQ ID NO: 44 and a VL-chain as depicted in SEQ ID NO: 46;
(d) a VH-chain as depicted in SEQ ID NO: 56 and a VL-chain as depicted in SEQ ID NO: 58;
(e) a VH-chain as depicted in SEQ ID NO: 68 and a VL-chain as depicted in SEQ ID NO: 70;
(f) a VH-chain as depicted in SEQ ID NO: 80 and a VL-chain as depicted in SEQ ID NO: 82;
(g) a VH-chain as depicted in SEQ ID NO: 92 and a VL-chain as depicted in SEQ ID NO: 94;
(h) a VH-chain as depicted in SEQ ID NO: 104 and a VL-chain as depicted in SEQ ID NO: 106;
(i) a VH-chain as depicted in SEQ ID NO: 116 and a VL-chain as depicted in SEQ ID NO: 118; and
(j) a VH-chain as depicted in SEQ ID NO: 128 and a VL-chain as depicted in SEQ ID NO: 130.

Also in one embodiment of the antibody construct of the invention the second binding domain comprises an amino acid sequence as depicted in SEQ ID NO: 24, SEQ ID NO: 36, SEQ ID NO: 48, SEQ ID NO: 60, SEQ ID NO: 72, SEQ ID NO: 84, SEQ ID NO: 96, SEQ ID NO: 108, SEQ ID NO: 120 or SEQ ID NO: 132.

In a further embodiment of the antibody construct of the invention, the first binding domain binds to a target cell surface antigen, which is a tumor antigen or a viral antigen on the surface of an infected host cell. In a preferred embodiment the tumor antigen is selected from the group consisting of CDH19, MSLN, DLL3, FLT3, EGFRvIII, CD33, CD19, CD20, and CD70. Preferred viral antigens are selected from a group consisting of Influenza A, CMV and HIV.

The invention further provides an antibody construct, wherein the antibody construct comprises an amino acid sequences selected from the group consisting of:
(a) SEQ ID NOs: 134-180;
(b) SEQ ID NOs: 181-227;

(c) SEQ ID NOs: 228-274;
(d) SEQ ID NOs: 275-321;
(e) SEQ ID NOs: 322-368;
(f) SEQ ID NOs: 369-415;
(g) SEQ ID NOs: 416-462;
(h) SEQ ID NOs: 463-509;
(i) SEQ ID NOs: 510-556; and
(j) SEQ ID NOs: 557-603.

The invention also provides an antibody construct, wherein the antibody construct comprises the following elements starting from the N-terminus:

(a) an scFv binding to the target cell surface antigen having an amino acid sequence selected from the group consisting of SEQ ID NOs: 629-675, 684, 694, 704, 714, 724, 734, 744, 754, 764, 774, 784, 794, 804, 814, 824, 834, 844, 854, 864, 874, 884, 894, 904, 914, 924, 934, 944, 954, 964, 974, 984, 994, 1004, 1014, 1024, 1034, 1044, 1054, 1064, 1074, 1084, 1094, 1104, 1114, 1124, 1134, 1144, 1154, 1164, 1174, 1184, 1194, 1204, 1214, 1224, 1234, 1244, 1254, 1264, 1274, 1284, 1294, 1304, 1314, 1324, 1334, 1344, 1354, 1364, 1374, 1384, 1394, 1404, 1414, 1424, 1434, 1444, 1454, 1464, 1474, 1484, 1494, 1504, 1514, 1524, 1534, 1544, 1554, 1564, 1574, 1584, 1594, 1604, 1614, 1624, 1634, 1644, 1654, 1664, 1674, 1684, 1694, 1704, 1714, 1724, 1734, 1744, 1754, 1764, 1774, 1784, 1794, 1804, 1814, 1824, 1834, 1844, 1854, 1864, 1874, 1884, 1894, 1904, 1914, 1924, 1934, 1944, 1954, 1964, 1974, 2004, 2014, 2024, 2034, 2044, 2054, 2064, 2074, 2084, 2094, 2104, 2114, 2124, 2134, 2144, 2154, 2164, 2174, 2184, 2194, 2204, 2214, 2224, 2234, 2244, 2254, 2264, 2274, 2284, 2294, 2304, 2314, 2324, 2334, 2344, 2354, 2364, 2374, 2384, 2394, 2404, 2414, 2424, 2434, 2444, 2454, 2464, 2474, 2484, 2494, 2504, 2514, 2524, 2534, 2544, 2554, 2564, 2574, 2584, 2594, 2604, 2614, 2624, 2634, 2644, 2654, 2664, 2674, 2684, 2694, and 2704;
(b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 13 and 2707-2709;
(c) an scFv binding to the T cell surface antigen CD3 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 24, 36, 48, 60, 72, 84, 96, 108, 120, 132 and 2706;
(d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 13 and 2707-2709;
(e) a serum albumin having an amino acid sequence selected from the group consting of SEQ ID NOs: 4 to 12 and 608 to 628; and

(f) optionally a His-tag.

It is particularly preferred that the elements defined in above items (a) to (f) are arranged in this sequence from the N-terminus to the C-terminus of the antibody construct.

Amino acid sequence modifications of the antibody constructs described herein are also contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody construct. Amino acid sequence variants of the antibody constructs are prepared by introducing appropriate nucleotide changes into the antibody constructs nucleic acid, or by peptide synthesis. All of the below described amino acd sequence modifications should result in an antibody construct which still retains the desired biological activity (binding to target cell antigen and to CD3) of the unmodified parental molecule.

The term "amino acid" or "amino acid residue" typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (GIn or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H); isoleucine (He or I): leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); pro line (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. Generally, amino acids can be grouped as having a nonpolar side chain (e.g., Ala, Cys, He, Leu, Met, Phe, Pro, Val); a negatively charged side chain (e.g., Asp, Glu); a positively charged sidechain (e.g., Arg, His, Lys); or an uncharged polar side chain (e.g., Asn, Cys, GIn, Gly, His, Met, Phe, Ser, Thr, Trp, and Tyr).

Amino acid modifications include, for example, deletions from, and/or insertions into, and/or substitutions of, residues within the amino acid sequences of the antibody constructs. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antibody constructs, such as changing the number or position of glycosylation sites.

For example, 1, 2, 3, 4, 5, or 6 amino acids may be inserted or deleted in each of the CDRs (of course, dependent on their length), while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be inserted or deleted in each of the FRs. Preferably, amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 residues to polypeptides containing a hundred or

more residues, as well as intra-sequence insertions of single or multiple amino acid residues. An insertional variant of the antibody construct of the invention includes the fusion to the N-terminus or to the C-terminus of the antibody construct to an enzyme or a fusion to a polypeptide which increases the serum half-life of the antibody construct.

The sites of greatest interest for substitutional mutagenesis include the CDRs of the heavy and/or light chain, in particular the hypervariable regions, but FR alterations in the heavy and/or light chain are also contemplated. The substitutions are preferably conservative substitutions as described herein. Preferably, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids may be substituted in a CDR, while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be substituted in the framework regions (FRs), depending on the length of the CDR or FR. For example, if a CDR sequence encompasses 6 amino acids, it is envisaged that one, two or three of these amino acids are substituted. Similarly, if a CDR sequence encompasses 15 amino acids it is envisaged that one, two, three, four, five or six of these amino acids are substituted.

A useful method for identification of certain residues or regions of the antibody constructs that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells in Science, 244: 1081-1085 (1989). Here, a residue or group of target residues within the antibody construct is/are identified (e.g. charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the epitope.

Those amino acid locations demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site or region for introducing an amino acid sequence variation is predetermined, the nature of the mutation *per se* needs not to be predetermined. For example, to analyze or optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at a target codon or region, and the expressed antibody construct variants are screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in the DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of target antigen binding activities.

Generally, if amino acids are substituted in one or more or all of the CDRs of the heavy and/or light chain, it is preferred that the then-obtained "substituted" sequence is at least

60%, more preferably 65%, even more preferably 70%, particularly preferably 75%, more particularly preferably 80% identical to the "original" CDR sequence. This means that it is dependent of the length of the CDR to which degree it is identical to the "substituted" sequence. For example, a CDR having 5 amino acids is preferably 80% identical to its substituted sequence in order to have at least one amino acid substituted. Accordingly, the CDRs of the antibody construct may have different degrees of identity to their substituted sequences, e.g., CDRL1 may have 80%, while CDRL3 may have 90%.

Preferred substitutions (or replacements) are conservative substitutions. However, any substitution (including non-conservative substitution or one or more from the "exemplary substitutions" listed in Table 1, below) is envisaged as long as the antibody construct retains its capability to bind to target cell antigen via the first binding domain and to CD3 epsilon via the second binding domain and/or its CDRs have an identity to the then substituted sequence (at least 60%, more preferably 65%, even more preferably 70%, particularly preferably 75%, more particularly preferably 80% identical to the "original" CDR sequence).

Conservative substitutions are shown in Table 1 under the heading of "preferred substitutions". If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table A, or as further described below in reference to amino acid classes, may be introduced and the products screened for a desired characteristic.

Table A: Amino acid substitutions

Original	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val, leu, ile	val
Arg (R)	lys, gln, asn	lys
Asn (N)	gln, his, asp, lys, arg	gln
Asp (D)	glu, asn	glu
Cys (C)	ser, ala	ser
Gln (Q)	asn, glu	asn
Glu (E)	asp, gln	asp
Gly (G)	Ala	ala
His (H)	asn, gln, lys, arg	arg
Ile (I)	leu, val, met, ala, phe	leu
Leu (L)	norleucine, ile, val, met, ala	ile
Lys (K)	arg, gln, asn	arg
Met (M)	leu, phe, ile	leu

Phe (F)	leu, val, ile, ala, tyr	tyr
Pro (P)	Ala	ala
Ser (S)	Thr	thr
Thr (T)	Ser	ser
Trp (W)	tyr, phe	tyr
Tyr (Y)	trp, phe, thr, ser	phe
Val (V)	ile, leu, met, phe, ala	leu

Substantial modifications in the biological properties of the antibody construct of the present invention are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties: (1) hydrophobic: norleucine, met, ala, val, leu, ile; (2) neutral hydrophilic: cys, ser, thr; (3) acidic: asp, glu; (4) basic: asn, gin, his, lys, arg; (5) residues that influence chain orientation: gly, pro; and (6) aromatic : trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Any cysteine residue not involved in maintaining the proper conformation of the antibody construct may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the antibody to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

For amino acid sequences, sequence identity and/or similarity is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman, 1988, *Proc. Nat. Acad. Sci. U.S.A.* 85:2444, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux *et al.*, 1984, *Nucl. Acid Res.* 12:387-395, preferably using the default settings, or by inspection. Preferably, percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30, "Current Methods in Sequence Comparison and Analysis," Macromolecule Sequencing and Synthesis, Selected Methods and Applications, pp 127-149 (1988), Alan R. Liss, Inc.

An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, 1987, *J. Mol. Evol.* 35:351-360; the method is similar to that described by Higgins and Sharp, 1989, *CABIOS* 5:151-153. Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in: Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402; and Karin *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5873-5787. A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul *et al.*, 1996, *Methods in Enzymology* 266:460-480. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=II. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

An additional useful algorithm is gapped BLAST as reported by Altschul *et al.*, 1993, *Nucl. Acids Res.* 25:3389-3402. Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9; the two-hit method to trigger ungapped extensions, charges gap lengths of k a cost of 10+k; Xu set to 16, and Xg set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

Generally, the amino acid homology, similarity, or identity between individual variant CDRs are at least 60% to the sequences depicted herein, and more typically with preferably increasing homologies or identities of at least 65% or 70%, more preferably at least 75% or 80%, even more preferably at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and almost 100%. In a similar manner, "percent (%) nucleic acid sequence identity" with respect to the nucleic acid sequence of the binding proteins identified herein is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the coding sequence of the antibody construct. A specific method

utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

Generally, the nucleic acid sequence homology, similarity, or identity between the nucleotide sequences encoding individual variant CDRs and the nucleotide sequences depicted herein are at least 60%, and more typically with preferably increasing homologies or identities of at least 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, and almost 100%. Thus, a "variant CDR" is one with the specified homology, similarity, or identity to the parent CDR of the invention, and shares biological function, including, but not limited to, at least 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the specificity and/or activity of the parent CDR.

It is furthermore envisaged that the bispecific antibody constructs of the present invention exhibit therapeutic efficacy or anti-tumor activity. This can *e.g.* be assessed in a study as disclosed in the following example of an advanced stage human tumor xenograft model:

On day 1 of the study, $5x10^6$ cells of a human target cell antigen positive cancer cell line are subcutaneously injected in the right dorsal flank of female NOD/SCID mice. When the mean tumor volume reaches about 100 mm^3, in vitro expanded human CD3 positive T cells are transplanted into the mice by injection of about $2x10^7$ cells into the peritoneal cavity of the animals. Mice of vehicle control group 1 do not receive effector cells and are used as an untransplanted control for comparison with vehicle control group 2 (receiving effector cells) to monitor the impact of T cells alone on tumor growth. The antibody treatment starts when the mean tumor volume reaches about 200 mm^3. The mean tumor size of each treatment group on the day of treatment start should not be statistically different from any other group (analysis of variance). Mice are treated with 0.5 mg/kg/day of a target cell antigen/CD3 bispecifc antibody construct by intravenous bolus injection for about 15 to 20 days. Tumors are measured by caliper during the study and progress evaluated by intergroup comparison of tumor volumes (TV). The tumor growth inhibition T/C [%] is determined by calculating TV as T/C% = 100 x (median TV of analyzed group) / (median TV of control group 2).

The skilled person knows how to modify or adapt certain parameters of this study, such as the number of injected tumor cells, the site of injection, the number of transplanted human T cells, the amount of bispecific antibody constructs to be administered, and the timelines, while still arriving at a meaningful and reproducible result. Preferably, the tumor growth

inhibition T/C [%] is ≤ 70 or ≤ 60, more preferably ≤ 50 or ≤ 40, even more preferably ≤ 30 or ≤ 20 and most preferably ≤ 10 or ≤ 5 or even ≤ 2.5.

In one embodiment, the bispecific antibody constructs of the present invention exhibit high monomer yields under standard research scale conditions, *e.g.,* in a standard two-step purification process. Preferably the monomer yield of the antibody constructs according to the invention is ≥ 0.25 mg/L supernatant, more preferably ≥ 0.5 mg/L, even more preferably ≥ 1 mg/L, and most preferably ≥ 3 mg/L supernatant.

Likewise, the yield of the dimeric antibody construct isoforms and the monomer percentage (*i.e.*, monomer : (monomer+dimer)) of the antibody constructs can be determined. The productivity of monomeric and dimeric antibody constructs and the calculated monomer percentage can *e.g.* be obtained in the SEC purification step of culture supernatant from standardized research-scale production in roller bottles. In one embodiment, the monomer percentage of the antibody constructs is ≥ 80%, more preferably ≥ 85%, even more preferably ≥ 90%, and most preferably ≥ 95%.

In a further embodiment, the percentage of identity to human germline of the antibody constructs according to the invention is ≥ 70% or ≥ 75%, more preferably ≥ 80% or ≥ 85%, even more preferably ≥ 90%, and most preferably ≥ 95%. Identity to human antibody germline gene products is thought to be an important feature to reduce the risk of therapeutic proteins to elicit an immune response against the drug in the patient during treatment. Hwang & Foote ("Immunogenicity of engineered antibodies"; Methods 36 (2005) 3-10) demonstrate that the reduction of non-human portions of drug antibody constructs leads to a decrease of risk to induce anti-drug antibodies in the patients during treatment. By comparing an exhaustive number of clinically evaluated antibody drugs and the respective immunogenicity data, the trend is shown that humanization of the V-regions of antibodies makes the protein less immunogenic (average 5.1 % of patients) than antibodies carrying unaltered non-human V regions (average 23.59 % of patients). A higher degree of identity to human sequences is hence desirable for V-region based protein therapeutics in the form of antibody constructs. For this purpose of determining the germline identity, the V-regions of VL can be aligned with the amino acid sequences of human germline V segments and J segments (http://vbase.mrc-cpe.cam.ac.uk/) using Vector NTI software and the amino acid sequence calculated by dividing the identical amino acid residues by the total number of amino acid residues of the VL in percent. The same can be for the VH segments (http://vbase.mrc-cpe.cam.ac.uk/) with the exception that the VH CDR3 may be excluded due to its high diversity and a lack of existing human germline VH CDR3 alignment partners.

Recombinant techniques can then be used to increase sequence identity to human antibody germline genes.

In one embodiment, the antibody constructs have a preferred plasma stability (ratio of EC50 with plasma to EC50 w/o plasma) of ≤ 5, more preferably ≤ 4, even more preferably ≤ 3, and most preferably ≤ 2. The plasma stability of an antibody construct can be tested by incubation of the construct in human plasma at 37°C for 24 hours followed by EC50 determination in a 51chromium release cytotoxicity assay. The effector cells in the cytotoxicity assay can be stimulated enriched human CD8 positive T cells. Target cells can e.g. be CHO cells transfected with the target antigen, *e.g.*, CDH19. The effector to target cell (E:T) ratio can be chosen as 10:1. The human plasma pool used for this purpose is derived from the blood of healthy donors collected by EDTA coated syringes. Cellular components are removed by centrifugation and the upper plasma phase is collected and subsequently pooled. As control, antibody constructs are diluted immediately prior to the cytotoxicity assay in RPMI-1640 medium. The plasma stability is calculated as ratio of EC50 (after plasma incubation) to EC50 (control).

It is preferred that the monomer to dimer conversion of antibody constructs of the invention is low. The conversion can be measured under different conditions and analyzed by high performance size exclusion chromatography. For example, incubation of the monomeric isoforms of the antibody constructs can be carried out for 7 days at 37°C and concentrations of e.g. 100 µg/ml or 250 µg/ml in an incubator. Under these conditions, it is preferred that the antibody constructs of the invention show a dimer percentage that is ≤5%, more preferably ≤4%, even more preferably ≤3%, even more preferably ≤2.5%, even more preferably ≤2%, even more preferably ≤1.5%, and most preferably ≤1%.

It is also preferred that the bispecific antibody constructs of the present invention present with very low dimer conversion after a number of freeze/thaw cycles. For example, the antibody construct monomer is adjusted to a concentration of 250 µg/ml *e.g.* in SEC running buffer and subjected to three freeze/thaw cycles (freezing at -80°C for 30 min followed by thawing for 30 min at room temperature), followed by high performance SEC to determine the percentage of initially monomeric antibody construct, which had been converted into dimeric antibody construct. Preferably the dimer percentages of the bispecific antibody constructs are ≤5%, more preferably ≤4%, even more preferably ≤3%, even more preferably ≤2.5%, even more preferably ≤2%, even more preferably ≤1.5%, and most preferably ≤1%, for example after three freeze/thaw cycles.

The bispecific antibody constructs of the present invention preferably show a favorable thermostability with melting temperatures above 60°C. This parameter can be determined as follows: Temperature melting curves are determined by Differential Scanning Calorimetry (DSC) to determine intrinsic biophysical protein stabilities of the antibody constructs. These experiments are performed using a MicroCal LLC (Northampton, MA, U.S.A) VP-DSC device. The energy uptake of a sample containing an antibody construct is recorded from 20°C to 90°C compared to a sample containing only the formulation buffer. The antibody constructs are adjusted to a final concentration of 250 µg/ml *e.g.* in SEC running buffer. For recording of the respective melting curve, the overall sample temperature is increased stepwise. At each temperature T energy uptake of the sample and the formulation buffer reference is recorded. The difference in energy uptake Cp (kcal/mole/°C) of the sample minus the reference is plotted against the respective temperature. The melting temperature is defined as the temperature at the first maximum of energy uptake.

In a further embodiment the antibody construct according to the invention is stable at acidic pH. The more tolerant the antibody construct behaves at unphysiologic pH such as pH 5.5 (a pH which is required to run e.g. a cation exchange chromatography), the higher is the recovery of the antibody construct eluted from an ion exchange column relative to the total amount of loaded protein. Recovery of the antibody construct from an ion (*e.g.*, cation) exchange column at pH 5.5 is preferably ≥ 30%, more preferably ≥ 40%, more preferably ≥ 50%, even more preferably ≥ 60%, even more preferably ≥ 70%, even more preferably ≥ 80%, and most preferably ≥ 90%.

It is furthermore envisaged that the bispecific antibody constructs of the present invention exhibit therapeutic efficacy or anti-tumor activity. This can *e.g.* be assessed in a study as disclosed in the following example of an advanced stage human tumor xenograft model.

In an alternative embodiment the invention provides a polynucleotide encoding an antibody construct of the invention.

A polynucleotide is a biopolymer composed of 13 or more nucleotide monomers covalently bonded in a chain. DNA (such as cDNA) and RNA (such as mRNA) are examples of polynucleotides with distinct biological function. Nucleotides are organic molecules that serve as the monomers or subunits of nucleic acid molecules like DNA or RNA. The nucleic acid molecule or polynucleotide can be double stranded and single stranded, linear and circular. It is preferably comprised in a vector which is preferably comprised in a host cell. Said host cell is, *e.g.* after transformation or transfection with the vector or the polynucleotide of the

invention, capable of expressing the antibody construct. For that purpose the polynucleotide or nucleic acid molecule is operatively linked with control sequences.

The genetic code is the set of rules by which information encoded within genetic material (nucleic acids) is translated into proteins. Biological decoding in living cells is accomplished by the ribosome which links amino acids in an order specified by mRNA, using tRNA molecules to carry amino acids and to read the mRNA three nucleotides at a time. The code defines how sequences of these nucleotide triplets, called codons, specify which amino acid will be added next during protein synthesis. With some exceptions, a three-nucleotide codon in a nucleic acid sequence specifies a single amino acid. Because the vast majority of genes are encoded with exactly the same code, this particular code is often referred to as the canonical or standard genetic code. While the genetic code determines the protein sequence for a given coding region, other genomic regions can influence when and where these proteins are produced.

In a further alternative embodiment the invention provides a vector comprising a polynucleotide of the invention.

A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell. The term “vector” encompasses – but is not restricted to – plasmids, viruses, cosmids and artificial chromosomes. In general, engineered vectors comprise an origin of replication, a multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the “backbone” of the vector. Modern vectors may encompass additional features besides the transgene insert and a backbone: promoter, genetic marker, antibiotic resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

A nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably

linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

“Transfection” is the process of deliberately introducing nucleic acid molecules or polynucleotides (including vectors) into target cells. The term is mostly used for non-viral methods in eukaryotic cells. Transduction is often used to describe virus-mediated transfer of nucleic acid molecules or polynucleotides. Transfection of animal cells typically involves opening transient pores or "holes" in the cell membrane, to allow the uptake of material. Transfection can be carried out using calcium phosphate, by electroporation, by cell squeezing or by mixing a cationic lipid with the material to produce liposomes, which fuse with the cell membrane and deposit their cargo inside.

The term “transformation” is used to describe non-viral transfer of nucleic acid molecules or polynucleotides (including vectors) into bacteria, and also into non-animal eukaryotic cells, including plant cells. Transformation is hence the genetic alteration of a bacterial or non-animal eukaryotic cell resulting from the direct uptake through the cell membrane(s) from its surroundings and subsequent incorporation of exogenous genetic material (nucleic acid molecules). Transformation can be effected by artificial means. For transformation to happen, cells or bacteria must be in a state of competence, which might occur as a time-limited response to environmental conditions such as starvation and cell density.

Moreover, in an additional alternative embodiment, the invention provides a host cell transformed or transfected with the polynucleotide of the invention or with the vector of the invention.

As used herein, the terms “host cell” or “recipient cell” are intended to include any individual cell or cell culture that can be or has/have been recipients of vectors, exogenous nucleic acid molecules, and polynucleotides encoding the antibody construct of the present invention; and/or recipients of the antibody construct itself. The introduction of the respective material into the cell is carried out by way of transformation, transfection and the like. The term “host

cell" is also intended to include progeny or potential progeny of a single cell. Because certain modifications may occur in succeeding generations due to either natural, accidental, or deliberate mutation or due to environmental influences, such progeny may not, in fact, be completely identical (in morphology or in genomic or total DNA complement) to the parent cell, but is still included within the scope of the term as used herein. Suitable host cells include prokaryotic or eukaryotic cells, and also include but are not limited to bacteria, yeast cells, fungi cells, plant cells, and animal cells such as insect cells and mammalian cells, e.g., murine, rat, macaque or human.

The antibody construct of the invention can be produced in bacteria. After expression, the antibody construct of the invention is isolated from the *E. coli* cell paste in a soluble fraction and can be purified through, e.g., affinity chromatography and/or size exclusion. Final purification can be carried out similar to the process for purifying antibody expressed *e.g.*, in CHO cells.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the antibody construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, Kluyveromyces hosts such as *K. lactis, K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickeramii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilarum* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; yarrowia (EP 402 226); *Pichia pastoris* (EP 183 070); Candida; *Trichoderma reesia* (EP 244 234); *Neurospora crassa*; Schwanniomyces such as *Schwanniomyces occidentalis*; and filamentous fungi such as Neurospora, Penicillium, Tolypocladium, and Aspergillus hosts such as *A. nidulans* and *A. niger*.

Suitable host cells for the expression of glycosylated antibody construct of the invention are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, *e.g.*, the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, Arabidopsis and tobacco can also be used as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See *e.g.* Hiatt *et al.*, Nature (1989) 342: 76-78, Owen *et al.* (1992) Bio/Technology 10: 790-794, Artsaenko *et al.* (1995) The Plant J 8: 745-750, and Fecker *et al.* (1996) Plant Mol Biol 32: 979-986.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al. , J. Gen Virol. 36 : 59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub *et al.*, Proc. Natl. Acad. Sci. USA 77: 4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23: 243-251 (1980)); monkey kidney cells (CVI ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,1413 8065); mouse mammary tumor (MMT 060562, ATCC CCL5 1); TRI cells (Mather *et al.*, Annals N. Y Acad. Sci. (1982) 383: 44-68); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

The invention also provides a process for the production of a antibody construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and recovering the produced antibody construct from the culture.

As used herein, the term "culturing" refers to the *in vitro* maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium. The term "expression" includes any step involved in the production of an antibody construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

When using recombinant techniques, the antibody construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10: 163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of

sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody construct of the invention prepared from the host cells can be recovered or purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™, chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromato-focusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered. Where the antibody construct of the invention comprises a CH3 domain, the Bakerbond ABX resin (J.T. Baker, Phillipsburg, NJ) is useful for purification.

Affinity chromatography is a preferred purification technique. The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly (styrenedivinyl) benzene allow for faster flow rates and shorter processing times than can be achieved with agarose.

Furthermore, the invention provides a pharmaceutical composition comprising an antibody construct of the invention, or an antibody construct produced according to the process of the invention.

According to one embodiment of the invention the antibody construct of the invention, or produced according to the process of the invention is used in the prevention, treatment or amelioration of a disease selected from a proliferative disease, a tumorous disease, a viral disease or an immunological disorder.

The formulations described herein are useful as pharmaceutical compositions in the treatment, amelioration and/or prevention of the pathological medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Treatment includes the application or administration of the formulation to the body, an isolated tissue, or cell from a patient who

has a disease/disorder, a symptom of a disease/disorder, or a predisposition toward a disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disease, the symptom of the disease, or the predisposition toward the disease.

The term "amelioration" as used herein refers to any improvement of the disease state of a patient, by the administration of an antibody construct according to the invention to a subject in need thereof. Such an improvement may also be seen as a slowing or stopping of the progression patient's disease. The term "prevention" as used herein means the avoidance of the occurrence or re-occurrence of a patient having a disease as specified herein, by the administration of an antibody construct according to the invention to a subject in need thereof.

The term "disease" refers to any condition that would benefit from treatment with the antibody construct or the pharmaceutic composition described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the mammal to the disease in question.

In one embodiment the invention provides a method for the treatment or amelioration of a proliferative disease, a tumorous disease, a viral disease or an immunological disorder, comprising the step of administering to a subject in need thereof the antibody construct of the invention, or produced according to the process of the invention.

The terms "subject in need" or those "in need of treatment" includes those already with the disorder, as well as those in which the disorder is to be prevented. The subject in need or "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

The antibody construct of the invention will generally be designed for specific routes and methods of administration, for specific dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. The materials of the composition are preferably formulated in concentrations that are acceptable for the site of administration.

Formulations and compositions thus may be designed in accordance with the invention for delivery by any suitable route of administration. In the context of the present invention, the routes of administration include, but are not limited to

- topical routes (such as epicutaneous, inhalational, nasal, opthalmic, auricular / aural, vaginal, mucosal);
- enteral routes (such as oral, gastrointestinal, sublingual, sublabial, buccal, rectal); and
- parenteral routes (such as intravenous, intraarterial, intraosseous, intramuscular, intracerebral, intracerebroventricular, epidural, intrathecal, subcutaneous, intraperitoneal, extra-amniotic, intraarticular, intracardiac, intradermal, intralesional, intrauterine, intravesical, intravitreal, transdermal, intranasal, transmucosal, intrasynovial, intraluminal).

The pharmaceutical compositions and the antibody construct of this invention are particularly useful for parenteral administration, e.g., subcutaneous or intravenous delivery, for example by injection such as bolus injection, or by infusion such as continuous infusion. Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163.

In particular, the present invention provides for an uninterrupted administration of the suitable composition. As a non-limiting example, uninterrupted or substantially uninterrupted, i.e. continuous administration may be realized by a small pump system worn by the patient for metering the influx of therapeutic agent into the body of the patient. The pharmaceutical composition comprising the antibody construct of the invention can be administered by using said pump systems. Such pump systems are generally known in the art, and commonly rely on periodic exchange of cartridges containing the therapeutic agent to be infused. When exchanging the cartridge in such a pump system, a temporary interruption of the otherwise uninterrupted flow of therapeutic agent into the body of the patient may ensue. In such a case, the phase of administration prior to cartridge replacement and the phase of administration following cartridge replacement would still be considered within the meaning of the pharmaceutical means and methods of the invention together make up one "uninterrupted administration" of such therapeutic agent.

The continuous or uninterrupted administration of the antibody constructs of the invention may be intravenous or subcutaneous by way of a fluid delivery device or small pump system including a fluid driving mechanism for driving fluid out of a reservoir and an actuating mechanism for actuating the driving mechanism. Pump systems for subcutaneous administration may include a needle or a cannula for penetrating the skin of a patient and

delivering the suitable composition into the patient's body. Said pump systems may be directly fixed or attached to the skin of the patient independently of a vein, artery or blood vessel, thereby allowing a direct contact between the pump system and the skin of the patient. The pump system can be attached to the skin of the patient for 24 hours up to several days. The pump system may be of small size with a reservoir for small volumes. As a non-limiting example, the volume of the reservoir for the suitable pharmaceutical composition to be administered can be between 0.1 and 50 ml.

The continuous administration may also be transdermal by way of a patch worn on the skin and replaced at intervals. One of skill in the art is aware of patch systems for drug delivery suitable for this purpose. It is of note that transdermal administration is especially amenable to uninterrupted administration, as exchange of a first exhausted patch can advantageously be accomplished simultaneously with the placement of a new, second patch, for example on the surface of the skin immediately adjacent to the first exhausted patch and immediately prior to removal of the first exhausted patch. Issues of flow interruption or power cell failure do not arise.

If the pharmaceutical composition has been lyophilized, the lyophilized material is first reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline, phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization.

The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. by dose escalating studies by administration of increasing doses of the antibody construct of the invention exhibiting cross-species specificity described herein to non-chimpanzee primates, for instance macaques. As set forth above, the antibody construct of the invention exhibiting cross-species specificity described herein can be advantageously used in identical form in preclinical testing in non-chimpanzee primates and as drug in humans. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is

defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts or doses effective for this use will depend on the condition to be treated (the indication), the delivered antibody construct, the therapeutic context and objectives, the severity of the disease, prior therapy, the patient's clinical history and response to the therapeutic agent, the route of administration, the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient, and the general state of the patient's own immune system. The proper dose can be adjusted according to the judgment of the attending physician such that it can be administered to the patient once or over a series of administrations, and in order to obtain the optimal therapeutic effect.

A typical dosage may range from about 0.1 µg/kg to up to about 30 mg/kg or more, depending on the factors mentioned above. In specific embodiments, the dosage may range from 1.0 µg/kg up to about 20 mg/kg, optionally from 10 µg/kg up to about 10 mg/kg or from 100 µg/kg up to about 5 mg/kg.

A therapeutic effective amount of an antibody construct of the invention preferably results in a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease affliction. For treating target cell antigen-expressing tumors, a therapeutically effective amount of the antibody construct of the invention, e.g. an anti-target cell antigen/anti-CD3 antibody construct, preferably inhibits cell growth or tumor growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may be evaluated in an animal model predictive of efficacy in human tumors.

The pharmaceutical composition can be administered as a sole therapeutic or in combination with additional therapies such as anti-cancer therapies as needed, e.g. other proteinaceous and non-proteinaceous drugs. These drugs may be administered simultaneously with the composition comprising the antibody construct of the invention as defined herein or separately before or after administration of said antibody construct in timely defined intervals and doses.

The term “effective and non-toxic dose” as used herein refers to a tolerable dose of an inventive antibody construct which is high enough to cause depletion of pathologic cells, tumor elimination, tumor shrinkage or stabilization of disease without or essentially without major toxic effects. Such effective and non-toxic doses may be determined e.g. by dose

escalation studies described in the art and should be below the dose inducing severe adverse side events (dose limiting toxicity, DLT).

The term "toxicity" as used herein refers to the toxic effects of a drug manifested in adverse events or severe adverse events. These side events might refer to a lack of tolerability of the drug in general and/or a lack of local tolerance after administration. Toxicity could also include teratogenic or carcinogenic effects caused by the drug.

The term "safety", "*in vivo* safety" or "tolerability" as used herein defines the administration of a drug without inducing severe adverse events directly after administration (local tolerance) and during a longer period of application of the drug. "Safety", "*in vivo* safety" or "tolerability" can be evaluated e.g. at regular intervals during the treatment and follow-up period. Measurements include clinical evaluation, e.g. organ manifestations, and screening of laboratory abnormalities. Clinical evaluation may be carried out and deviations to normal findings recorded/coded according to NCI-CTC and/or MedDRA standards. Organ manifestations may include criteria such as allergy/immunology, blood/bone marrow, cardiac arrhythmia, coagulation and the like, as set forth e.g. in the Common Terminology Criteria for adverse events v3.0 (CTCAE). Laboratory parameters which may be tested include for instance hematology, clinical chemistry, coagulation profile and urine analysis and examination of other body fluids such as serum, plasma, lymphoid or spinal fluid, liquor and the like. Safety can thus be assessed e.g. by physical examination, imaging techniques (i.e. ultrasound, x-ray, CT scans, Magnetic Resonance Imaging (MRI), other measures with technical devices (i.e. electrocardiogram), vital signs, by measuring laboratory parameters and recording adverse events. For example, adverse events in non-chimpanzee primates in the uses and methods according to the invention may be examined by histopathological and/or histochemical methods.

The above terms are also referred to *e.g.* in the Preclinical safety evaluation of biotechnology-derived pharmaceuticals S6; ICH Harmonised Tripartite Guideline; ICH Steering Committee meeting on July 16, 1997.

Finally, the invention provides a kit comprising an antibody construct of the invention or produced according to the process of the invention, a vector of the invention and/or a host cell of the invention.

In the context of the present invention, the term "kit" means two or more components – one of which corresponding to the antibody construct, the pharmaceutical composition, the vector

or the host cell of the invention – packaged together in a container, recipient or otherwise. A kit can hence be described as a set of products and/or utensils that are sufficient to achieve a certain goal, which can be marketed as a single unit.

The kit may comprise one or more recipients (such as vials, ampoules, containers, syringes, bottles, bags) of any appropriate shape, size and material (preferably waterproof, *e.g.* plastic or glass) containing the antibody construct or the pharmaceutical composition of the present invention in an appropriate dosage for administration (see above). The kit may additionally contain directions for use (*e.g.* in the form of a leaflet or instruction manual), means for administering the antibody construct of the present invention such as a syringe, pump, infuser or the like, means for reconstituting the antibody construct of the invention and/or means for diluting the antibody construct of the invention.

The invention also provides kits for a single-dose administration unit. The kit of the invention may also contain a first recipient comprising a dried / lyophilized antibody construct and a second recipient comprising an aqueous formulation. In certain embodiments of this invention, kits containing single-chambered and multi-chambered pre-filled syringes (*e.g.*, liquid syringes and lyosyringes) are provided.

Brief description of the drawings

Figure 1:
T activation of BiTE® antibody constructs in the absence of an albumin fusion at the C-terminus of the molecule. Expression of CD25 and CD69 on $CD4^+$ (panel A and C) and $CD8^+$ (panel B and D) T cells was determined by flow cytometry.

Figure 2:
T activation of BiTE® antibody constructs in the presence (lower panel) of an albumin fusion at the C-terminus of the molecule. Expression of CD25 and CD69 on $CD4^+$ (panel A and C) and $CD8^+$ (panel B and D) T cells was determined by flow cytometry.

Figure 3:
FACS analysis of CDH19/CD3 bispecific antibodies on indicated cell lines: 1) CHO cells stably transfected with human CDH19, 2) human CD3 positive human T cell line HBP-ALL, 3) CHO cells stably transfected with cynomolgus CDH19, 4) macaque T cell line 4119 LnPx, 5) human melanoma cell line CHL-1 expressing native human CDH19, 6) untransfected CHO

cells. Negative controls [1) to 6)]: detection antibodies without prior CDH19/CD3 bispecific antibody.

Figure 4:

Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in a 48-hour FACS-based cytotoxicity assay. Effector cells: CD3-expressing macaque T cell line 4119LnPx. Target cells: cynomolgus CDH19-transfected CHO cells. Effector to target cell (E:T)-ratio: 10:1. The figure shows the results for CDH19 2G6 302xI2C HALB and for a negative control.

Figure 5:

Pharmacokinetics of BiTE® antibody constructs

Four molecules named 1) 2G6-156; 2) 2G6-LFcBy; 3) 2G6-LFcBy-156; 4) 2G6-D3HSA were tested in the cynomolgus monkey in the context of a pharmacokinetic (PK) study. The figure shows the results in connection with Example 4.

Figure 6:

Absence of "unspecific" T cell activation for bispecific single chain antibody constructs comprising a human/chimpanzee specific CD3 binding domain using AMG 110.

Figure 7:

T activation in the by bispecific antibody constructs binding to different cell surface target structures in absence and presence of an albumin fusion at the C-terminus of the molecule. Expression of CD25 and CD69 on T cells was determined by flow cytometry.

7a FACS-based activation assay (48 h) with human PBMC (donors #669, #729, #736) and Influenza specific BITE® antibody constructs; BiTE® start concentration = 1 µg/mL (1:10 dilution);

7b FACS-based activation assay (48 h) with human PBMC (donors #453, #458, #551) and DLL3 specific BITE® antibody constructs; BiTE® start concentration = 1 µg/mL (1:10 dilution);

7c Human PBMC were cultured in the absence of target cells with Mesothelin BiTE® or the HSA-variant of the Mesothelin BiTE® antibody construct for 48 h. The expression of the activation marker CD69 on T cells was determined by immunostaining and flow cytometry;

Figure 8:

T activation in the by bispecific antibody constructs binding to different cell surface target structures in absence and presence of target cells. Expression of CD25 and CD69 on T cells was determined by flow cytometry.

8a: Isolated T cells from healthy human donors were co-cultured in the presence or absence of target cells (Raji) (E:T cell ratio 10:1) and Full length HSA-CD19 BITE® for 48 h. The expression of the activation markers CD69 or CD25 on T cells was determined by immunostaining and flow cytometry;
8b: Isolated T cells from healthy human donors were co-cultured in the presence or absence of target cells (Raji) (E:T cell ratio 10:1) and Full length HSA-CD20 BITE® for 48 h. The expression of the activation markers CD69 or CD25 on T cells was determined by immunostaining and flow cytometry;
8c: Human PBMC were co-cultured in the presence or absence of target cells (U251vIII) (E:T cell ratio 10:1) and EGFRvIII-BiTE® or the HSA-variant of the EGFRvIII-BITE® for 48 h. The expression of the activation markers CD69 on T cells was determined by immunostaining and flow cytometry.

Figure 9:
Tumor-accumulation of CDH19-HALB BiTE® antibody construct.

Figure 10:
Mean PK profiles of six BiTE®-HALB fusion proteins after single dose administration in cynomolgus monkeys.

Figure 11:
Pharmacokinetic profiles of CD33-1 x I2C-HALB and CD33-2 x I2C6-HALB constructs administered in repeated dose schedules at different doses and different consecutive schedules. For reasons of comparability, described repeated dose profiles are dose-normalized to 120 µg/kg. The PK profile of the reference compound 8 administered at 30 µg/kg/day, cIV for 7 days, is shown in orange.

Figure 12:
Pharmacokinetic profiles of modified HALB HLE modalities based on the EGFRvIII-BiTE antibody construct. Seven different EGFRvIII-HLE BiTE antibody constructs generated by mutations within the HALB wild-type sequence were tested in the cynomolgus monkey in the context of a pharmacokinetic (PK) study. Differences in the hALB variants are based on different, increased FcRn-binding affinities.

It should be understood that the inventions herein are not limited to particular methodology, protocols, or reagents, as such can vary. The discussion and examples provided herein are

presented for the purpose of describing particular embodiments only and are not intended to limit the scope of the present invention, which is defined solely by the claims.

All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supersede any such material.

Examples:

The following examples are provided for the purpose of illustrating specific embodiments or features of the present invention. These examples should not be construed as to limit the scope of this invention. The examples are included for purposes of illustration, and the present invention is limited only by the claims.

