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(54) Title: CYTOSOLIC PROTEIN TARGETING ENGINEERED DEUBIQUITINASES AND METHODS OF USE THEREOF

(57) Abstract: Provided herein are fusion protein comprising: an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof; and a targeting domain comprising a moiety that specifically binds a cytosolic protein. Also provided herein are methods of using the fusion proteins to treat a disease, including genetic diseases.

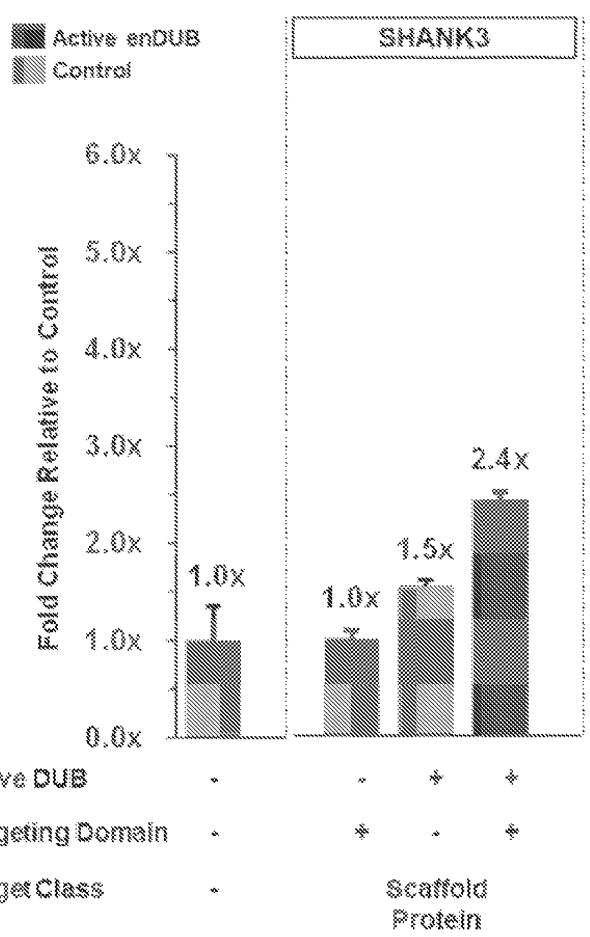

FIG. 3

[Continued on next page]

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CYTOSOLIC PROTEIN TARGETING ENGINEERED DEUBIQUITINASES AND METHODS OF USE THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Patent Application No. 63/110,622, filed November 6, 2020, the entire disclosure of which is incorporated herein by reference.

1. FIELD

[0001] This disclosure relates to fusion proteins comprising an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof; and a targeting domain comprising a moiety that specifically binds a target cytosolic protein. The disclosure further relates to therapeutic methods of using the same.

2. BACKGROUND

[0002] A subset of genetic diseases are associated with a decrease in the level of expression of a functional cytosolic protein or a decrease in the stability of a cytosolic protein. For example, haploinsufficiency genetic diseases are caused by the presence a single copy of a wild-type allele in heterozygous combination with a loss of function variant allele, wherein the level of functional protein expressed is insufficient to produce the standard phenotype. Haploinsufficiency can arise from a de novo or inherited loss-of-function mutation in the variant allele, such that it produces little or no functional protein. Despite recent developments in gene therapy, there are still no curative treatments for these diseases, and treatment typically centers on the management of symptoms. Therefore, new treatments are needed for diseases, e.g., genetic diseases, that are associated with decreased functional cytosolic protein expression or stability.

3. SUMMARY

[0003] Provided herein are, *inter alia*, engineered deubiquitinases (enDubs) that comprise a targeting moiety that specifically binds a cytosolic target protein and a catalytic domain of a deubiquitinase. The targeting moiety directs that deubiquitinase catalytic domain to the specific target cytosolic protein for deubiquitination. The fusion proteins described herein are particularly

useful in methods of treating genetic diseases, particularly those associated with or caused by decreased expression or stability of a specific cytosolic protein.

[0004] In one aspect, provided herein are fusion proteins comprising: an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein.

[0005] In some embodiments, the deubiquitinase is a cysteine protease or a metalloprotease.

[0006] In some embodiments, the deubiquitinase is a cysteine protease. In some embodiments, the cysteine protease is a ubiquitin-specific protease (USP), a ubiquitin C-terminal hydrolase (UCH), a Machado-Josephin domain protease (MJD), an ovarian tumour protease (OTU), a MINDY protease, or a ZUFSP protease. In some embodiments, the cysteine protease is a USP. In some embodiments, the USP is USP1, USP2, USP3, USP4, USP5, USP6, USP7, USP8, USP9X, USP9Y, USP10, USP11, USP12, USP13, USP14, USP15, USP16, USP17, USP17L2, USP17L3, USP17L4, USP17L5, USP17L7, USP17L8, USP18, USP19, USP20, USP21, USP22, USP23, USP24, USP25, USP26, USP27X, USP28, USP29, USP30, USP31, USP32, USP33, USP34, USP35, USP36, USP37, USP38, USP39, USP40, USP41, USP42, USP43, USP44, USP45, or USP46.

[0007] In some embodiments, the cysteine protease is a UCH. In some embodiments, the UCH is BAP1, UCHL1, UCHL3, or UCHL5.

[0008] In some embodiments, the cysteine protease is a MJD. In some embodiments, the MJD is ATXN3 or ATXN3L.

[0009] In some embodiments, the cysteine protease is an OTU. In some embodiments, the OTU is OTUB1 or OTUB2.

[0010] In some embodiments, the cysteine protease is a MINDY. In some embodiments, the MINDY MINDY1, MINDY2, MINDY3, or MINDY4.

[0011] In some embodiments, the cysteine protease is a ZUFSP. In some embodiments, the ZUFSP is ZUP1.

[0012] In some embodiments, the deubiquitinase is a metalloprotease. In some embodiments, the metalloprotease is a Jab1/Mov34/Mpr1 Pad1 N-terminal+ (MPN+) (JAMM) domain protease.

[0013] In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112.

[0014] In some embodiments, the catalytic domain comprises a catalytic domain derived from a deubiquitinase comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112.

[0015] In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286.

[0016] In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286.

[0017] In some embodiments, the catalytic domain comprises an amino acid sequence that is a functional fragment of the amino acid sequence of any one of SEQ ID NOS: 1-112.

[0018] In some embodiments, the catalytic domain comprises an amino acid sequence that is a functional fragment of the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286.

[0019] In some embodiments, the moiety that specifically binds a cytosolic protein comprises an antibody, or functional fragment or functional variant thereof. In some embodiments, the antibody, or functional fragment or functional variant thereof, comprises a full-length antibody, a single chain variable fragment (scFv), a scFv2, a scFv-Fc, a Fab, a Fab', a F(ab')2, a F(v), a VHH, or a $(VHH)_2$. In some embodiments, the antibody, or functional fragment or functional variant thereof, comprises a VHH or a $(VHH)_2$.

[0020] In some embodiments, the cytosolic protein is cyclin-dependent kinase-like 5 (CDKL5), copper-transporting ATPase 2 (ATP7B), syntaxin-binding protein 1 (STXBP1), Ras/Rap GTPase-activating protein (SYNGAP1), progranulin (GRN), protein jagged-1 (JAG1), GATOR complex protein DEPDC5 (DEPDC5), tuberin (TSC2), hamartin (TSC1), kinesin-like protein KIF1A (KIF1A), dynamin-1 (DNM1), SH3 and multiple ankyrin repeat domains protein 3 (SHANK3), dystrophin (DMD), oxygen-regulated protein 1 (RP1), titin (TTN), cytoplasmic dynein 1 heavy chain 1 (DYNC1H1), TRIO and F-actin-binding protein (TRIO), probable ubiquitin carboxyl-terminal hydrolase FAF-X (USP9X), cystatin-B (CSTB), or pterin-4-alpha-carbinolamine dehydratase (PCBD1).

[0021] In some embodiments, the cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 221-328 or 287-289.

[0022] In some embodiments, the effector domain is directly fused to the targeting domain. In some embodiments, the effector domain is indirectly fused to the targeting domain. In some embodiments, the effector domain is indirectly fused to the targeting domain via a peptide linker. In some embodiments, the effector domain is indirectly fused to the targeting domain via a peptide linker of sufficient length such that the effector domain and the targeting domain can simultaneous bind the respective target proteins. In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications. In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications.