Example 1:

T cell activation of BiTE® molecules in the presence and the absence of an albumin fusion at the C-terminus of the molecule

- BiTE® constructs (serial dilutions: 0.1 pg/mL – 1 µg/mL):
    1. CDH19 2G6 302 x I2C -H6; 258.7 µg/mL (SoW0416; Aliquot Lot: 140514_APu01); Untagged BiTE®
    2. CDH19 2G6 302 x I2C -HALB -DY -H6; 260 µg/mL (SoW0445; Aliquot Lot: 140514_APu03); Half-life extended full length
- Human PBMC effector cells (4 donors; #875, #889, #891, #895)
- 48 h incubation time
- Determination of CD25 and CD69 expression on CD4+ and CD8+ T cells with flow cytometer and antigen-specific conjugates mAb

In a similar setting the capacity of different BiTE® antibody constructs to activate T cell was analyzed. Those BiTE® antibody constructs do not comprise the CD3 specific binding domain of bispecific single chain antibody constructs of the invention but merely a human/chimpanzee specific CD3 binding domain. The corresponding BiTE® antibody construct is AMG 110, which is an EpCAM and CD3 specific BiTE® antibody construct. PBMC were incubated with increasing AMG 110 concentrations for 24 or 48hrs, T cell

activation was determined by staining for CD25 or CD69 surface expression by by flow cytometry on a BD FACSCanto II instrument. The result of this analysis is shown in Figure 6. Moreover, the generic modality of eliminating the target independent T cell activation in the defined extreme high BiTE® antibody construct concentrations was demonstrated for a greater number of additional bispecific antibody constructs with specificity for different target structures as shown in figure 7 (7a: Influenza A antigen; 7b: DLL3 ; 7c: mesothelin (MSLN)).

Example 2:

Bispecific binding and interspecies cross-reactivity:

For confirmation of binding to human and cyno CDH19 and to human and macaque CD3, bispecific antibodies were tested by flow cytometry using indicated cell lines. CHO cells transfected with human CDH19, with cyno CDH19, the human melanoma cell line CHL-1 expressing native human CDH19, CD3-expressing human T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) and the CD3-expressing macaque T cell line 4119LnPx (Knappe A, et al., Blood, 2000, 95, 3256-3261) were used as antigen positive cell lines. Moreover, untransfected CHO cells were used as negative control.

For flow cytometry 200,000 cells of the respective cell lines were incubated for 30 min on ice with 50 µl of purified bispecific antibody at a concentration of 5 µg/ml. The cells were washed twice in PBS/10% FCS and binding of the constructs was detected with a murine anti-His antibody (AbD Serotec; diluted 1:1000 in 50 µl PBS/10% FCS). After washing, bound anti-His antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS/10% FCS. Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

The CDH19/CD3 bispecific antibodies stained CHO cells transfected with human CDH19, cyno CDH19, the human CDH19-expressing melanoma cell lines CHL-1 as well as human and macaque T cells. Moreover, there was no staining of untransfected CHO cells (see Figure 3).

Example 3:

Cytotoxic activity

Target cell labeling

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye $DiOC_{18}$ (DiO) (Molecular Probes, #V22886) was used to label cynomolgus CDH19 positive CHO cells - as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10^6 cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 µL/10^6 cells). After incubation for 3 min at 37°C, cells were washed

twice in complete RPMI medium and the cell number adjusted to 1.25 x 10^5 cells/mL. The vitality of cells was determined using 0.5 % (v/v) isotonic EosinG solution (Roth, #45380).

Flow cytometry based analysis

This assay was designed to quantify the lysis of cynomolgus CDH19-transfected CHO cells in the presence of serial dilutions of CDH19 bispecific antibodies.

Equal volumes of DiO-labeled target cells and effector cells (i.e. CD3-expressing macaque T cell line 4119LnPx) were mixed, resulting in an E:T cell ratio of 10:1. 160 µL of this suspension were transferred to each well of a 96-well plate. 40 µL of serial dilutions of the CDH19 bispecific antibodies and a negative control bispecific (an CD3-based bispecific antibody recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control were added. The bispecific antibody-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO_2 humidified incubator. Then cells were transferred to a new 96-well plate and loss of target cell membrane integrity was monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

Target cells were identified as DiO-positive cells. PI-negative target cells were classified as living target cells. Percentage of cytotoxicity was calculated according to the following formula:

$$\text{Cytotoxicity}[\%] = \frac{n_{\text{dead target cells}}}{n_{\text{target cells}}} \times 100$$

n = number of events

Using GraphPad Prism 6 software (Graph Pad Software, San Diego), the percentage of cytotoxicity was plotted against the corresponding bispecific antibody concentrations. Dose response curves were analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC_{50} values were calculated.

The cytotox results using the above described system for CDH19 2G6 302xI2C HALB and for a negative control are shown in figure 4

Example 4

Pharmacokinetics of BiTE® antibody constructs

Four molecules named 1) 2G6-156; 2) 2G6-LFcBy; 3) 2G6-LFcBy-156; 4) 2G6-D3HSA were tested in the cynomolgus monkey in the context of a pharmacokinetic (PK) study. In this PK study a dose of 6 µg/kg was administered as a single intravenous bolus injection. For each of

the above compounds, a group of 2 animals were used. Blood samples were collected and serum was prepared for determination of serum concentration for each drug in both animals. Serum drug levels were measured using an immunoassay. The serum concentration-time data were used to determine PK parameters. Blood sample was collected at the following time points: predose, 0.05, 0.25, 0.5, 1, 4, 8, 24, 48, 72, 168, 240, and 336 hours post dose. The PK parameters were determined using standard non-compartmental analysis (NCA) methods.

For all drugs tested, serum levels were quantifiable for the vast majority of time points in all animals after drug administration. The PK profiles showed a biphasic exponential decline for all drugs tested. Using NCA methods, the following parameters were estimated: AUC_{inf} (Area under the serum concentration-time curve), V_{ss} (volume of distribution at steady state), CL (systemic clearance), MRT (mean residence time), and Terminal $t_{1/2}$ (half-life estimated from terminal phase). The PK parameters (mean of n=2) of each compound tested are summarized below:

The AUC_{inf} was 568 hr*ng/mL, 366 hr*ng/mL, 1796 hr*ng/mL, and 1383 hr*ng/mL respectively for compounds 1, 2, 3 and 4. The V_{ss} was 446 mL/kg, 594 mL/kg, 193 mL/kg, and 80.7 mL/kg respectively for compounds 1, 2, 3 and 4. Systemic clearance was 11.3 mL/hr/kg, 16.1 mL/hr/kg, 4.3 mL/hr/kg, and 4.9 mL/hr/kg respectively for compounds 1, 2, 3 and 4. The MRT value for compounds 1, 2, 3 and 4 were 42.3 hr, 39.8 hr, 48.7 hr, and 18.1 hr respectively and that for terminal half-life was 44.3 hr, 31.2 hr, 40.3 hr, and 13.5 hr respectively for compounds 1, 2, 3 and 4.

The terminal half- life and MRT of each of compounds 1, 2 and 3 were much higher (> 2-folds) than those for compound 4. Compounds 1, 2 and 3 present a longer half-life version of BiTE® antibody constructs.

Results see figure 5.

Example 5

BiTE® induced CD69 or CD25 Expression on T Cells in Presence and Absence of Target Cells

Isolated T cells from healthy human donors were co-cultured in the presence or absence of target cells

For CD19/CD3 and CD20/CD3 bispecific antibody constructs Raji cells were used as target cells. An E:T cell ratio of 10:1 was used and CD19-HALB-BITE (Figure 8a) and CD20-HALB-BiTE (Figure 8b) were incubated for 48 h. The expression of the activation markers CD69 or CD25 on T cells was determined by immunostaining and flow cytometry and antigen-specific conjugates mAb.

For EGFRvIII/CD3 bispecific antibody constructs U251vIII cells were used as target cells. At an E:T of 10:1 EGFRvIII-BiTE or the HSA-variant of the EGFRvIII-BITE were incubated for 48 h. The expression of the activation markers CD69 on T cells was determined by immunostaining and flow cytometry (Figure 8c).

Example 6

Tumor-accumulation of CDH19-HALB BiTE

CDH19-HALB BiTE, labeled with CW800 (nearinfrared dye), injected i.v. into the lateral tail vein of tumor-bearing mice (CDH19-positive tumor), in vivo analysis using „In Vivo Xtreme Imager" (Bruker) at the indicated time post injection (Figure 9).

Example 7

Pharmacokinetics of BiTE® antibody constructs after single administration

Different target binding BiTE® antibodies were fused to a single wild type human Albumin (HALB) moiety and were tested in the cynomolgus monkey in the context of pharmacokinetic (PK) studies. The pharmacokinetics of six BiTE®-HALB antibodies are shown exemplarily. The corresponding nomenclature of these molecules is briefly summarized in Table 2, below.

Table 2: Compound nomenclature of five single dosed BiTE®-HALB antibodies

compound synonym	test compound name
Compound 1	MS-3 x I2C6-HALB
Compound 2	MS-4 x I2C6-HALB
Compound 3	MS-5 x I2C6-HALB
Compound 4	CD33-1 x I2C6-HALB
Compound 5	CDH19cc x I2C6-HALB
Compound 6	CDH19 x I2C6-HALB

The BiTE®-HALB antibodies were administered as intravenous short (30 min) infusions at 12 µg/kg (compounds 1-3 and 5) and 15 µg/kg (compounds 4 and 6), respectively. For each of the above named compounds a group of three animals was used. Blood samples were collected and serum was prepared for determination of serum concentrations. Serum BiTE® antibody construct levels were measured using an immunoassay. The assay is performed by capturing the BiTE® via its target moiety, while an antibody directed against the CD3-binding part of the construct was used for detection. The serum concentration-time profiles were used to determine PK parameters. Blood sampling time points are listed in Table 3 below.

Table 3 Blood sampling time points during the PK study

blood sampling time points cmpd. 1-3 [h]	**blood sampling time points cmpd. 4-5 [h]**	**blood sampling time points cmpd. 6 [h]**
0	0	0
0.05	0.08	0.08
0.25	0.25	0.25
0.5	1	1
1	4	2
4	8	4
8	16	8
24	24	24
48	48	48
72	72	72
168	120	96
240	168	168
	240	240

The pharmacokinetic parameters were determined using standard non-compartmental analysis (NCA) methods.

For all tested proteins serum levels were quantifiable for all time points in all animals after BiTE® antibody construct administration. The PK profiles describe a biphasic, exponential decline after each of the single test item administrations (Figure 10).

Using non compartmental analysis, the following PK parameters were estimated: AUCinf (Area under the serum concentration- time curve), Vss (volume of distribution at steady state), CL (systemic clearance) and terminal t1/2 (terminal half-life).

The PK parameter as mean of n=3 for each tested compound are summarized in Table 4 below.

Table 4: Pharmacokinetic parameters after single dose administration of six various BiTE®-HALB proteins in cynomolgus monkeys.

test item	terminal t1/2 [h]	AUCinf [h*ng/mL]	Cl [mL/h/kg]	Vss [mL/kg]
MS-3 x I2C6-HALB	75	11419	1.1	66
MS-4 x I2C6-HALB	77	11593	1.0	65
MS-5 x I2C6-HALB	70	10262	1.2	64
CD33-1 x I2C6-HALB	48	4498	3.3	161
CDH19cc x I2C6-HALB	53	2226	6.7	303

test item	terminal t1/2 [h]	AUCinf [h*ng/mL]	Cl [mL/h/kg]	Vss [mL/kg]
CDH19 x I2C6-HALB	52	3199	3.8	349

The AUCinf for the different BiTE®-HALB variants ranged between 2226 h*ng/mL and 11593 h*ng/mL, depending on the BiTE® target context. All analyzed HALB fusions achieved terminal half-lives of at least 48 hours after single low dose administration at 12 and 15 µg/kg. Systemic clearance values were 1.1 mL/h/kg, 1.0 mL/h/kg, 1.2 mL/h/kg, 3.3 mL/h/kg, 6.7 mL/h/kg and 3.8 mL/h/kg respectively for compounds 1-6. The corresponding volume of distribution was 66 mL/kg, 65 mL/kg, 64 mL/kg, 161 mL/kg, 303 mL/kg and 349 mL/kg, respectively.

The differences in pharmacokinetic behavior of the various BiTE®-HALB antibodies was clearly related to the different BiTE® moieties and their targets, respectively. The HALB-moiety of each of the analyzed was represented by the wild type human Albumin and was not changed between the constructs.

Example 8

Pharmacokinetics of BiTE® antibody constructs after repeated administration

Three molecules, CD33-1 x I2C6-HALB (compound 4) and CD33-2 x I2C6-HALB (compound 7) were tested in the cynomolgus monkey in the context of repeated dose pharmacokinetic (PK) studies. Each molecule represents a BiTE® moiety directed against one common target protein fused one copy of the wild type human serum albumin (HALB) moiety. Compound 8 represents a naked, non HALB-fused version of compound 7 and is named CD33-2 x I2C6

The compounds were administered at different concentrations and in different dose schedules as described in Table 5 below.

Table 5: Administered doses with corresponding dose schedules analyzed in repeated dose set up of CD33-1 x I2C6 BiTE® variants

test item	Administered dose [µg/kg]	Dose schedule	Consecutive doses
CD33-1 x I2C6-HALB	60	Q2D (every other day)	4
	80		
	180		
CD33-2 x I2C6-HALB	120	Q3D (every third day)	2

test item	Administered dose [µg/kg]	Dose schedule	Consecutive doses
	120	Q5D (every fifth day)	
CD33-2 x I2C6	30 µg/kg/day	cIV	1

In these studies two or four consecutive doses of 60 µg/kg, 80 µg/kg, 180 µg/kg and 120 µg/kg were administered as intravenous short (30 min) infusions for compounds 4 and 7. Compound 8 was administered as continuous infusion (cIV) at 30 µg/kg/day for 7 days. For each of the above compounds a group of three animals were used. Blood samples were collected and serum was prepared for determination of serum concentrations. Serum BiTE® antibody construct levels were measured using an immunoassay. The assay is performed by capturing the BiTE® via its target moiety, while an antibody directed against the CD3-binding part of the construct was used for detection. The serum concentration-time profiles are described in Figure 11.

Repeated administration of BiTE®-HALB antibodies leads to accumulation of serum trough levels over dosing, whereas the maximum achieved serum concentrations (cmax) stays nearly stable over repeated dosing (Table 6**Fehler! Verweisquelle konnte nicht gefunden werden.**). For all described administered doses and dose schedules the exposures over 7 days of the CD33-1 x I2C6-HALB compounds were clearly increased compared to the exposure of a single cIV administered CD33-1 x I2C6 naked, BiTE® antibody construct within the same time frame (Figure 11).

Table 6: Maximum and trough serum concentrations of CD33 x I2C6 BiTE® antibody construct variations administered at different dose schedules and various doses

test item	Dose [µg/kg]	Dose schedule	C_{max} after dosing [ng/mL]			
			1st	2nd	3rd	4th
CD33-1 x I2C6-HALB	60	Q2D (every other day)	1447	1092	1230	1214
	80		1961	1701	1691	1333
	180		5053	3871	4163	2171
CD33-2 x I2C6-HALB	120	Q3D (every third day)	3631	2891	-	-
		Q5D (every fifth day)	3133	2630	-	-

test item	Dose [µg/kg]	Dose schedule	C_{trough} after dosing [ng/mL]			
			1st	2nd	3rd	4th
CD33-1 x I2C6-HALB	60	Q2D (every other day)	84	147	190	395
	80		132	229	231	412
	180		394	735	676	1052
CD33-2 x I2C6-HALB	120	Q3D (every third day)	243	380	-	-
		Q5D (every fifth day)	100	22	-	-

Every other day administration of compound 4 at different dose levels shows dose linear behavior with stable AUC/Dose values (Table 7Table) of the BiTE®-HALB antibody construct in a dose range of 60 µg/kg to 180 µg/kg.

Table 7: Exposure over dose of CD33-1 x I2C6-HALB BiTE® antibodies administered at 60, 80 and 180 µg/kg compared to canonical CD33-2 x I2C6 BiTE®

test item	Administered dose [µg/kg]	AUC_{0-168h}/Dose
CD33-1 x I2C6-HALB	60	0.341
	80	0.341
	180	0.416
CD33-2 x I2C6	30 µg/kg/day	0.027

The mean AUC/Dose of the CD33-1 x I2C6-HALB BiTE® antibody construct is 10-fold increased, compared to the AUC/Dose of the corresponding canonical BiTE® antibody construct.

Example 9

Pharmacokinetics of BiTE® antibody constructs with different albumin-based half-life extensions

Eight molecules were tested in the cynomolgus monkey in the context of a pharmacokinetic (PK) study. Each molecule represents a fusion of the same BiTE® protein to wild type or FcRn-affinity modified human serum albumin (HALB). The names of the test compounds are briefly summarized in Table 8, below.

Table 8 Compound nomenclature

compound synonym	test compound name
Compound 9	EvIII-1 x I2C6-HALB
Compound 10	EvIII-1 x I2C6-HALB098
Compound 11	EvIII-1 x I2C6-HALB114
Compound 12	EvIII-1 x I2C6-HALB131
Compound 13	EvIII-1 x I2C6-HALB133
Compound 14	EvIII-1 x I2C6-HALB135
Compound 15	EvIII-1 x I2C6-HALB253
Compound 16	EvIII-1 x I2C6-HALB254

In this study two consecutive doses of 80 µg/kg were administered as intravenous short (30 min) infusions. For each of the above compounds a group of three animals were used. Blood samples were collected and serum was prepared for determination of serum concentrations. Serum BiTE® antibody levels were measured using an immunoassay. The assay is performed by capturing the BiTE® via its target moiety, while an antibody directed against the CD3-binding part of the construct was used for detection. The serum concentration-time profiles were used to determine PK parameters. Blood sampling time points are listed in Table 9, below.

Table 9: Blood sampling time points during the PK study

blood sampling time points [h]
0.08
1
2
4
8
16
24
48
72
96
96
97
100
120

144
168
192
216
240

The pharmacokinetic parameters were determined using standard non-compartmental analysis (NCA) methods. The pharmacokinetic terminal phase of the single drugs was described using the decay period of the second test item administration.
For all tested proteins serum levels were quantifiable for all time points in all animals after BiTE® antibody administration. The PK profiles describe a biphasic, exponential decline after each of the single test item administrations (Figure 12).

Using non compartmental analysis, the following PK parameters were estimated: AUCinf (Area under the serum concentration- time curve), Vss (volume of distribution at steady state), CL (systemic clearance) and terminal t1/2 (terminal half-life).
The PK parameter as mean of n=3 for each tested compound are summarized in the table below.

test item	terminal t1/2 [h]	AUCinf [h*ng/mL]	Cl [mL/h/kg]	Vss [mL/kg]	x-fold increase in t1/2 compared to EGFRvIII-HALB
EvIII-1 x I2C6-HALB	51.2	169109	0.95	110.21	1
EvIII-1 x I2C6-HALB098	67.6	208504	0.77	109.03	1.32
EvIII-1 x I2C6-HALB114	79.7	248438	0.64	99.87	1.56
EvIII-1 x I2C6-HALB131	69.8	194542	0.82	118.34	1.36
EvIII-1 x I2C6-HALB133	54.2	203041	0.79	98.35	1.06
EvIII-1 x I2C6-HALB135	71.1	246928	0.65	95.05	1.39
EvIII-1 x I2C6-HALB253	71.2	216000	0.74	106.44	1.39
EvIII-1 x I2C6-HALB254	66.8	189131	0.85	117.72	1.30

In respect to terminal half-life, all tested affinity-increased EGFRvIII-HALB variants achieve a factor of up to 1.56 fold (compound 11) longer half-life then the wild-type HALB fusion protein

in the cyno repeated dose setting. They thereby all represent a half-life extended (HLE) version of the corresponding wild-type albumin.

SEQ ID NO:	Description	SEQUENCE
1.	N-terminus of CD3ε	QDGNE
2.	CDH19 14302 x I2C-HALB SEQ ID 1575 of PCT/EP2014/051550	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLDYHHHHHH
3.	CDH19 14302 CC x I2C-HALB SEQ ID 2222 of PCT/EP2014/051550	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLDYHHHHHH
4.	HALB	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV

		LHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL
5.	HALB7	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL
6.	HALB098	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKLVAASQAALGL
7.	HALB114	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHLVAASKAALGL
8.	HALB254	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKLVAASQAALGL
9.	HALB253	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ

		NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKLVAASQAALGL
10.	HALB131	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHLVAASQAALGL
11.	HALB135	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHLVAASKAALGL
12.	HALB133	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV ATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPEL LFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEV SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQ NLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCV LHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKLVAASKAALGL
13.	Peptide linker	GGGGS
14.	CDR-L1 of F6A	GSSTGAVTSGYYPN
15.	CDR-L2 of F6A	GTKFLAP
16.	CDR-L3 of F6A	ALWYSNRWV
17.	CDR-H1 of F6A	IYAMN
18.	CDR-H2 of F6A	RIRSKYNNYATYYADSVKS
19.	CDR-H3 of F6A	HGNFGNSYVSFFAY
20.	VH of F6A	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSS
21.	VH of F6A	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG

		ATTCACCTTCAATATCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAAGCAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACGTATCCTTCTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
22.	VL of F6A	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
23.	VL of F6A	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
24.	VH-VL of F6A	EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
25.	VH-VL of F6A	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATATCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAAGCAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACGTATCCTTCTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
26.	CDR-L1 of H2C	GSSTGAVTSGYYPN
27.	CDR-L2 of H2C	GTKFLAP
28.	CDR-L3 of H2C	ALWYSNRWV
29.	CDR-H1 of H2C	KYAMN
30.	CDR-H2 of H2C	RIRSKYNNYATYYADSVKD
31.	CDR-H3 of H2C	HGNFGNSYISYWAY
32.	VH of H2C	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
33.	VH of H2C	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA

34.	VL of H2C	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
35.	VL of H2C	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
36.	VH-VL of H2C	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
37.	VH-VL of H2C	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
38.	CDR-L1 of H1E	GSSTGAVTSGYYPN
39.	CDR-L2 of H1E	GTKFLAP
40.	CDR-L3 of H1E	ALWYSNRWV
41.	CDR-H1 of H1E	SYAMN
42.	CDR-H2 of H1E	RIRSKYNNYATYYADSVKG
43.	CDR-H3 of H1E	HGNFGNSYLSFWAY
44.	VH of H1E	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSS
45.	VH of H1E	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGAGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATTCGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACCTATCCTTCTGGGCTTACTGGGCCAAGGGACTCTGGTCACCGTCTCCTC
46.	VL of H1E	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
47.	VL of H1E	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG

		GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
48.	VH-VL of H1E	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
49.	VH-VL of H1E	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGAGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATTCGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACCTATCCTTCTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
50.	CDR-L1 of G4H	GSSTGAVTSGYYPN
51.	CDR-L2 of G4H	GTKFLAP
52.	CDR-L3 of G4H	ALWYSNRWV
53.	CDR-H1 of G4H	RYAMN
54.	CDR-H2 of G4H	RIRSKYNNYATYYADSVKG
55.	CDR-H3 of G4H	HGNFGNSYLSYFAY
56.	VH of G4H	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSS
57.	VH of G4H	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATCGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACTTATCCTACTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
58.	VL of G4H	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
59.	VL of G4H	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA

60.	VH-VL of G4H	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
61.	VH-VL of G4H	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATCGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACTTATCCTACTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
62.	CDR-L1 of A2J	RSSTGAVTSGYYPN
63.	CDR-L2 of A2J	ATDMRPS
64.	CDR-L3 of A2J	ALWYSNRWV
65.	CDR-H1 of A2J	VYAMN
66.	CDR-H2 of A2J	RIRSKYNNYATYYADSVKK
67.	CDR-H3 of A2J	HGNFGNSYLSWWAY
68.	VH of A2J	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSS
69.	VH of A2J	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATGTCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACTTATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
70.	VL of A2J	QTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
71.	VL of A2J	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTCGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG CCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
72.	VH-VL of A2J	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL

73.	VH-VL of A2J	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATGTCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACTTATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTCGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGAGGAACCAAACTGACTGTCCTA
74.	CDR-L1 of E1L	GSSTGAVTSGYYPN
75.	CDR-L2 of E1L	GTKFLAP
76.	CDR-L3 of E1L	ALWYSNRWV
77.	CDR-H1 of E1L	KYAMN
78.	CDR-H2 of E1L	RIRSKYNNYATYYADSVKS
79.	CDR-H3 of E1L	HGNFGNSYTSYYAY
80.	VH of E1L	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSS
81.	VH of E1L	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAATCGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACACATCCTACTACGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
82.	VL of E1L	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
83.	VL of E1L	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
84.	VH-VL of E1L	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKSRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
85.	VH-VL of E1L	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAATCGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA

		CTTCGGTAATAGCTACACATCCTACTACGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
86.	CDR-L1 of E2M	RSSTGAVTSGYYPN
87.	CDR-L2 of E2M	ATDMRPS
88.	CDR-L3 of E2M	ALWYSNRWV
89.	CDR-H1 of E2M	GYAMN
90.	CDR-H2 of E2M	RIRSKYNNYATYYADSVKE
91.	CDR-H3 of E2M	HRNFGNSYLSWFAY
92.	VH of E2M	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKERFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSS
93.	VH of E2M	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATGGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGAGGAGGTTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATAGGAA CTTCGGTAATAGCTACTTATCCTGGTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
94.	VL of E2M	QTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
95.	VL of E2M	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTCGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG CCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
96.	VH-VL of E2M	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKERFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
97.	VH-VL of E2M	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATGGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGAGGAGGTTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATAGGAA CTTCGGTAATAGCTACTTATCCTGGTTCGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTCGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGCCACTGACATGAGGCCCTCTGGTACTCCTGCCAGATTCTCAG

		GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
98.	CDR-L1 of F7O	GSSTGAVTSGYYPN
99.	CDR-L2 of F7O	GTKFLAP
100.	CDR-L3 of F7O	ALWYSNRWV
101.	CDR-H1 of F7O	VYAMN
102.	CDR-H2 of F7O	RIRSKYNNYATYYADSVKK
103.	CDR-H3 of F7O	HGNFGNSYISWWAY
104.	VH of F7O	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSS
105.	VH of F7O	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATGTGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
106.	VL of F7O	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
107.	VL of F7O	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
108.	VH-VL of F7O	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKKRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
109.	VH-VL of F7O	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATGTGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAAAGAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCTACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGCT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
110.	CDR-L1 of F12Q	GSSTGAVTSGNYPN

111.	CDR-L2 of F12Q	GTKFLAP
112.	CDR-L3 of F12Q	VLWYSNRWV
113.	CDR-H1 of F12Q	SYAMN
114.	CDR-H2 of F12Q	RIRSKYNNYATYYADSVKG
115.	CDR-H3 of F12Q	HGNFGNSYVSWWAY
116.	VH of F12Q	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSS
117.	VH of F12Q	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
118.	VL of F12Q	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
119.	VL of F12Q	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
120.	VH-VL of F12Q	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
121.	VH-VL of F12Q	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAGCTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACGTTTCCTGGTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
122.	CDR-L1 of I2C	GSSTGAVTSGNYPN
123.	CDR-L2 of I2C	GTKFLAP
124.	CDR-L3 of I2C	VLWYSNRWV
125.	CDR-H1 of I2C	KYAMN

126.	CDR-H2 of I2C	RIRSKYNNYATYYADSVKD
127.	CDR-H3 of I2C	HGNFGNSYISYWAY
128.	VH of I2C	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS
129.	VH of I2C	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA
130.	VL of I2C	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
131.	VL of I2C	CAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCTGGTGGAACAGTCACACTCACTTGTGGCTCCTCGAC TGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACAAAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTG GGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAGGCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTC TCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTTCTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGG AACCAAACTGACTGTCCTA
132.	VH-VL of I2C	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
133.	VH-VL of I2C	GAGGTGCAGCTGGTCGAGTCTGGAGGAGGATTGGTGCAGCCTGGAGGGTCATTGAAACTCTCATGTGCAGCCTCTGG ATTCACCTTCAATAAGTACGCCATGAACTGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAA GAAGTAAATATAATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCA AAAAACACTGCCTATCTACAAATGAACAACTTGAAAACTGAGGACACTGCCGTGTACTACTGTGTGAGACATGGGAA CTTCGGTAATAGCTACATATCCTACTGGGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCAGGTGGTGGTG GTTCTGGCGGCGGCGGCTCCGGTGGTGGTTCTCAGACTGTTGTGACTCAGGAACCTTCACTCACCGTATCACCT GGTGGAACAGTCACACTCACTTGTGGCTCCTCGACTGGGGCTGTTACATCTGGCAACTACCCAAACTGGGTCCAACA AAAACCAGGTCAGGCACCCCGTGGTCTAATAGGTGGGACTAAGTTCCTCGCCCCCGGTACTCCTGCCAGATTCTCAG GCTCCCTGCTTGGAGGCAAGGCTGCCCTCACCCTCTCAGGGGTACAGCCAGAGGATGAGGCAGAATATTACTGTGTT CTATGGTACAGCAACCGCTGGGTGTTCGGTGGAGGAACCAAACTGACTGTCCTA
134.	CH19_2G6_302_VKGxI2C 6-HALBwD	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR

		DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
135.	CH19_0-E11xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
136.	CH19_5-G4xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH

137.	CH19_8-H6xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
138.	CH19_2-C11xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
139.	CH19_2-A10xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
140.	CH19_1-D11xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
141.	CH19_9-F9xI2C6-HALBwD	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL

		VAASQAALGLHHHHHH
142.	CH19_1-H8xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
143.	CH19_1-B12xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
144.	CH19_0-C4xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG

		GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
145.	CH19_3-F2xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
146.	CH19_3-B10xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST

		PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
147.	CH19_0-G4xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
148.	CH19_0-H5xI2C6-HALBwD	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
149.	CH19_0-B8xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP

		TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
150.	CH19_2-D9xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
151.	CH19_8-H7xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
152.	CH19_9-C2xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
153.	CH19_3-D5xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
154.	CH19_1-G11xI2C6-	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

	HALBwD	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
155.	CH19_1-H11xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
156.	CH19_9-F3xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL

		PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
157.	CH19_2-G6xI2C6-HALBwD	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
158.	CH19_2-H7xI2C6-HALBwD	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH

159.	CH19_5-B3xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
160.	CH19_5-E10xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
161.	CH19_6-G10xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA

		ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
162.	CH19_4-H8xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
163.	CH19_2-E4xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
164.	CH19_6-B8xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
165.	CH19_0-B4xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
166.	CH19_9-F1xI2C6-HALBwD	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
167.	CH19_4-A7xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
168.	CH19_6-E12xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV

		VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
169.	CH19_6-C12xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
170.	CH19_6-A7xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
171.	CH19_6-G8xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC

		RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
172.	CH19_6-F9xI2C6-HALBwD	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
173.	CH19_0-C11xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL

		RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAE EGKKLVAASQAALGLHHHHHH
174.	CH19_8-F6xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
175.	CH19_0-G9xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH

176.	CH19_1-E11xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
177.	CH19_0-F5xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEG KKLVAASQAALGLHHHHHH
178.	CH19_1-E1xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ

		QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
179.	CH19_1-E6xI2C6-HALBwD	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
180.	CH19_2G6_302xI2C6-HALBwD	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGDGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE

		GKKLVAASQAALGLHHHHHH
181.	CH19_2G6_302_VKGxI2C6-HALB	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIGTGIYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
182.	CH19_0-E11xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
183.	CH19_5-G4xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
184.	CH19_8-H6xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
185.	CH19_2-C11xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
186.	CH19_2-A10xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK

		NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
187.	CH19_1-D11xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
188.	CH19_9-F9xI2C6-HALB	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN

		QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
189.	CH19_1-H8xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
190.	CH19_1-B12xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
191.	CH19_0-C4xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT

		YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
192.	CH19_3-F2xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
193.	CH19_3-B10xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
194.	CH19_0-G4xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
195.	CH19_0-H5xI2C6-HALB	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
196.	CH19_0-B8xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF

		EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
197.	CH19_2-D9xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
198.	CH19_8-H7xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
199.	CH19_9-C2xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK

		NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
200.	CH19_3-D5xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
201.	CH19_1-G11xI2C6-HALB	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
202.	CH19_1-H11xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
203.	CH19_9-F3xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
204.	CH19_2-G6xI2C6-HALB	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK

		YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
205.	CH19_2-H7xI2C6-HALB	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
206.	CH19_5-B3xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
207.	CH19_5-E10xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
208.	CH19_6-G10xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
209.	CH19_4-H8xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
210.	CH19_2-E4xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
211.	CH19_6-B8xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
212.	CH19_0-B4xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS

		TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
213.	CH19_9-F1xI2C6-HALB	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
214.	CH19_4-A7xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
215.	CH19_6-E12xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
216.	CH19_6-C12xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
217.	CH19_6-A7xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
218.	CH19_6-G8xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
219.	CH19_6-F9xI2C6-HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
220.	CH19_0-C11xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAE EGKKLVAASQAALGLHHHHHH
221.	CH19_8-F6xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
222.	CH19_0-G9xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY

		LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
223.	CH19_1-E11xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
224.	CH19_0-F5xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEG KKLVAASQAALGLHHHHHH
225.	CH19_1-E1xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN

		TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
226.	CH19_1-E6xI2C6-HALB	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
227.	CH19_2G6_302xI2C6-HALB	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY

		ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
228.	CH19_2G6_302_VKGxI2C6-HALB7	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
229.	CH19_0-E11xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
230.	CH19_5-G4xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
231.	CH19_8-H6xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
232.	CH19_2-C11xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
233.	CH19_2-A10xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
234.	CH19_1-D11xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
235.	CH19_9-F9xI2C6-HALB7	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF

		EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
236.	CH19_1-H8xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
237.	CH19_1-B12xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
238.	CH19_0-C4xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

		NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
239.	CH19_3-F2xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
240.	CH19_3-B10xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
241.	CH19_0-G4xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
242.	CH19_0-H5xI2C6-HALB7	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
243.	CH19_0-B8xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT

		YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
244.	CH19_2-D9xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
245.	CH19_8-H7xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
246.	CH19_9-C2xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
247.	CH19_3-D5xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
248.	CH19_1-G11xI2C6-HALB7	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
249.	CH19_1-H11xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
250.	CH19_9-F3xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
251.	CH19_2-G6xI2C6-HALB7	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ

		FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
252.	CH19_2-H7xI2C6-HALB7	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKKL VAASQAALGLHHHHHH
253.	CH19_5-B3xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
254.	CH19_5-E10xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
255.	CH19_6-G10xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
256.	CH19_4-H8xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
257.	CH19_2-E4xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
258.	CH19_6-B8xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
259.	CH19_0-B4xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
260.	CH19_9-F1xI2C6-HALB7	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
261.	CH19_4-A7xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
262.	CH19_6-E12xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
263.	CH19_6-C12xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
264.	CH19_6-A7xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS

		TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
265.	CH19_6-G8xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
266.	CH19_6-F9xI2C6-HALB7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEGKK LVAASQAALGLHHHHHH
267.	CH19_0-C11xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV DETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAE EGKKLVAASQAALGLHHHHHH
268.	CH19_8-F6xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
269.	CH19_0-G9xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK

		YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
270.	CH19_1-E11xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFA EEGKKLVAASQAALGLHHHHHH
271.	CH19_0-F5xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE

		TYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEEG KKLVAASQAALGLHHHHHH
272.	CH19_1-E1xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
273.	CH19_1-E6xI2C6-HALB7	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
274.	CH19_2G6_302xI2C6-HALB7	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ

		QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCKADDKETCFAEE GKKLVAASQAALGLHHHHHH
275.	CH19_2G6_302_VKGxI2C6-HALB098	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
276.	CH19_0-E11xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
277.	CH19_5-G4xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK

	HALB098	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
278.	CH19_8-H6xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
279.	CH19_2-C11xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
280.	CH19_2-A10xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
281.	CH19_1-D11xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
282.	CH19_9-F9xI2C6-HALB098	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT

		YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
283.	CH19_1-H8xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
284.	CH19_1-B12xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV

		PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
285.	CH19_0-C4xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
286.	CH19_3-F2xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
287.	CH19_3-B10xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
288.	CH19_0-G4xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
289.	CH19_0-H5xI2C6-HALB098	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
290.	CH19_0-B8xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

	HALB098	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
291.	CH19_2-D9xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE
292.	CH19_8-H7xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
293.	CH19_9-C2xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
294.	CH19_3-D5xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
295.	CH19_1-G11xI2C6-HALB098	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
296.	CH19_1-H11xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
297.	CH19_9-F3xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
298.	CH19_2-G6xI2C6-HALB098	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
299.	CH19_2-H7xI2C6-HALB098	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
300.	CH19_5-B3xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
301.	CH19_5-E10xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
302.	CH19_6-G10xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
303.	CH19_4-H8xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS

	HALB098	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
304.	CH19_2-E4xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
305.	CH19_6-B8xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
306.	CH19_0-B4xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
307.	CH19_9-F1xI2C6-HALB098	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
308.	CH19_4-A7xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
309.	CH19_6-E12xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
310.	CH19_6-C12xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
311.	CH19_6-A7xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
312.	CH19_6-G8xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
313.	CH19_6-F9xI2C6-HALB098	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
314.	CH19_0-C11xI2C6-HALB098	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAE EGPKLVAASQAALGLHHHHHH
315.	CH19_8-F6xI2C6-HALB098	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
316.	CH19_0-G9xI2C6-	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN

	HALB098	TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
317.	CH19_1-E11xI2C6-HALB098	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
318.	CH19_0-F5xI2C6-HALB098	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI

		CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEG PKLVAASQAALGLHHHHHH
319.	CH19_1-E1xI2C6-HALB098	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
320.	CH19_1-E6xI2C6-HALB098	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
321.	CH19_2G6_302xI2C6-HALB098	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN

		NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
322.	CH19_2G6_302_VKGxI2C6-HALB114	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
323.	CH19_0-E11xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
324.	CH19_5-G4xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
325.	CH19_8-H6xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
326.	CH19_2-C11xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
327.	CH19_2-A10xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
328.	CH19_1-D11xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
329.	CH19_9-F9xI2C6-	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK

	HALB114	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
330.	CH19_1-H8xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
331.	CH19_1-B12xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN

		QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
332.	CH19_0-C4xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
333.	CH19_3-F2xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
334.	CH19_3-B10xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
335.	CH19_0-G4xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
336.	CH19_0-H5xI2C6-HALB114	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
337.	CH19_0-B8xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
338.	CH19_2-D9xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
339.	CH19_8-H7xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
340.	CH19_9-C2xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
341.	CH19_3-D5xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
342.	CH19_1-G11xI2C6-	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

	HALB114	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
343.	CH19_1-H11xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
344.	CH19_9-F3xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
345.	CH19_2-G6xI2C6-HALB114	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
346.	CH19_2-H7xI2C6-HALB114	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
347.	CH19_5-B3xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
348.	CH19_5-E10xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
349.	CH19_6-G10xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
350.	CH19_4-H8xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
351.	CH19_2-E4xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
352.	CH19_6-B8xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
353.	CH19_0-B4xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
354.	CH19_9-F1xI2C6-HALB114	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
355.	CH19_4-A7xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS

	HALB114	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
356.	CH19_6-E12xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
357.	CH19_6-C12xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
358.	CH19_6-A7xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
359.	CH19_6-G8xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
360.	CH19_6-F9xI2C6-HALB114	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
361.	CH19_0-C11xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAE EGPHLVAASKAALGLHHHHHH
362.	CH19_8-F6xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD

		VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
363.	CH19_0-G9xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
364.	CH19_1-E11xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
365.	CH19_0-F5xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ

		CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEG PHLVAASKAALGLHHHHHH
366.	CH19_1-E1xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
367.	CH19_1-E6xI2C6-HALB114	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
368.	CH19_2G6_302xI2C6-	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN

	HALB114	TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
369.	CH19_2G6_302_VKGxI2C6-HALB254	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
370.	CH19_0-E11xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
371.	CH19_5-G4xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
372.	CH19_8-H6xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
373.	CH19_2-C11xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
374.	CH19_2-A10xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
375.	CH19_1-D11xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
376.	CH19_9-F9xI2C6-HALB254	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
377.	CH19_1-H8xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
378.	CH19_1-B12xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF

		EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
379.	CH19_0-C4xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
380.	CH19_3-F2xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
381.	CH19_3-B10xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK

	HALB254	NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
382.	CH19_0-G4xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
383.	CH19_0-H5xI2C6-HALB254	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
384.	CH19_0-B8xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
385.	CH19_2-D9xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
386.	CH19_8-H7xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
387.	CH19_9-C2xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
388.	CH19_3-D5xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
389.	CH19_1-G11xI2C6-HALB254	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
390.	CH19_1-H11xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
391.	CH19_9-F3xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
392.	CH19_2-G6xI2C6-HALB254	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALG VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
393.	CH19_2-H7xI2C6-HALB254	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
394.	CH19_5-B3xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS

	HALB254	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
395.	CH19_5-E10xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
396.	CH19_6-G10xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
397.	CH19_4-H8xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
398.	CH19_2-E4xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
399.	CH19_6-B8xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
400.	CH19_0-B4xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
401.	CH19_9-F1xI2C6-HALB254	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
402.	CH19_4-A7xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
403.	CH19_6-E12xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
404.	CH19_6-C12xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
405.	CH19_6-A7xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
406.	CH19_6-G8xI2C6-HALB254	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
407.	CH19_6-F9xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS

	HALB254	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
408.	CH19_0-C11xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAE EGPKLVAASQAALGLHHHHHH
409.	CH19_8-F6xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA

		KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALG VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
410.	CH19_0-G9xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALG VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
411.	CH19_1-E11xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALG VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
412.	CH19_0-F5xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN

		YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEG PKLVAASQAALGL HHHHHH
413.	CH19_1-E1xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
414.	CH19_1-E6xI2C6-HALB254	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVD

		ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
415.	CH19_2G6_302xI2C6-HALB254	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
416.	CH19_2G6_302_VKGxI2C6-HALB253	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
417.	CH19_0-E11xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
418.	CH19_5-G4xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
419.	CH19_8-H6xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
420.	CH19_2-C11xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK

	HALB253	NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
421.	CH19_2-A10xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
422.	CH19_1-D11xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
423.	CH19_9-F9xI2C6-HALB253	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
424.	CH19_1-H8xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
425.	CH19_1-B12xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT

		YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
426.	CH19_0-C4xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
427.	CH19_3-F2xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV

		PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
428.	CH19_3-B10xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
429.	CH19_0-G4xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
430.	CH19_0-H5xI2C6-HALB253	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
431.	CH19_0-B8xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
432.	CH19_2-D9xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
433.	CH19_8-H7xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK

	HALB253	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
434.	CH19_9-C2xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
435.	CH19_3-D5xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
436.	CH19_1-G11xI2C6-HALB253	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
437.	CH19_1-H11xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
438.	CH19_9-F3xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
439.	CH19_2-G6xI2C6-HALB253	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
440.	CH19_2-H7xI2C6-HALB253	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYV

		PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASQAALGLHHHHHH
441.	CH19_5-B3xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
442.	CH19_5-E10xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
443.	CH19_6-G10xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
444.	CH19_4-H8xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
445.	CH19_2-E4xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
446.	CH19_6-B8xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN

	HALB253	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
447.	CH19_0-B4xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
448.	CH19_9-F1xI2C6-HALB253	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
449.	CH19_4-A7xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
450.	CH19_6-E12xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
451.	CH19_6-C12xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
452.	CH19_6-A7xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
453.	CH19_6-G8xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
454.	CH19_6-F9xI2C6-HALB253	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASQAALGLHHHHHH
455.	CH19_0-C11xI2C6-HALB253	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAE EGPKLVAASQAALGLHHHHHH
456.	CH19_8-F6xI2C6-HALB253	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY

		LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
457.	CH19_0-G9xI2C6-HALB253	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
458.	CH19_1-E11xI2C6-HALB253	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALD VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASQAALGLHHHHHH
459.	CH19_0-F5xI2C6-	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN

	HALB253	TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEG PKLVAASQAALGLHHHHHH
460.	CH19_1-E1xI2C6-HALB253	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
461.	CH19_1-E6xI2C6-HALB253	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY

		ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
462.	CH19_2G6_302xI2C6-HALB253	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASQAALGLHHHHHH
463.	CH19_2G6_302_VKGxI2C6-HALB131	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPHLVAASQAALGLHHHHHH
464.	CH19_0-E11xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
465.	CH19_5-G4xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
466.	CH19_8-H6xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
467.	CH19_2-C11xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
468.	CH19_2-A10xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
469.	CH19_1-D11xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
470.	CH19_9-F9xI2C6-HALB131	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
471.	CH19_1-H8xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
472.	CH19_1-B12xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

	HALB131	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
473.	CH19_0-C4xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
474.	CH19_3-F2xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN

		QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
475.	CH19_3-B10xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
476.	CH19_0-G4xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
477.	CH19_0-H5xI2C6-HALB131	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
478.	CH19_0-B8xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
479.	CH19_2-D9xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH
		LVAASQAALGLHHHHHH
480.	CH19_8-H7xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK
		NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA
		TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
		LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA
		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG
		GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA
		ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP
		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL
		PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG
		KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE
		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV
		VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
		PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY
		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH
		LVAASQAALGLHHHHHH
481.	CH19_9-C2xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK
		NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA
		TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
		LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA
		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG
		GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA
		ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP
		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL
		PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG
		KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE
		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV
		VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
		PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY
		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH
		LVAASQAALGLHHHHHH
482.	CH19_3-D5xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK
		NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA
		TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
		LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA
		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG
		GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA
		ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
483.	CH19_1-G11xI2C6-HALB131	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
484.	CH19_1-H11xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
485.	CH19_9-F3xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK

	HALB131	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
486.	CH19_2-G6xI2C6-HALB131	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPHLVAASQAALGLHHHHHH
487.	CH19_2-H7xI2C6-HALB131	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN

		QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPHL VAASQAALGLHHHHHH
488.	CH19_5-B3xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
489.	CH19_5-E10xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
490.	CH19_6-G10xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
491.	CH19_4-H8xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
492.	CH19_2-E4xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
493.	CH19_6-B8xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
494.	CH19_0-B4xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
495.	CH19_9-F1xI2C6-HALB131	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
496.	CH19_4-A7xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
497.	CH19_6-E12xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
498.	CH19_6-C12xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN

	HALB131	TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
499.	CH19_6-A7xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
500.	CH19_6-G8xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
501.	CH19_6-F9xI2C6-HALB131	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPH LVAASQAALGLHHHHHH
502.	CH19_0-C11xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAE EGPHLVAASQAALGLHHHHHH
503.	CH19_8-F6xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK

		YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPHLVAASQAALGLHHHHHH
504.	CH19_0-G9xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPHLVAASQAALGLHHHHHH
505.	CH19_1-E11xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE

		VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPHLVAASQAALGLHHHHHH
506.	CH19_0-F5xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEG PHLVAASQAALGLHHHHHH
507.	CH19_1-E1xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPHLVAASQAALGLHHHHHH
508.	CH19_1-E6xI2C6-HALB131	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ

		QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPHLVAASQAALGLHHHHHH
509.	CH19_2G6_302xI2C6-HALB131	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
510.	CH19_2G6_302_VKGxI2C6-HALB135	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
511.	CH19_0-E11xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK

	HALB135	NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
512.	CH19_5-G4xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
513.	CH19_8-H6xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
514.	CH19_2-C11xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
515.	CH19_2-A10xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
516.	CH19_1-D11xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
517.	CH19_9-F9xI2C6-HALB135	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
518.	CH19_1-H8xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
519.	CH19_1-B12xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
520.	CH19_0-C4xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
521.	CH19_3-F2xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF

		EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
522.	CH19_3-B10xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
523.	CH19_0-G4xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
524.	CH19_0-H5xI2C6-	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

	HALB135	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
525.	CH19_0-B8xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
526.	CH19_2-D9xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
527.	CH19_8-H7xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
528.	CH19_9-C2xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
529.	CH19_3-D5xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
530.	CH19_1-G11xI2C6-HALB135	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
531.	CH19_1-H11xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV

		PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
532.	CH19_9-F3xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
533.	CH19_2-G6xI2C6-HALB135	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
534.	CH19_2-H7xI2C6-HALB135	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF

		EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPHL VAASKAALGLHHHHHH
535.	CH19_5-B3xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
536.	CH19_5-E10xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
537.	CH19_6-G10xI2C6-	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS

	HALB135	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
538.	CH19_4-H8xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
539.	CH19_2-E4xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
540.	CH19_6-B8xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
541.	CH19_0-B4xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
542.	CH19_9-F1xI2C6-HALB135	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
543.	CH19_4-A7xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
544.	CH19_6-E12xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
545.	CH19_6-C12xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
546.	CH19_6-A7xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
547.	CH19_6-G8xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
548.	CH19_6-F9xI2C6-HALB135	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGPH LVAASKAALGLHHHHHH
549.	CH19_0-C11xI2C6-HALB135	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAE EGPHLVAASKAALGLHHHHHH
550.	CH19_8-F6xI2C6-	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN

	HALB135	TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
551.	CH19_0-G9xI2C6-HALB135	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
552.	CH19_1-E11xI2C6-HALB135	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA

		KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFA EEGPHLVAASKAALGLHHHHHH
553.	CH19_0-F5xI2C6-HALB135	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEG PHLVAASKAALGLHHHHHH
554.	CH19_1-E1xI2C6-HALB135	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
555.	CH19_1-E6xI2C6-HALB135	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN

		NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
556.	CH19_2G6_302xI2C6-HALB135	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEE GPHLVAASKAALGLHHHHHH
557.	CH19_2G6_302_VKGxI2C6-HALB133	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD

		ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASKAALGLHHHHHH
558.	CH19_0-E11xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
559.	CH19_5-G4xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
560.	CH19_8-H6xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
561.	CH19_2-C11xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
562.	CH19_2-A10xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSP RTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
563.	CH19_1-D11xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK

	HALB133	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
564.	CH19_9-F9xI2C6-HALB133	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
565.	CH19_1-H8xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
566.	CH19_1-B12xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
567.	CH19_0-C4xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
568.	CH19_3-F2xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT

		YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
569.	CH19_3-B10xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
570.	CH19_0-G4xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP SFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV

		PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
571.	CH19_0-H5xI2C6-HALB133	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
572.	CH19_0-B8xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
573.	CH19_2-D9xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
574.	CH19_8-H7xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
575.	CH19_9-C2xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
576.	CH19_3-D5xI2C6-	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSK

	HALB133	NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
577.	CH19_1-G11xI2C6-HALB133	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP LTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
578.	CH19_1-H11xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP TFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN

		QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
579.	CH19_9-F3xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSK NQFSLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP ITFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
580.	CH19_2-G6xI2C6-HALB133	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQ FSLKLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLS PGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQ YGSSPFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASKAALGLHHHHHH
581.	CH19_2-H7xI2C6-HALB133	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSK NQFSLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQ AFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT

		YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPF EDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLP RLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGK ASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTP TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPKL VAASKAALGLHHHHHH
582.	CH19_5-B3xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
583.	CH19_5-E10xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY

		VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
584.	CH19_6-G10xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
585.	CH19_4-H8xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
586.	CH19_2-E4xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN TAYMELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP

		FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
587.	CH19_6-B8xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTN TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
588.	CH19_0-B4xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
589.	CH19_9-F1xI2C6-	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTN

	HALB133	TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
590.	CH19_4-A7xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
591.	CH19_6-E12xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE

		NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
592.	CH19_6-C12xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTN TAYMELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
593.	CH19_6-A7xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
594.	CH19_6-G8xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTS TAYMELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA

		TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
595.	CH19_6-F9xI2C6-HALB133	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISC RSSQSLLHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP FTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICE NQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEGPK LVAASKAALGLHHHHHH
596.	CH19_0-C11xI2C6-HALB133	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YDNLPTFGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY NNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYL QQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDD NPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAK YICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHP DYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVP QVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEV

		DETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAE EGPKLVAASKAALGLHHHHHH
597.	CH19_8-F6xI2C6-HALB133	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQ YYSTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASKAALGLHHHHHH
598.	CH19_0-G9xI2C6-HALB133	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKN TLYLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQ YDNLPLTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASKAALGLHHHHHH
599.	CH19_1-E11xI2C6-HALB133	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKN TLFLQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSA SVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQ YVNLPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK YNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQY

		LQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKD DNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDE LRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRH PDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFA EEGPKLVAASKAALGLHHHHHH
600.	CH19_0-F5xI2C6-HALB133	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNS APLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGG SGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQ CPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRD EGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEEG PKLVAASKAALGLHHHHHH
601.	CH19_1-E1xI2C6-HALB133	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYG TSPLTFGGGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASKAALGLHHHHHH
602.	CH19_1-E6xI2C6-	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKN

	HALB133	TLYLQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYG SSPFTFGPGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASKAALGLHHHHHH
603.	CH19_2G6_302xI2C6-HALB133	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKN TLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWE SSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQ QCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDN PNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPD YSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCKADDKETCFAEE GPKLVAASKAALGLHHHHHH
604.	human CD3 ε (1-27)	QDGNEEMGGITQTPYKVSISGTTVILT
605.	Human CD3ε extracellular domain	QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLK EFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMD
606.	Human Cadherin-19	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSF QYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYE AIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIG QPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITN HETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQ GSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVLN INDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFN

		LQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTL GLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSA IFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQS NN
607.	Cyno Cadherin-19 Macaca fascicularis	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSF QYKLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYE AIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIG QPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITN HETQEGIVILKKKVNFEHQNHYGIRAKVKNHHVDEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQ GSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTITTTNSLDREISAWYNLSITATEKYNIEQISSIPVYVQVLN INDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNSSSFTIIDNQDNTAVILTNRTGFN LQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFKTEVIIAILICIMVIFGFIFLTL GLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSA IFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQS NN

SEQ ID NO:	Description	Source	Sequence
608.	HALB234	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPKLVAASKAALGL
609.	HALB C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGKKLVAASQAALGL
610.	HALB7 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE

			YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCCK ADDKETCFAEEGKKLVAASQAALGL
611.	HALB098 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPKLVAASQAALGL
612.	HALB114 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPHLVAASKAALGL
613.	HALB254 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALGVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPKLVAASQAALGL
614.	HALB253 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPKLVAASQAALGL
615.	HALB131 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA

			EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPHLVAASQAALGL
616.	HALB135 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPHLVAASKAALGL
617.	HALB133 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPKLVAASKAALGL
618.	HALB234 C34S	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPKLVAASKAALGL
619.	HALB C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGKKLVAASQAALGL
620.	HALB7 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK

			VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGKKLVAASQAALGL
621.	HALB098 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFTLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPKLVAASQAALGL
622.	HALB114 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFTLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPHLVAASKAALGL
623.	HALB254 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALGVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPKLVAASQAALGL
624.	HALB253 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPKLVAASQAALGL
625.	HALB131 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR

			YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPHLVAASQAALGL
626.	HALB135 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPHLVAASKAALGL
627.	HALB133 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCK ADDKETCFAEEGPKLVAASKAALGL
628.	HALB234 C34A	artificial	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATL RETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKR YKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGE YKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES LVNRRPCFSALDVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCK ADDKETCFAEEGPKLVAASKAALGL
629.	CH19-1	bispecific molecule	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASI TCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGG TKLTVL
630.	CH19-2	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQFPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKL EIK
631.	CH19-3	bispecifi	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSKNQF

		c molecule	SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGTSNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKL EIK
632.	CH19-4	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKL EIK
633.	CH19-5	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSKNQF SLKLRSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKL EIK
634.	CH19-6	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLRSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARDSSSSRALDYWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDSSPRTFGQGTKL EIK
635.	CH19-7	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKL EIK
636.	CH19-8	bispecifi c molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTFGGGTKVE IK
637.	CH19-9	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
638.	CH19-10	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTFGPGTKVE IK
639.	CH19-11	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTFGGGTKVE IK
640.	CH19-12	bispecifi c molecule	QVQLQESGPGLVKPSQTLSLTCTISGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSKNQF SLKLTSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTFGGGTKVE IK

641.	CH19-13	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLDWIGYIFYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVNSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
642.	CH19-14	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPSFGQGTKVE IK
643.	CH19-15	bispecific molecule	QVQLQESGPGLVRPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSPLTFGGGTKV EIK
644.	CH19-16	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTFGGGTKVE IK
645.	CH19-17	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
646.	CH19-18	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWVRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVIISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
647.	CH19-19	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
648.	CH19-20	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGRTYYNPSLKSRVSISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
649.	CH19-21	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKV EIK
650.	CH19-22	bispecific	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYRGRTYYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTFGQGTRLE

		molecule	IK
651.	CH19-23	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIFYSGKTYYNPSLKSRVSISVDTSKNQF SLKLSSVTAADTAVYYCARVYSNYGWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTRL EIK
652.	CH19-24	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTMSIDTSKNQFSL KLISVTAADTAVYYCARDQRRIVAAGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERAT LSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFG PGTKVDIK
653.	CH19-25	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSNDYYWSWIRQHPGKGLEWIGYIYYSGSTFYNPSLKSRGAISVDTSKNQF SLKLTSVTAADTAVYYCARGVYRTGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDIATYYCQQSYSTPQAFGGGTKVD IK
654.	CH19-26	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYGGETNYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSL LHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
655.	CH19-27	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYSGATNYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSL LHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
656.	CH19-28	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSL LHSNGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
657.	CH19-29	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
658.	CH19-30	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTNTAY MELSSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTLGQPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKL EIK
659.	CH19-31	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQDRVTMTTDTSTNTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
660.	CH19-32	bispecific	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMATDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSL

		c molecule	LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKL EIK
661.	CH19-33	bispecifi c molecule	QVQLVQSGAEVKEPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQDRVTMTTDTSTNTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKL EIK
662.	CH19-34	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV EIK
663.	CH19-35	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGITWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLSVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
664.	CH19-36	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKFQGRVTMTTDTSTNTAY MELSSLRSEDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
665.	CH19-37	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMGWINPYTGNRNYAQKVQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV EIK
666.	CH19-38	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKVQGRVTMTTDTSTSTAY MELRNLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
667.	CH19-39	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTYYGISWVRQAPGQGLEWMGWINPYTGKTNYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARGSGGFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISCRSSQSL LHSVGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKV DIK
668.	CH19-40	bispecifi c molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKNTLY LQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPTFGQ GTRLEIK
669.	CH19-41	bispecifi c molecule	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKNTLY LQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTEFTLTISSLQAEDVAVYYCQQYYSTPLTFG GGTKVDIK

670.	CH19-42	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFRNYAMHWVRQAPGKGLEWVAGISYSGTNKYYASSVKGRFTISRDNSKNTLY LQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTEFTLTISSLQPEDIATYYCQQYDNLPLTFG GGTKVDIK
671.	CH19-43	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCVASGFTFRNYAMHWVRQAPGKGLEWVAVISYSGNNKYYASSVKGRFTISRDNSKNTLF LQLNSLRAEDTAVYYCAREFYYDSTGYDYSTPGNYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRV TITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYVNLPLTFG GGTKLEIK
672.	CH19-44	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMQWVRQAPGKGLEWVAVIWYSGSNKYYASSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT CRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPLTFGGGT KVEIK
673.	CH19-45	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYSGSNKYYASSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYPIFYRYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLS CRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDLAVYYCQQYGTSPLTFGGG TKLEIK
674.	CH19-46	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFIWYSGSNKYYASSVKGRVTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYPIFYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLS CRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPG TRLEIK
675.	CH19-47	bispecific molecule	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASI TCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGG TKLTVL
676.	MS_1	VH CDR1	SSSYYWG
677.	MS_1	VH CDR2	SIYYSGITNYNPSLKS
678.	MS_1	VH CDR3	PSNYDAFDI
679.	MS_1	VL CDR1	TGSSSNIGAGYDVH
680.	MS_1	VL CDR2	GNSKRPS
681.	MS_1	VL CDR3	QSYDSSLGGWV

682.	MS_1	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGITNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARPSNYDAFDIWGQGTMVTVSS
683.	MS_1	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQVPGTAPKLLIYGNSKRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLGGWVFGGGTKLTVL
684.	MS_1	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGITNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARPSNYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSS SNIGAGYDVHWYQQVPGTAPKLLIYGNSKRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLGGWVFGGGT KLTVL
685.	MS_1	bispecifi cmolecul e	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYYSGITNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARPSNYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSS SNIGAGYDVHWYQQVPGTAPKLLIYGNSKRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLGGWVFGGGT KLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
686.	MS_2	VH CDR1	DHYMS
687.	MS_2	VH CDR2	YISSSGSTIYYADSVKG
688.	MS_2	VH CDR3	DLGPSFDY
689.	MS_2	VL CDR1	RASQGISSWLA
690.	MS_2	VL CDR2	AASRLQS
691.	MS_2	VL CDR3	QQANSFPRT
692.	MS_2	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDHYMSWIRQTPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDLGPSFDYWGQGSLVTVSS
693.	MS_2	VL	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIDAASRLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQANSFPRTFGQGTKVEIK
694.	MS_2	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDHYMSWIRQTPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDLGPSFDYWGQGSLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQG ISSWLAWYQQKPGKAPKLLIDAASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPRTFGQGTKVEIK
695.	MS_2	bispecifi c	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDHYMSWIRQTPGKGLEWVSYISSSGSTIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDLGPSFDYWGQGSLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQG

		molecule	
696.	MS_3	VH CDR1	ISSWLAWYQQKPGKAPKLLIDAASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPRTFGQGTKVEIKS GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTKLTVL
697.	MS_3	VH CDR2	YISSSGSTIYYADSVKG
698.	MS_3	VH CDR3	DRNSHFDY
699.	MS_3	VL CDR1	RASQGITRWLA
700.	MS_3	VL CDR2	AASVLQS
701.	MS_3	VL CDR3	QQSNSFPRT
702.	MS_3	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWISYISSSGSTIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDRNSHFDYWGQGTLVTVSS
703.	MS_3	VL	DIQMTQSPSSVSASVGDRVTITCRASQGITRWLAWYQQKPGKAPKLLIYAASVLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSNSFPRTFGQGTKVEIK
704.	MS_3	scFv	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWISYISSSGSTIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDRNSHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQG ITRWLAWYQQKPGKAPKLLIYAASVLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNSFPRTFGQGTKVEIK
705.	MS_3	bispecific molecule	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWISYISSSGSTIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDRNSHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQG ITRWLAWYQQKPGKAPKLLIYAASVLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNSFPRTFGQGTKVEIKS GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTKLTVL
706.	MS_4	VH CDR1	DYYMT
707.	MS_4	VH CDR2	YISSSGSTIYYADSVKG

708.	MS_4	VH CDR3	DRNSHFDY
709.	MS_4	VL CDR1	RASQGINTWLA
710.	MS_4	VL CDR2	GASGLQS
711.	MS_4	VL CDR3	QQAKSFPRT
712.	MS_4	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISRDNAKNSLF LQMNSLRAEDTAVYYCARDRNSHFDYWGQGTLVTVSS
713.	MS_4	VL	DIQMTQSPSSVSASVGDRVTITCRASQGINTWLAWYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQAKSFPRTFGQGTKVEIK
714.	MS_4	scFv	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISRDNAKNSLF LQMNSLRAEDTAVYYCARDRNSHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQG INTWLAWYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAKSFPRTFGQGTKVEIK
715.	MS_4	bispecific molecule	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMTWIRQAPGKGLEWLSYISSSGSTIYYADSVKGRFTISRDNAKNSLF LQMNSLRAEDTAVYYCARDRNSHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQG INTWLAWYQQKPGKAPKLLIYGASGLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAKSFPRTFGQGTKVEIKS GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTKLTVL
716.	MS_5	VH CDR1	DHYMS
717.	MS_5	VH CDR2	YISSSGGIIYYADSVKG
718.	MS_5	VH CDR3	DVGSHFDY
719.	MS_5	VL CDR1	RASQDISRWLA
720.	MS_5	VL CDR2	AASRLQS
721.	MS_5	VL CDR3	QQAKSFPRT

722.	MS_5	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMSWIRQAPGKGLEWFSYISSSGGIIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDVGSHFDYWGQGTLVTVSS
723.	MS_5	VL	DIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLISAASRLQSGVPSRFSGSGSGTDFTLTISSLQP EDFAIYYCQQAKSFPRTFGQGTKVEIK
724.	MS_5	scFv	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMSWIRQAPGKGLEWFSYISSSGGIIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDVGSHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQD ISRWLAWYQQKPGKAPKLLISAASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAIYYCQQAKSFPRTFGQGTKVEIK
725.	MS_5	bispecific molecule	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMSWIRQAPGKGLEWFSYISSSGGIIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDVGSHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQD ISRWLAWYQQKPGKAPKLLISAASRLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAIYYCQQAKSFPRTFGQGTKVEIKS GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTKLTVL
726.	MS_6	VH CDR1	DHYMS
727.	MS_6	VH CDR2	YISNSGSIIYYVDSVKG
728.	MS_6	VH CDR3	DVRTAFDY
729.	MS_6	VL CDR1	RASQSIGSWLA
730.	MS_6	VL CDR2	AASSLQS
731.	MS_6	VL CDR3	QQANSFPRT
732.	MS_6	VH	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMSWIRQAPGKGLEWISYISNSGSIIYYVDSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDVRTAFDYWGQGTLVTVSS
733.	MS_6	VL	DIQMTQSPSSVSASVGDRVTITCRASQSIGSWLAWYQQKPGKAPNLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQANSFPRTFGQGTKVDIK
734.	MS_6	scFv	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMSWIRQAPGKGLEWISYISNSGSIIYYVDSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDVRTAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQS IGSWLAWYQQKPGKAPNLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPRTFGQGTKVDIK
735.	MS_6	bispecific molecule	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDHYMSWIRQAPGKGLEWISYISNSGSIIYYVDSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARDVRTAFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQS IGSWLAWYQQKPGKAPNLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPRTFGQGTKVDIKS

			GGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS NRWVFGGGTKLTVL
736.	MS_7	VH CDR1	SKFMT
737.	MS_7	VH CDR2	VIYSGGKTYYADSVKG
738.	MS_7	VH CDR3	DSGGWGYFDY
739.	MS_7	VL CDR1	KSSQSVLYSSNNKNYLA
740.	MS_7	VL CDR2	WASTRES
741.	MS_7	VL CDR3	QQYYSTPPT
742.	MS_7	VH	EVQLVESGGGLIQPGGSLRLSCAVSGFTVSSKFMTWVRQAPGKGLEWVSVIYSGGKTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDSGGWGYFDYWGQGTLVTVSS
743.	MS_7	VL	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCQQYYSTPPTFGQGTKVEIK
744.	MS_7	scFv	EVQLVESGGGLIQPGGSLRLSCAVSGFTVSSKFMTWVRQAPGKGLEWVSVIYSGGKTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDSGGWGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLAVSLGERATINCKSSQ SVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGQG TKVEIK
745.	MS_7	bispecific molecule	EVQLVESGGGLIQPGGSLRLSCAVSGFTVSSKFMTWVRQAPGKGLEWVSVIYSGGKTYYADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARDSGGWGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLAVSLGERATINCKSSQ SVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGQG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
746.	MS_8	VH CDR1	SYYWN
747.	MS_8	VH CDR2	RIYYNGNTYYNPSLKS

748.	MS_8	VH CDR3	PKLGIDAFDI
749.	MS_8	VL CDR1	TGSSSNIGAGYDVH
750.	MS_8	VL CDR2	GNSNRPS
751.	MS_8	VL CDR3	QSYDSSLSGWV
752.	MS_8	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWNWIRQPPGKGLEWIGRIYYNGNTYYNPSLKSRVTISGDTSKNQFSL KLSSVTAADTAVYYCARPKLGIDAFDIWGQGTMVTVSS
753.	MS_8	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGL QAEDEADYYCQSYDSSLSGWVFGGGTKLTVL
754.	MS_8	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWNWIRQPPGKGLEWIGRIYYNGNTYYNPSLKSRVTISGDTSKNQFSL KLSSVTAADTAVYYCARPKLGIDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSS NIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTK LTVL
755.	MS_8	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWNWIRQPPGKGLEWIGRIYYNGNTYYNPSLKSRVTISGDTSKNQFSL KLSSVTAADTAVYYCARPKLGIDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSS NIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTK LTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
756.	DL_1	VH CDR1	SYGMH
757.	DL_1	VH CDR2	VISYHGRDTYYARSVKG
758.	DL_1	VH CDR3	DGATVTSYYYSGMDV
759.	DL_1	VL CDR1	RASQGISNYLA
760.	DL_1	VL CDR2	LASSLQS
761.	DL_1	VL CDR3	QQYNFYPFT

762.	DL_1	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGRDTYYARSVKGRFTISRDNSKNTLY LHMNSLRAEDTAVYYCARDGATVTSYYYSGMDVWGQGTTVTVSSK
763.	DL_1	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYLASSLQSGVPSKFSGSGSGTDFTLTISSLQP EDFATYYCQQYNFYPFTFGPGTKVDIK
764.	DL_1	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGRDTYYARSVKGRFTISRDNSKNTLY LHMNSLRAEDTAVYYCARDGATVTSYYYSGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWFQQKPGKAPKSLIYLASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYNFYPFTFGPG TKVDIK
765.	DL_1	bispecifi c molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGRDTYYARSVKGRFTISRDNSKNTLY LHMNSLRAEDTAVYYCARDGATVTSYYYSGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWFQQKPGKAPKSLIYLASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYNFYPFTFGPG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
766.	DL_2	VH CDR1	SYYWS
767.	DL_2	VH CDR2	YVYYSGTTNYNPSLKS
768.	DL_2	VH CDR3	IAVTGFYFDY
769.	DL_2	VL CDR1	RASQRVNNNYLA
770.	DL_2	VL CDR2	GASSRAT
771.	DL_2	VL CDR3	QQYDRSPLT
772.	DL_2	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYVYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCASIAVTGFYFDYWGQGTLVTVSS
773.	DL_2	VL	EIVLTQSPGTLSLSPGERVTLSCRASQRVNNNYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDRSPLTFGGGTKLEIK
774.	DL_2	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYVYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCASIAVTGFYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERVTLSCRASQ RVNNNYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEI K
775.	DL_2	bispecifi	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYVYYSGTTNYNPSLKSRVTISVDTSKNQFSL

		c molecule	KLSSVTAADTAVYYCASIAVTGFYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERVTLSCRASQ RVNNNYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL
776.	DL_3	VH CDR1	SYYWS
777.	DL_3	VH CDR2	YIYYSGRTNYYPSLKS
778.	DL_3	VH CDR3	IAVAGFFFDY
779.	DL_3	VL CDR1	RASQSVNKNYLA
780.	DL_3	VL CDR2	GASSRAT
781.	DL_3	VL CDR3	QQYDRSPLT
782.	DL_3	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGRTNYYPSLKSRVTISIDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSS
783.	DL_3	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDRSPLTFGGGTKLEIK
784.	DL_3	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGRTNYYPSLKSRVTISIDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEI K
785.	DL_3	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGRTNYYPSLKSRVTISIDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL
786.	DL_4	VH CDR1	SFYWS
787.	DL_4	VH	YIYYSGTTNYNPSLKS

		CDR2	
788.	DL_4	VH CDR3	IAVAGFFFDY
789.	DL_4	VL CDR1	RASQSVNKNYLA
790.	DL_4	VL CDR2	GASSRAT
791.	DL_4	VL CDR3	QQYDRSPLT
792.	DL_4	VH	QVQLQESGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSS
793.	DL_4	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDRSPLTFGGGTKVEIK
794.	DL_4	scFv	QVQLQESGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKVEI K
795.	DL_4	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKVEI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL
796.	DL_5	VH CDR1	SFYWS
797.	DL_5	VH CDR2	YIYYSGTTNYNPSLKS
798.	DL_5	VH CDR3	IAVAGFFFDY
799.	DL_5	VL CDR1	RASQSVNKNYLA
800.	DL_5	VL CDR2	GASSRAT

801.	DL_5	VL CDR3	QQYDRSPLT	
802.	DL_5	VH	QVQLQESGPGLVKPSQTLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSS	
803.	DL_5	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDRSPLTFGGGTKVEIK	
804.	DL_5	scFv	QVQLQESGPGLVKPSQTLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKVEI K	
805.	DL_5	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKVEI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL	
806.	DL_6	VH CDR1	SFYWS	
807.	DL_6	VH CDR2	YIYYSGTTNYNPSLKS	
808.	DL_6	VH CDR3	IAVAGFFFDY	
809.	DL_6	VL CDR1	RASQSVNKNYLA	
810.	DL_6	VL CDR2	GASSRAT	
811.	DL_6	VL CDR3	QQYDRSPLT	
812.	DL_6	VH	QVQLQEWGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQLSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSK	
813.	DL_6	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDRSPLTFGGGTKVDIK	
814.	DL_6	scFv	QVQLQEWGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQLSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKVDI	

815.	DL_6	bispecific molecule	K QVQLQEWGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQLSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKVDI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL
816.	DL_7	VH CDR1	SFYWS
817.	DL_7	VH CDR2	YIYYSGTTNYNPSLKS
818.	DL_7	VH CDR3	IAVAGFFFDY
819.	DL_7	VL CDR1	RASQSVNKNYLA
820.	DL_7	VL CDR2	GASSRAT
821.	DL_7	VL CDR3	QQYDRSPLT
822.	DL_7	VH	QVQLQESGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSS
823.	DL_7	VL	EIVLTQSPGTLSLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDRSPLTFGGGTRLEIK
824.	DL_7	scFv	QVQLQESGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGESATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTRLEI K
825.	DL_7	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARIAVAGFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGESATLSCRASQ SVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTRLEI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL
826.	DL_8	VH	SYYWS

		CDR1	
827.	DL_8	VH CDR2	YIFYNGITNYNPSLKS
828.	DL_8	VH CDR3	IHSGSFSFDY
829.	DL_8	VL CDR1	RASQSVSRGYLA
830.	DL_8	VL CDR2	GASSRAT
831.	DL_8	VL CDR3	QQYDTSPIT
832.	DL_8	VH	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYNPSLKSRVTISLDTSKNQFSL KLSSVTAADTAKYYCARIHSGSFSFDYWDQGTLVTVSS
833.	DL_8	VL	EIVMTQSPGTLSLSPGERATLSCRASQSVSRGYLAWYQQKPGQAPRLLIYGASSRATDIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYDTSPITFGQGTKVEIK
834.	DL_8	scFv	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYNPSLKSRVTISLDTSKNQFSL KLSSVTAADTAKYYCARIHSGSFSFDYWDQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTLSLSPGERATLSCRASQ SVSRGYLAWYQQKPGQAPRLLIYGASSRATDIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSPITFGQGTKVEI K
835.	DL_8	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYNPSLKSRVTISLDTSKNQFSL KLSSVTAADTAKYYCARIHSGSFSFDYWDQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTLSLSPGERATLSCRASQ SVSRGYLAWYQQKPGQAPRLLIYGASSRATDIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSPITFGQGTKVEI KSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW YSNRWVFGGGTKLTVL
836.	DL_9	VH CDR1	SYYMH
837.	DL_9	VH CDR2	IINPSDGSTNYAQNFQG
838.	DL_9	VH CDR3	GGNSAFYSYYDMDV
839.	DL_9	VL CDR1	RSSQSLVYRDGNTYLS

840.	DL_9	VL CDR2	KVSNWQS
841.	DL_9	VL CDR3	MQGTHWPPT
842.	DL_9	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSDGSTNYAQNFQGRVTMTRDTSTNTVY MELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSS
843.	DL_9	VL	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYFCMQGTHWPPTFGQGTKVEIK
844.	DL_9	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSDGSTNYAQNFQGRVTMTRDTSTNTVY MELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDVVMTQSPLSLPVTLGQPASIS CRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPT FGQGTKVEIK
845.	DL_9	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSDGSTNYAQNFQGRVTMTRDTSTNTVY MELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDVVMTQSPLSLPVTLGQPASIS CRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPT FGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVL
846.	DL_10	VH CDR1	NYYMH
847.	DL_10	VH CDR2	IINPSDGSTSYAQKFQG
848.	DL_10	VH CDR3	GGNSAFYSYYDMDV
849.	DL_10	VL CDR1	RSSQSLVYRDGNTYLS
850.	DL_10	VL CDR2	KVSNWQS
851.	DL_10	VL CDR3	MQGTHWPPT
852.	DL_10	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQKFQGRVTMTRDTSTNTVY MDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSS
853.	DL_10	VL	DVVMTQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGGGSGTDFTLKI SRVEAEDVGVYYCMQGTHWPPTFGQGTKVEIK

854.	DL_10	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQKFQGRVTMTRDTSTNTVY MDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDVVMTQTPLSLPVTLGQPASIS CRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPT FGQGTKVEIK
855.	DL_10	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQKFQGRVTMTRDTSTNTVY MDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDVVMTQTPLSLPVTLGQPASIS CRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPT FGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVL
856.	DL_11	VH CDR1	GYYIH
857.	DL_11	VH CDR2	IINPSDGSTSYGQNFQG
858.	DL_11	VH CDR3	GGNSAFYSYYDMDV
859.	DL_11	VL CDR1	RSSQSLAYRDGNTYLS
860.	DL_11	VL CDR2	KVSNWQS
861.	DL_11	VL CDR3	MQGTHWPPT
862.	DL_11	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGIINPSDGSTSYGQNFQGRVTMTRDTSTNTVY MELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSS
863.	DL_11	VL	DVVMTQSPLSLPVTLGQPASISCRSSQSLAYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYFCMQGTHWPPTFGQGTKVEIK
864.	DL_11	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGIINPSDGSTSYGQNFQGRVTMTRDTSTNTVY MELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDVVMTQSPLSLPVTLGQPASIS CRSSQSLAYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPT FGQGTKVEIK
865.	DL_11	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGLEWMGIINPSDGSTSYGQNFQGRVTMTRDTSTNTVY MELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDVVMTQSPLSLPVTLGQPASIS CRSSQSLAYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPT FGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV

			TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVL
866.	DL_12	VH CDR1	NYGMH
867.	DL_12	VH CDR2	VISHHGSSKYYARSVKG
868.	DL_12	VH CDR3	DWWELVFDY
869.	DL_12	VL CDR1	KSSQSLLHSDGKTFLY
870.	DL_12	VL CDR2	EVSNRFS
871.	DL_12	VL CDR3	LQGIHLPFT
872.	DL_12	VH	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISHHGSSKYYARSVKGRFTISRDNSKNTLY LEMNSLRAEDTAVYYCARDWWELVFDYWGQGTLVTVSS
873.	DL_12	VL	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTFLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCLQGIHLPFTFGPGTKVEIK
874.	DL_12	scFv	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISHHGSSKYYARSVKGRFTISRDNSKNTLY LEMNSLRAEDTAVYYCARDWWELVFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISCKSSQ SLLHSDGKTFLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGIHLPFTFGPGT KVEIK
875.	DL_12	bispecific molecule	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISHHGSSKYYARSVKGRFTISRDNSKNTLY LEMNSLRAEDTAVYYCARDWWELVFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISCKSSQ SLLHSDGKTFLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGIHLPFTFGPGT KVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
876.	DL_13	VH CDR1	NSRMGVS
877.	DL_13	VH CDR2	HIFSNDGKSYSTSLKS
878.	DL_13	VH CDR3	YNYDSSGYYYSFFDY

879.	DL_13	VL CDR1	RASQSISSYLN
880.	DL_13	VL CDR2	AASSLQS
881.	DL_13	VL CDR3	QQGYSSPFT
882.	DL_13	VH	QVTLKESGPMLVKPTETLTLTCTVSGFSLSNSRMGVSWIRQPPGRALEWLAHIFSNDGKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARYNYDSSGYYYSFFDYWGQGTLVTVSS
883.	DL_13	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQGYSSPFTFGGGTKVEIK
884.	DL_13	scFv	QVTLKESGPMLVKPTETLTLTCTVSGFSLSNSRMGVSWIRQPPGRALEWLAHIFSNDGKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARYNYDSSGYYYSFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSSPFTFGG GTKVEIK
885.	DL_13	bispecific molecule	QVTLKESGPMLVKPTETLTLTCTVSGFSLSNSRMGVSWIRQPPGRALEWLAHIFSNDGKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARYNYDSSGYYYSFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSSPFTFGG GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
886.	DL_14	VH CDR1	NARMGVS
887.	DL_14	VH CDR2	HIFSTDEKSYSTSLKS
888.	DL_14	VH CDR3	YYYDSSGYYYSFFDY
889.	DL_14	VL CDR1	RASQSIRSYLN
890.	DL_14	VL CDR2	GASNLQS
891.	DL_14	VL CDR3	QQSYSSPFT
892.	DL_14	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWLRQPPGKALEWLAHIFSTDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARYYYDSSGYYYSFFDYWGQGTLVTVSS

893.	DL_14	VL	DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQKPGKAPKLLIYGASNLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSSPFTFGGGTKVEIK
894.	DL_14	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWLRQPPGKALEWLAHIFSTDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARYYYDSSGYYYSFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQSIRSYLNWYQQKPGKAPKLLIYGASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSPFTFGG GTKVEIK
895.	DL_14	bispecifi c molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWLRQPPGKALEWLAHIFSTDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARYYYDSSGYYYSFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQSIRSYLNWYQQKPGKAPKLLIYGASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSPFTFGG GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
896.	DL_15	VH CDR1	SYYIH
897.	DL_15	VH CDR2	IINPSGGSKSYAQKFRG
898.	DL_15	VH CDR3	SMSTVTSDAFDI
899.	DL_15	VL CDR1	RASQSISNYLN
900.	DL_15	VL CDR2	AASSLQS
901.	DL_15	VL CDR3	QQSYSAPLT
902.	DL_15	VH	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYYIHWVRQAPGQGLEWMGIINPSGGSKSYAQKFRGRVTMTRDTSTSTVY MELSSLTSEDTAVYYCARSMSTVTSDAFDIWGQGTMVTVSS
903.	DL_15	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCQQSYSAPLTFGGGTKVDIK
904.	DL_15	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYYIHWVRQAPGQGLEWMGIINPSGGSKSYAQKFRGRVTMTRDTSTSTVY MELSSLTSEDTAVYYCARSMSTVTSDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCR ASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQSYSAPLTFGGGTKV DIK
905.	DL_15	bispecifi c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYYIHWVRQAPGQGLEWMGIINPSGGSKSYAQKFRGRVTMTRDTSTSTVY MELSSLTSEDTAVYYCARSMSTVTSDAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCR ASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQSYSAPLTFGGGTKV

			DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
906.	DL_16	VH CDR1	DYGIH
907.	DL_16	VH CDR2	VISYHGSNKYYARSVKG
908.	DL_16	VH CDR3	EIPFGMDV
909.	DL_16	VL CDR1	RSSQSLLHSDGYNYLD
910.	DL_16	VL CDR2	LGSNRAS
911.	DL_16	VL CDR3	MQALQTPLT
912.	DL_16	VH	QVQLVESGGGVVQSGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSNKYYARSVKGRFTVSRDNSKNTLY LQMNSLRAEDTAVYYCAREIPFGMDVWGQGTTVTVSS
913.	DL_16	VL	DIVMTQTPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLTI SRVEAEDVGVYYCMQALQTPLTFGGGTKVDIK
914.	DL_16	scFv	QVQLVESGGGVVQSGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSNKYYARSVKGRFTVSRDNSKNTLY LQMNSLRAEDTAVYYCAREIPFGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISCRSSQS LLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLTISRVEAEDVGVYYCMQALQTPLTFGGGTK VDIK
915.	DL_16	bispecific molecule	QVQLVESGGGVVQSGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSNKYYARSVKGRFTVSRDNSKNTLY LQMNSLRAEDTAVYYCAREIPFGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISCRSSQS LLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLTISRVEAEDVGVYYCMQALQTPLTFGGGTK VDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
916.	DL_17	VH CDR1	GYYMH
917.	DL_17	VH CDR2	WINPNSGDTNYAQKFQG