[0023] In some embodiments, the effector domain is operably connected either directly or indirectly to the C terminus of the targeting domain. In some embodiments, the effector moiety is operably connected either directly or indirectly to the N terminus of the targeting domain.

[0024] In some embodiments, the targeting domain comprises a VHH of any one of claims 62-69, or a $(VHH)_2$ of any one of claims 70-81.

[0025] In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286.

[0026] In some embodiments, the effector domain is indirectly fused to the targeting domain via a peptide linker of sufficient length such that the effector domain and the targeting domain can simultaneous bind the respective target proteins. In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications. In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications.

[0027] In some embodiments, the effector domain is operably connected either directly or

indirectly to the C terminus of the targeting domain. In some embodiments, the effector moiety is operably connected either directly or indirectly to the N terminus of the targeting domain.

[0028] In some embodiments, the fusion protein comprises an amino acid sequence at least at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 320-367.

[0029] In one aspect, provided herein are nucleic acid molecules encoding a fusion protein described herein. In some embodiments, the nucleic acid molecule is a DNA molecule. In some embodiments, the nucleic acid molecule is an RNA molecule.

[0030] In one aspect, provided herein are vectors comprising a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a fusion protein described herein). In some embodiments, the vector is a plasmid or a viral vector.

[0031] In one aspect, provided herein are viral particles comprising a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a fusion protein described herein).

[0032] In one aspect, provided herein are in vitro cell or population of cells comprising a fusion protein described herein, a nucleic acid molecule described herein, or a vector described herein.

[0033] In one aspect, provided herein are pharmaceutical compositions comprising a fusion protein described herein, a nucleic acid described herein, a vector described herein, or a viral particle described herein, and an excipient.

[0034] In one aspect, provided herein are methods of making a fusion protein described herein, comprising introducing into an in vitro cell or population of cells a nucleic acid molecule described herein, a vector described herein, or a viral particle described herein; culturing the cell or population of cells in a culture medium under conditions suitable for expression of the fusion protein, isolating the fusion protein from the culture medium, and optionally purifying the fusion protein.

[0035] In one aspect, provided herein are methods of treating or preventing a disease in a subject comprising administering a fusion protein described herein, a nucleic acid molecule described herein, a vector described herein, a viral particle described herein, or a pharmaceutical composition described herein, to a subject in need thereof. In some embodiments, the subject is human.

[0036] In some embodiments, the disease is associated with decreased expression of a

functional version of the cytosolic protein relative to a non-diseased control. In some embodiments, the disease is associated with decreased stability of a functional version of the cytosolic protein relative to a non-diseased control. In some embodiments, the disease is associated with increased ubiquitination of the cytosolic protein relative to a non-diseased control. In some embodiments, the disease is associated with increased ubiquitination and degradation of the cytosolic protein relative to a non-diseased control. In some embodiments, disease is a genetic disease. In some embodiments, the disease is a haploinsufficiency disease.

[0037] In some embodiments, the disease is SYNGAP1 encephalopathy, CDKL5 deficiency disorder, STXBP1 encephalopathy, early infantile epileptic encephalopathy type 2, Wilson disease, early infantile epileptic encephalopathy type 4, mental retardation autosomal dominant 5, aphasia, alagille syndrome 1, epilepsy, tuberous sclerosis-2, tuberous sclerosis-1, KIF1A-associated neurological disorder, encephalopathy, Phelan-McDermid syndrome, Becker Muscular Dystrophy, RP1, retinitis pigmentosa 1, dilated cardiomyopathy 1G, DYNC1H1 Syndrome, TRIO-Related intellectual disability (ID), USP9X Development Disorder, epilepsy, progressive myoclonic 1 (EPM1), or hyperphenylalaninemia BH4-deficient D (HPABH4D).