918.	DL_17	VH CDR3	DANIAALDAFEI
919.	DL_17	VL CDR1	RASQSISSYLN
920.	DL_17	VL CDR2	AASSLQS
921.	DL_17	VL CDR3	QQSYSTPLT
922.	DL_17	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGDTNYAQKFQGRVTMTRDTSISTAY MELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMVTVSS
923.	DL_17	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPLTFGGGTKVEIK
924.	DL_17	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGDTNYAQKFQGRVTMTRDTSISTAY MELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKV EIK
925.	DL_17	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGDTNYAQKFQGRVTMTRDTSISTAY MELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCR ASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
926.	FL_1	VH CDR1	NARMGVS
927.	FL_1	VH CDR2	HIFSNAEKSYRTSLKS
928.	FL_1	VH CDR3	IPGYGGNGDYHYYGMDV
929.	FL_1	VL CDR1	RASQGIRNDLG
930.	FL_1	VL CDR2	ASSTLQS
931.	FL_1	VL CDR3	LQHNNFPWT

932.	FL_1	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLINARMGVSWIRQPPGKALEWLAHIFSNAEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNGDYHYYGMDVWGQGTTVTVSS
933.	FL_1	VL	DIQMTQSPSSLSASLGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYASSTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNNFPWTFGQGTKVEIK
934.	FL_1	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLINARMGVSWIRQPPGKALEWLAHIFSNAEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNGDYHYYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASLGDR VTITCRASQGIRNDLGWYQQKPGKAPKRLIYASSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNFPWTF GQGTKVEIK
935.	FL_1	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLINARMGVSWIRQPPGKALEWLAHIFSNAEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNGDYHYYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASLGDR VTITCRASQGIRNDLGWYQQKPGKAPKRLIYASSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNFPWTF GQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
936.	FL_2	VH CDR1	NARMGVS
937.	FL_2	VH CDR2	HIFSNDEKTYSTSLKS
938.	FL_2	VH CDR3	IPYYGSGSHNYGMDV
939.	FL_2	VL CDR1	RASQDIRNDFG
940.	FL_2	VL CDR2	AASTLQS
941.	FL_2	VL CDR3	LQYNTYPWT
942.	FL_2	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNDEKTYSTSLKSRLTISRDTSKGQV VLTMTKMDPVDTATYYCARIPYYGSGSHNYGMDVWGQGTTVTVSS
943.	FL_2	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRNDFGWYQQKPGKAPQRLLYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQYNTYPWTFGQGTKVEIK
944.	FL_2	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNDEKTYSTSLKSRLTISRDTSKGQV VLTMTKMDPVDTATYYCARIPYYGSGSHNYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQDIRNDFGWYQQKPGKAPQRLLYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQYNTYPWTFGQ GTKVEIK
945.	FL_2	bispecifi	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKALEWLAHIFSNDEKTYSTSLKSRLTISRDTSKGQV

		c molecule	VLTMTKMDPVDTATYYCARIPYYGSGSHNYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQDIRNDFGWYQQKPGKAPQRLLYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQYNTYPWTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
946.	FL_3	VH CDR1	NARMAVS
947.	FL_3	VH CDR2	HIFSNGEKSYSTSLKS
948.	FL_3	VH CDR3	IVGYSDWLLPFDH
949.	FL_3	VL CDR1	RASQNINRFLN
950.	FL_3	VL CDR2	AASSLQS
951.	FL_3	VL CDR3	LQHNSYPWT
952.	FL_3	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMAVSWIRQPPGKALEWLAHIFSNGEKSYSTSLKSRLTISKDTSKTQV VLTMTNTDPVDTATYFCARIVGYSDWLLPFDHWGQGIMVTVSS
953.	FL_3	VL	DIQMTQSPSSLSASVGDRVTITCRASQNINRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCLQHNSYPWTFGQGTKVDIK
954.	FL_3	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMAVSWIRQPPGKALEWLAHIFSNGEKSYSTSLKSRLTISKDTSKTQV VLTMTNTDPVDTATYFCARIVGYSDWLLPFDHWGQGIMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT CRASQNINRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPWTFGQGT KVDIK
955.	FL_3	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMAVSWIRQPPGKALEWLAHIFSNGEKSYSTSLKSRLTISKDTSKTQV VLTMTNTDPVDTATYFCARIVGYSDWLLPFDHWGQGIMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT CRASQNINRFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPWTFGQGT KVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
956.	FL_4	VH CDR1	NAKMGVS
957.	FL_4	VH	HIFSNDEKSYSTSLKS

		CDR2	
958.	FL_4	VH CDR3	IVGYGSGWYGYFDY
959.	FL_4	VL CDR1	RASQDIRDDLG
960.	FL_4	VL CDR2	GASTLQS
961.	FL_4	VL CDR3	LQHNSYPLT
962.	FL_4	VH	QVTLKESGPALVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
963.	FL_4	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK
964.	FL_4	scFv	QVTLKESGPALVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIK
965.	FL_4	bispecific molecule	QVTLKESGPALVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
966.	FL_5	VH CDR1	NARMGVS
967.	FL_5	VH CDR2	HIFWNDEKSYSTSLKS
968.	FL_5	VH CDR3	IPYYGSGSYNYGMDV
969.	FL_5	VL CDR1	RASQGIRNDLG
970.	FL_5	VL CDR2	AASSLQS

971.	FL_5	VL CDR3	LQHNTYPLT
972.	FL_5	VH	QVTLKESGPMLVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSS
973.	FL_5	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNTYPLTFGGGTKVDIK
974.	FL_5	scFv	QVTLKESGPMLVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPLTFGG GTKVDIK
975.	FL_5	bispecific molecule	QVTLKESGPMLVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPLTFGG GTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
976.	FL_6	VH CDR1	NARMAVS
977.	FL_6	VH CDR2	HIFSNDEKSYSPSLKS
978.	FL_6	VH CDR3	IVGYGTGWYGFFDY
979.	FL_6	VL CDR1	RASQGIRNDLG
980.	FL_6	VL CDR2	AASVLQS
981.	FL_6	VL CDR3	LQHNSYPLT
982.	FL_6	VH	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSPSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSS
983.	FL_6	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWFQQKPGKAPKRLIYAASVLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK
984.	FL_6	scFv	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSPSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWFQQKPGKAPKRLIYAASVLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG

			TKVDIK
985.	FL_6	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSPSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWFQQKPGKAPKRLIYAASVLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
986.	FL_7	VH CDR1	NARMGVS
987.	FL_7	VH CDR2	HIFSNDEKSYSTSLKN
988.	FL_7	VH CDR3	IVGYGTGWFGYFDY
989.	FL_7	VL CDR1	RASQDIRTDLA
990.	FL_7	VL CDR2	AASSLQS
991.	FL_7	VL CDR3	LQHNRYPLT
992.	FL_7	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWFGYFDYWGQGTQVTVSS
993.	FL_7	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNRYPLTFGGGTKVDIK
994.	FL_7	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWFGYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNRYPLTFGGG TKVDIK
995.	FL_7	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWFGYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNRYPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
996.	FL_8	VH	YARMGVS

		CDR1	
997.	FL_8	VH CDR2	QIFSNDEKSYSTSLKS
998.	FL_8	VH CDR3	IVGYGTGWYGFFDY
999.	FL_8	VL CDR1	RASQGIRNDLG
1000	FL_8	VL CDR2	AASSLQS
1001	FL_8	VL CDR3	LQHNSYPLT
1002	FL_8	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKGTSNSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSS
1003	FL_8	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK
1004	FL_8	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKGTSNSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIK
1005	FL_8	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKGTSNSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1006	FL_9	VH CDR1	NARMGVS
1007	FL_9	VH CDR2	HIFSNDEKSYSTSLKS
1008	FL_9	VH CDR3	IPGYGGNFYYHYYGMDV
1009	FL_9	VL CDR1	RASQGIRNDLA

1010	FL_9	VL CDR2	AASTVQS
1011	FL_9	VL CDR3	LQHNSFPWT
1012	FL_9	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSS
1013	FL_9	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISSLQP EDFATYYCLQHNSFPWTFGQGTKVDIK
1014	FL_9	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDR VTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISSLQPEDFATYYCLQHNSFPWTF GQGTKVDIK
1015	FL_9	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDR VTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISSLQPEDFATYYCLQHNSFPWTF GQGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1016	FL_10	VH CDR1	NARMGVS
1017	FL_10	VH CDR2	HIFSNDEKSYSTSLKS
1018	FL_10	VH CDR3	MPEYSSGWSGAFDI
1019	FL_10	VL CDR1	RASQDIRDDLG
1020	FL_10	VL CDR2	GASTLQS
1021	FL_10	VL CDR3	LQHNSYPLT
1022	FL_10	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1023	FL_10	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK

1024	FL_10	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIK
1025	FL_10	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1026	FL_11	VH CDR1	NAKMGVS
1027	FL_11	VH CDR2	QIFSNGEKSYSTSLKS
1028	FL_11	VH CDR3	IVGYGSGWYGYFDY
1029	FL_11	VL CDR1	RASQGIRNDLG
1030	FL_11	VL CDR2	GASTLQS
1031	FL_11	VL CDR3	LQHNSYPLT
1032	FL_11	VH	QVTLKESGPVLVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAQIFSNGEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCSRIVGYGSGWYGYFDYWGQGTLVTVSS
1033	FL_11	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1034	FL_11	scFv	QVTLKESGPVLVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAQIFSNGEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCSRIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1035	FL_11	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTLSGFSLNNAKMGVSWIRQPPGKALEWLAQIFSNGEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCSRIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP

			SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1036	FL_12	VH CDR1	NARMGVS
1037	FL_12	VH CDR2	NIFSNDEKSYSTSLKS
1038	FL_12	VH CDR3	IVGYGSGWYGYFDY
1039	FL_12	VL CDR1	RASQGIRNDLG
1040	FL_12	VL CDR2	AASSLQS
1041	FL_12	VL CDR3	LQHNSYPLT
1042	FL_12	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNMDPEDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1043	FL_12	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPQRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1044	FL_12	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNMDPEDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPQRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1045	FL_12	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNMDPEDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPQRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1046	FL_13	VH CDR1	NARMGVS
1047	FL_13	VH CDR2	HIFSNDEKSYSTSLKN
1048	FL_13	VH CDR3	IVGYGSGWYGFFDY

1049	FL_13	VL CDR1	RASQGIRNDLG
1050	FL_13	VL CDR2	AASTLQS
1051	FL_13	VL CDR3	LQHNSYPLT
1052	FL_13	VH	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGSGWYGFFDYWGQGTLVTVSS
1053	FL_13	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1054	FL_13	scFv	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGSGWYGFFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1055	FL_13	bispecifi c molecule	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGSGWYGFFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1056	FL_14	VH CDR1	NARMAVS
1057	FL_14	VH CDR2	HIFSNDEKSYSTSLKS
1058	FL_14	VH CDR3	IVGYGSGWYGYFDY
1059	FL_14	VL CDR1	RASQDIRNDLG
1060	FL_14	VL CDR2	AASTLQS
1061	FL_14	VL CDR3	LQHNSYPLT
1062	FL_14	VH	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS

1063	FL_14	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1064	FL_14	scFv	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1065	FL_14	bispecifi c molecule	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1066	FL_15	VH CDR1	NARMAVS
1067	FL_15	VH CDR2	HIFSNDEKSYSTSLKS
1068	FL_15	VH CDR3	IVGYGSGWYGYFDY
1069	FL_15	VL CDR1	RASQDIGNDLG
1070	FL_15	VL CDR2	AASSLQS
1071	FL_15	VL CDR3	LQHNSYPLT
1072	FL_15	VH	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1073	FL_15	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIGNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1074	FL_15	scFv	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIGNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1075	FL_15	bispecifi c molecule	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIGNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG

			TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1076	FL_16	VH CDR1	NARMAVS
1077	FL_16	VH CDR2	HIFSNDEKSYSTSLKS
1078	FL_16	VH CDR3	IVGYGSGWYGYFDY
1079	FL_16	VL CDR1	RASQDIRYDLA
1080	FL_16	VL CDR2	AASSLQS
1081	FL_16	VL CDR3	LQHNFYPLT
1082	FL_16	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1083	FL_16	VL	DIQMTQSPSSVSASVGDRVTITCRASQDIRYDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNFYPLTFGGGTKVEIK
1084	FL_16	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTI TCRASQDIRYDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNFYPLTFGGG TKVEIK
1085	FL_16	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTI TCRASQDIRYDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNFYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1086	FL_17	VH CDR1	NARMGVS
1087	FL_17	VH CDR2	NIFSNDEKSYSTSLKS

1088	FL_17	VH CDR3	IVGYGSGWYGYFDY
1089	FL_17	VL CDR1	RASQDIRNDLG
1090	FL_17	VL CDR2	ATSIRQS
1091	FL_17	VL CDR3	LQHNSFPLT
1092	FL_17	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNVNPVDTGTYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1093	FL_17	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQP EDFATYFCLQHNSFPLTFGGGTKVEIK
1094	FL_17	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNVNPVDTGTYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPGKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGGG TKVEIK
1095	FL_17	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNVNPVDTGTYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPGKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1096	FL_18	VH CDR1	NARMGVS
1097	FL_18	VH CDR2	HIFSNDEKSFSTSLKN
1098	FL_18	VH CDR3	MVGYGSGWYAYFDY
1099	FL_18	VL CDR1	RASQSISSYLN
1100	FL_18	VL CDR2	AASSLQS
1101	FL_18	VL CDR3	LQHNSYPLT

1102	FL_18	VH	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTQVTVSS
1103	FL_18	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1104	FL_18	scFv	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1105	FL_18	bispecific molecule	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1106	FL_19	VH CDR1	YARMGVS
1107	FL_19	VH CDR2	QIFSNDEKSYSTSLKS
1108	FL_19	VH CDR3	IVGYGTGWYGYFDY
1109	FL_19	VL CDR1	RASQDIGDDLG
1110	FL_19	VL CDR2	AASTLQS
1111	FL_19	VL CDR3	LQHNSYPLT
1112	FL_19	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSS
1113	FL_19	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIGDDLGWYQQKPGKAPKRLIYAASTLQSGVPFRFSGSGSGTDFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1114	FL_19	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIGDDLGWYQQKPGKAPKRLIYAASTLQSGVPFRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1115	FL_19	bispecifi	QVTLKESGPTLVKPTETLTLTCTVSGFSLSYARMGVSWIRQPPGKALEWLAQIFSNDEKSYSTSLKSRLTISKDTSKSQV

		c molecule	VLTMTDMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIGDDLGWYQQKPGKAPKRLIYAASTLQSGVPFRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1116	FL_20	VH CDR1	NARMAVS
1117	FL_20	VH CDR2	HIFSNDEKSYSTSLKS
1118	FL_20	VH CDR3	IVGYGTGWYGFFDY
1119	FL_20	VL CDR1	RASQGIRNDLA
1120	FL_20	VL CDR2	AASSLQS
1121	FL_20	VL CDR3	LQHNSYPLT
1122	FL_20	VH	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSS
1123	FL_20	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1124	FL_20	scFv	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1125	FL_20	bispecific molecule	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1126	FL_21	VH CDR1	NARMGVS
1127	FL_21	VH	HIFSNDEKSYSTSLKS

1128	FL_21	VH CDR3	IPGYGGNFYYHYYGMDV
1129	FL_21	VL CDR1	RTSRGIRNDLG
1130	FL_21	VL CDR2	AASTLQS
1131	FL_21	VL CDR3	LQHNNFPWT
1132	FL_21	VH	QVTLKESGPALVKPTETLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSS
1133	FL_21	VL	DIQMTQSPSSLSASVGDRVTITCRTSRGIRNDLGWYQQIPGRAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNNFPWTFGQGTKVEIK
1134	FL_21	scFv	QVTLKESGPALVKPTETLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDR VTITCRTSRGIRNDLGWYQQIPGRAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNFPWTF GQGTKVEIK
1135	FL_21	bispecific molecule	QVTLKESGPALVKPTETLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDR VTITCRTSRGIRNDLGWYQQIPGRAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNNFPWTF GQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1136	FL_22	VH CDR1	NARMGVS
1137	FL_22	VH CDR2	HIFSNDEKSYSTSLKS
1138	FL_22	VH CDR3	MPEYSSGWSGAFDI
1139	FL_22	VL CDR1	RASQGISNYLA
1140	FL_22	VL CDR2	AASTLQS

1141	FL_22	VL CDR3	LQHNTYPWT
1142	FL_22	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1143	FL_22	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNTYPWTFGQGTKVEIK
1144	FL_22	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPWTFGQG TKVEIK
1145	FL_22	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPWTFGQG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1146	FL_23	VH CDR1	NARMGVS
1147	FL_23	VH CDR2	HIFSNDEKSYSTSLKS
1148	FL_23	VH CDR3	MPEYSSGWSGAFDI
1149	FL_23	VL CDR1	RASQDIGYDLG
1150	FL_23	VL CDR2	AASTLQS
1151	FL_23	VL CDR3	LQHNSFPWT
1152	FL_23	VH	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1153	FL_23	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIGYDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLIISSLQP EDFATYYCLQHNSFPWTFGQGTKVEIK
1154	FL_23	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIGYDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLIISSLQPEDFATYYCLQHNSFPWTFGQG

			TKVEIK
1155	FL_23	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIGYDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLIISSLQPEDFATYYCLQHNSFPWTFGQG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1156	FL_24	VH CDR1	NVRMGVS
1157	FL_24	VH CDR2	HIFSNDEKSYSTSLKS
1158	FL_24	VH CDR3	MPEYSSGWSGAFDI
1159	FL_24	VL CDR1	RASQDIRDDLV
1160	FL_24	VL CDR2	AASTLQS
1161	FL_24	VL CDR3	LQHHSYPWT
1162	FL_24	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLILTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1163	FL_24	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRDDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHHSYPWTFGQGTKVEIK
1164	FL_24	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLILTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHHSYPWTFGQG TKVEIK
1165	FL_24	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLILTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHHSYPWTFGQG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1166	FL_25	VH	NARMGVS

		CDR1	
1167	FL_25	VH CDR2	HIFSNDEKSYSTSLKS
1168	FL_25	VH CDR3	MPEYSSGWSGAFDI
1169	FL_25	VL CDR1	RASQDIRDDLG
1170	FL_25	VL CDR2	AASTLQS
1171	FL_25	VL CDR3	LQHNSFPFT
1172	FL_25	VH	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1173	FL_25	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRDDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFTGGGSGTEFTLTISSLQP EDFATYYCLQHNSFPFTFGGGTKVEIK
1174	FL_25	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFTGGGSGTEFTLTISSLQPEDFATYYCLQHNSFPFTFGGG TKVEIK
1175	FL_25	bispecific molecule	QVTLKESGPALVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFTGGGSGTEFTLTISSLQPEDFATYYCLQHNSFPFTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1176	FL_26	VH CDR1	NARMGVS
1177	FL_26	VH CDR2	HIFSNDEKSYSTSLKS
1178	FL_26	VH CDR3	MPEYSSGWSGAFDI
1179	FL_26	VL CDR1	RASQGIRNDLV

1180	FL_26	VL CDR2	GTSTLQS
1181	FL_26	VL CDR3	LQHNSYPLT
1182	FL_26	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1183	FL_26	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1184	FL_26	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1185	FL_26	bispecifi c molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1186	FL_27	VH CDR1	NARMGVS
1187	FL_27	VH CDR2	HIFSNDEKSYSTSLKS
1188	FL_27	VH CDR3	MPEYSSGWSGAFDI
1189	FL_27	VL CDR1	RTSQGIRNDLV
1190	FL_27	VL CDR2	AASTLQS
1191	FL_27	VL CDR3	LQHYSYPLT
1192	FL_27	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1193	FL_27	VL	DIQMTQSPSSLSASVGDRVTITCRTSQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYFCLQHYSYPLTFGGGTKVEIK

1194	FL_27	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHYSYPLTFGGG TKVEIK
1195	FL_27	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHYSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1196	FL_28	VH CDR1	NARMGVS
1197	FL_28	VH CDR2	HIFSNDEKSYSTSLKS
1198	FL_28	VH CDR3	MPEYSSGWSGAFDI
1199	FL_28	VL CDR1	RASQGIGDDLG
1200	FL_28	VL CDR2	ATSVLQS
1201	FL_28	VL CDR3	LQHNSYPLT
1202	FL_28	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1203	FL_28	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1204	FL_28	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1205	FL_28	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP

			SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1206	FL_29	VH CDR1	NARMGVS
1207	FL_29	VH CDR2	HIFSNDEKSYRTSLKS
1208	FL_29	VH CDR3	IVGYGSGWYAYFDY
1209	FL_29	VL CDR1	RASQGIRNDLG
1210	FL_29	VL CDR2	AASSLQS
1211	FL_29	VL CDR3	LQHNSYPLT
1212	FL_29	VH	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYAYFDYWGQGTLVTVSS
1213	FL_29	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1214	FL_29	scFv	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1215	FL_29	bispecific molecule	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1216	FL_30	VH CDR1	NARMGVS
1217	FL_30	VH CDR2	LIYWNDDKRYSPSLKS
1218	FL_30	VH CDR3	MVGYGSGWYAYFDY

1219	FL_30	VL CDR1	RASQGIRNDLG
1220	FL_30	VL CDR2	AASSLQS
1221	FL_30	VL CDR3	LQHNSYPLT
1222	FL_30	VH	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSS
1223	FL_30	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1224	FL_30	scFv	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1225	FL_30	bispecific molecule	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1226	FL_31	VH CDR1	NARMGVS
1227	FL_31	VH CDR2	HIFSNDEKSYSTSLKS
1228	FL_31	VH CDR3	IVGYGTGWYGFFDY
1229	FL_31	VL CDR1	RTSQGIRNDLG
1230	FL_31	VL CDR2	AASSLQS
1231	FL_31	VL CDR3	LQHNSYPLT
1232	FL_31	VH	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSS

1233	FL_31	VL	DIQMTQSPSSLSASVGDRVTITCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1234	FL_31	scFv	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1235	FL_31	bispecifi c molecule	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1236	FL_32	VH CDR1	NARMGVS
1237	FL_32	VH CDR2	HIFSNDEKSYSTSLKS
1238	FL_32	VH CDR3	IVGYGSGWYGYFDY
1239	FL_32	VL CDR1	RASQGIRNDLV
1240	FL_32	VL CDR2	AASTLQS
1241	FL_32	VL CDR3	LQHYSYPLT
1242	FL_32	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1243	FL_32	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFILTISSLQP EDFATYFCLQHYSYPLTFGGGTKLEIK
1244	FL_32	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFILTISSLQPEDFATYFCLQHYSYPLTFGGG TKLEIK
1245	FL_32	bispecifi c molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFILTISSLQPEDFATYFCLQHYSYPLTFGGG

			TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1246	FL_33	VH CDR1	NARMGVS
1247	FL_33	VH CDR2	HIFSNDEKSYSTSLKS
1248	FL_33	VH CDR3	IVGYGSGWYGYFDY
1249	FL_33	VL CDR1	RASQGIGDDLG
1250	FL_33	VL CDR2	ATSVLQS
1251	FL_33	VL CDR3	LQHNSYPLT
1252	FL_33	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1253	FL_33	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKLEIK
1254	FL_33	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKLEIK
1255	FL_33	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNARMGVSWIRQPPGKTLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKGQV VLTMTNMDPVDTATYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIGDDLGWYQQIPGKAPKRLIYATSVLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1256	FL_34	VH CDR1	NARMGVS
1257	FL_34	VH CDR2	HIFWNDEKSYSTSLKS

1258	FL_34	VH CDR3	IPYYGSGSYNYGMDV
1259	FL_34	VL CDR1	RASQGIRNDLG
1260	FL_34	VL CDR2	AASSLQS
1261	FL_34	VL CDR3	LQHNSYPLT
1262	FL_34	VH	QVTLKESGPALVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSS
1263	FL_34	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKLEIK
1264	FL_34	scFv	QVTLKESGPALVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGG GTKLEIK
1265	FL_34	bispecifi c molecule	QVTLKESGPALVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKALEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGG GTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
1266	FL_35	VH CDR1	NARMGVS
1267	FL_35	VH CDR2	HIFSNDEKSYSTSLKN
1268	FL_35	VH CDR3	IVGYGTGWYGFFDY
1269	FL_35	VL CDR1	RASQDIRDDLV
1270	FL_35	VL CDR2	GTSTLQS
1271	FL_35	VL CDR3	LQHHSYPLT

1272	FL_35	VH	QVTLKESGPALVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWYGFFDYWGQGTQVTVSS
1273	FL_35	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRDDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHHSYPLTFGGGTKLEIK
1274	FL_35	scFv	QVTLKESGPALVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWYGFFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHHSYPLTFGGG TKLEIK
1275	FL_35	bispecifi c molecule	QVTLKESGPALVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWYGFFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHHSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1276	FL_36	VH CDR1	YARMGVS
1277	FL_36	VH CDR2	HIFSNDEKSYSTSLKS
1278	FL_36	VH CDR3	MPEYSSGWSGAFDI
1279	FL_36	VL CDR1	RASQDIRNDLA
1280	FL_36	VL CDR2	AASSLQS
1281	FL_36	VL CDR3	LQHNSYPLT
1282	FL_36	VH	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1283	FL_36	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKLEIK
1284	FL_36	scFv	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKLEIK
1285	FL_36	bispecifi	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV

		c molecule	VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL	
1286	FL_37	VH CDR1	NIKMGVS
1287	FL_37	VH CDR2	HIFSNDEKSYSTSLKS
1288	FL_37	VH CDR3	MPEYSSGWSGAFDI
1289	FL_37	VL CDR1	RASQDISNYLA
1290	FL_37	VL CDR2	AASSLQS
1291	FL_37	VL CDR3	LQHNSFPLT
1292	FL_37	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNIKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1293	FL_37	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSFPLTFGGGTKLEIK
1294	FL_37	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNIKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDISNYLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSFPLTFGGG TKLEIK
1295	FL_37	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNIKMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDISNYLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSFPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1296	FL_38	VH CDR1	NARMGVS
1297	FL_38	VH	HIFSNDEKSYSTSLKS

		CDR2	
1298	FL_38	VH CDR3	MPEYSSGWSGAFDI
1299	FL_38	VL CDR1	RASQGIRNDLG
1300	FL_38	VL CDR2	AASSLQS
1301	FL_38	VL CDR3	LQHNSYPLT
1302	FL_38	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTLVTVSS
1303	FL_38	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKLEIK
1304	FL_38	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKLEIK
1305	FL_38	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1306	FL_39	VH CDR1	NARMGVS
1307	FL_39	VH CDR2	HIFSNDEKSYSTSLKN
1308	FL_39	VH CDR3	IVGYGSGWYGFFDY
1309	FL_39	VL CDR1	RASQGIRNDLG
1310	FL_39	VL CDR2	AASTLQS

1311	FL_39	VL CDR3	LQHNSYPLT
1312	FL_39	VH	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGSGWYGFFDYWGQGTLVTVSS
1313	FL_39	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1314	FL_39	scFv	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGSGWYGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1315	FL_39	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTLSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGSGWYGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1316	FL_40	VH CDR1	NARMGVS
1317	FL_40	VH CDR2	NIFSNDEKSYSTSLKS
1318	FL_40	VH CDR3	IVGYGSGWYGYFDY
1319	FL_40	VL CDR1	RASQDIRNDLG
1320	FL_40	VL CDR2	ATSIRQS
1321	FL_40	VL CDR3	LQHNSFPLT
1322	FL_40	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKCLEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNVNPVDTGTYYCARIVGYGSGWYGYFDYWGQGTLVTVSS
1323	FL_40	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQP EDFATYFCLQHNSFPLTFGCGTKVEIK
1324	FL_40	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKCLEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNVNPVDTGTYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPGKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGCG

			TKVEIK
1325	FL_40	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKCLEWLANIFSNDEKSYSTSLKSRLTISKGTSKSQV VLTMTNVNPVDTGTYYCARIVGYGSGWYGYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPGKAPKRLIYATSIRQSGVPSRFTGSGSGTEFTLTISGLQPEDFATYFCLQHNSFPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1326	FL_41	VH CDR1	NARMGVS
1327	FL_41	VH CDR2	HIFSNDEKSFSTSLKN
1328	FL_41	VH CDR3	MVGYGSGWYAYFDY
1329	FL_41	VL CDR1	RASQSISSYLN
1330	FL_41	VL CDR2	AASSLQS
1331	FL_41	VL CDR3	LQHNSYPLT
1332	FL_41	VH	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTQVTVSS
1333	FL_41	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1334	FL_41	scFv	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1335	FL_41	bispecific molecule	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSFSTSLKNRLTISKDTSKSQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTQVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1336	FL_42	VH	NARMAVS

		CDR1	
1337	FL_42	VH CDR2	HIFSNDEKSYSTSLKS
1338	FL_42	VH CDR3	IVGYGTGWYGFFDY
1339	FL_42	VL CDR1	RASQGIRNDLA
1340	FL_42	VL CDR2	AASSLQS
1341	FL_42	VL CDR3	LQHNSYPLT
1342	FL_42	VH	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSS
1343	FL_42	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1344	FL_42	scFv	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1345	FL_42	bispecific molecule	QVTLKESGPALVKPTETLTLTCTLSGFSLNNARMAVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1346	FL_43	VH CDR1	NARMGVS
1347	FL_43	VH CDR2	HIFSNDEKSYSTSLKS
1348	FL_43	VH CDR3	MPEYSSGWSGAFDI
1349	FL_43	VL CDR1	RASQGIRNDLV

1350	FL_43	VL CDR2	GTSTLQS
1351	FL_43	VL CDR3	LQHNSYPLT
1352	FL_43	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1353	FL_43	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1354	FL_43	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1355	FL_43	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLVWYQQKPGKAPKRLIYGTSTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1356	FL_44	VH CDR1	NARMGVS
1357	FL_44	VH CDR2	HIFSNDEKSYSTSLKS
1358	FL_44	VH CDR3	MPEYSSGWSGAFDI
1359	FL_44	VL CDR1	RTSQGIRNDLV
1360	FL_44	VL CDR2	AASTLQS
1361	FL_44	VL CDR3	LQHYSYPLT
1362	FL_44	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1363	FL_44	VL	DIQMTQSPSSLSASVGDRVTITCRTSQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYFCLQHYSYPLTFGCGTKVEIK

1364	FL_44	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHYSYPLTFGCG TKVEIK
1365	FL_44	bispecifi c molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSFRNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLVWYQQKPGKAPKRLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHYSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1366	FL_45	VH CDR1	NARMGVS
1367	FL_45	VH CDR2	HIFSNDEKSYRTSLKS
1368	FL_45	VH CDR3	IVGYGSGWYAYFDY
1369	FL_45	VL CDR1	RASQGIRNDLG
1370	FL_45	VL CDR2	AASSLQS
1371	FL_45	VL CDR3	LQHNSYPLT
1372	FL_45	VH	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYAYFDYWGQGTLVTVSS
1373	FL_45	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1374	FL_45	scFv	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1375	FL_45	bispecifi c molecule	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYRTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP

			SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1376	FL_46	VH CDR1	NARMGVS
1377	FL_46	VH CDR2	LIYWNDDKRYSPSLKS
1378	FL_46	VH CDR3	MVGYGSGWYAYFDY
1379	FL_46	VL CDR1	RASQGIRNDLG
1380	FL_46	VL CDR2	AASSLQS
1381	FL_46	VL CDR3	LQHNSYPLT
1382	FL_46	VH	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSS
1383	FL_46	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1384	FL_46	scFv	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1385	FL_46	bispecific molecule	QVTLKESGPVLVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1386	FL_47	VH CDR1	NARMGVS
1387	FL_47	VH CDR2	HIFSNDEKSYSTSLKS
1388	FL_47	VH CDR3	IVGYGTGWYGFFDY

1389	FL_47	VL CDR1	RTSQGIRNDLG
1390	FL_47	VL CDR2	AASSLQS
1391	FL_47	VL CDR3	LQHNSYPLT
1392	FL_47	VH	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSS
1393	FL_47	VL	DIQMTQSPSSLSASVGDRVTITCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1394	FL_47	scFv	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1395	FL_47	bispecific molecule	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTDMDPEDTATYYCARIVGYGTGWYGFFDYWGQGILVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1396	FL_48	VH CDR1	NARMGVS
1397	FL_48	VH CDR2	HIFWNDEKSYSTSLKS
1398	FL_48	VH CDR3	IPYYGSGSYNYGMDV
1399	FL_48	VL CDR1	RASQGIRNDLG
1400	FL_48	VL CDR2	AASSLQS
1401	FL_48	VL CDR3	LQHNTYPLT
1402	FL_48	VH	QVTLKESGPMLVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKCLEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSS

1403	FL_48	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNTYPLTFGCGTKVDIK
1404	FL_48	scFv	QVTLKESGPMLVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKCLEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPLTFGC GTKVDIK
1405	FL_48	bispecific molecule	QVTLKESGPMLVKPTETLTLTCTFSGFSLRNARMGVSWIRQPPGKCLEWLAHIFWNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPYYGSGSYNYGMDVWGQGTTVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNTYPLTFGC GTKVDIKSGGGGSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
1406	FL_49	VH CDR1	NARMGVS
1407	FL_49	VH CDR2	HIFSNDEKSYSTSLKN
1408	FL_49	VH CDR3	IVGYGTGWFGYFDY
1409	FL_49	VL CDR1	RASQDIRTDLA
1410	FL_49	VL CDR2	AASSLQS
1411	FL_49	VL CDR3	LQHNRYPLT
1412	FL_49	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWFGYFDYWGQGTQVTVSS
1413	FL_49	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNRYPLTFGCGTKVDIK
1414	FL_49	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWFGYFDYWGQGTQVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNRYPLTFGCG TKVDIK
1415	FL_49	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLNNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKNRLTISKDSSKTQV VLTMTNVDPVDTATYYCARIVGYGTGWFGYFDYWGQGTQVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRTDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNRYPLTFGCG

			TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1416	FL_50	VH CDR1	NARMGVS
1417	FL_50	VH CDR2	HIFSNDEKSYSTSLKS
1418	FL_50	VH CDR3	IPGYGGNFYYHYYGMDV
1419	FL_50	VL CDR1	RASQGIRNDLA
1420	FL_50	VL CDR2	AASTVQS
1421	FL_50	VL CDR3	LQHNSFPWT
1422	FL_50	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSS
1423	FL_50	VL	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISSLQP EDFATYYCLQHNSFPWTFGCGTKVDIK
1424	FL_50	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDR VTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISSLQPEDFATYYCLQHNSFPWTF GCGTKVDIK
1425	FL_50	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTMTNMDPVDTATYYCARIPGYGGNFYYHYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDR VTITCRASQGIRNDLAWYQQKPGKAPKRLIYAASTVQSGVPSRFSGSGSGTEFALTISSLQPEDFATYYCLQHNSFPWTF GCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1426	FL_51	VH CDR1	NVRMGVS
1427	FL_51	VH CDR2	HISSNDEKSYSTSLRS

1428	FL_51	VH CDR3	MPGDSNTWRGFFDY
1429	FL_51	VL CDR1	RTSQSVNNNLA
1430	FL_51	VL CDR2	GASTRAT
1431	FL_51	VL CDR3	LQHNSYPLT
1432	FL_51	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKCLEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSS
1433	FL_51	VL	EIVMTQSPATLSVSPGERATLSCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVEIK
1434	FL_51	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKCLEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL SCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIK
1435	FL_51	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKCLEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL SCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1436	FL_52	VH CDR1	YARMGVS
1437	FL_52	VH CDR2	HIFSNDEKSYSTSLKS
1438	FL_52	VH CDR3	MPEYSSGWSGAFDI
1439	FL_52	VL CDR1	RASQDIRNDLA
1440	FL_52	VL CDR2	AASSLQS
1441	FL_52	VL CDR3	LQHNSYPLT

1442	FL_52	VH	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1443	FL_52	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKLEIK
1444	FL_52	scFv	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKLEIK
1445	FL_52	bispecifi c molecule	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKCLEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLAWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGCG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1446	FL_53	VH CDR1	SYGMH
1447	FL_53	VH CDR2	VISYDGSNEFYADSVKG
1448	FL_53	VH CDR3	GGEITMVRGVIGYYYYGMDV
1449	FL_53	VL CDR1	RTSQSISSYLN
1450	FL_53	VL CDR2	AASSLQS
1451	FL_53	VL CDR3	LQHNSYPLT
1452	FL_53	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSS
1453	FL_53	VL	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGCGTKVDIK
1454	FL_53	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGCGTKVDIK
1455	FL_53	bispecifi	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY

		c molecule	LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1456	FL_54	VH CDR1	SYGMH
1457	FL_54	VH CDR2	VISYDGSNEFYADSVKG
1458	FL_54	VH CDR3	GGEITMVRGVIGYYYYGMDV
1459	FL_54	VL CDR1	RASQGVRNNLV
1460	FL_54	VL CDR2	GASTRAT
1461	FL_54	VL CDR3	LQHNSYPLT
1462	FL_54	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSS
1463	FL_54	VL	EIVMTQSPATLSVSPGERATLSCRASQGVRNNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFATYYCLQHNSYPLTFGCGTKVEIK
1464	FL_54	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRNNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPL TFGCGTKVEIK
1465	FL_54	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRNNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPL TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1466	FL_55	VH CDR1	SYGMH
1467	FL_55	VH	VISYDGSNKYYADSVKG

		CDR2	
1468	FL_55	VH CDR3	SYGMDV
1469	FL_55	VL CDR1	RASQGISSWLA
1470	FL_55	VL CDR2	AASSLQS
1471	FL_55	VL CDR3	QQANSFPWT
1472	FL_55	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQGTTVTVSS
1473	FL_55	VL	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQANSFPWTFGCGTKLEIK
1474	FL_55	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGCGTKLEIK
1475	FL_55	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGCGTKLEIKSGG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR WVFGGGTKLTVL
1476	FL_56	VH CDR1	NVRMGVS
1477	FL_56	VH CDR2	HIFSNDEKLYTTSLKS
1478	FL_56	VH CDR3	IVGYGTGWYGYFDY
1479	FL_56	VL CDR1	RASQDIRDDLG
1480	FL_56	VL CDR2	ATSIRQS
1481	FL_56	VL	LQHHSFPLT

		CDR3	
1482	FL_56	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKLYTTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSS
1483	FL_56	VL	DIQMTQSPSSLSASIGDRVTITCRASQDIRDDLGWYQREPGKAPKRLIYATSIRQSGVPSRFSGSGSGTEFTLTISGLQP EDFATYFCLQHHSFPLTFGGGTKVDIK
1484	FL_56	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKLYTTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSSGGGGSGGGGSDIQMTQSPSSLSASIGDRVTI TCRASQDIRDDLGWYQREPGKAPKRLIYATSIRQSGVPSRFSGSGSGTEFTLTISGLQPEDFATYFCLQHHSFPLTFGGG TKVDIK
1485	FL_56	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKLYTTSLKSRLTISKDTSKSQV VLTMTNMDPEDTATYYCARIVGYGTGWYGYFDYWGQGTQVTVSSGGGGSGGGGSDIQMTQSPSSLSASIGDRVTI TCRASQDIRDDLGWYQREPGKAPKRLIYATSIRQSGVPSRFSGSGSGTEFTLTISGLQPEDFATYFCLQHHSFPLTFGGG TKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1486	FL_57	VH CDR1	YARMGVS
1487	FL_57	VH CDR2	HISSNDEKSFSTALES
1488	FL_57	VH CDR3	MPGDSNTWRGFFDY
1489	FL_57	VL CDR1	RTSQTVTNSYIA
1490	FL_57	VL CDR2	GTSTRAT
1491	FL_57	VL CDR3	QKYGSSPLT
1492	FL_57	VH	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHISSNDEKSFSTALESRLTISTDTSKSQM VLTMTNVDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSS
1493	FL_57	VL	EIVMTQSPGTLSLSPGERATLSCRTSQTVTNSYIAWYQQRPGQAPRLLIYGTSTRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQKYGSSPLTFGGGTKLEIK
1494	FL_57	scFv	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHISSNDEKSFSTALESRLTISTDTSKSQM VLTMTNVDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTLSLSPGERATL SCRTSQTVTNSYIAWYQQRPGQAPRLLIYGTSTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGSSPLTFGG GTKLEIK

1495	FL_57	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTFSGFSLRYARMGVSWIRQPPGKALEWLAHISSNDEKSFSTALESRLTISTDTSKSQM VLTMTNVDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPGTLSLSPGERATL SCRTSQTVTNSYIAWYQQRPGQAPRLLIYGTSTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGSSPLTFGG GTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
1496	FL_58	VH CDR1	NVRMGVS
1497	FL_58	VH CDR2	HISSNDEKSYSTSLRS
1498	FL_58	VH CDR3	MPGDSNTWRGFFDY
1499	FL_58	VL CDR1	RTSQSVNNNLA
1500	FL_58	VL CDR2	GASTRAT
1501	FL_58	VL CDR3	LQHNSYPLT
1502	FL_58	VH	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSS
1503	FL_58	VL	EIVMTQSPATLSVSPGERATLSCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1504	FL_58	scFv	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL SCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIK
1505	FL_58	bispecific molecule	QVTLKESGPTLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHISSNDEKSYSTSLRSRLTISTDTSKSQV VLTMTNMDPVDTATYYCARMPGDSNTWRGFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPGERATL SCRTSQSVNNNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1506	FL_59	VH CDR1	NVRMGVS

1507	FL_59	VH CDR2	HIFSNDEKSYSTSLKS
1508	FL_59	VH CDR3	MPEYSSGWSGAFDI
1509	FL_59	VL CDR1	RASQDIRDDLG
1510	FL_59	VL CDR2	GASTLQS
1511	FL_59	VL CDR3	LQHNSYPLT
1512	FL_59	VH	QVTLKESGPMLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSS
1513	FL_59	VL	DIQMTQSPSSLSASVGDRVTITCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTRLEIK
1514	FL_59	scFv	QVTLKESGPMLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TRLEIK
1515	FL_59	bispecific molecule	QVTLKESGPMLVKPTETLTLTCTVSGFSLRNVRMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQV VLTLTNMDPVDTATYFCARMPEYSSGWSGAFDIWGQGTMVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQDIRDDLGWYQQKPGNAPKRLIYGASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGG TRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1516	FL_60	VH CDR1	NARMGVS
1517	FL_60	VH CDR2	HIFSNDEKSYSTSLKS
1518	FL_60	VH CDR3	MVGYGSGWYAYFDY
1519	FL_60	VL CDR1	RSSQSLLHSNGYNYLY
1520	FL_60	VL CDR2	EVSNRFS

1521	FL_60	VL CDR3	MQALQTPLT
1522	FL_60	VH	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKRQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSS
1523	FL_60	VL	DIVMTQTPLSLSVTPGQPASISCRSSQSLLHSNGYNYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK
1524	FL_60	scFv	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKRQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASI SCRSSQSLLHSNGYNYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPL TFGGGTKVEIK
1525	FL_60	bispecific molecule	QVTLKESGPALVKPTQTLTLTCTFSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKRQV VLTMTNMDPVDTATYYCARMVGYGSGWYAYFDYWGQGTLVTVSSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASI SCRSSQSLLHSNGYNYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPL TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1526	FL_61	VH CDR1	SYGMH
1527	FL_61	VH CDR2	VISYDGSNEFYADSVKG
1528	FL_61	VH CDR3	GGEITMVRGVIGYYYYGMDV
1529	FL_61	VL CDR1	RASQSISSYLN
1530	FL_61	VL CDR2	AASSLQS
1531	FL_61	VL CDR3	LQHNSYPLT
1532	FL_61	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSS
1533	FL_61	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVEIK
1534	FL_61	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL

			TFGGGTKVEIK
1535	FL_61	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1536	FL_62	VH CDR1	SYGMH
1537	FL_62	VH CDR2	VISYDGSNEFYADSVKG
1538	FL_62	VH CDR3	GGEITMVRGVIGYYYYGMDV
1539	FL_62	VL CDR1	RASQGVRNNLV
1540	FL_62	VL CDR2	GASTRAT
1541	FL_62	VL CDR3	LQHNSYPLT
1542	FL_62	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSS
1543	FL_62	VL	EIVMTQSPATLSVSPGERATLSCRASQGVRNNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQS EDFATYYCLQHNSYPLTFGGGTKVEIK
1544	FL_62	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRNNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPL TFGGGTKVEIK
1545	FL_62	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPATLSVSPG ERATLSCRASQGVRNNLVWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFATYYCLQHNSYPL TFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1546	FL_63	VH	SYGMH

		CDR1	
1547	FL_63	VH CDR2	VISYDGSNEFYADSVKG
1548	FL_63	VH CDR3	GGEITMVRGVIGYYYYGMDV
1549	FL_63	VL CDR1	RTSQSISSYLN
1550	FL_63	VL CDR2	AASSLQS
1551	FL_63	VL CDR3	LQHNSYPLT
1552	FL_63	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSS
1553	FL_63	VL	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK
1554	FL_63	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGGGTKVDIK
1555	FL_63	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG DRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1556	FL_64	VH CDR1	SYGMH
1557	FL_64	VH CDR2	VISYDGSNEFYADSVKG
1558	FL_64	VH CDR3	GGEITMVRGVIGYYYYGMDV
1559	FL_64	VL CDR1	RASQSISSYLN

1560	FL_64	VL CDR2	AASSLQS
1561	FL_64	VL CDR3	LQHNSYPLT
1562	FL_64	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSS
1563	FL_64	VL	DIQMTQSPSSLSASVGNRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQHNSYPLTFGGGTKVDIK
1564	FL_64	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG NRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGGGTKVDIK
1565	FL_64	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNEFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGGEITMVRGVIGYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVG NRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPL TFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1566	FL_66	VH CDR1	SYGMH
1567	FL_66	VH CDR2	VISYDGSNKYYADSVKG
1568	FL_66	VH CDR3	SYGMDV
1569	FL_66	VL CDR1	RASQGISSWLA
1570	FL_66	VL CDR2	AASSLQS
1571	FL_66	VL CDR3	QQANSFPWT
1572	FL_66	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQGTTVTVSS
1573	FL_66	VL	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQANSFPWTFGQGTKLEIK

1574	FL_66	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGQGTKLEIK
1575	FL_66	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARSYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQGIS SWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGQGTKLEIKSGG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR WVFGGGTKLTVL
1576	CD33_1	VH CDR1	NYGMN
1577	CD33_1	VH CDR2	WINTYTGEPTYADKFQG
1578	CD33_1	VH CDR3	WSWSDGYYVYFDY
1579	CD33_1	VL CDR1	KSSQSVLDSSTNKNSLA
1580	CD33_1	VL CDR2	WASTRES
1581	CD33_1	VL CDR3	QQSAHFPIT
1582	CD33_1	VH	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAY MEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSS
1583	CD33_1	VL	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLT IDSPQPEDSATYYCQQSAHFPITFGQGTRLEIK
1584	CD33_1	scFv	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAY MEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINC KSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIT FGQGTRLEIK
1585	CD33_1	bispecific molecule	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAY MEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINC KSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIT FGQGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED

			EAEYYCVLWYSNRWVFGGGTKLTVL
1586	CD33_2	VH CDR1	NYGMN
1587	CD33_2	VH CDR2	WINTYTGEPTYADKFQG
1588	CD33_2	VH CDR3	WSWSDGYYVYFDY
1589	CD33_2	VL CDR1	KSSQSVLDSSTNKNSLA
1590	CD33_2	VL CDR2	WASTRES
1591	CD33_2	VL CDR3	QQSAHFPIT
1592	CD33_2	VH	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQCLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAY MEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSS
1593	CD33_2	VL	DIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLT IDSPQPEDSATYYCQQSAHFPITFGCGTRLEIK
1594	CD33_2	scFv	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQCLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAY MEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINC KSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIT FGCGTRLEIK
1595	CD33_2	bispecific molecule	QVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQCLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAY MEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINC KSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIT FGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVL
1596	CD19-1	VH CDR1	SYWMN
1597	CD19-1	VH CDR2	QIWPGDGDTNYNGKFKG
1598	CD19-1	VH CDR3	RETTTVGRYYYAMDY
1599	CD19-1	VL	KASQSVDYDGSSYLN

		CDR1	
1600	CD19-1	VL CDR2	DASNLVS
1601	CD19-1	VL CDR3	QQSTEDPWT
1602	CD19-1	VH	QVQLVQSGAEVKKPGASVKISCKASGYAFTSYWMNWVRQAPGQGLEWIGQIWPGDGDTNYNGKFKGRVTLTADTSTSTAY MELSSLQSEDTAVYYCARRETTVGRYYYAMDYWGQGTTVTVSS
1603	CD19-1	VL	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLVSGVPPRFSGSGSGTDFTLTIH SLQPEDFATYYCQQSTEDPWTFGQGTKVEIK
1604	CD19-1	scFv	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLVSGVPPRFSGSGSGTDFTLTIH SLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKISCKASGYAFTSYWM NWVRQAPGQGLEWIGQIWPGDGDTNYNGKFKGRVTLTADTSTSTAYMELSSLQSEDTAVYYCARRETTVGRYYYAMDYW GQGTTVTVSS
1605	CD19-1	bispecific molecule	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLVSGVPPRFSGSGSGTDFTLTIH SLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKISCKASGYAFTSYWM NWVRQAPGQGLEWIGQIWPGDGDTNYNGKFKGRVTLTADTSTSTAYMELSSLQSEDTAVYYCARRETTVGRYYYAMDYW GQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1606	CD19-2	VH CDR1	SYWMN
1607	CD19-2	VH CDR2	QIWPGDGDTNYNGKFKG
1608	CD19-2	VH CDR3	RETTTVGRYYYAMDY
1609	CD19-2	VL CDR1	KASQSVDYDGSSYLN
1610	CD19-2	VL CDR2	DASNLVS
1611	CD19-2	VL CDR3	QQSTEDPWT
1612	CD19-2	VH	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAY MELSSLRSEDTAVYYCARRETTVGRYYYAMDYWGQGTTVTVSS
1613	CD19-2	VL	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLVSGVPPRFSGSGSGTDFTLTIH

			SLQPEDFATYYCQQSTEDPWTFGQGTKVEIK
1614	CD19-2	scFv	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLVSGVPPRFSGSGSGTDFTLTIH SLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWM NWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSS
1615	CD19-2	bispecific molecule	DIQMTQSPSSLSASVGERVTITCKASQSVDYDGSSYLNWYQQKPGKAPKLLIYDASNLVSGVPPRFSGSGSGTDFTLTIH SLQPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWM NWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1616	CD19-3	VH CDR1	SYWMN
1617	CD19-3	VH CDR2	QIWPGDGDTNYNGKFKG
1618	CD19-3	VH CDR3	RETTTVGRYYYAMDY
1619	CD19-3	VL CDR1	KASQSVDYDGLSYLN
1620	CD19-3	VL CDR2	DASNLVS
1621	CD19-3	VL CDR3	QQSTEDPWT
1622	CD19-3	VH	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAY MELSSLRSEDTAVYYCARRETTTVGRYYYAMDYWGQGTTVTVSS
1623	CD19-3	VL	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGLSYLNWYQQKPGQAPKLLIYDASNLVSGIPSRFSGSGSGTDFTLTIS SLEPEDFATYYCQQSTEDPWTFGQGTKVEIK
1624	CD19-3	scFv	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGLSYLNWYQQKPGQAPKLLIYDASNLVSGIPSRFSGSGSGTDFTLTIS SLEPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWM NWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSS
1625	CD19-3	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGLSYLNWYQQKPGQAPKLLIYDASNLVSGIPSRFSGSGSGTDFTLTIS SLEPEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWM NWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS

			VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1626	CD19-4	VH CDR1	SYWMN
1627	CD19-4	VH CDR2	QIWPGDGDTNYNGKFKG
1628	CD19-4	VH CDR3	RETTTVGRYYYAMDY
1629	CD19-4	VL CDR1	KASQSVDYDGTSYLN
1630	CD19-4	VL CDR2	DASNLVS
1631	CD19-4	VL CDR3	QQSTEDPWT
1632	CD19-4	VH	QVQLVQSGAEVVKPGASVKISCKASGYAFTSYWMNWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAY MELSSLRSEDTAVYYCARRETTTVGRYYYAMDYWGQGTTVTVSS
1633	CD19-4	VL	DIQMTQSPSSLAASVGERVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLVSGVPSRFSGSGSGTDFTLTIN SLEKEDFATYYCQQSTEDPWTFGQGTKVEIK
1634	CD19-4	scFv	DIQMTQSPSSLAASVGERVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLVSGVPSRFSGSGSGTDFTLTIN SLEKEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWM NWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSS
1635	CD19-4	bispecific molecule	DIQMTQSPSSLAASVGERVTITCKASQSVDYDGTSYLNWYQQKPGKAPKLLIYDASNLVSGVPSRFSGSGSGTDFTLTIN SLEKEDFATYYCQQSTEDPWTFGQGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVVKPGASVKISCKASGYAFTSYWM NWVRQRPGQGLEWIGQIWPGDGDTNYNGKFKGRVTMTADESTSTAYMELSSLRSEDTAVYYCARRETTTVGRYYYAMDYW GQGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1636	CD19-5	VH CDR1	TYAMN
1637	CD19-5	VH CDR2	RIRSKGNNYATYYADSVKG
1638	CD19-5	VH	HIPYASNNEGIYYAMDY

		CDR3	
1639	CD19-5	VL CDR1	RASQDISNYLN
1640	CD19-5	VL CDR2	YTSRLHS
1641	CD19-5	VL CDR3	QQGNKLPYT
1642	CD19-5	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARHIPYASNNEGIYYAMDYWGQGTLVTVSS
1643	CD19-5	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGNKLPYTFGQGTKLEIK
1644	CD19-5	scFv	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGNKLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARHIPYASNNEGIYYAMDYWGQGTLVTVSS
1645	CD19-5	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGNKLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARHIPYASNNEGIYYAMDYWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1646	CD19-6	VH CDR1	TYAMN
1647	CD19-6	VH CDR2	RIRSKGNNYATYYADSVKG
1648	CD19-6	VH CDR3	HIPYASNNEGIYYAMDY
1649	CD19-6	VL CDR1	RASQDISNYLN
1650	CD19-6	VL CDR2	YTSRLHS
1651	CD19-6	VL CDR3	QQGNVLPYT

1652	CD19-6	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVARIRSKGNNYATYYADSVKGRFTISRDDSKNT LYLQMNSLRAEDTAVYYCVKHIPYASNNEGIYYAMDYWGQGTLVTVSS
1653	CD19-6	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLEP EDFATYYCQQGNVLPYTFGQGTKLEIK
1654	CD19-6	scFv	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLEP EDFATYYCQQGNVLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVR QAPGKGLEWVARIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVKHIPYASNNEGIYYAMDYW GQGTLVTVSS
1655	CD19-6	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLEP EDFATYYCQQGNVLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVR QAPGKGLEWVARIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVKHIPYASNNEGIYYAMDYW GQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1656	CD19-7	VH CDR1	TYAMN
1657	CD19-7	VH CDR2	RIRSKGNNYATYYADSVKG
1658	CD19-7	VH CDR3	HIPYASNNEGIYYAMDY
1659	CD19-7	VL CDR1	RASQDISNYLN
1660	CD19-7	VL CDR2	YTSRLHS
1661	CD19-7	VL CDR3	QQGNYLPYT
1662	CD19-7	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNT LYLQMNSLRAEDTAVYYCVKHIPYASNNEGIYYAMDYWGQGTLVTVSS
1663	CD19-7	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQGNYLPYTFGQGTKLEIK
1664	CD19-7	scFv	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQGNYLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVR QAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVKHIPYASNNEGIYYAMDYW GQGTLVTVSS
1665	CD19-7	bispecifi	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQP

		c molecule	EDFATYYCQQGNYLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVR QAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVKHIPYASNNEGIYYAMDYW GQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1666	CD19-8	VH CDR1	TYAMN
1667	CD19-8	VH CDR2	RIRSKGNNYATYYADSVKG
1668	CD19-8	VH CDR3	HIPYASNNEGIYYAMDY
1669	CD19-8	VL CDR1	RASQDISNYLN
1670	CD19-8	VL CDR2	YTSRLHS
1671	CD19-8	VL CDR3	QQGNSLPYT
1672	CD19-8	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNT LYLQMNNLRAEDTAVYYCVRHIPYASNNEGIYYAMDYWGQGTLVTVSS
1673	CD19-8	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGRAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQGNSLPYTFGQGTKLEIK
1674	CD19-8	scFv	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGRAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQGNSLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVR QAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNNLRAEDTAVYYCVRHIPYASNNEGIYYAMDYW GQGTLVTVSS
1675	CD19-8	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGRAPKLLIYYTSRLHSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQGNSLPYTFGQGTKLEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVR QAPGKGLEWVSRIRSKGNNYATYYADSVKGRFTISRDDSKNTLYLQMNNLRAEDTAVYYCVRHIPYASNNEGIYYAMDYW GQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCVLWYSNRWVFGGGTKLTVL
1676	CD19-9	VH CDR1	SYAMG
1677	CD19-9	VH	VINTGGSAYYASWAKG

		CDR2	
1678	CD19-9	VH CDR3	GDNYIGTARWNFAYFTW
1679	CD19-9	VL CDR1	QASQSISSRYLA
1680	CD19-9	VL CDR2	GASTLAT
1681	CD19-9	VL CDR3	LYGHYSASDSDYP
1682	CD19-9	VH	EVQLVESGGGLVTPGGSLTLSCAASGFTFSSYAMGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFTWWGQGTLVTVSS
1683	CD19-9	VL	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIK
1684	CD19-9	scFv	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSS
1685	CD19-9	bispecific molecule	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1686	CD19-10	VH CDR1	SYAMG
1687	CD19-10	VH CDR2	IINTGGSAYYASWAKG
1688	CD19-10	VH CDR3	GDNYIGTARWNFAYFTY
1689	CD19-10	VL CDR1	QASQSISSRYLA
1690	CD19-10	VL CDR2	GASTLAT

1691	CD19-10	VL CDR3	LYGHYSASDSDYP
1692	CD19-10	VH	EVQLVESEGGLVKPGGSLRLSCAASGFTFSSYAMGWVRQAPGKGLEWVGIINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCVTGDNYIGTARWNFAYFTYWGQGTLVTVSS
1693	CD19-10	VL	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIK
1694	CD19-10	scFv	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESEGGLVKPGGSLRLSCAASGFTFSSYA MGWVRQAPGKGLEWVGIINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVTGDNYIGTARWNFAYFT YWGQGTLVTVSS
1695	CD19-10	bispecific molecule	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESEGGLVKPGGSLRLSCAASGFTFSSYA MGWVRQAPGKGLEWVGIINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVTGDNYIGTARWNFAYFT YWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1696	CD19-11	VH CDR1	SYAMG
1697	CD19-11	VH CDR2	VINTGGSAYYASWAKG
1698	CD19-11	VH CDR3	GDNYIGTARWNFAYFTY
1699	CD19-11	VL CDR1	QASQSISSRYLA
1700	CD19-11	VL CDR2	GASTLAA
1701	CD19-11	VL CDR3	LYGHYSASDSDYP
1702	CD19-11	VH	EVQLVESGGGLVTPGGSLTLSCAASGFTFSSYAMGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCITGDNYIGTARWNFAYFTYWSQGTLVTVSS
1703	CD19-11	VL	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLAAGVPSKFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIK
1704	CD19-11	scFv	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLAAGVPSKFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCITGDNYIGTARWNFAYFT

			YWSQGTLVTVSS
1705	CD19-11	bispecific molecule	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLAAGVPSKFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCITGDNYIGTARWNFAYFT YWSQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1706	CD19-12	VH CDR1	SYAMG
1707	CD19-12	VH CDR2	VINTGGSAYYASWAKG
1708	CD19-12	VH CDR3	GDNYIGTARWNFAYFTW
1709	CD19-12	VL CDR1	QASQSISSRYLA
1710	CD19-12	VL CDR2	GASTLAM
1711	CD19-12	VL CDR3	LYGHYSASDSDYP
1712	CD19-12	VH	EVQLVESGGGLVTPGGSLTLSCAASGFTFSSYAMGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCITGDNYIGTARWNFAYFTWWGQGTLVTVSS
1713	CD19-12	VL	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGQAPKLLIYGASTLAMGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIK
1714	CD19-12	scFv	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGQAPKLLIYGASTLAMGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSS
1715	CD19-12	bispecific molecule	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGQAPKLLIYGASTLAMGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGQGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKGLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1716	CD19-13	VH	SYGVS

		CDR1	
1717	CD19-13	VH CDR2	YNDPVFGSIYYASWVKG
1718	CD19-13	VH CDR3	DRSYVSSSGYHFNL
1719	CD19-13	VL CDR1	QASETIYSSLA
1720	CD19-13	VL CDR2	GASNLES
1721	CD19-13	VL CDR3	QSGVYSAGLT
1722	CD19-13	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1723	CD19-13	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKPPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGGGTKVEIK
1724	CD19-13	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKPPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1725	CD19-13	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKPPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1726	CD19-14	VH CDR1	SYGVS
1727	CD19-14	VH CDR2	YNDPVFGSIYYASWVKG
1728	CD19-14	VH CDR3	DRSYVSSSGYHFNL
1729	CD19-14	VL CDR1	QASETIYSSLA

1730	CD19-14	VL CDR2	GASNLES
1731	CD19-14	VL CDR3	QSGVYSAGLT
1732	CD19-14	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1733	CD19-14	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSMQP EDIATYYCQSGVYSAGLTFGGGTKVEIK
1734	CD19-14	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSMQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1735	CD19-14	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSMQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1736	CD19-15	VH CDR1	SYGVS
1737	CD19-15	VH CDR2	YNDPVFGSIYYASWVKG
1738	CD19-15	VH CDR3	DRSYVSSSGYHFNL
1739	CD19-15	VL CDR1	QASETIYSSLA
1740	CD19-15	VL CDR2	GASNLES
1741	CD19-15	VL CDR3	QSGVYSAGLT
1742	CD19-15	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1743	CD19-15	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISGLQP EDIATYYCQSGVYSAGLTFGGGTKVEIK

1744	CD19-15	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISGLQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1745	CD19-15	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISGLQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1746	CD19-16	VH CDR1	SYGVS
1747	CD19-16	VH CDR2	YNDPVFGSIYYASWVKG
1748	CD19-16	VH CDR3	DRSYVSSSGYHFNL
1749	CD19-16	VL CDR1	QASETIYSSLA
1750	CD19-16	VL CDR2	GASNLES
1751	CD19-16	VL CDR3	QSGVYSAGLT
1752	CD19-16	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKGLEWVGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1753	CD19-16	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGGGTKVEIK
1754	CD19-16	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWVGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1755	CD19-16	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGGGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKGLEWVGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS

			LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1756	CD19-17	VH CDR1	SYAMG
1757	CD19-17	VH CDR2	VINTGGSAYYASWAKG
1758	CD19-17	VH CDR3	GDNYIGTARWNFAYFTW
1759	CD19-17	VL CDR1	QASQSISSRYLA
1760	CD19-17	VL CDR2	GASTLAT
1761	CD19-17	VL CDR3	LYGHYSASDSDYP
1762	CD19-17	VH	EVQLVESGGGLVTPGGSLTLSCAASGFTFSSYAMGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFTWWGQGTLVTVSS
1763	CD19-17	VL	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIK
1764	CD19-17	scFv	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSS
1765	CD19-17	bispecific molecule	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1766	CD19-18	VH CDR1	SYAMG
1767	CD19-18	VH CDR2	IINTGGSAYYASWAKG
1768	CD19-18	VH CDR3	GDNYIGTARWNFAYFTY

1769	CD19-18	VL CDR1	QASQSISSRYLA
1770	CD19-18	VL CDR2	GASTLAT
1771	CD19-18	VL CDR3	LYGHYSASDSDYP
1772	CD19-18	VH	EVQLVESEGGLVKPGGSLRLSCAASGFTFSSYAMGWVRQAPGKCLEWVGIINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCVTGDNYIGTARWNFAYFTVSS
1773	CD19-18	VL	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIK
1774	CD19-18	scFv	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESEGGLVKPGGSLRLSCAASGFTFSSYA MGWVRQAPGKCLEWVGIINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVTGDNYIGTARWNFAYFT YWGQGTLVTVSS
1775	CD19-18	bispecifi c molecule	DIQMTQSPSSVSASVGGRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLATGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESEGGLVKPGGSLRLSCAASGFTFSSYA MGWVRQAPGKCLEWVGIINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVTGDNYIGTARWNFAYFT YWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1776	CD19-19	VH CDR1	SYAMG
1777	CD19-19	VH CDR2	VINTGGSAYYASWAKG
1778	CD19-19	VH CDR3	GDNYIGTARWNFAYFTY
1779	CD19-19	VL CDR1	QASQSISSRYLA
1780	CD19-19	VL CDR2	GASTLAA
1781	CD19-19	VL CDR3	LYGHYSASDSDYP
1782	CD19-19	VH	EVQLVESGGGLVTPGGSLTLSCAASGFTFSSYAMGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCITGDNYIGTARWNFAYFTYWSQGTLVTVSS

1783	CD19-19	VL	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLAAGVPSKFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIK
1784	CD19-19	scFv	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLAAGVPSKFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCITGDNYIGTARWNFAYFT YWSQGTLVTVSS
1785	CD19-19	bispecific molecule	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGKAPKLLIYGASTLAAGVPSKFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCITGDNYIGTARWNFAYFT YWSQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1786	CD19-20	VH CDR1	SYAMG
1787	CD19-20	VH CDR2	VINTGGSAYYASWAKG
1788	CD19-20	VH CDR3	GDNYIGTARWNFAYFTW
1789	CD19-20	VL CDR1	QASQSISSRYLA
1790	CD19-20	VL CDR2	GASTLAM
1791	CD19-20	VL CDR3	LYGHYSASDSDYP
1792	CD19-20	VH	EVQLVESGGGLVTPGGSLTLSCAASGFTFSSYAMGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCITGDNYIGTARWNFAYFTWWGQGTLVTVSS
1793	CD19-20	VL	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGQAPKLLIYGASTLAMGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIK
1794	CD19-20	scFv	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGQAPKLLIYGASTLAMGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT WWGQGTLVTVSS
1795	CD19-20	bispecific molecule	DIQMTQSPSSVSASVGDRVTINCQASQSISSRYLAWYQQKPGQAPKLLIYGASTLAMGVPSRFSGSGSGTDFTLTISSLQ PEDFATYYCLYGHYSASDSDYPFGCGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVTPGGSLTLSCAASGFTFSSYA MGWVRQAPGKCLEWVGVINTGGSAYYASWAKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGDNYIGTARWNFAYFT

			WWGQGTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1796	CD19-21	VH CDR1	SYGVS
1797	CD19-21	VH CDR2	YNDPVFGSIYYYASWVKG
1798	CD19-21	VH CDR3	DRSYVSSSGYHFNL
1799	CD19-21	VL CDR1	QASETIYSSLA
1800	CD19-21	VL CDR2	GASNLES
1801	CD19-21	VL CDR3	QSGVYSAGLT
1802	CD19-21	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKGLEWIGYNDPVFGSIYYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1803	CD19-21	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKPPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGCGTKVEIK
1804	CD19-21	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKPPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1805	CD19-21	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKPPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1806	CD19-22	VH CDR1	SYGVS
1807	CD19-22	VH CDR2	YNDPVFGSIYYASWVKG

1808	CD19-22	VH CDR3	DRSYVSSSGYHFNL
1809	CD19-22	VL CDR1	QASETIYSSLA
1810	CD19-22	VL CDR2	GASNLES
1811	CD19-22	VL CDR3	QSGVYSAGLT
1812	CD19-22	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1813	CD19-22	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSMQP EDIATYYCQSGVYSAGLTFGCGTKVEIK
1814	CD19-22	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSMQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1815	CD19-22	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSMQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1816	CD19-23	VH CDR1	SYGVS
1817	CD19-23	VH CDR2	YNDPVFGSIYYASWVKG
1818	CD19-23	VH CDR3	DRSYVSSSGYHFNL
1819	CD19-23	VL CDR1	QASETIYSSLA
1820	CD19-23	VL CDR2	GASNLES
1821	CD19-23	VL CDR3	QSGVYSAGLT

1822	CD19-23	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1823	CD19-23	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISGLQP EDIATYYCQSGVYSAGLTFGCGTKVEIK
1824	CD19-23	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISGLQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1825	CD19-23	bispecific molecule	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISGLQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWIGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1826	CD19-24	VH CDR1	SYGVS
1827	CD19-24	VH CDR2	YNDPVFGSIYYASWVKG
1828	CD19-24	VH CDR3	DRSYVSSSGYHFNL
1829	CD19-24	VL CDR1	QASETIYSSLA
1830	CD19-24	VL CDR2	GASNLES
1831	CD19-24	VL CDR3	QSGVYSAGLT
1832	CD19-24	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWVRQAPGKCLEWVGYNDPVFGSIYYASWVKGRFTISSDNSKNTLY LQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGTLVTVSS
1833	CD19-24	VL	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGCGTKVEIK
1834	CD19-24	scFv	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWVGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSS
1835	CD19-24	bispecifi	DIQMTQSPSSLSASVGDRVTITCQASETIYSSLAWYQQKPGKAPKLLIYGASNLESGVPSRFSGSGSGTDFTFTISSLQP

		c molecule	EDIATYYCQSGVYSAGLTFGCGTKVEIKGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGVSWV RQAPGKCLEWVGYNDPVFGSIYYASWVKGRFTISSDNSKNTLYLQMNSLRAEDTAVYYCAKDRSYVSSSGYHFNLWGQGT LVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1836	CD19-25	VH CDR1	SYVMH
1837	CD19-25	VH CDR2	YINPYNDGTKYNEKFQG
1838	CD19-25	VH CDR3	GTYYYGTRVFDY
1839	CD19-25	VL CDR1	RSSKSLQNSNGNTYLY
1840	CD19-25	VL CDR2	RMSNLNS
1841	CD19-25	VL CDR3	MQHLEYPIT
1842	CD19-25	VH	EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPGKGLEWIGYINPYNDGTKYNEKFQGRVTISSDKSISTAY MELSSLRESDTAMYYCARGTYYYGTRVFDYWGQGTLVTVSS
1843	CD19-25	VL	DIVMTQSPATLSLSPGERATLSCRSSKSLQNSNGNTYLYWFQQKPGQSPQLLIYRMSNLNSGVPDRFSGSGSGTEFTLTI SSLEPEDFAVYYCMQHLEYPITFGAGTKLEIK
1844	CD19-25	scFv	DIVMTQSPATLSLSPGERATLSCRSSKSLQNSNGNTYLYWFQQKPGQSPQLLIYRMSNLNSGVPDRFSGSGSGTEFTLTI SSLEPEDFAVYYCMQHLEYPITFGAGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLKLSCAASGYTFTSYV MHWVRQAPGKGLEWIGYINPYNDGTKYNEKFQGRVTISSDKSISTAYMELSSLRESDTAMYYCARGTYYYGTRVFDYWGQ GTLVTVSS
1845	CD19-25	bispecific molecule	DIVMTQSPATLSLSPGERATLSCRSSKSLQNSNGNTYLYWFQQKPGQSPQLLIYRMSNLNSGVPDRFSGSGSGTEFTLTI SSLEPEDFAVYYCMQHLEYPITFGAGTKLEIKGGGGSGGGGSGGGGSEVQLVESGGGLVKPGGSLKLSCAASGYTFTSYV MHWVRQAPGKGLEWIGYINPYNDGTKYNEKFQGRVTISSDKSISTAYMELSSLRESDTAMYYCARGTYYYGTRVFDYWGQ GTLVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
1846	CD19-26	VH CDR1	NYGMH
1847	CD19-26	VH	VISYDGSNKYYAEPVKG

		CDR2	
1848	CD19-26	VH CDR3	DRGTIFGYYGMDV
1849	CD19-26	VL CDR1	RSSQSLLHSNGYNYLD
1850	CD19-26	VL CDR2	LGSNRAS
1851	CD19-26	VL CDR3	MQALQTPFT
1852	CD19-26	VH	ESGGGVVQPGRSLRLSCEASGFIVSNYGMHWVRQAPGKGLEWVAVISYDGSNKYYAEPVKGRFTISRDKSKNTVSLQMSS LRAEDTALYYCARDRGTIFGYYGMDVWGQGTTVTVSS
1853	CD19-26	VL	DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPFTFGPGTKVEIK
1854	CD19-26	scFv	DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPFTFGPGTKVEIKGGGGSGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCEASGFIVSNYG MHWVRQAPGKGLEWVAVISYDGSNKYYAEPVKGRFTISRDKSKNTVSLQMSSLRAEDTALYYCARDRGTIFGYYGMDVWG QGTTVTVSS
1855	CD19-26	bispecific molecule	DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPFTFGPGTKVEIKGGGGSGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCEASGFIVSNYG MHWVRQAPGKGLEWVAVISYDGSNKYYAEPVKGRFTISRDKSKNTVSLQMSSLRAEDTALYYCARDRGTIFGYYGMDVWG QGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEA EYYCVLWYSNRWVFGGGTKLTVL
1856	CD19-27	VH CDR1	NYGMH
1857	CD19-27	VH CDR2	VISYDGSNKYYAEPVKG
1858	CD19-27	VH CDR3	DRGTIFGYYGMDV
1859	CD19-27	VL CDR1	RSSQSLLHSNGFNYLD
1860	CD19-27	VL CDR2	LGSNRAS

1861	CD19-27	VL CDR3	MQALQTPLT
1862	CD19-27	VH	ESGGGVVQPGRSLRLSCEASGFIVSNYGMHWVRQAPGKGLEWVAVISYDGSNKYYAEPVKGRFTISRDKSKNTLSLQMSS LRAEDTALYYCARDRGTIFGYYGMDVWGQGTTVTVSS
1863	CD19-27	VL	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGFNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPLTFAGGTKVEIK
1864	CD19-27	scFv	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGFNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPLTFAGGTKVEIKGGGGSGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCEASGFIVSNYG MHWVRQAPGKGLEWVAVISYDGSNKYYAEPVKGRFTISRDKSKNTLSLQMSSLRAEDTALYYCARDRGTIFGYYGMDVWG QGTTVTVSS
1865	CD19-27	bispecific molecule	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGFNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCMQALQTPLTFAGGTKVEIKGGGGSGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCEASGFIVSNYG MHWVRQAPGKGLEWVAVISYDGSNKYYAEPVKGRFTISRDKSKNTLSLQMSSLRAEDTALYYCARDRGTIFGYYGMDVWG QGTTVTVSSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEA EYYCVLWYSNRWVFGGGTKLTVL
1866	CD20-1	VH CDR1	SYNMH
1867	CD20-1	VH CDR2	AIYPLTGDTSYNQKSKL
1868	CD20-1	VH CDR3	STYVGGDWQFDV
1869	CD20-1	VL CDR1	RASSSVPYIH
1870	CD20-1	VL CDR2	ATSALAS
1871	CD20-1	VL CDR3	QQWLSNPPT
1872	CD20-1	VH	EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTGDTSYNQKSKLQVTISADKSISTAY LQWSSLKASDTAMYYCARSTYVGGDWQFDVWGKGTTVTVSS
1873	CD20-1	VL	EIVLTQSPGTLSLSPGERATLSCRASSSVPYIHWYQQKPGQAPRLLIYATSALASGIPDRFSGSGSGTDFTLTISRLEPE DFAVYYCQQWLSNPPTFGQGTKLEIK
1874	CD20-1	scFv	EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTGDTSYNQKSKLQVTISADKSISTAY LQWSSLKASDTAMYYCARSTYVGGDWQFDVWGKGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCR ASSSVPYIHWYQQKPGQAPRLLIYATSALASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLE

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1875	CD20-1	bispecific molecule	EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTGDTSYNQKSKLQVTISADKSISTAY LQWSSLKASDTAMYYCARSTYVGGDWQFDVWGKGTTVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCR ASSSVPYIHWYQQKPGQAPRLLIYATSALASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
1876	CD20-2	VH CDR1	YSWIN
1877	CD20-2	VH CDR2	RIFPGDGDTDYNGKFKG
1878	CD20-2	VH CDR3	NVFDGYWLVY
1879	CD20-2	VL CDR1	RSSKSLLHSNGITYLY
1880	CD20-2	VL CDR2	QMSNLVS
1881	CD20-2	VL CDR3	AQNLELPYT
1882	CD20-2	VH	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSYSWINWVRQAPGQGLEWMGRIFPGDGDTDYNGKFKGRVTITADKSTSTAY MELSSLRSEDTAVYYCARNVFDGYWLVYWGQGTLVTVSS
1883	CD20-2	VL	DIVMTQTPLSLPVTPGEPASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLVSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCAQNLELPYTFGGGTKVEIK
1884	CD20-2	scFv	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSYSWINWVRQAPGQGLEWMGRIFPGDGDTDYNGKFKGRVTITADKSTSTAY MELSSLRSEDTAVYYCARNVFDGYWLVYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISCRSS KSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLVSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCAQNLELPYTFGGG TKVEIK
1885	CD20-2	bispecific molecule	QVQLVQSGAEVKKPGSSVKVSCKASGYAFSYSWINWVRQAPGQGLEWMGRIFPGDGDTDYNGKFKGRVTITADKSTSTAY MELSSLRSEDTAVYYCARNVFDGYWLVYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLPVTPGEPASISCRSS KSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLVSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCAQNLELPYTFGGG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1886	EvIII-1	VH	NYGMH

		CDR1	
1887	EvIII-1	VH CDR2	VIWYDGSDKYYADSVRG
1888	EvIII-1	VH CDR3	DGYDILTGNPRDFDY
1889	EvIII-1	VL CDR1	RSSQSLVHSDGNTYLS
1890	EvIII-1	VL CDR2	RISRRFS
1891	EvIII-1	VL CDR3	MQSTHVPRT
1892	EvIII-1	VH	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQGTLVTVSS
1893	EvIII-1	VL	DTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEI SRVEAEDVGVYYCMQSTHVPRTFGCGTKVEIK
1894	EvIII-1	scFv	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDTVMTQTPLSSHVTLGQPASI SCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEISRVEAEDVGVYYCMQSTHVPR TFGCGTKVEIK
1895	EvIII-1	bispecific molecule	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKCLEWVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDTVMTQTPLSSHVTLGQPASI SCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEISRVEAEDVGVYYCMQSTHVPR TFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1896	EvIII-2	VH CDR1	NYGMH
1897	EvIII-2	VH CDR2	VIWYDGSDKYYADSVRG
1898	EvIII-2	VH CDR3	DGYDILTGNPRDFDY
1899	EvIII-2	VL CDR1	RSSQSLVHSDGNTYLS

1900	EvIII-2	VL CDR2	RISRRFS
1901	EvIII-2	VL CDR3	MQSTHVPRT
1902	EvIII-2	VH	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKGLEWVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQGTLVTVSS
1903	EvIII-2	VL	DTVMTQTPLSSHVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEI SRVEAEDVGVYYCMQSTHVPRTFGQGTKVEIK
1904	EvIII-2	scFv	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKGLEWVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQGTLVTVSSGGGGSGGGGSDTVMTQTPLSSHVTLGQPASI SCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEISRVEAEDVGVYYCMQSTHVPR TFGQGTKVEIK
1905	EvIII-2	bispecifi c molecule	QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKGLEWVAVIWYDGSDKYYADSVRGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGYDILTGNPRDFDYWGQGTLVTVSSGGGGSGGGGSDTVMTQTPLSSHVTLGQPASI SCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYRISRRFSGVPDRFSGSGAGTDFTLEISRVEAEDVGVYYCMQSTHVPR TFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVL
1906	CD70-1	VH CDR1	TYGMH
1907	CD70-1	VH CDR2	VIWYDGSNKYYGDSVKG
1908	CD70-1	VH CDR3	DNSHYYYGMDV
1909	CD70-1	VL CDR1	TGSSSNIGAGYDVN
1910	CD70-1	VL CDR2	VNNNRPS
1911	CD70-1	VL CDR3	QSYDTSLSASV
1912	CD70-1	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTTVTVSS
1913	CD70-1	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDRFSGSTSGTSASLAITGL QAEDEADYYCQSYDTSLSASVFGGGTRLTVL

1914	CD70-1	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGS SSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDRFSGSTSGTSASLAITGLQAEDEADYYCQSYDTSLSASVFGGG TRLTVLS
1915	CD70-1	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTTVTVSSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGS SSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDRFSGSTSGTSASLAITGLQAEDEADYYCQSYDTSLSASVFGGG TRLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1916	CD70-2	VH CDR1	SYGMH
1917	CD70-2	VH CDR2	VIWYDGSDKYFADSVKG
1918	CD70-2	VH CDR3	DGIAGARYVYFDY
1919	CD70-2	VL CDR1	RASQGISNYLA
1920	CD70-2	VL CDR2	AASSLQG
1921	CD70-2	VL CDR3	QQYYNYPFT
1922	CD70-2	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSDKYFADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGTLVTVSS
1923	CD70-2	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFSGSGSGTDFTLTISSLQP EDFATYYCQQYYNYPFTFGPGTTVDIK
1924	CD70-2	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSDKYFADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITC RASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGPGTT VDIK
1925	CD70-2	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSDKYFADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITC RASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGPGTT VDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL

			TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
1926	CD70-3	VH CDR1	SYGMH
1927	CD70-3	VH CDR2	VTWYDGSNKYYGDSVKG
1928	CD70-3	VH CDR3	DLLRGVKGYAMDV
1929	CD70-3	VL CDR1	RASQSLRRIYLA
1930	CD70-3	VL CDR2	DVFDRAT
1931	CD70-3	VL CDR3	QQYSDSPFT
1932	CD70-3	VH	QEQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVTWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDLLRGVKGYAMDVWGQGTTVTVSS
1933	CD70-3	VL	EIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLAWYQQKPGQAPRLLIYDVFDRATGIPDRFSGGGSGTDFTLTISRLE PEDFAVYYCQQYSDSPFTFGPGTKVDIK
1934	CD70-3	scFv	QEQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVTWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDLLRGVKGYAMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSC RASQSLRRIYLAWYQQKPGQAPRLLIYDVFDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSDSPFTFGPGT KVDIK
1935	CD70-3	bispecific molecule	QEQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVTWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDLLRGVKGYAMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSC RASQSLRRIYLAWYQQKPGQAPRLLIYDVFDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSDSPFTFGPGT KVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVL
1936	CD70-4	VH CDR1	SYGIS
1937	CD70-4	VH CDR2	WISAYNGYTHYAQKLQG
1938	CD70-4	VH CDR3	DYGGNDYYGMDV

1939	CD70-4	VL CDR1	SGSSSNIGINYVY
1940	CD70-4	VL CDR2	RSDQRPS
1941	CD70-4	VL CDR3	AAWDDSLSGVV
1942	CD70-4	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGYTHYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTTVTVSS
1943	CD70-4	VL	QSVLTQPPSASGTPGQRVTISCSGSSSNIGINYVYWYQQLPGTAPKLLIYRSDQRPSGVPDRFSGSKSGTSASLALSGLR SEDEADYYCAAWDDSLSGVVFGGGTKLTVL
1944	CD70-4	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGYTHYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSG SSSNIGINYVYWYQQLPGTAPKLLIYRSDQRPSGVPDRFSGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFGGG TKLTVL
1945	CD70-4	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGYTHYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSG SSSNIGINYVYWYQQLPGTAPKLLIYRSDQRPSGVPDRFSGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFGGG TKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1946	CD70-5	VH CDR1	SGGYYWS
1947	CD70-5	VH CDR2	YIFYSGSTDYNPSLKS
1948	CD70-5	VH CDR3	SGYSYALFDH
1949	CD70-5	VL CDR1	RASQFIGRYFN
1950	CD70-5	VL CDR2	AESSLQS
1951	CD70-5	VL CDR3	QQSYSTPWT
1952	CD70-5	VH	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKGLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSS

1953	CD70-5	VL	DIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFARYYCQQSYSTPWTFGQGTKVEIK
1954	CD70-5	scFv	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKGLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTISCRA SQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFARYYCQQSYSTPWTFGQGTKVE IK
1955	CD70-5	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKGLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTISCRA SQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFARYYCQQSYSTPWTFGQGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
1956	CD70-6	VH CDR1	SGGYYWS
1957	CD70-6	VH CDR2	YIFYSGSTDYNPSLKS
1958	CD70-6	VH CDR3	SGYSYALFDH
1959	CD70-6	VL CDR1	RASQFIGRYFN
1960	CD70-6	VL CDR2	AESSLQS
1961	CD70-6	VL CDR3	QQSYSTPFT
1962	CD70-6	VH	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSS
1963	CD70-6	VL	DIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFARYYCQQSYSTPFTFGCGTKVEIK
1964	CD70-6	scFv	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTISCRA SQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFARYYCQQSYSTPFTFGCGTKVE IK
1965	CD70-6	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSSGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTISCRA SQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFARYYCQQSYSTPFTFGCGTKVE

			IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
1966	CD70-7	VH CDR1	SYYLH
1967	CD70-7	VH CDR2	IVDPSGGSTSYDQKFQG
1968	CD70-7	VH CDR3	DYGDYVFDY
1969	CD70-7	VL CDR1	SGSSSNIGTNTVN
1970	CD70-7	VL CDR2	INNQRPS
1971	CD70-7	VL CDR3	ATWDDSLNGPV
1972	CD70-7	VH	QVHLVQSGAEVKKPGASVRVSCKASGYTFTSYYLHWVRQAPGQCLEWMGIVDPSGGSTSYDQKFQGRFTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYGDYVFDYWGQGTLVTVSS
1973	CD70-7	VL	QSVLTQPPSASGTPGQRVTISCSGSSSNIGTNTVNWYQQLPGTAPQLLIYINNQRPSGVPDRFSGSKSGTSASLAISGLQ SEDEADYYCATWDDSLNGPVVGCGTKLTVL
1974	CD70-7	scFv	QVHLVQSGAEVKKPGASVRVSCKASGYTFTSYYLHWVRQAPGQCLEWMGIVDPSGGSTSYDQKFQGRFTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYGDYVFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSSS NIGTNTVNWYQQLPGTAPQLLIYINNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSLNGPVVGCGTKL TVL
1975	CD70-7	bispecific molecule	QVHLVQSGAEVKKPGASVRVSCKASGYTFTSYYLHWVRQAPGQCLEWMGIVDPSGGSTSYDQKFQGRFTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYGDYVFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSSS NIGTNTVNWYQQLPGTAPQLLIYINNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSLNGPVVGCGTKL TVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
1976	CD70-8	VH CDR1	SYGMH
1977	CD70-8	VH CDR2	VIWYDGSDKYFADSVKG

1978	CD70-8	VH CDR3	DGIAGARYVYFDY
1979	CD70-8	VL CDR1	RASQGISNYLA
1980	CD70-8	VL CDR2	AASSLQG
1981	CD70-8	VL CDR3	QQYYNYPFT
1982	CD70-8	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVIWYDGSDKYFADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGTLVTVSS
1983	CD70-8	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFSGSGSGTDFTLTISSLQP EDFATYYCQQYYNYPFTFGCGTTVDIK
1984	CD70-8	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVIWYDGSDKYFADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITC RASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGCGTT VDIK
1985	CD70-8	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVIWYDGSDKYFADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITC RASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGCGTT VDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL
1986	CD70-9	VH CDR1	SYGIS
1987	CD70-9	VH CDR2	WISAYNGYTHYAQKLQG
1988	CD70-9	VH CDR3	DYGGNDYYGMDV
1989	CD70-9	VL CDR1	SGSSSNIGINYVY
1990	CD70-9	VL CDR2	RSDQRPS
1991	CD70-9	VL CDR3	AAWDDSLSGVV

1992	CD70-9	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYNGYTHYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTTVTVSS
1993	CD70-9	VL	QSVLTQPPSASGTPGQRVTISCSGSSSNIGINYVYWYQQLPGTAPKLLIYRSDQRPSGVPDRFSGSKSGTSASLALSGLR SEDEADYYCAAWDDSLSGVVFGCGTKLTVL
1994	CD70-9	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYNGYTHYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSG SSSNIGINYVYWYQQLPGTAPKLLIYRSDQRPSGVPDRFSGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFGCG TKLTVL
1995	CD70-9	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYNGYTHYAQKLQGRVTMTTDTSTSTAY MELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSG SSSNIGINYVYWYQQLPGTAPKLLIYRSDQRPSGVPDRFSGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFGCG TKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
1996	CD70-10	VH CDR1	SGGYYWS
1997	CD70-10	VH CDR2	YIFYSGSTDYNPSLKS
1998	CD70-10	VH CDR3	SGYSYALFDH
1999	CD70-10	VL CDR1	RASQFIGRYFN
2000	CD70-10	VL CDR2	AESSLQS
2001	CD70-10	VL CDR3	QQSYSTPWT
2002	CD70-10	VH	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSS
2003	CD70-10	VL	DIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQP EDFARYYCQQSYSTPWTFGCGTKVEIK
2004	CD70-10	scFv	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTISCRA SQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFARYYCQQSYSTPWTFGCGTKVE IK
2005	CD70-10	bispecifi	QVQLQESGPGLVKPSQTLSLTCTVSGDSIISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNPSLKSRVTISVDTSKNQF

		c molecule	SLKLSSVTAADTAVYYCARSGYSYALFDHWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTISCRA SQFIGRYFNWYQQQPGKAPKVLIYAESSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFARYYCQQSYSTPWTFGCGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2006	CD70-11	VH CDR1	TYGMH
2007	CD70-11	VH CDR2	VIWYDGSNKYYGDSVKG
2008	CD70-11	VH CDR3	DNSHYYYGMDV
2009	CD70-11	VL CDR1	TGSSSNIGAGYDVN
2010	CD70-11	VL CDR2	VNNNRPS
2011	CD70-11	VL CDR3	QSYETSLSASV
2012	CD70-11	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKCLEWVAVIWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTTVTVSS
2013	CD70-11	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDRFSGSTSGTSASLAITGL QAEDEADYYCQSYETSLSASVFGCGTRLTVL
2014	CD70-11	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKCLEWVAVIWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTTVTVSSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGS SSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDRFSGSTSGTSASLAITGLQAEDEADYYCQSYETSLSASVFGCG TRLTVL
2015	CD70-11	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKCLEWVAVIWYDGSNKYYGDSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTTVTVSSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGS SSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDRFSGSTSGTSASLAITGLQAEDEADYYCQSYETSLSASVFGCG TRLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
2016	CD70-12	VH CDR1	YYGMH
2017	CD70-12	VH	VIWYDGSNKYYADSVKG

		CDR2	
2018	CD70-12	VH CDR3	DREMGSRGDFDY
2019	CD70-12	VL CDR1	RASQGINNYLA
2020	CD70-12	VL CDR2	AVSILQS
2021	CD70-12	VL CDR3	QQYNFYPFS
2022	CD70-12	VH	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGTLVTVSS
2023	CD70-12	VL	DIQMTQSPSSLSASVGDRVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSILQSGVPSKFSGSGSGTDFTLTIGNLQP EDFATYYCQQYNFYPFSFGCGTKVDIK
2024	CD70-12	scFv	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCR ASQGINNYLAWFQQKPGKAPKSLIYAVSILQSGVPSKFSGSGSGTDFTLTIGNLQPEDFATYYCQQYNFYPFSFGCGTKV DIK
2025	CD70-12	bispecific molecule	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCR ASQGINNYLAWFQQKPGKAPKSLIYAVSILQSGVPSKFSGSGSGTDFTLTIGNLQPEDFATYYCQQYNFYPFSFGCGTKV DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2026	CD70-13	VH CDR1	SYAMS
2027	CD70-13	VH CDR2	VISGSGGRPNYADSVKG
2028	CD70-13	VH CDR3	VDYSNYLFFDY
2029	CD70-13	VL CDR1	RAGQSVRSSYLG
2030	CD70-13	VL CDR2	GASSRAT

2031	CD70-13	VL CDR3	QQYGYSPPT
2032	CD70-13	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGRPNYADSVKGRFTISRDNSKNTLY LQMNSLRDEDTAVYYCAKVDYSNYLFFDYWGQGTLVTVSS
2033	CD70-13	VL	EIVLTQSPGTLSLSPGEGATLSCRAGQSVRSSYLGWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGYSPPTFGGGTKLEIK
2034	CD70-13	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGRPNYADSVKGRFTISRDNSKNTLY LQMNSLRDEDTAVYYCAKVDYSNYLFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGEGATLSCRA GQSVRSSYLGWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGYSPPTFGGGTKL EIK
2035	CD70-13	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGRPNYADSVKGRFTISRDNSKNTLY LQMNSLRDEDTAVYYCAKVDYSNYLFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGEGATLSCRA GQSVRSSYLGWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGYSPPTFGGGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2036	CD70-14	VH CDR1	IYAMS
2037	CD70-14	VH CDR2	AISGSGGSTFYADSVKG
2038	CD70-14	VH CDR3	HDYSNYPYFDY
2039	CD70-14	VL CDR1	RASQSVRSSYLA
2040	CD70-14	VL CDR2	GASSRAT
2041	CD70-14	VL CDR3	QQYGDLPFT
2042	CD70-14	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2043	CD70-14	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKLEIK
2044	CD70-14	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKL

			EIK
2045	CD70-14	bispecific molecule	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2046	CD70-15	VH CDR1	SYAMS
2047	CD70-15	VH CDR2	AISGSGGRTFYADSVEG
2048	CD70-15	VH CDR3	HDYSNYPYFDY
2049	CD70-15	VL CDR1	RASQSVRSSYLA
2050	CD70-15	VL CDR2	GASSRAT
2051	CD70-15	VL CDR3	QQYGSSPFT
2052	CD70-15	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLF LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2053	CD70-15	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPFTFGPGTKLEIK
2054	CD70-15	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLF LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKL EIK
2055	CD70-15	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLF LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2056	CD70-16	VH	SYAMS

		CDR1	
2057	CD70-16	VH CDR2	AISGSGGRTFYADSVEG
2058	CD70-16	VH CDR3	HDYSNYPYFDY
2059	CD70-16	VL CDR1	RASQSIRSSYLA
2060	CD70-16	VL CDR2	GASSRAT
2061	CD70-16	VL CDR3	QQYGDLPFT
2062	CD70-16	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2063	CD70-16	VL	EIVLTQSPGTLSLSPGERATLSCRASQSIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKLEIK
2064	CD70-16	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKL EIK
2065	CD70-16	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2066	CD70-17	VH CDR1	SYAMS
2067	CD70-17	VH CDR2	AISGSGGRTHYADSVKG
2068	CD70-17	VH CDR3	HDYSNYPYFDY
2069	CD70-17	VL CDR1	RASQSVRSSYLA

2070	CD70-17	VL CDR2	GASSRAT
2071	CD70-17	VL CDR3	QQYGSSPFT
2072	CD70-17	VH	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2073	CD70-17	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPFTFGPGTKLEIK
2074	CD70-17	scFv	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKL EIK
2075	CD70-17	bispecific molecule	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2076	CD70-18	VH CDR1	SYAMS
2077	CD70-18	VH CDR2	LISGSGGRTHYADSVKG
2078	CD70-18	VH CDR3	HDYSNYPYFDY
2079	CD70-18	VL CDR1	RASQSVRSTYLA
2080	CD70-18	VL CDR2	DASSRAT
2081	CD70-18	VL CDR3	QQYGSSPPT
2082	CD70-18	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSLISGSGGRTHYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2083	CD70-18	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYFCQQYGSSPPTFGGGTKLEIK

2084	CD70-18	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSLISGSGGRTHYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSTYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTKL EIK
2085	CD70-18	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSLISGSGGRTHYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSTYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2086	CD70-19	VH CDR1	TYAMS
2087	CD70-19	VH CDR2	AISGSGGSTFYADSVKG
2088	CD70-19	VH CDR3	HDYSNYPYFDY
2089	CD70-19	VL CDR1	RASQSVRSSYLA
2090	CD70-19	VL CDR2	GASSRAT
2091	CD70-19	VL CDR3	QQYGDLPFT
2092	CD70-19	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLS LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2093	CD70-19	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKLEIK
2094	CD70-19	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLS LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKL EIK
2095	CD70-19	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLS LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT

			VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2096	CD70-20	VH CDR1	TYAMS
2097	CD70-20	VH CDR2	LISGSGGRTYYADSVKG
2098	CD70-20	VH CDR3	HDYSNYPYFDY
2099	CD70-20	VL CDR1	RASQGVRSDYLA
2100	CD70-20	VL CDR2	GASSRAT
2101	CD70-20	VL CDR3	QQYGSTPPT
2102	CD70-20	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2103	CD70-20	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRSDYLAWYQQKPGQALRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYHCQQYGSTPPTFGGGTKLEIK
2104	CD70-20	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSDYLAWYQQKPGQALRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGGGTKL EIK
2105	CD70-20	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSDYLAWYQQKPGQALRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGGGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2106	CD70-21	VH CDR1	TYAMS
2107	CD70-21	VH CDR2	AISGSGGRTFYADSVEG
2108	CD70-21	VH CDR3	HDYSNYPYFDY

2109	CD70-21	VL CDR1	RASQSVRSTYLA
2110	CD70-21	VL CDR2	GASSRAT
2111	CD70-21	VL CDR3	QQYGDLPFT
2112	CD70-21	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2113	CD70-21	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYSCQQYGDLPFTFGPGTKLEIK
2114	CD70-21	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKL EIK
2115	CD70-21	bispecifi c molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2116	CD70-22	VH CDR1	SYAMS
2117	CD70-22	VH CDR2	AISGSGGYTYYADSVKG
2118	CD70-22	VH CDR3	HDYSNYPYFDY
2119	CD70-22	VL CDR1	RASQSVRSNYLA
2120	CD70-22	VL CDR2	GASSRAT
2121	CD70-22	VL CDR3	QQYGDLPFT
2122	CD70-22	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGYTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS

2123	CD70-22	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKVEIK
2124	CD70-22	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGYTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIK
2125	CD70-22	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGYTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2126	CD70-23	VH CDR1	VYAMS
2127	CD70-23	VH CDR2	TISDSGGSTFYADSVKG
2128	CD70-23	VH CDR3	HDYSNYAYFDY
2129	CD70-23	VL CDR1	RASQSVRSSYLA
2130	CD70-23	VL CDR2	GASSRAT
2131	CD70-23	VL CDR3	QQYGDLPFT
2132	CD70-23	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLVTVSS
2133	CD70-23	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKVEIK
2134	CD70-23	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIK
2135	CD70-23	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV

			EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2136	CD70-24	VH CDR1	SYAMS
2137	CD70-24	VH CDR2	AISGSGGSTFYADSVKG
2138	CD70-24	VH CDR3	HDYSNYPYFDY
2139	CD70-24	VL CDR1	RASQSVRSSYLA
2140	CD70-24	VL CDR2	GASSRAT
2141	CD70-24	VL CDR3	QQYGDLPFT
2142	CD70-24	VH	EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYFCAKHDYSNYPYFDYWGQGTLVTVSS
2142	CD70-24	VH	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKVEIK
2143	CD70-24	VL	EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYFCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIK
2144	CD70-24	scFv	
2145	CD70-24	bispecific molecule	EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYFCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2146	CD70-25	VH CDR1	SYAMS
2147	CD70-25	VH CDR2	AISGSGGRTFYADSVEG

2148	CD70-25	VH CDR3	HDYSNYPYFDY
2149	CD70-25	VL CDR1	RASQSVRSNYLA
2150	CD70-25	VL CDR2	GASSRAT
2151	CD70-25	VL CDR3	QQYGDLPFT
2152	CD70-25	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2153	CD70-25	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKVEIK
2154	CD70-25	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIK
2155	CD70-25	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2156	CD70-26	VH CDR1	SYAMS
2157	CD70-26	VH CDR2	AISGSGGRTFYADSVEG
2158	CD70-26	VH CDR3	HDYSNYPYFDY
2159	CD70-26	VL CDR1	RASQSVRSSYLA
2160	CD70-26	VL CDR2	GASSRAT
2161	CD70-26	VL CDR3	QQYGSSPFT

2162	CD70-26	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2163	CD70-26	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPFTFGPGTKVEIK
2164	CD70-26	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKV EIK
2165	CD70-26	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2166	CD70-27	VH CDR1	TYAMS
2167	CD70-27	VH CDR2	AISGSGGGTFYADSVKG
2168	CD70-27	VH CDR3	HDYSNYPYFDY
2169	CD70-27	VL CDR1	RASQSIRSNYLA
2170	CD70-27	VL CDR2	GASSRAT
2171	CD70-27	VL CDR3	QQYGSSPFT
2172	CD70-27	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGGTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2173	CD70-27	VL	EIVLTQSPGTLSLSPGERATLSCRASQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPFTFGPGTKVEIK
2174	CD70-27	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGGTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKV EIK
2175	CD70-27	bispecifi	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGGTFYADSVKGRFTISRDNSKNTLY

		c molecule	LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2176	CD70-28	VH CDR1	TYAMS
2177	CD70-28	VH CDR2	LISGSGGRTYYADSVKG
2178	CD70-28	VH CDR3	HDYSNYPYFDY
2179	CD70-28	VL CDR1	RASQSVRSNYLA
2180	CD70-28	VL CDR2	GASNRAT
2181	CD70-28	VL CDR3	QQYGISPPT
2182	CD70-28	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2183	CD70-28	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASNRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYSCQQYGISPPTFGGGTKVEIK
2184	CD70-28	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGGGTKV EIK
2185	CD70-28	bispecifi c molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASNRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGGGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2186	CD70-29	VH CDR1	SYAMS
2187	CD70-29	VH	VISGSGGRTHYADSGKG

		CDR2	
2188	CD70-29	VH CDR3	HDYSNYPYFDY
2189	CD70-29	VL CDR1	RASQSVRSSYLA
2190	CD70-29	VL CDR2	GASSRAT
2191	CD70-29	VL CDR3	EQYGNSPPT
2192	CD70-29	VH	EVQLLESGGGLVQPGGSLRLSCAASGFNFASYAMSWVRQAPGKGLEWVSVISGSGGRTHYADSGKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2193	CD70-29	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSESGTDFTLTINRLE PEDFAVYYCEQYGNSPPTFGGGTKVEIK
2194	CD70-29	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFNFASYAMSWVRQAPGKGLEWVSVISGSGGRTHYADSGKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSESGTDFTLTINRLEPEDFAVYYCEQYGNSPPTFGGGTKV EIK
2195	CD70-29	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFNFASYAMSWVRQAPGKGLEWVSVISGSGGRTHYADSGKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSESGTDFTLTINRLEPEDFAVYYCEQYGNSPPTFGGGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2196	CD70-30	VH CDR1	TYAMS
2197	CD70-30	VH CDR2	LISGSGGRTYYADSVKG
2198	CD70-30	VH CDR3	HDYSNYPYFDY
2199	CD70-30	VL CDR1	RASQSVRSSYLA
2200	CD70-30	VL CDR2	GASSRAT

2201	CD70-30	VL CDR3	QQYGSSPPP
2202	CD70-30	VH	EVQLLESGGGVVQPGRSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2203	CD70-30	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPPPFGGGTKVEIK
2204	CD70-30	scFv	EVQLLESGGGVVQPGRSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPPFGGGTKV EIK
2205	CD70-30	bispecifi c molecule	EVQLLESGGGVVQPGRSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPPFGGGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2206	CD70-31	VH CDR1	SYAMS
2207	CD70-31	VH CDR2	AISGSGGRAQYADSVQG
2208	CD70-31	VH CDR3	HDYSNYPYFDY
2209	CD70-31	VL CDR1	RASQSVSSNLA
2210	CD70-31	VL CDR2	GSSSRAT
2211	CD70-31	VL CDR3	QQYGSSPPP
2212	CD70-31	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYADSVQGRFTVSRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2213	CD70-31	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFSGSGSGTDFTLTISRLEP EDFAVYYCQQYGSSPPPFGGGTKVEIK
2214	CD70-31	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYADSVQGRFTVSRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPPFGGGTKVE

2215	CD70-31	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYADSVQGRFTVSRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPPFGGGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2216	CD70-32	VH CDR1	SYAMS
2217	CD70-32	VH CDR2	AISGSGGRTFYADSVEG
2218	CD70-32	VH CDR3	HDYSNYPYFDY
2219	CD70-32	VL CDR1	RASQGVRSDYLA
2220	CD70-32	VL CDR2	GASSRAT
2221	CD70-32	VL CDR3	QQYGSTPPT
2222	CD70-32	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLVTVSS
2223	CD70-32	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRSDYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGGGTKV EIK
2224	CD70-32	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSDYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGGGTKV EIK
2225	CD70-32	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSDYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGGGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2226	CD70-33	VH	TYAMS

		CDR1	
2227	CD70-33	VH CDR2	TISDSGGSTFYADSVMG
2228	CD70-33	VH CDR3	HDYSNYAFFDY
2229	CD70-33	VL CDR1	RASQSVSSNLA
2230	CD70-33	VL CDR2	GASSRAT
2231	CD70-33	VL CDR3	QQYYSTPFT
2232	CD70-33	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVMGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLVTVSS
2233	CD70-33	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLQA EDVAVYYCQQYYSTPFTFGPGTKVEIK
2234	CD70-33	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVMGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPFTFGPGTKVE IK
2235	CD70-33	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVMGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPFTFGPGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2236	CD70-34	VH CDR1	TYAMS
2237	CD70-34	VH CDR2	TISDSGGSTFYADSVMG
2238	CD70-34	VH CDR3	HDYSNYAFFDY
2239	CD70-34	VL CDR1	RASQSVSSNLA

2240	CD70-34	VL CDR2	GASTRAT
2241	CD70-34	VL CDR3	QQYYSTPFT
2242	CD70-34	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVMGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLVTVSS
2243	CD70-34	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLAISRLEP EDFAVYYCQQYYSTPFTFGGGTKVEIK
2244	CD70-34	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVMGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLAISRLEPEDFAVYYCQQYYSTPFTFGGGTKVE IK
2245	CD70-34	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSTISDSGGSTFYADSVMGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSVSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLAISRLEPEDFAVYYCQQYYSTPFTFGGGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2246	CD70-35	VH CDR1	TYAMS
2247	CD70-35	VH CDR2	AISGSGGYTYYADSVEG
2248	CD70-35	VH CDR3	HDYSNYAWFDP
2249	CD70-35	VL CDR1	RASQSVSSAYLA
2250	CD70-35	VL CDR2	GASSRAT
2251	CD70-35	VL CDR3	QQFGSSPFT
2252	CD70-35	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSS
2253	CD70-35	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQFGSSPFTFGPGTKVEIK

2254	CD70-35	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGPGTKV EIK
2255	CD70-35	bispecifi c molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2256	CD70-36	VH CDR1	SYAMS
2257	CD70-36	VH CDR2	AISGSGGRTYYADSVKG
2258	CD70-36	VH CDR3	HDYSNYPYFDY
2259	CD70-36	VL CDR1	RASQSVRGSYLA
2260	CD70-36	VL CDR2	SASSRAT
2261	CD70-36	VL CDR3	QQYGDSPFT
2262	CD70-36	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQGLEWVSAISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2263	CD70-36	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDSPFTFGPGTKVEIK
2264	CD70-36	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQGLEWVSAISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGPGTKV EIK
2265	CD70-36	bispecifi c molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQGLEWVSAISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT

			VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2266	CD70-37	VH CDR1	SYAMS
2267	CD70-37	VH CDR2	AIGDGGGYTYYADSVKG
2268	CD70-37	VH CDR3	HDYSNYPYFDY
2269	CD70-37	VL CDR1	RASQGVRSSYFA
2270	CD70-37	VL CDR2	GASTRAT
2271	CD70-37	VL CDR3	QQYGSSPPT
2272	CD70-37	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAIGDGGGYTYYADSVKGRFTISRDNSKNTLS LLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLVTVSS
2273	CD70-37	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRSSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPPTFGQGTKVEIK
2274	CD70-37	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAIGDGGGYTYYADSVKGRFTISRDNSKNTLS LLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGQGTKV EIK
2275	CD70-37	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAIGDGGGYTYYADSVKGRFTISRDNSKNTLS LLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGQGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2276	CD70-38	VH CDR1	SYAMS
2277	CD70-38	VH CDR2	AISGSGGRTFYADSVEG
2278	CD70-38	VH CDR3	HDYSNYPYFDY

2279	CD70-38	VL CDR1	RASQSIRSNYLA
2280	CD70-38	VL CDR2	GASSRAT
2281	CD70-38	VL CDR3	QQYGSSPPS
2282	CD70-38	VH	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2283	CD70-38	VL	EIVLTQSPGTLSLSPGERATLSCRASQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGSSPPSFGQGTKVEIK
2284	CD70-38	scFv	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPSFGQGTKV EIK
2285	CD70-38	bispecific molecule	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPSFGQGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2286	CD70-39	VH CDR1	SYAMS
2287	CD70-39	VH CDR2	AISGSGGGTFYADSVEG
2288	CD70-39	VH CDR3	HDYSNYPYFDY
2289	CD70-39	VL CDR1	RASQSVRSSYLA
2290	CD70-39	VL CDR2	GASSRAT
2291	CD70-39	VL CDR3	QQYGDLPFT
2292	CD70-39	VH	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYPYFDYWGLGTLVTVSS

2293	CD70-39	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYSCQQYGDLPFTFGPGTKVEIK
2294	CD70-39	scFv	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYPYFDYWGLGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKV EIK
2295	CD70-39	bispecific molecule	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNYPYFDYWGLGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2296	CD70-40	VH CDR1	SYAMS
2297	CD70-40	VH CDR2	AISGSGGRTFYADSVEG
2298	CD70-40	VH CDR3	HDYSNYPYFDY
2299	CD70-40	VL CDR1	RASQSIRSSYLA
2300	CD70-40	VL CDR2	GASSRAT
2301	CD70-40	VL CDR3	QQYGDLPFT
2302	CD70-40	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2303	CD70-40	VL	EIVLTQSPGTLSLSPGERATLSCRASQSIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKVDIK
2304	CD70-40	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV DIK
2305	CD70-40	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV

			DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2306	CD70-41	VH CDR1	SYAMS
2307	CD70-41	VH CDR2	AISGSGGRTFYADSVEG
2308	CD70-41	VH CDR3	HDYSNYPYFDY
2309	CD70-41	VL CDR1	RASQSVRSSYLA
2310	CD70-41	VL CDR2	GASSRAT
2311	CD70-41	VL CDR3	QQYGDLPFT
2312	CD70-41	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLVTVSS
2313	CD70-41	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTKVDIK
2314	CD70-41	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV DIK
2315	CD70-41	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKV DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2316	CD70-42	VH CDR1	TYAMS
2317	CD70-42	VH CDR2	LISGSGGRTYYADSVKG

2318	CD70-42	VH CDR3	HDYSNYPYFDY
2319	CD70-42	VL CDR1	RASQGVRSSYLA
2320	CD70-42	VL CDR2	GASSRAT
2321	CD70-42	VL CDR3	QQYGSSPPT
2322	CD70-42	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2323	CD70-42	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTINRLE PEDFAVYYCQQYGSSPPTFGGGTKVDIK
2324	CD70-42	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKV DIK
2325	CD70-42	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQGVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKV DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2326	CD70-43	VH CDR1	SYAMS
2327	CD70-43	VH CDR2	AISGSGGRTFYADSVEG
2328	CD70-43	VH CDR3	HDYSNYPYFDY
2329	CD70-43	VL CDR1	RASQSVRSNYLA
2330	CD70-43	VL CDR2	GASSRAT
2331	CD70-43	VL CDR3	QQYGSSPPT

2332	CD70-43	VH	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2333	CD70-43	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTINRLE PEDFAVYYCQQYGSSPPTFGGGTKVDIK
2334	CD70-43	scFv	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKV DIK
2335	CD70-43	bispecific molecule	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKV DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2336	CD70-44	VH CDR1	SYAMS
2337	CD70-44	VH CDR2	VISDSGGITDFADSVKG
2338	CD70-44	VH CDR3	HDYSNYFFFDY
2339	CD70-44	VL CDR1	RASQDISNYLN
2340	CD70-44	VL CDR2	AASSLQS
2341	CD70-44	VL CDR3	QQSYISPPT
2342	CD70-44	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFIISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2343	CD70-44	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYISPPTFGQGTKVEIK
2344	CD70-44	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFIISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQDISNYLNWYQQKSGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVE IK
2345	CD70-44	bispecifi	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFIISRDNSRNTLY

		c molecule	LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQDISNYLNWYQQKSGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2346	CD70-45	VH CDR1	SYAMS
2347	CD70-45	VH CDR2	VISDSGGITDFADSVKG
2348	CD70-45	VH CDR3	HDYSNYFFFDY
2349	CD70-45	VL CDR1	RASQSISSYLN
2350	CD70-45	VL CDR2	AASSLQS
2351	CD70-45	VL CDR3	QQSYISPPT
2352	CD70-45	VH	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2353	CD70-45	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYISPPTFGQGTKVEIK
2354	CD70-45	scFv	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVE IK
2355	CD70-45	bispecifi c molecule	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2356	CD70-46	VH CDR1	SYAMS
2357	CD70-46	VH	VISGSGGRTDYADSVKG

		CDR2	
2358	CD70-46	VH CDR3	HDYSNRFYFDY
2359	CD70-46	VL CDR1	RASQSISSYLN
2360	CD70-46	VL CDR2	AASSLQS
2361	CD70-46	VL CDR3	QQSYSAPPT
2362	CD70-46	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQVPGKGLEWVSVISGSGGRTDYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNRFYFDYWGQGTLVTVSS
2363	CD70-46	VL	DIQMTQSPSSLSASVGDRVSITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSAPPTFGGGTKVEIK
2364	CD70-46	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQVPGKGLEWVSVISGSGGRTDYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNRFYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVSITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSAPPTFGGGTKVE IK
2365	CD70-46	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQVPGKGLEWVSVISGSGGRTDYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARHDYSNRFYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVSITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSAPPTFGGGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2366	CD70-47	VH CDR1	SYAMS
2367	CD70-47	VH CDR2	VISDSGGITDYADSVKG
2368	CD70-47	VH CDR3	HDYSNRYYFDY
2369	CD70-47	VL CDR1	RASQSISSYLN
2370	CD70-47	VL CDR2	AASSLQS

2371	CD70-47	VL CDR3	QQSYSTPLT
2372	CD70-47	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDYADSVKGRFTISRDNSKNTLY LQMNSLRAEDRAVYYCARHDYSNRYYFDYWGQGTLVTVSS
2373	CD70-47	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPLTFGGGTKVEIK
2374	CD70-47	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDYADSVKGRFTISRDNSKNTLY LQMNSLRAEDRAVYYCARHDYSNRYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVE IK
2375	CD70-47	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDYADSVKGRFTISRDNSKNTLY LQMNSLRAEDRAVYYCARHDYSNRYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2376	CD70-48	VH CDR1	SYAMS
2377	CD70-48	VH CDR2	VISDSGGITDFADSVKG
2378	CD70-48	VH CDR3	HDYSNYFFFDY
2379	CD70-48	VL CDR1	RASQGISNYLA
2380	CD70-48	VL CDR2	AASILQS
2381	CD70-48	VL CDR3	QQYFAYPIT
2382	CD70-48	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2383	CD70-48	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFSGSGSGTDFTLTISSLQP EDFAIYYCQQYFAYPITFGQGTRLEIK
2384	CD70-48	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFSGSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGQGTRLE

2385	CD70-48	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFSGSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGQGTRLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2386	CD70-49	VH CDR1	SYAMS
2387	CD70-49	VH CDR2	VISDSGGITDFADSVKG
2388	CD70-49	VH CDR3	HDYSNYFFFDY
2389	CD70-49	VL CDR1	RASQSISSYLN
2390	CD70-49	VL CDR2	AASSLQS
2391	CD70-49	VL CDR3	QQSYSTPIT
2392	CD70-49	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRSTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2393	CD70-49	VL	DIQMTQSPSSVSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPITFGQGTRLEIK
2394	CD70-49	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRSTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQGTRLE IK
2395	CD70-49	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRSTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQGTRLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2396	CD70-50	VH	TYAMS

		CDR1	
2397	CD70-50	VH CDR2	AISGSGGYTYYADSVEG
2398	CD70-50	VH CDR3	HDYSNYAWFDP
2399	CD70-50	VL CDR1	RASQSISSYLN
2400	CD70-50	VL CDR2	AASSLQS
2401	CD70-50	VL CDR3	QQSYSTPFT
2402	CD70-50	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSS
2403	CD70-50	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPFTFGPGTRLEIK
2404	CD70-50	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTRLE IK
2405	CD70-50	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTRLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2406	CD70-51	VH CDR1	TDGYYWS
2407	CD70-51	VH CDR2	YIYYSGSTNYNPSLKS
2408	CD70-51	VH CDR3	GIGLGFEY
2409	CD70-51	VL CDR1	GGNNIGSKSVH

2410	CD70-51	VL CDR2	DDSDRPS
2411	CD70-51	VL CDR3	QVWDRSSDQDVV
2412	CD70-51	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARGIGLGFEYWGQGTLVTVSS
2413	CD70-51	VL	SYVLTQLTSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAG DEADFYCQVWDRSSDQDVVFGGGTKLTVL
2414	CD70-51	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARGIGLGFEYWGQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQLTSVSVAPGQTARITCGGNNI GSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADFYCQVWDRSSDQDVVFGGGTKLT VL
2415	CD70-51	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARGIGLGFEYWGQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQLTSVSVAPGQTARITCGGNNI GSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADFYCQVWDRSSDQDVVFGGGTKLT VLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2416	CD70-52	VH CDR1	TDGYYWS
2417	CD70-52	VH CDR2	YIYYSGSTNYNPSLKS
2418	CD70-52	VH CDR3	GIGLGFEY
2419	CD70-52	VL CDR1	GGNNIGSKSVH
2420	CD70-52	VL CDR2	DDSDRPS
2421	CD70-52	VL CDR3	QVWDRSSDQDVV
2422	CD70-52	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARGIGLGFEYWGQGTLVTVSS
2423	CD70-52	VL	SYVLTQLSSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAG DEADYYCQVWDRSSDQDVVFGGGTKLTVL

2424	CD70-52	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARGIGLGFEYWGQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQLSSVSVAPGQTARITCGGNNI GSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDRSSDQDVVFGGGTKLT VL
2425	CD70-52	bispecifi c molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARGIGLGFEYWGQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQLSSVSVAPGQTARITCGGNNI GSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDRSSDQDVVFGGGTKLT VLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQ SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2426	CD70-53	VH CDR1	SYAMS
2427	CD70-53	VH CDR2	AISGSGGRTFYADSVEG
2428	CD70-53	VH CDR3	HDYSNYPYFDY
2429	CD70-53	VL CDR1	RASQSVRSSYLA
2430	CD70-53	VL CDR2	GASSRAT
2431	CD70-53	VL CDR3	QQYGSSPPT
2432	CD70-53	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2433	CD70-53	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYFCQQYGSSPPTFGGGTRLEIK
2434	CD70-53	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTRL EIK
2435	CD70-53	bispecifi c molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVEGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTRL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSQTVVTQEPSLT

			VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2436	CD70-54	VH CDR1	IYAMS
2437	CD70-54	VH CDR2	AIGDSGGSTFYADSVKG
2438	CD70-54	VH CDR3	HDYSNYPYFDY
2439	CD70-54	VL CDR1	RASQSVRSSYVA
2440	CD70-54	VL CDR2	GASSRAT
2441	CD70-54	VL CDR3	QQYGDLPFT
2442	CD70-54	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2443	CD70-54	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYVAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGPGTRLEIK
2444	CD70-54	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYVAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTRL EIK
2445	CD70-54	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYVAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTRL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2446	CD70-55	VH CDR1	SYGMH
2447	CD70-55	VH CDR2	VISYDGSNKYYADSVKG
2448	CD70-55	VH CDR3	GRYYGSGNYNHGMDV

2449	CD70-55	VL CDR1	RASQSISSYLN
2450	CD70-55	VL CDR2	AASSLQS
2451	CD70-55	VL CDR3	QQSYSTPFT
2452	CD70-55	VH	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGNYNHGMDVWGQGTTVTVSS
2453	CD70-55	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQP EDFATYYCQQSYSTPFTFGPGTKVEIK
2454	CD70-55	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGNYNHGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPG TKVEIK
2455	CD70-55	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGNYNHGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
2456	CD70-56	VH CDR1	SYGMH
2457	CD70-56	VH CDR2	VISYDGSNKYYADSVKG
2458	CD70-56	VH CDR3	GRYYGSGSYNYGMDV
2459	CD70-56	VL CDR1	RASQSIFDYLN
2460	CD70-56	VL CDR2	AASSLQS
2461	CD70-56	VL CDR3	QQSYSTPLT
2462	CD70-56	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGTTVTVSS

2463	CD70-56	VL	DIQMTQSPSSLSASVGDRVTITCRASQSIFDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTISSLQP EDFATYYCQQSYSTPLTFGGGTKLEIK
2464	CD70-56	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSIFDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGG TKLEIK
2465	CD70-56	bispecifi c molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSIFDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
2466	CD70-57	VH CDR1	SYGMH
2467	CD70-57	VH CDR2	VIWYDGSSEYYADSVKG
2468	CD70-57	VH CDR3	DNSYNYYGMDV
2469	CD70-57	VL CDR1	TGSSSNIGAAYDVH
2470	CD70-57	VL CDR2	VNSHRPP
2471	CD70-57	VL CDR3	LSYDNSLSGSV
2472	CD70-57	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSSEYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSYNYYGMDVWGQGTTVTVSS
2473	CD70-57	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAAYDVHWYQQFPGTAPKLLIYVNSHRPPGVPDRFSGSKSGTSASLAITGL QAEDEADYYCLSYDNSLSGSVFGGGTKLTVL
2474	CD70-57	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSSEYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSYNYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGS SSNIGAAYDVHWYQQFPGTAPKLLIYVNSHRPPGVPDRFSGSKSGTSASLAITGLQAEDEADYYCLSYDNSLSGSVFGGG TKLTVL
2475	CD70-57	bispecifi c molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSSEYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDNSYNYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGS SSNIGAAYDVHWYQQFPGTAPKLLIYVNSHRPPGVPDRFSGSKSGTSASLAITGLQAEDEADYYCLSYDNSLSGSVFGGG

			TKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
2476	CD70-58	VH CDR1	SSSYYWG
2477	CD70-58	VH CDR2	SIYHSGGTYFNPSLKS
2478	CD70-58	VH CDR3	HYEILTGYYPDVFDI
2479	CD70-58	VL CDR1	RASQSISSYLN
2480	CD70-58	VL CDR2	AASNLQS
2481	CD70-58	VL CDR3	QQSFSSPRT
2482	CD70-58	VH	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYHSGGTYFNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARHYEILTGYYPDVFDIWGQGTMVTVSS
2483	CD70-58	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLQSGVSSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSFSSPRTFGQGTKVEIK
2484	CD70-58	scFv	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYHSGGTYFNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARHYEILTGYYPDVFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLQSGVSSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGQ GTKVEIK
2485	CD70-58	bispecific molecule	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGSIYHSGGTYFNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARHYEILTGYYPDVFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVT ITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLQSGVSSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGQ GTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVL
2486	CD70-59	VH CDR1	GFYWS
2487	CD70-59	VH CDR2	EIDHSGSTNYNPSLKS

2488	CD70-59	VH CDR3	NGYSGYLFDY
2489	CD70-59	VL CDR1	RASQIISSYLN
2490	CD70-59	VL CDR2	GASSMQS
2491	CD70-59	VL CDR3	QQSYSIPRT
2492	CD70-59	VH	QVQLQQWGAGLLKPSETLSLTCAVYDGSVSGFYWSWIRQPPGKGLEWIGEIDHSGSTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADSAVYYCARNGYSGYLFDYWGQGTLVTVSS
2493	CD70-59	VL	DIQMTQSPSSLSASVGDRVTITCRASQIISSYLNWYQQKPGKAPKVLIYGASSMQSGVPSRFSGSGYGTDFTLTISSLQP EDFATYYCQQSYSIPRTFGQGTKLEIK
2494	CD70-59	scFv	QVQLQQWGAGLLKPSETLSLTCAVYDGSVSGFYWSWIRQPPGKGLEWIGEIDHSGSTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADSAVYYCARNGYSGYLFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQ IISSYLNWYQQKPGKAPKVLIYGASSMQSGVPSRFSGSGYGTDFTLTISSLQPEDFATYYCQQSYSIPRTFGQGTKLEIK
2495	CD70-59	bispecific molecule	QVQLQQWGAGLLKPSETLSLTCAVYDGSVSGFYWSWIRQPPGKGLEWIGEIDHSGSTNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADSAVYYCARNGYSGYLFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQ IISSYLNWYQQKPGKAPKVLIYGASSMQSGVPSRFSGSGYGTDFTLTISSLQPEDFATYYCQQSYSIPRTFGQGTKLEIK SGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWY SNRWVFGGGTKLTVL
2496	CD70-60	VH CDR1	TYYWS
2497	CD70-60	VH CDR2	RIYPTGITNYNPSLKS
2498	CD70-60	VH CDR3	DRRFLEPSYYYYYGMDV
2499	CD70-60	VL CDR1	RSSQSLLHSNGYNYLD
2500	CD70-60	VL CDR2	LGSNRAS
2501	CD70-60	VL CDR3	MQGLRTPFT

2502	CD70-60	VH	QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAGKGLEWIGRIYPTGITNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARDRRFLEPSYYYYYGMDVWGQGTTVTVSS
2503	CD70-60	VL	DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSVSGTDFTLKI SRVEAEDVGVYYCMQGLRTPFTFGPGTKLEIK
2504	CD70-60	scFv	QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAGKGLEWIGRIYPTGITNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARDRRFLEPSYYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPLSLPVTPGEPAS ISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQGLRTP FTFGPGTKLEIK
2505	CD70-60	bispecifi c molecule	QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAGKGLEWIGRIYPTGITNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARDRRFLEPSYYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPLSLPVTPGEPAS ISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQGLRTP FTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVL
2506	CD70-61	VH CDR1	SYAMS
2507	CD70-61	VH CDR2	VISDSGGITDFADSVKG
2508	CD70-61	VH CDR3	HDYSNYFFFDY
2509	CD70-61	VL CDR1	RASQSISNYLN
2510	CD70-61	VL CDR2	AASSLQS
2511	CD70-61	VL CDR3	QQSYIIPPT
2512	CD70-61	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2513	CD70-61	VL	DIQMTQSPSSLSASVGDRITITCRASQSISNYLNWYQQKPGKAPKLLISAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYIIPPTFGQGTKVDIK
2514	CD70-61	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRITITCRA SQSISNYLNWYQQKPGKAPKLLISAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYIIPPTFGQGTKVD IK
2515	CD70-61	bispecifi	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY

		c molecule	LQMNSLRAEDTAVYFCARHDYSNYFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRITITCRA SQSISNYLNWYQQKPGKAPKLLISAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYIIPPTFGQGTKVD IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2516	CD70-62	VH CDR1	SYSMN
2517	CD70-62	VH CDR2	YISSSGGYIYYADSVKG
2518	CD70-62	VH CDR3	GDYSNYAYFDY
2519	CD70-62	VL CDR1	RASQGISNYLA
2520	CD70-62	VL CDR2	AASTLQS
2521	CD70-62	VL CDR3	QQYYSTPLT
2522	CD70-62	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLVTVSS
2523	CD70-62	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQA EDVAVYYCQQYYSTPLTFGGGTKVEIK
2524	CD70-62	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVE IK
2525	CD70-62	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLVTVSSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2526	CD70-63	VH CDR1	TYTMN
2527	CD70-63	VH	SISSSSGYIYYADSVKG

		CDR2	
2528	CD70-63	VH CDR3	GDYSNYLYFDL
2529	CD70-63	VL CDR1	RASQSFRSSYLA
2530	CD70-63	VL CDR2	GASSRAT
2531	CD70-63	VL CDR3	QLYGSLPIT
2532	CD70-63	VH	EVQLVESGGGLVKPGGSLRLSCAASGITFSTYTMNWVRQAPGKGLEWVSSISSSSGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARGDYSNYLYFDLWGRGTLVTVSS
2533	CD70-63	VL	EIVLTQSPGTLSLSPGERATLSCRASQSFRSSYLAWYQQKPGQAPRLLIHGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQLYGSLPITFGQGTRLEIK
2534	CD70-63	scFv	EVQLVESGGGLVKPGGSLRLSCAASGITFSTYTMNWVRQAPGKGLEWVSSISSSSGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARGDYSNYLYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSFRSSYLAWYQQKPGQAPRLLIHGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQLYGSLPITFGQGTRL EIK
2535	CD70-63	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGITFSTYTMNWVRQAPGKGLEWVSSISSSSGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARGDYSNYLYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSFRSSYLAWYQQKPGQAPRLLIHGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQLYGSLPITFGQGTRL EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2536	CD70-64	VH CDR1	VYAMS
2537	CD70-64	VH CDR2	TISDSGGSTFYADSVKG
2538	CD70-64	VH CDR3	HDYSNYAYFDY
2539	CD70-64	VL CDR1	RASQSVRSSYLA
2540	CD70-64	VL CDR2	GASSRAT

2541	CD70-64	VL CDR3	QQYGDLPFT
2542	CD70-64	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLVTVSS
2543	CD70-64	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDLPFTFGCGTKVEIK
2544	CD70-64	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKV EIK
2545	CD70-64	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADSVKGRFTISRDNSKNTLY LQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2546	CD70-65	VH CDR1	TYAMS
2547	CD70-65	VH CDR2	AISGSGGYTYYADSVEG
2548	CD70-65	VH CDR3	HDYSNYAWFDP
2549	CD70-65	VL CDR1	RASQSVSSAYLA
2550	CD70-65	VL CDR2	GASSRAT
2551	CD70-65	VL CDR3	QQFGSSPFT
2552	CD70-65	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSS
2553	CD70-65	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQFGSSPFTFGCGTKVEIK
2554	CD70-65	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGCGTKV

			EIK
2555	CD70-65	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKCLDWVSAISGSGGYTYYADSVEGRFTISRDNSRNTLY LQMNSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGCGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2556	CD70-66	VH CDR1	SYAMS
2557	CD70-66	VH CDR2	AISGSGGRTYYADSVKG
2558	CD70-66	VH CDR3	HDYSNYPYFDY
2559	CD70-66	VL CDR1	RASQSVRGSYLA
2560	CD70-66	VL CDR2	SASSRAT
2561	CD70-66	VL CDR3	QQYGDSPFT
2562	CD70-66	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQCLEWVSAISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSS
2563	CD70-66	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGDSPFTFGCGTKVEIK
2564	CD70-66	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQCLEWVSAISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGCGTKV EIK
2565	CD70-66	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQCLEWVSAISGSGGRTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGCGTKV EIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2566	CD70-67	VH	SYAMS

		CDR1	
2567	CD70-67	VH CDR2	VISDSGGITDFADSVKG
2568	CD70-67	VH CDR3	HDYSNYFFFDY
2569	CD70-67	VL CDR1	RASQDISNYLN
2570	CD70-67	VL CDR2	AASSLQS
2571	CD70-67	VL CDR3	QQSYISPPT
2572	CD70-67	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADSVKGRFIISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2573	CD70-67	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYISPPTFGCGTKVEIK
2574	CD70-67	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADSVKGRFIISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQDISNYLNWYQQKSGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYISPPTFGCGTKVE IK
2575	CD70-67	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADSVKGRFIISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQDISNYLNWYQQKSGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYISPPTFGCGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2576	CD70-68	VH CDR1	SYAMS
2577	CD70-68	VH CDR2	VISDSGGITDFADSVKG
2578	CD70-68	VH CDR3	HDYSNYFFFDY
2579	CD70-68	VL CDR1	RASQGISNYLA

2580	CD70-68	VL CDR2	AASILQS
2581	CD70-68	VL CDR3	QQYFAYPIT
2582	CD70-68	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSS
2583	CD70-68	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFSGSGSGTDFTLTISSLQP EDFAIYYCQQYFAYPITFGCGTRLEIK
2584	CD70-68	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFSGSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLE IK
2585	CD70-68	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADSVKGRFTISRDNSRNTLY LQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFSGSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2586	CD70-69	VH CDR1	TDGYYWS
2587	CD70-69	VH CDR2	YIYYSGSTNYNPSLKS
2588	CD70-69	VH CDR3	GIGLGFEY
2589	CD70-69	VL CDR1	GGNNIGSKSVH
2590	CD70-69	VL CDR2	DDSDRPS
2591	CD70-69	VL CDR3	QVWDRSSDQDVV
2592	CD70-69	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKCLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLISVTAADTAVYYCARGIGLGFEYWGQGTLVTVSS
2593	CD70-69	VL	SYVLTQLSSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAG DEADYYCQVWDRSSDQDVVFGCGTKLTVL

2594	CD70-69	scFv	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKCLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLISVTAADTAVYYCARGIGLGFEYWGQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQLSSVSVAPGQTARITCGGNNI GSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDRSSDQDVVFGCGTKLT VL
2595	CD70-69	bispecifi c molecule	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYWSWIRQPPGKCLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLISVTAADTAVYYCARGIGLGFEYWGQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQLSSVSVAPGQTARITCGGNNI GSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDRSSDQDVVFGCGTKLT VLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2596	CD70-70	VH CDR1	SYGMH
2597	CD70-70	VH CDR2	VISYDGSNKYYADSVKG
2598	CD70-70	VH CDR3	GRYYGSGNYNHGMDV
2599	CD70-70	VL CDR1	RASQSISSYLN
2600	CD70-70	VL CDR2	AASSLQS
2601	CD70-70	VL CDR3	QQSYSTPFT
2602	CD70-70	VH	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGNYNHGMDVWGQGTTVTVSS
2603	CD70-70	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQP EDFATYYCQQSYSTPFTFGCGTKVEIK
2604	CD70-70	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGNYNHGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCG TKVEIK
2605	CD70-70	bispecifi c molecule	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGNYNHGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGRGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCG TKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSQTVVTQEP

			SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
2606	CD70-71	VH CDR1	SYGMH
2607	CD70-71	VH CDR2	VISYDGSNKYYADSVKG
2608	CD70-71	VH CDR3	GRYYGSGSYNYGMDV
2609	CD70-71	VL CDR1	RASQSIFDYLN
2610	CD70-71	VL CDR2	AASSLQS
2611	CD70-71	VL CDR3	QQSYSTPLT
2612	CD70-71	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGTTVTVSS
2613	CD70-71	VL	DIQMTQSPSSLSASVGDRVTITCRASQSIFDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTISSLQP EDFATYYCQQSYSTPLTFGCGTKLEIK
2614	CD70-71	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSIFDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGCG TKLEIK
2615	CD70-71	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGTTVTVSSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTI TCRASQSIFDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGCG TKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVL
2616	CD70-72	VH CDR1	TYYWS
2617	CD70-72	VH CDR2	RIYPTGITNYNPSLKS
2618	CD70-72	VH CDR3	DRRFLEPSYYYYYGMDV

2619	CD70-72	VL CDR1	RSSQSLLHSNGYNYLD
2620	CD70-72	VL CDR2	LGSNRAS
2621	CD70-72	VL CDR3	MQGLRTPFT
2622	CD70-72	VH	QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAGKCLEWIGRIYPTGITNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARDRRFLEPSYYYYYGMDVWGQGTTVTVSS
2623	CD70-72	VL	DIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSVSGTDFTLKI SRVEAEDVGVYYCMQGLRTPFTFGCGTKLEIK
2624	CD70-72	scFv	QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAGKCLEWIGRIYPTGITNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARDRRFLEPSYYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPLSLPVTPGEPAS ISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQGLRTP FTFGCGTKLEIK
2625	CD70-72	bispecific molecule	QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAGKCLEWIGRIYPTGITNYNPSLKSRVTISVDTSKNQFSL KLSSVTAADTAVYYCARDRRFLEPSYYYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPLSLPVTPGEPAS ISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQGLRTP FTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVL
2626	CD70-73	VH CDR1	SYSMN
2627	CD70-73	VH CDR2	YISSSGGYIYYADSVKG
2628	CD70-73	VH CDR3	GDYSNYAYFDY
2629	CD70-73	VL CDR1	RASQGISNYLA
2630	CD70-73	VL CDR2	AASTLQS
2631	CD70-73	VL CDR3	QQYYSTPLT
2632	CD70-73	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYISSSGGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLVTVSS

2633	CD70-73	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQA EDVAVYYCQQYYSTPLTFGCGTKVEIK
2634	CD70-73	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYISSSGGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGCGTKVE IK
2635	CD70-73	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYISSSGGYIYYADSVKGRFTISRDNAKNSLY LQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA SQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGCGTKVE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
2636	CD70-74	VH CDR1	SYAMS
2637	CD70-74	VH CDR2	AISGSGGSTFYADSVQG
2638	CD70-74	VH CDR3	HDYSNYPYFDY
2639	CD70-74	VL CDR1	RASQSVRGNYLA
2640	CD70-74	VL CDR2	GASSRAT
2641	CD70-74	VL CDR3	QQYGYSPFT
2642	CD70-74	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVQGRFTISRDNSKNTLY LQVNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLVTVSS
2643	CD70-74	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE PEDFAVYYCQQYGYSPFTFGPGTKVDIK
2644	CD70-74	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVQGRFTISRDNSKNTLY LQVNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGPGTKV DIK
2645	CD70-74	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVQGRFTISRDNSKNTLY LQVNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRA SQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGPGTKV

			DIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV LWYSNRWVFGGGTKLTVL
2646	IVA-1	VH CDR1	TYAMS
2647	IVA-1	VH CDR2	SMSSGGSLYYPDTVKG
2648	IVA-1	VH CDR3	GGYGTSY
2649	IVA-1	VL CDR1	RSSQSIVHSIGDTYLE
2650	IVA-1	VL CDR2	KVSNRFS
2651	IVA-1	VL CDR3	FQGSHFPYT
2652	IVA-1	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPGKRLEWVASMSSGGSLYYPDTVKGRFTISRDTSKNTVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSS
2653	IVA-1	VL	DIVMTQTPLSLSVTPGEPASISCRSSQSIVHSIGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCFQGSHFPYTFGQGTKLEIK
2654	IVA-1	scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPGKRLEWVASMSSGGSLYYPDTVKGRFTISRDTSKNTVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSIV HSIGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHFPYTFGQGTKLE IK
2655	IVA-1	bispecific molecule	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPGKRLEWVASMSSGGSLYYPDTVKGRFTISRDTSKNTVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSIV HSIGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHFPYTFGQGTKLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQTPGKRLEWVASMSSGGSLYYPDTVKGRFTISRDTSKNTVYL SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADE SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKK

			YLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVA RLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDE MPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEF KPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVL NQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKP KATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2656	IVA-2	VH CDR1	TYAMS
2657	IVA-2	VH CDR2	SMSSGGSLYYPDTVKG
2658	IVA-2	VH CDR3	GGYGTSY
2659	IVA-2	VL CDR1	RSSQSIVHSIGDTYLE
2660	IVA-2	VL CDR2	KVSNRFS
2661	IVA-2	VL CDR3	FQGSHFPYT
2662	IVA-2	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPEKRLEWVASMSSGGSLYYPDTVKGRFTISRDNSKNIVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSS
2663	IVA-2	VL	DIVMTQTPLSLSVTPGEPASISCRSSQSIVHSIGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCFQGSHFPYTFGQGTKLEIK
2664	IVA-2	scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPEKRLEWVASMSSGGSLYYPDTVKGRFTISRDNSKNIVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSIV HSIGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHFPYTFGQGTKLE IK
2665	IVA-2	bispecific molecule	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPEKRLEWVASMSSGGSLYYPDTVKGRFTISRDNSKNIVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSIV HSIGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHFPYTFGQGTKLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL

			WYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADE SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKK YLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVA RLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDE MPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEF KPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVL NQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKP KATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2666	IVA-3	VH CDR1	TYAMS
2667	IVA-3	VH CDR2	SMSSGGSLYYPDTVKG
2668	IVA-3	VH CDR3	GGYGTSY
2669	IVA-3	VL CDR1	RSSQSIVHSIGDTYLE
2670	IVA-3	VL CDR2	KVSNRFS
2671	IVA-3	VL CDR3	FQGSHFPYT
2672	IVA-3	VH	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPEKRLEWVASMSSGGSLYYPDTVKGRFTISRDNSKNIVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSS
2673	IVA-3	VL	DIVMTQTPLSLSVTPGEPASISCRSSQSIVHSIGDTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKI SRVEAEDVGVYYCFQGSHFPYTFGQGTKLEIK
2674	IVA-3	scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPEKRLEWVASMSSGGSLYYPDTVKGRFTISRDNSKNIVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSIV HSIGDTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHFPYTFGQGTKLE IK
2675	IVA-3	bispecific molecule	EVQLVESGGGLVQPGGSLRLSCAASGFTVSTYAMSWVRQTPEKRLEWVASMSSGGSLYYPDTVKGRFTISRDNSKNIVYL QMNSLRAEDTAVYYCVRGGYGTSYWGQGTLVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGEPASISCRSSQSIV HSIGDTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHFPYTFGQGTKLE IKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTI

			SRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTV SPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADE SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKK YLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVA RLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDE MPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEF KPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVL NQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKP KATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2676	CMV-1	VH CDR1	GSWMN
2677	CMV-1	VH CDR2	RIYPGDGDTNYNGKFKG
2678	CMV-1	VH CDR3	DDGYYVAFDYYAMDY
2679	CMV-1	VL CDR1	KSSQSLSRASYSYLH
2680	CMV-1	VL CDR2	YASNRES
2681	CMV-1	VL CDR3	QHSWEIPYT
2682	CMV-1	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSS
2683	CMV-1	VL	DIVMTQTPLSLSVSPGQPASISCKSSQSLSRASYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCQHSWEIPYTFGQGTKLEIK
2684	CMV-1	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVSPGQPASI SCKSSQSLSRASYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHSWEIPYT FGQGTKLEIK
2685	CMV-1	bispecific	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVSPGQPASI

		molecule	
			SCKSSQSLSRASYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHSWEIPYT FGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEF AKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHD NEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGER AFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHC IAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTAL VELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2686	CMV-2	VH CDR1	GSWMN
2687	CMV-2	VH CDR2	RIYPGDGDTNYNGKFKG
2688	CMV-2	VH CDR3	DDGYYVAFDYYAMDY
2689	CMV-2	VL CDR1	RSSQSLSRSSYSYLH
2690	CMV-2	VL CDR2	YASNRES
2691	CMV-2	VL CDR3	QHSWEIPYT
2692	CMV-2	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSS
2693	CMV-2	VL	DIVMTQTPLSLSVTPGQPASISCRSSQSLSRSSYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCQHSWEIPYTFGQGTKLEIK
2694	CMV-2	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASI SCRSSQSLSRSSYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHSWEIPYT FGQGTKLEIK

2695	CMV-2	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASI SCRSSQSLSRSSYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHSWEIPYT FGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEF AKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHD NEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGER AFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHC IAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTAL VELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2696	CMV-3	VH CDR1	GSWMN
2697	CMV-3	VH CDR2	RIYPGDGDTNYNGKFKG
2698	CMV-3	VH CDR3	DDGYYVAFDYYAMDY
2699	CMV-3	VL CDR1	KSSQSLSRSSYSYLH
2700	CMV-3	VL CDR2	YASNRES
2701	CMV-3	VL CDR3	QHSWEIPYT
2702	CMV-3	VH	QVQLAQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSS
2703	CMV-3	VL	DIVMTQTPLSLSVTPGQPASTSCKSSQSLSRSSYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCQHSWEIPYTFGQGTKLEIK
2704	CMV-3	scFv	QVQLAQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPAST

			SCKSSQSLSRSSYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHSWEIPYT FGQGTKLEIK
2705	CMV-3	bispecific molecule	QVQLAQSGAEVKKPGASVKVSCKASGYTFTGSWMNWVRQAPGQGLEWMGRIYPGDGDTNYNGKFKGRVTMTADKSTSTAY MELSRLRSDDTAVYYCARDDGYYVAFDYYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPAST SCKSSQSLSRSSYSYLHWYLQKPGQPPKLLIKYASNRESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQHSWEIPYT FGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEF AKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHD NEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGER AFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHC IAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTAL VELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH	
2706	F12q	scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNT AYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTL TCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF GGGTKLTVL
2707	Peptide linker	artificial	PGGGGS
2708	Peptide linker	artificial	PGGDGS
2709	Peptide linker	artificial	SGGGGS

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Claims

1. A bispecific single chain antibody construct binding to a target cell surface antigen via a first binding domain and the T cell surface antigen CD3 via a second binding domain, wherein:

- the second binding domain binds to an epitope of the human and *Callithrix jacchus, Saguinus oedipus* or *Saimiri sciureus* CD3ε chain, wherein the epitope comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu (SEQ ID NO: **1**), and
- a serum albumin is fused to the C-terminus of the construct;

wherein the bispecific single chain antibody construct does not have an amino acid sequence as depicted in SEQ ID NOs: 2 and 3, and wherein the bispecific single chain antibody construct does not have the amino acid sequence:

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADS
  VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
  GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
  DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGS
  EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
  DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
  GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
  IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
  GGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP
  EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA
  ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETC
  FAEEGKKLVAASQAALGLHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADS
  VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
  GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
  DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGS
  EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
  DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG

GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLG
KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD
ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEK
CCKADDKETCFAEEGKKLVAASQAALGLHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADS
VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGS
EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP
EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA
ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETC
FAEEGKKLVAASQAALGLGGGGSGGGSRDWDFDVFGGGTPVGGHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADS
VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGS
EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLG
KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD
ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEK
CCKADDKETCFAEEGKKLVAASQAALGLGGGGSGGGSRDWDFDVFGGGTPVGGHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADS
VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGS

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP
EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA
ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETC
FAEEGKKLVAASQAALGLGGGGSGGGSRLIEDICLPRWGCLWEDDHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADS
VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGS
EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLG
KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD
ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEK
CCKADDKETCFAEEGKKLVAASQAALGLGGGGSGGGSRLIEDICLPRWGCLWEDDHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADS
VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG
GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGS
EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP
EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA
ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETC
FAEEGKKLVAASQAALGLHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADS
VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG

GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ
DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGS
EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG
GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL
IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG
GGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLG
KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD
ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEK
CCKADDKETCFAEEGKKLVAASQAALGLHHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADS
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EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA
ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETC
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- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADS
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KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD
ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEK
CCKADDKETCFAEEGKKLVAASQAALGL GGGGSGGGS RDWDFDVFGGGTPVGG HHHHHH,

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADS VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG GGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETC FAEEGKKLVAASQAALGL GGGGSGGGS RLIEDICLPRWGCLWEDD HHHHHH, and

- QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADS VKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSG GGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQ DTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG GGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLG KVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEK CCKADDKETCFAEEGKKLVAASQAALGL GGGGSGGGS RLIEDICLPRWGCLWEDD HHHHHH.

2. The antibody construct according to claim 1, wherein the serum albumin is a human serum albumin or an FcRn binding optimized variant thereof.

3. The antibody construct according to claim 1 or 2, wherein the serum albumin comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 4 to 12 and 608 to 628.

4. The antibody construct according to any one of the preceding claims, wherein the serum albumin is linked to the antibody construct via a peptide linker.

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5. The antibody construct according to claim 4, wherein the peptide linker has the amino acid sequence $(GGGGS)_n$ (SEQ ID NO: 13)$_n$ wherein n is an integer in the range of 1 to 5.

6. The antibody construct according to any one of the preceding claims, wherein the second binding domain comprises a VL region having CDR-L1-L3 and a VH region having CDR-H1 -H3 selected from the group consisting of:
   (a) CDR-L1-L3 as depicted in SEQ ID NOs: 14-16 and CDR-H1-H3 as depicted in SEQ ID NOs: 17-19;
   (b) CDR-L1-L3 as depicted in SEQ ID NOs: 26-28 and CDR-H1-H3 as depicted in SEQ ID NOs: 29-31;
   (c) CDR-L1-L3 as depicted in SEQ ID NOs: 38-40 and CDR-H1-H3 as depicted in SEQ ID NOs: 41-43;
   (d) CDR-L1-L3 as depicted in SEQ ID NOs: 50-52 and CDR-H1-H3 as depicted in SEQ ID NOs: 53-55;
   (e) CDR-L1-L3 as depicted in SEQ ID NOs: 62-64 and CDR-H1-H3 as depicted in SEQ ID NOs: 65-67;
   (f) CDR-L1-L3 as depicted in SEQ ID NOs: 74-76 and CDR-H1-H3 as depicted in SEQ ID NOs: 77-79;
   (g) CDR-L1-L3 as depicted in SEQ ID NOs: 86-88 and CDR-H1-H3 as depicted in SEQ ID NOs: 89-91;
   (h) CDR-L1-L3 as depicted in SEQ ID NOs: 98-100 and CDR-H1-H3 as depicted in SEQ ID NOs: 101-103;
   (i) CDR-L1-L3 as depicted in SEQ ID NOs: 110-112 and CDR-H1-H3 as depicted in SEQ ID NOs: 113-115; and
   (j) CDR-L1-L3 as depicted in SEQ ID NOs: 122-124 and CDR-H1-H3 as depicted in SEQ ID NOs: 125-127.

7. The antibody construct according to any one of the preceding claims, wherein the second binding domain comprises pairs of VH and VL chains selected from the group consisting of:
   (a) a VH-chain as depicted in SEQ ID NO: 20 and a VL-chain as depicted in SEQ ID NO: 22;

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(b) a VH-chain as depicted in SEQ ID NO: 32 and a VL-chain as depicted in SEQ ID NO: 34;

(c) a VH-chain as depicted in SEQ ID NO: 44 and a VL-chain as depicted in SEQ ID NO: 46;

(d) a VH-chain as depicted in SEQ ID NO: 56 and a VL-chain as depicted in SEQ ID NO: 58;

(e) a VH-chain as depicted in SEQ ID NO: 68 and a VL-chain as depicted in SEQ ID NO: 70;

(f) a VH-chain as depicted in SEQ ID NO: 80 and a VL-chain as depicted in SEQ ID NO: 82;

(g) a VH-chain as depicted in SEQ ID NO: 92 and a VL-chain as depicted in SEQ ID NO: 94;

(h) a VH-chain as depicted in SEQ ID NO: 104 and a VL-chain as depicted in SEQ ID NO: 106;

(i) a VH-chain as depicted in SEQ ID NO: 116 and a VL-chain as depicted in SEQ ID NO: 118; and

(j) a VH-chain as depicted in SEQ ID NO: 128 and a VL-chain as depicted in SEQ ID NO: 130.

8. The antibody construct according to any one of the preceding claims, wherein the second binding domain comprises an amino acid sequence as depicted in SEQ ID NO: 24, SEQ ID NO: 36, SEQ ID NO: 48, SEQ ID NO: 60, SEQ ID NO: 72, SEQ ID NO: 84, SEQ ID NO: 96, SEQ ID NO: 108, SEQ ID NO: 120 or SEQ ID NO: 132.

9. The antibody construct according to any one of the preceding claims, wherein the target cell surface antigen is a tumor antigen or a viral antigen on the surface of an infected host cell.

10. The antibody construct according to claim 9, wherein the tumor antigen is selected from the group consisting of CDH19, MSLN, DLL3, FLT3, EGFRvIII, CD33, CD19, CD20, and CD70.

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11. The antibody construct according to claims 1 to 8, wherein the antibody construct comprises the following elements starting from the N-terminus:

(a) an scFv binding to the target cell surface antigen having an amino acid sequence selected from the group consisting of SEQ ID NOs: 629-675, 684, 694, 704, 714, 724, 734, 744, 754, 764, 774, 784, 794, 804, 814, 824, 834, 844, 854, 864, 874, 884, 894, 904, 914, 924, 934, 944, 954, 964, 974, 984, 994, 1004, 1014, 1024, 1034, 1044, 1054, 1064, 1074, 1084, 1094, 1104, 1114, 1124, 1134, 1144, 1154, 1164, 1174, 1184, 1194, 1204, 1214, 1224, 1234, 1244, 1254, 1264, 1274, 1284, 1294, 1304, 1314, 1324, 1334, 1344, 1354, 1364, 1374, 1384, 1394, 1404, 1414, 1424, 1434, 1444, 1454, 1464, 1474, 1484, 1494, 1504, 1514, 1524, 1534, 1544, 1554, 1564, 1574, 1584, 1594, 1604, 1614, 1624, 1634, 1644, 1654, 1664, 1674, 1684, 1694, 1704, 1714, 1724, 1734, 1744, 1754, 1764, 1774, 1784, 1794, 1804, 1814, 1824, 1834, 1844, 1854, 1864, 1874, 1884, 1894, 1904, 1914, 1924, 1934, 1944, 1954, 1964, 1974, 2004, 2014, 2024, 2034, 2044, 2054, 2064, 2074, 2084, 2094, 2104, 2114, 2124, 2134, 2144, 2154, 2164, 2174, 2184, 2194, 2204, 2214, 2224, 2234, 2244, 2254, 2264, 2274, 2284, 2294, 2304, 2314, 2324, 2334, 2344, 2354, 2364, 2374, 2384, 2394, 2404, 2414, 2424, 2434, 2444, 2454, 2464, 2474, 2484, 2494, 2504, 2514, 2524, 2534, 2544, 2554, 2564, 2574, 2584, 2594, 2604, 2614, 2624, 2634, 2644, 2654, 2664, 2674, 2684, 2694, and 2704;

(b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 13 and 2707-2709;

(c) an scFv binding to the T cell surface antigen CD3 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 24, 36, 48, 60, 72, 84, 96, 108, 120, 132 and 2706;

(d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 13 and 2707-2709;

(e) a serum albumin having an amino acid sequence selected from the group consisting of SEQ ID NOs: 4 to 12 and 608 to 628; and

(f) optionally a His-tag.

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12. A polynucleotide encoding an antibody construct as defined in any one of claims 1 to 11.

13. A vector comprising a polynucleotide as defined in claim 12.

14. A host cell transformed or transfected with the polynucleotide as defined in claim 12 or with the vector as defined in claim 13.

15. A process for the production of an antibody construct according to any one of claims 1 to 11, said process comprising culturing a host cell as defined in claim 14 under conditions allowing the expression of the antibody construct as defined in any one of claims 1 to 11 and recovering the produced antibody construct from the culture.

16. A pharmaceutical composition comprising an antibody construct according to any one of claims 1 to 11, or produced according to the process of claim 15.

17. The antibody construct according to any one of claims 1 to 11, or produced according to the process of claim 15, for use in the prevention, treatment or amelioration of a disease selected from a proliferative disease, a tumorous disease, a viral disease or an immunological disorder.

18. A method for the treatment or amelioration of a proliferative disease, a tumorous disease, a viral disease or an immunological disorder, comprising the step of administering to a subject in need thereof the antibody construct according to any one of claims 1 to 11, or produced according to the process of claim 15.

19. A kit comprising an antibody construct according to any one of claims 1 to 11, or produced according to the process of claim 15, a vector as defined in claim 13, and/or a host cell as defined in claim 14.

20. Use of an antibody construct according to any one of claims 1-11 or produced according to the process of claim 15 in the preparation of a medicament for the treatment or amelioration of a proliferative disease, a tumorous disease, a viral disease or an immunological disorder.

Figure 1

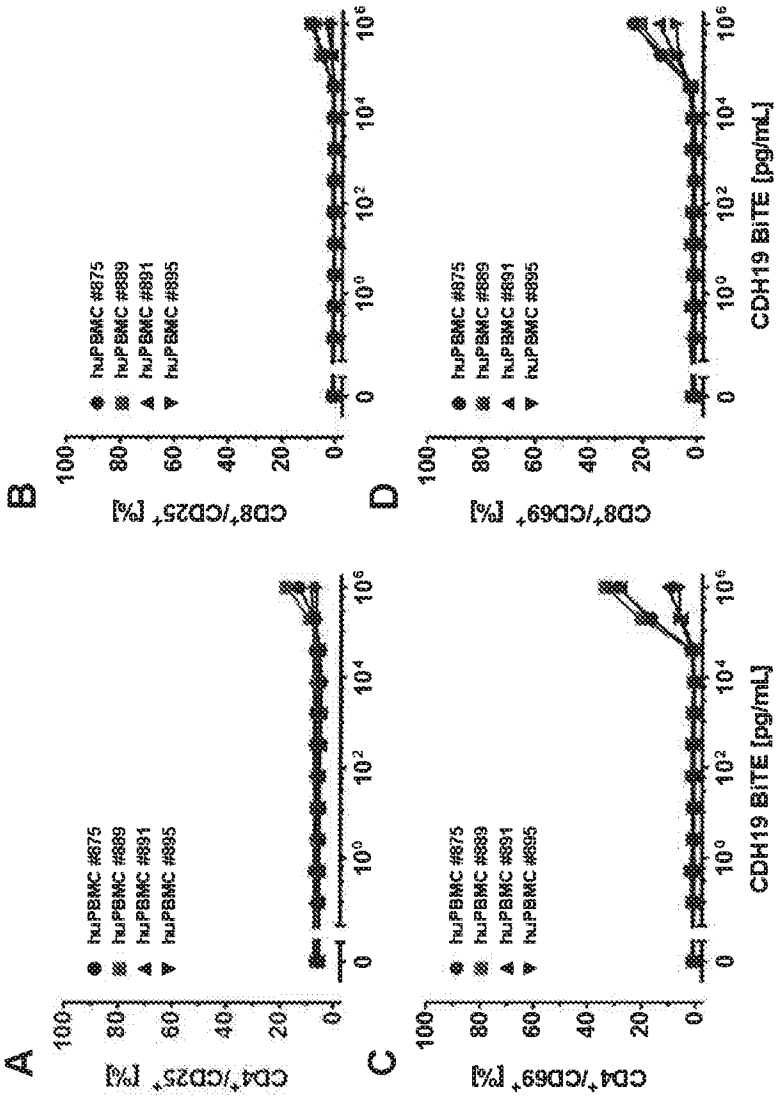

A
B
C
D
huPBMC #875
huPBMC #889
huPBMC #891
huPBMC #895
CD4+/CD25+ [%]
CD8+/CD25+ [%]
CD4+/CD69+ [%]
CD8+/CD69+ [%]
CDH19 BiTE [pg/mL]
0
20
40
60
80
100
10^0
10^2
10^4
10^6

Figure 2

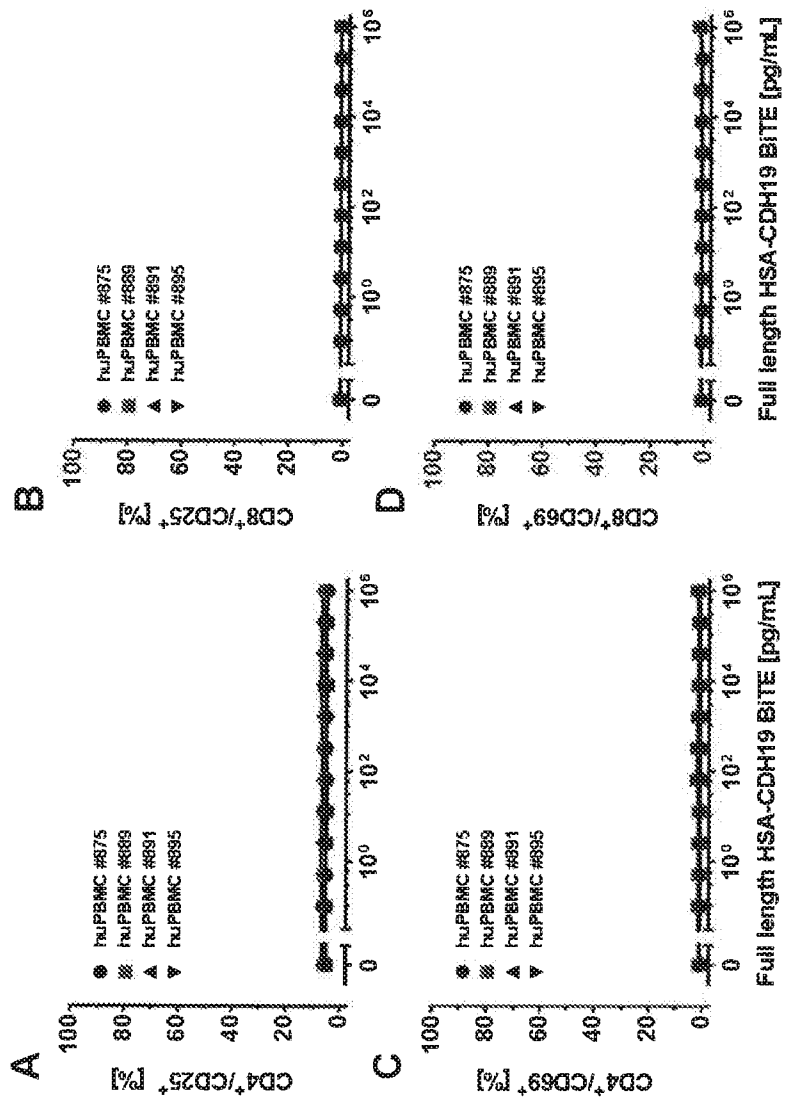

A
B
C
D
huPBMC #875
huPBMC #889
huPBMC #891
huPBMC #895
CD4+/CD25+ [%]
CD8+/CD25+ [%]
CD4+/CD69+ [%]
CD8+/CD69+ [%]
Full length HSA-CDH19 BiTE [pg/mL]
0
20
40
60
80
100
10^0
10^2
10^4
10^6

Figure 3

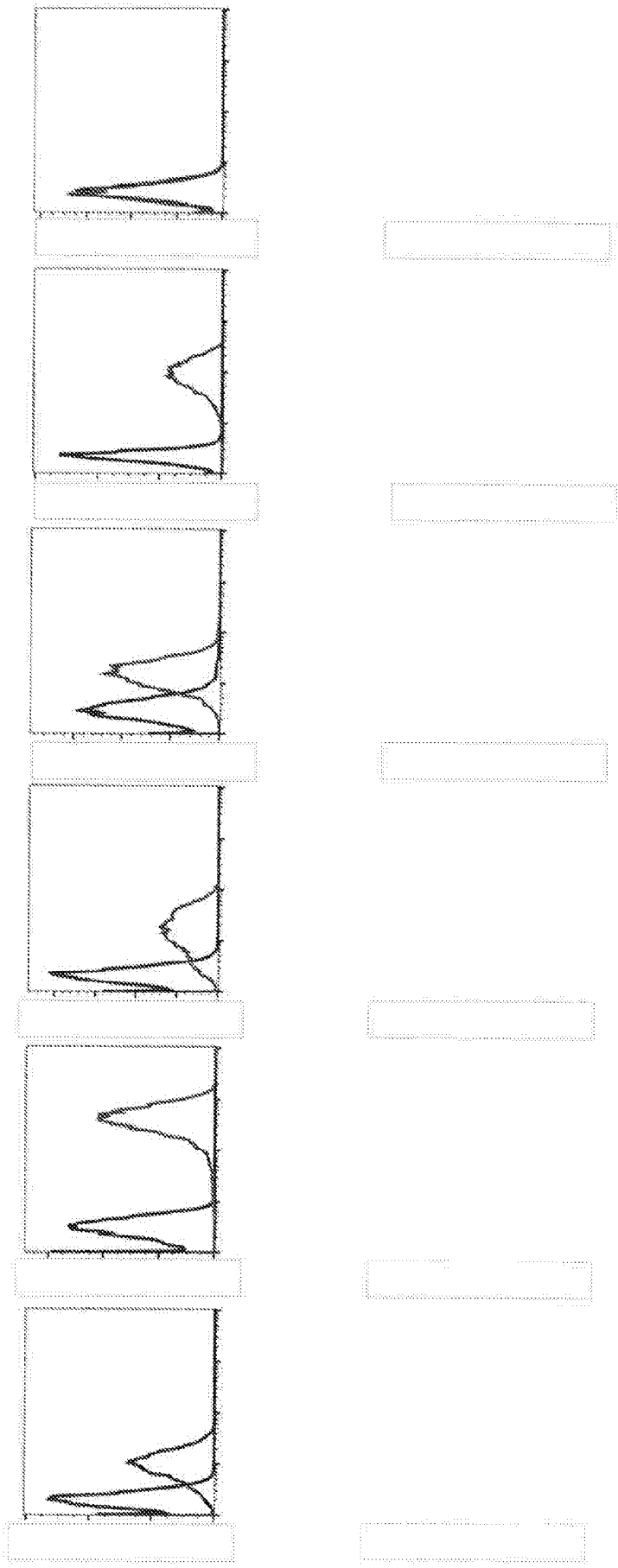

CHO human CDH19
HPB-ALL human CD3
CHO macaque CDH19
LnPx4119 macaque CD3
CHL-1 native CDH19
CHO untrans-fected
2G6 302 x I2C6-HALB

Figure 4

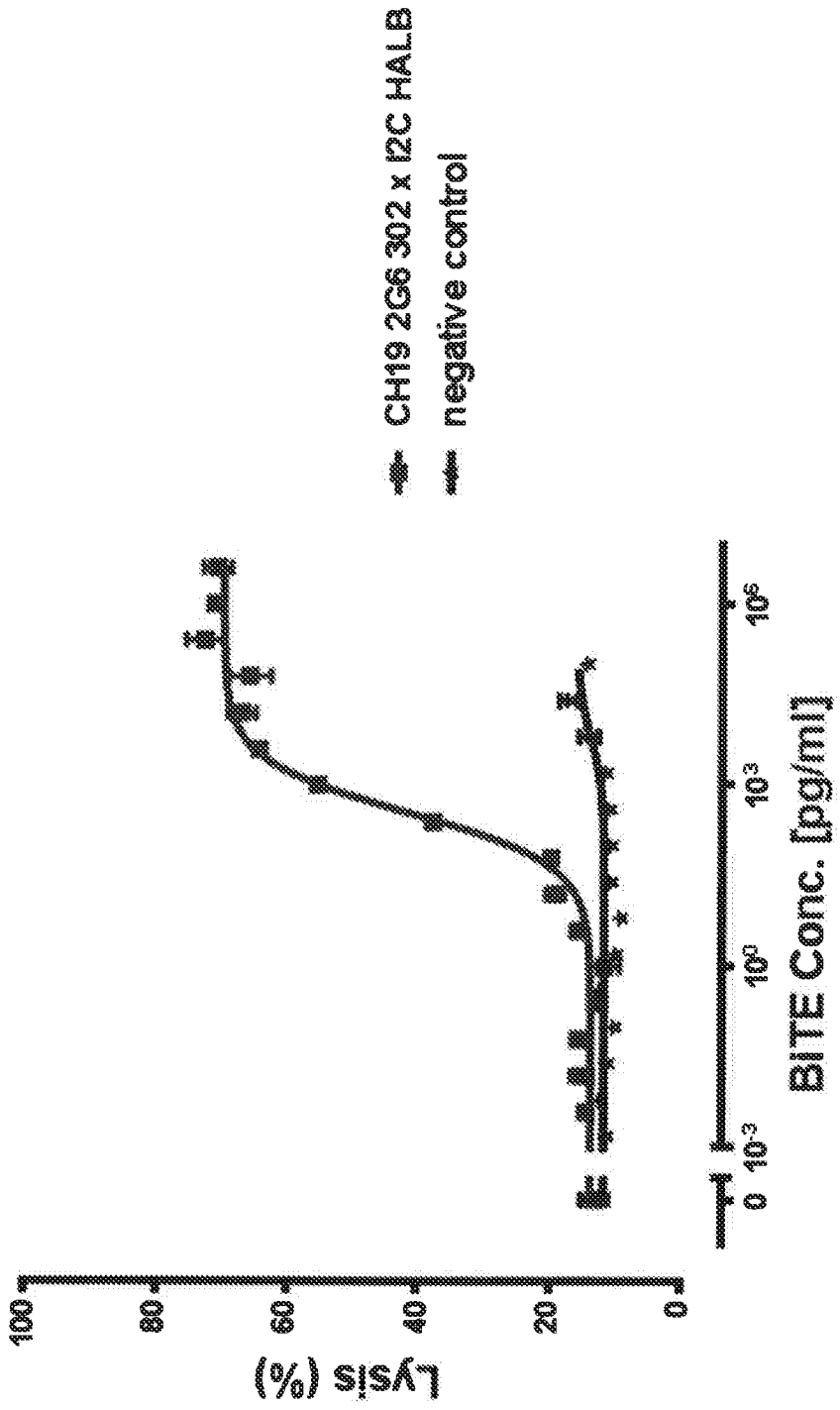
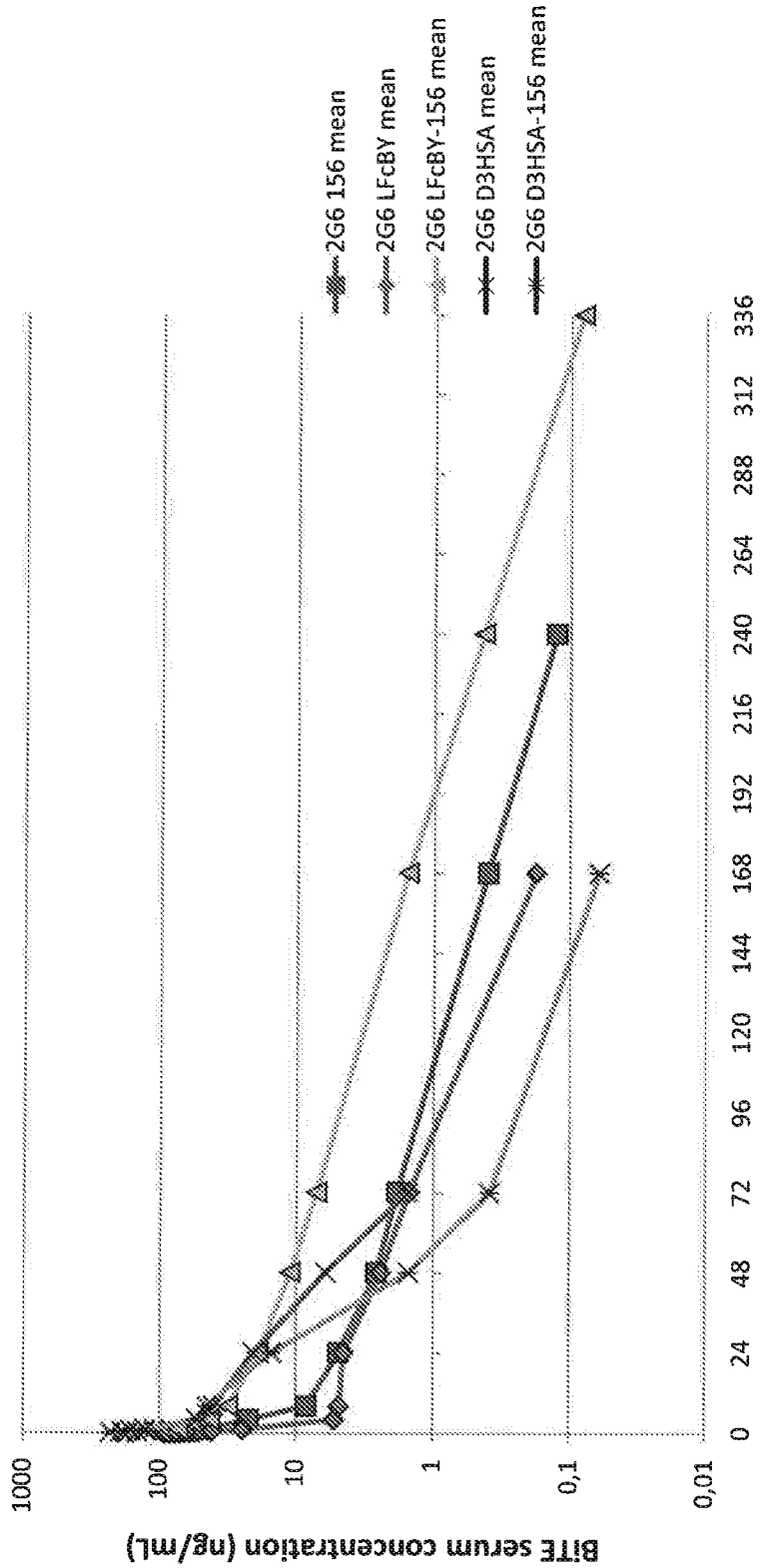
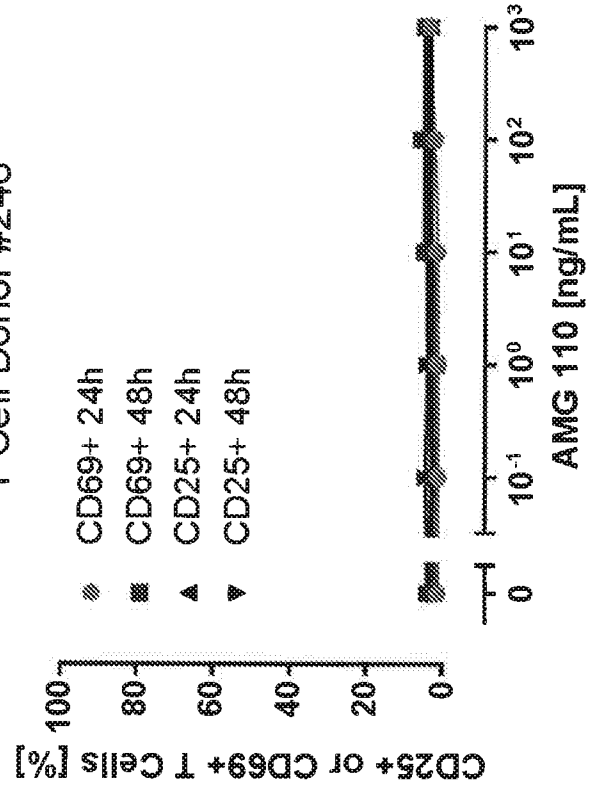

CH19 2G6 302 x I2C HALB
negative control
Lysis (%)
100
80
60
40
20
0
0
10-2
100
10-3
10-6
BITE Conc. [pg/ml]

Figure 5



BiTE	Dose (µg/kg)	AUC_{inf} (ng·h/mL)	V_{ss} (mL/kg)	CL (mL/h/kg)	MRT (h)	$t_{1/2}$ (h)
2G6 156 mean	6	568	446	11.3	42.3	44.3
2G6 LFcBy mean	6	366	594	16.1	39.8	31.2
2G6 LFcBy-156 mean*	6	1796	193	4.3	48.7	40.3
2G6 D3HSA mean	6	1383	80.7	4.9	18.1	13.5
2G6 D3HSA-156 mean*	6	1216	58.9	5.2	12.3	17.3

Figure 6


T Cell Donor #246
CD69+ 24h
CD69+ 48h
CD25+ 24h
CD25+ 48h
CD25+ or CD69+ T cells [%]
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80
60
40
20
0
0
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
AMG 110 [ng/mL]

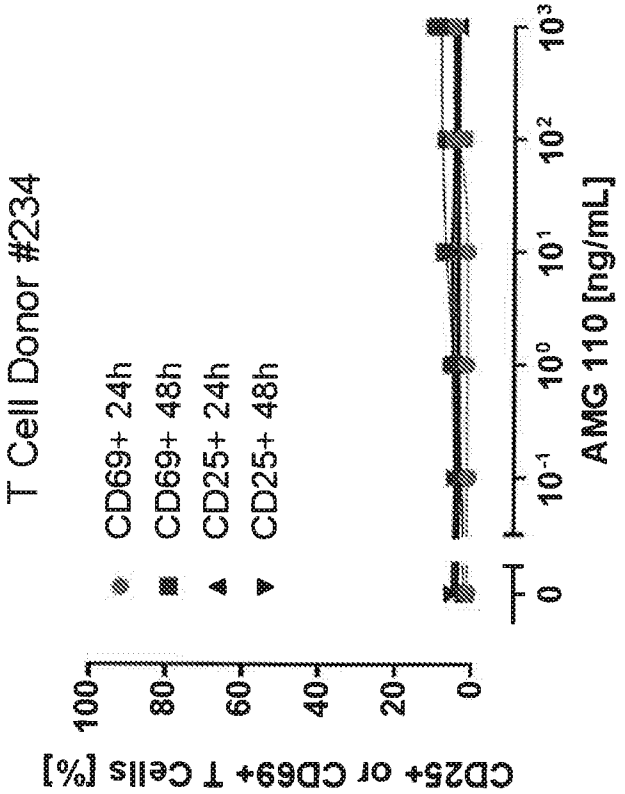
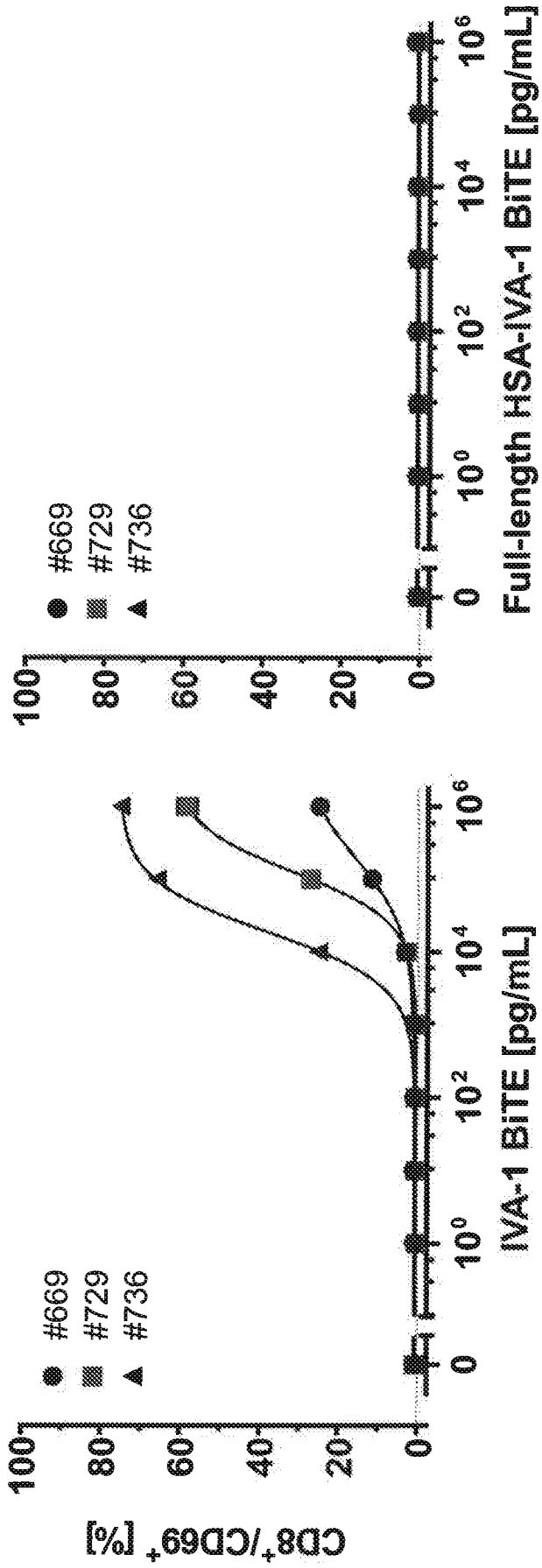

T Cell Donor #234
CD69+ 24h
CD69+ 48h
CD25+ 24h
CD25+ 48h
CD25+ or CD69+ T cells [%]
100
80
60
40
20
0
0
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
AMG 110 [ng/mL]

Figure 7a


CD8+/CD69+ [%]
100
80
60
40
20
0
#669
#729
#736
0
10^0
10^2
10^4
10^6
IVA-1 BiTE [pg/mL]
Full-length HSA-IVA-1 BiTE [pg/mL]

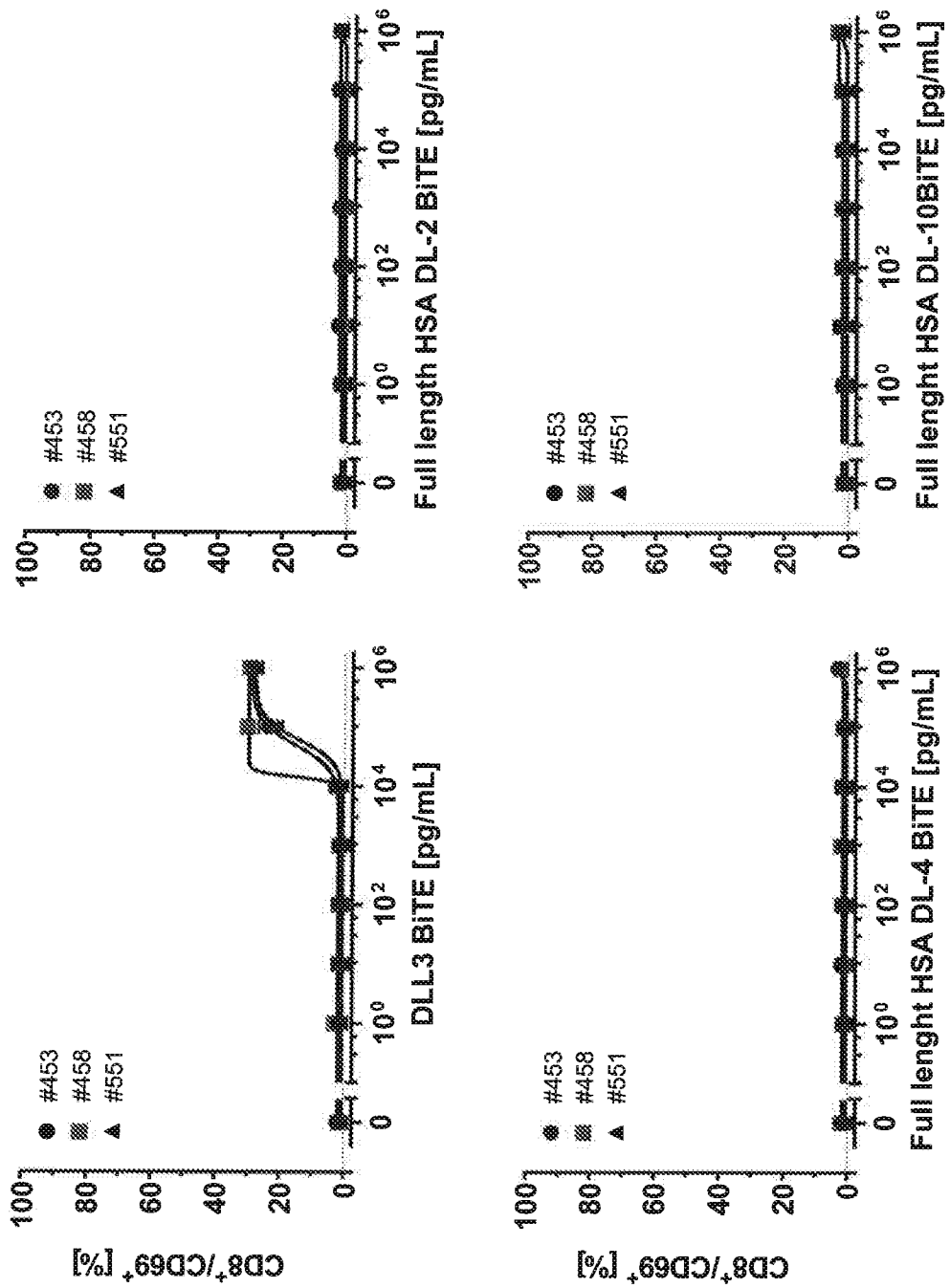
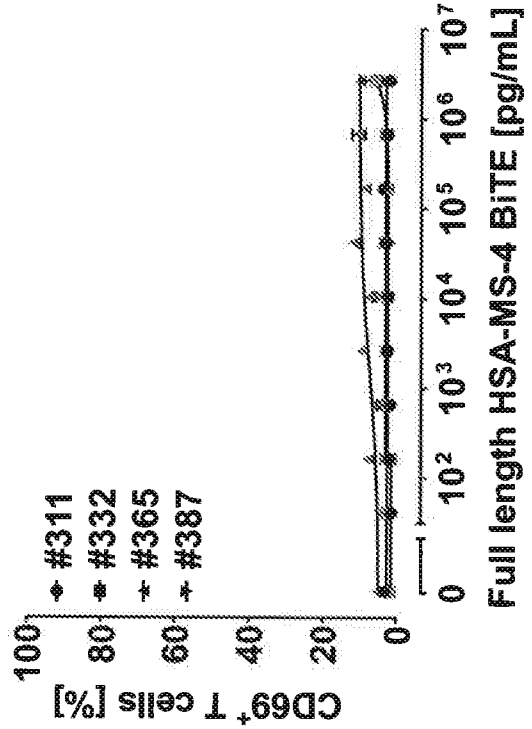

CD8+/CD69+ [%]
#453
#458
#551
DLL3 BiTE [pg/mL]
Full length HSA DL-2 BiTE [pg/mL]
Full lenght HSA DL-4 BiTE [pg/mL]
Full lenght HSA DL-10BiTE [pg/mL]

Figure 7b


CD69+ T cells [%]
100
80
60
40
20
0
#311
#332
#365
#387
0
10^2
10^3
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10^5
10^6
10^7
Full length HSA-MS-4 BiTE [pg/mL]

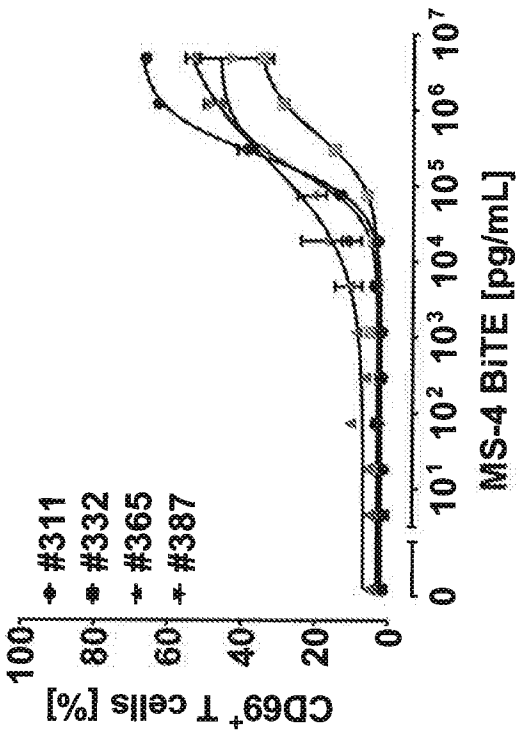

CD69+ T cells [%]
100
80
60
40
20
0
#311
#332
#365
#387
0
10^1
10^2
10^3
10^4
10^5
10^6
10^7
MS-4 BiTE [pg/mL]

Figure 7c

Figure 8a

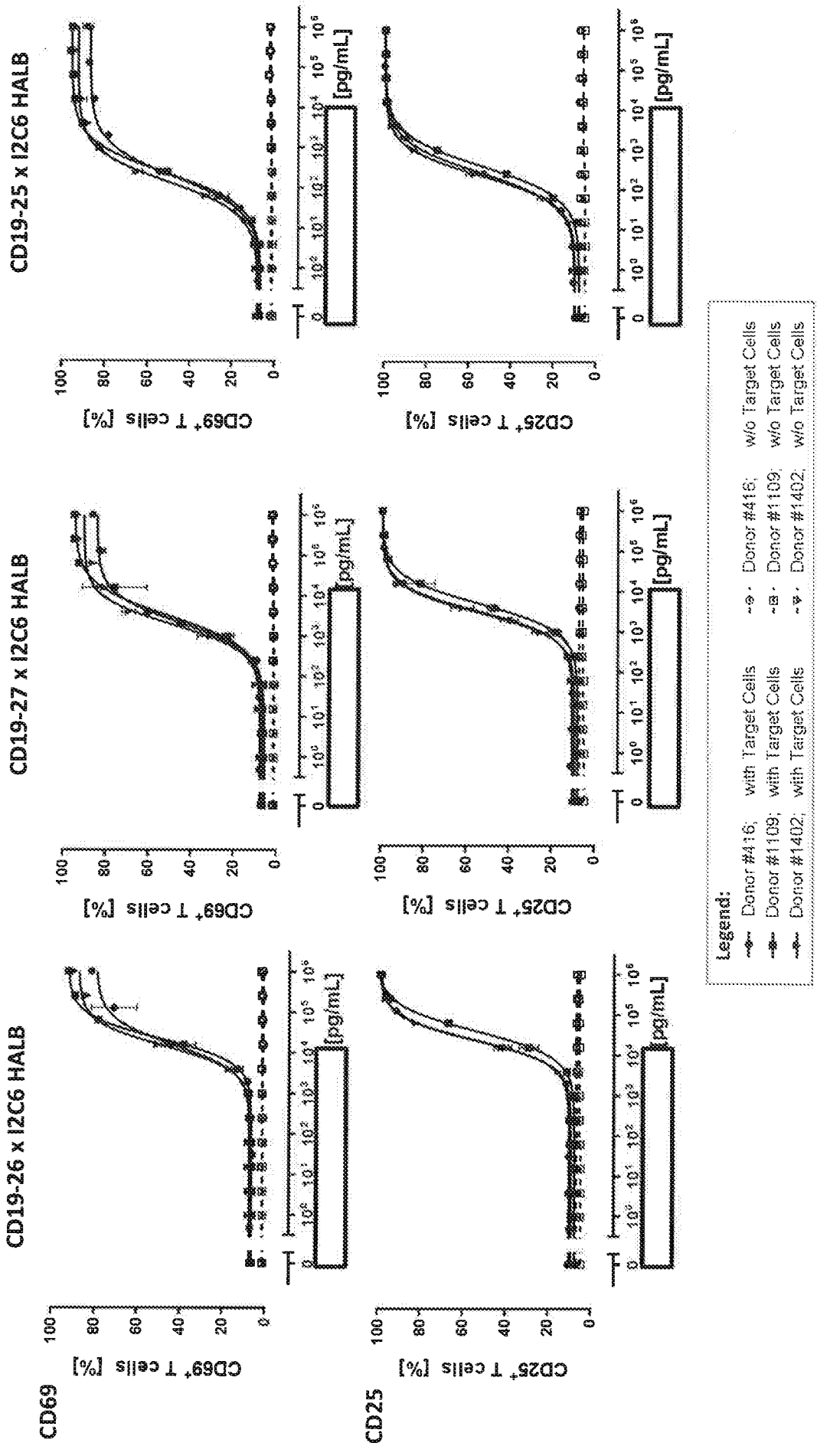

CD69
CD25
CD19-26 x I2C6 HALB
CD19-27 x I2C6 HALB
CD19-25 x I2C6 HALB
CD69+ T cells [%]
CD25+ T cells [%]
[pg/mL]
Legend:
Donor #416; with Target Cells
Donor #1109; with Target Cells
Donor #1402; with Target Cells
Donor #416; w/o Target Cells
Donor #1109; w/o Target Cells
Donor #1402; w/o Target Cells

Figure 8b

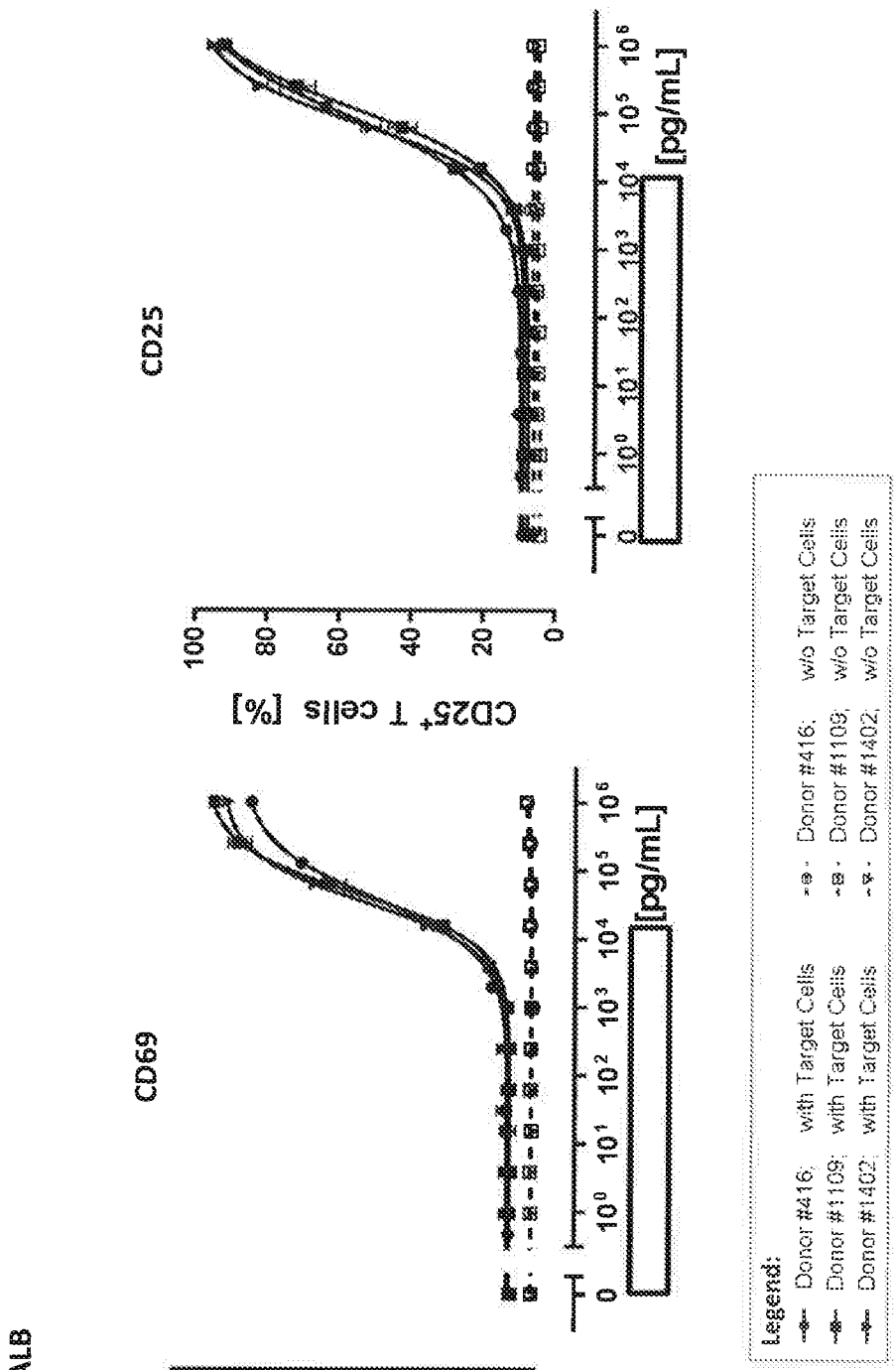
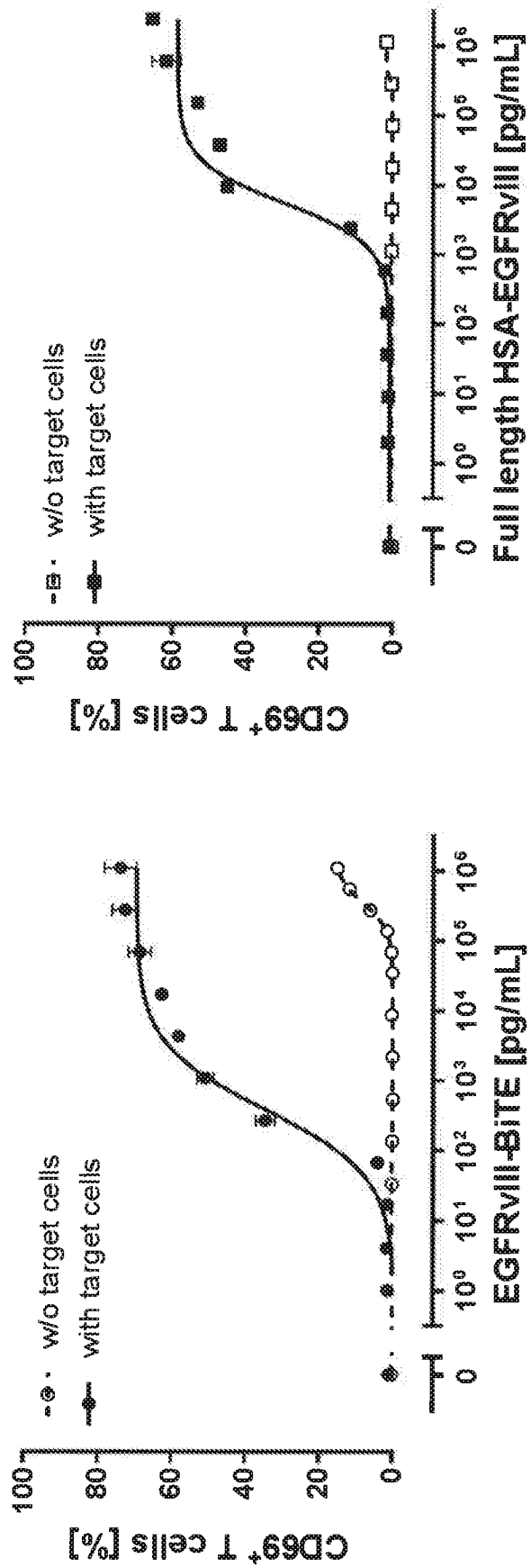

CD20-2 x I2C6 HALB
CD69
CD25
CD69+ T cells [%]
CD25+ T cells [%]
[pg/mL]
Legend:
Donor #416; with Target Cells
Donor #1109; with Target Cells
Donor #1402; with Target Cells
Donor #416; w/o Target Cells
Donor #1109; w/o Target Cells
Donor #1402; w/o Target Cells

Figure 8c


CD69+ T cells [%]
w/o target cells
with target cells
EGFRvIII-BiTE [pg/mL]
Full length HSA-EGFRvIII [pg/mL]

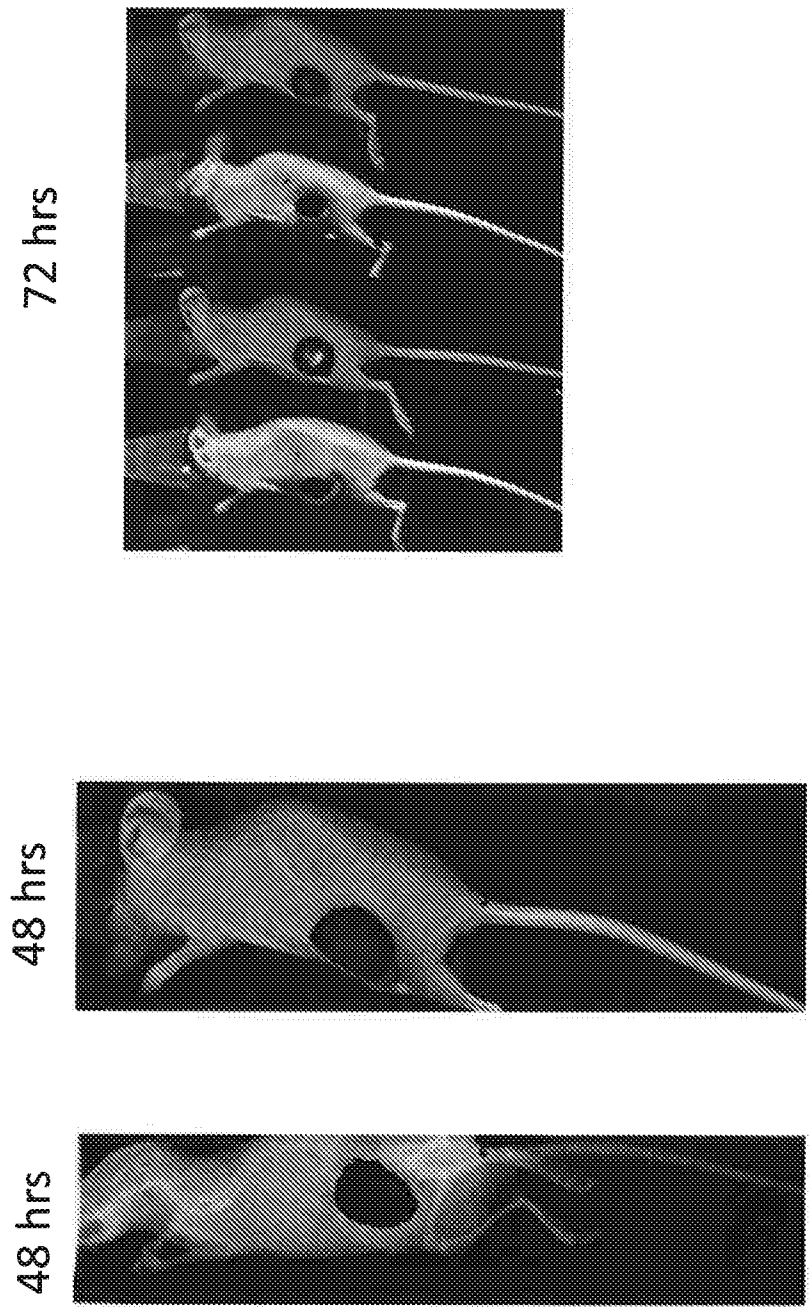


Figure 9

Figure 10

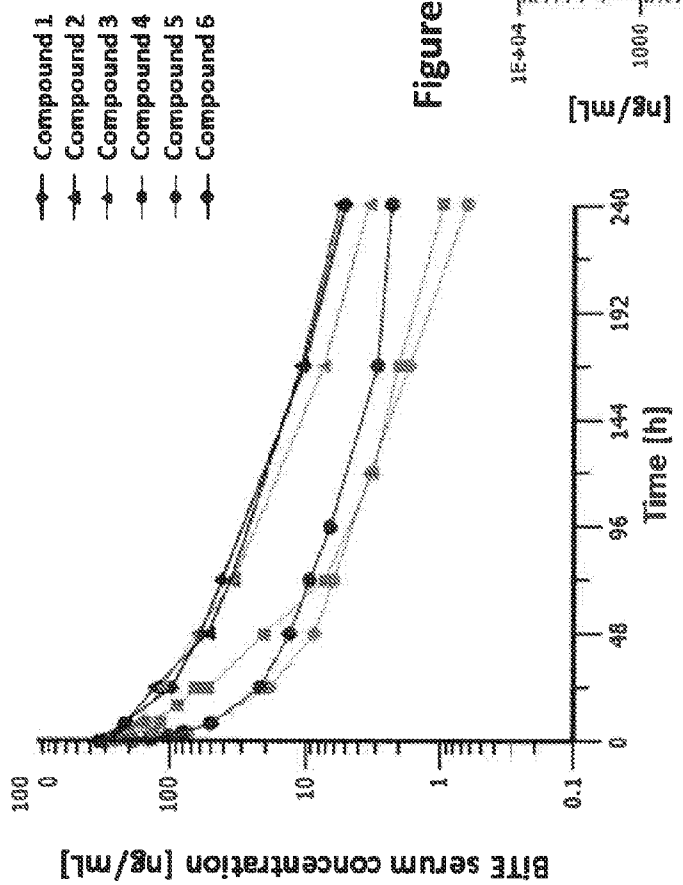
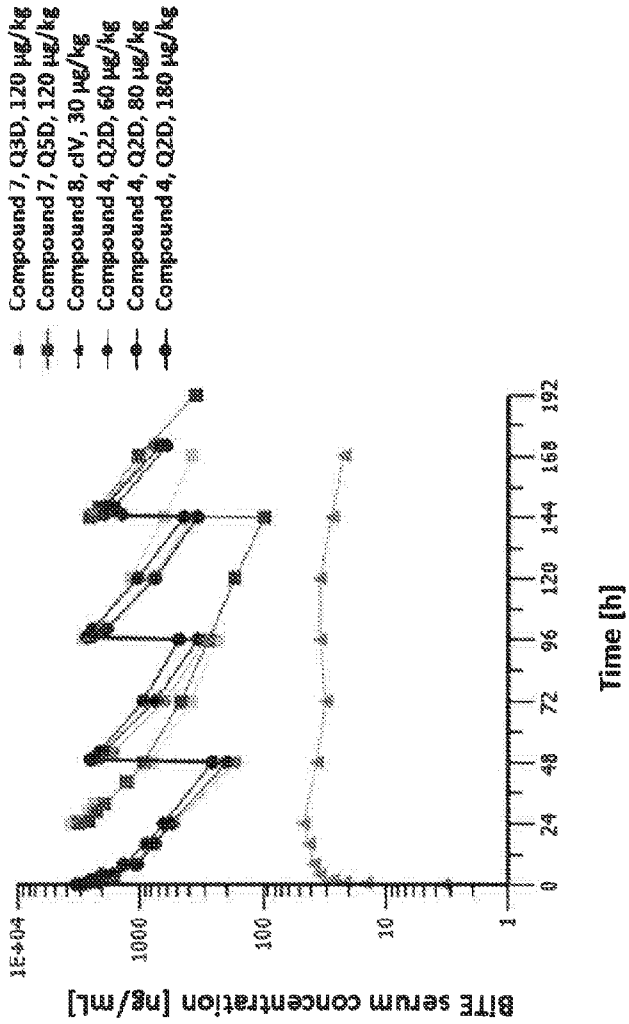


Figure 11



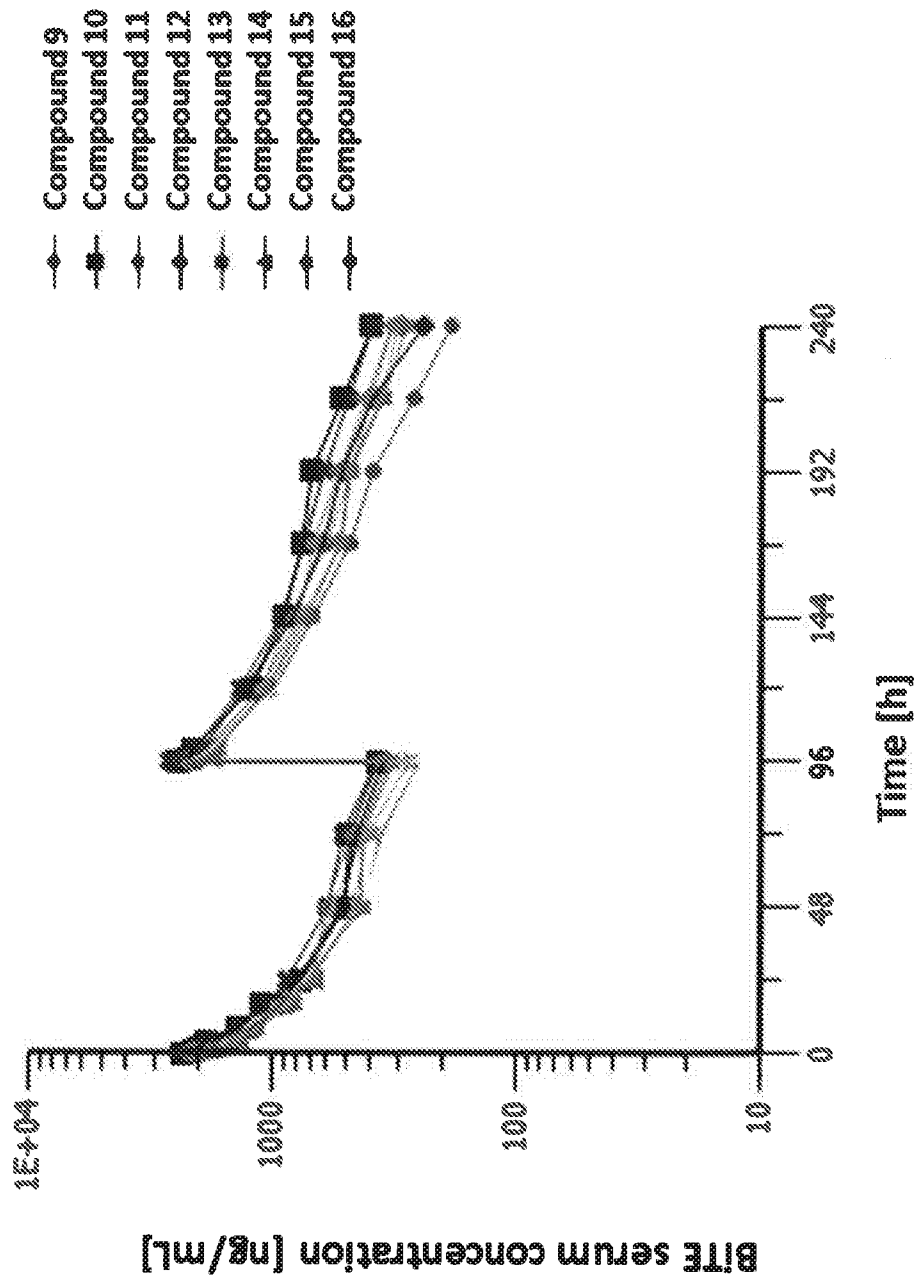

Compound 9
Compound 10
Compound 11
Compound 12
Compound 13
Compound 14
Compound 15
Compound 16
BiTE serum concentration [ng/mL]
1E+04
1000
100
10
0
48
96
144
192
240
Time [h]

Figure 12