[0100] In some embodiments, the target cytosolic protein is SYNGAP1, and the disease is SYNGAP1 encephalopathy; the target cytosolic protein is SYNGAP1, and the disease is Mental retardation autosomal dominant 5; the target cytosolic protein is CDKL5, and the disease is CDKL5 deficiency disorder; the target cytosolic protein is CDKL5, and the disease is an early infantile epileptic encephalopathy; the target cytosolic protein is CDKL5, and the disease is early infantile epileptic encephalopathy type 2; the target cytosolic protein is ATP7B, and the disease is Wilson disease; the target cytosolic protein is STXBP1, and the disease is STXBP1 encephalopathy; the target cytosolic protein is STXBP1, and the disease is an early infantile epileptic encephalopathy; the target cytosolic protein is STXBP1, and the disease is early infantile epileptic encephalopathy type 4; the target cytosolic protein is GRN, and the disease is aphasia primary progressive & FTD (frontotemporal degeneration); the target cytosolic protein is JAG1, and the disease is alagille syndrome 1; the target cytosolic protein is DEPDC5, and the disease is epilepsy (e.g., familial focal, with variable foci 1); the target cytosolic protein is TSC2, and the disease is tuberous sclerosis; the target cytosolic protein is TSC2, and the disease is tuberous sclerosis type 2; the target cytosolic protein is TSC2, and the disease is tuberous sclerosis type 1; the target cytosolic protein is TSC1, and the disease is tuberous sclerosis; the target cytosolic

protein is TSC1, and the disease is tuberous sclerosis type 1; the target cytosolic protein is TSC1, and the disease is tuberous sclerosis type 2; the target cytosolic protein is KIF1A, and the disease is KIF1A-associated neurological disorder; the target cytosolic protein is DNM1, and the disease is a DNM1 encephalopathy; the target cytosolic protein is DNM1, and the disease is encephalopathy; the target cytosolic protein is SHANK3, and the disease is Phelan-McDermid syndrome; the target cytosolic protein is DMD, and the disease is Becker Muscular Dystrophy; the target cytosolic protein is RP1, and the disease is retinitis pigmentosa 1; the target cytosolic protein is TTN, and the disease is dilated cardiomyopathy 1G; the target cytosolic protein is DYNC1H1, and the disease is DYNC1H1 Syndrome; the target cytosolic protein is TRIO, and the disease is TRIO-Related intellectual disability (ID); the target cytosolic protein is USP9X, and the disease is USP9X development disorder; the target cytosolic protein is CSTB, and the disease is epilepsy, progressive myoclonic 1 (EPM1); or the target cytosolic protein is PCBD1, and the disease is hyperphenylalaninemia, BH4-deficient, D (HPABH4D). In some embodiments, the target cytosolic protein is SYNGAP1, and the disease is SYNGAP1 encephalopathy.

[0038] In some embodiments, the fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered at a therapeutically effective dose. In some embodiments, the disease is a haploinsufficiency disease. the fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered systematically or locally. In some embodiments, the disease is a haploinsufficiency disease. In some embodiments the fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered intravenously, subcutaneously, or intramuscularly.

[0039] In one aspect, provided herein are fusion proteins described herein, polynucleotides described herein, DNA described herein, RNA described herein, vectors described herein, viral particles described herein, and pharmaceutical compositions described herein for use as a medicament.

[0040] In one aspect, provided herein are fusion proteins described herein, polynucleotides described herein, DNA described herein, RNA described herein, vectors described herein, viral particles described herein, and pharmaceutical compositions described herein for use in treating or inhibiting a genetic disorder.

[0041] In one aspect, provided herein are single variable domain antibodies (VHHs) that specifically binds SYNGAP1 comprising three complementarity determining regions: CDR1,

CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312, or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 comprising 1, 2, or 3 amino acid modifications.

[0100] In some embodiments, the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 comprising 1, 2, or 3 amino acid modifications.

[0101] In some embodiments, the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 comprising 1, 2, or 3 amino acid modifications.

[0102] In some embodiments, the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 comprising 1, 2, or 3 amino acid modifications.

[0042] In some embodiments, the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 comprising 1, 2,

or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 comprising 1, 2, or 3 amino acid modifications.

[0100] In some embodiments, the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 comprising 1, 2, or 3 amino acid modifications.

[0101] In some embodiments, the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 comprising 1, 2, or 3 amino acid modifications.

[0043] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313.

[0044] In one aspect, provided herein are nucleic acid molecules encoding a VHH described herein. In some embodiments, the nucleic acid molecule is a DNA molecule. In some embodiments, the nucleic acid molecule is an RNA molecule.

[0045] In one aspect, provided herein are vectors comprising a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a VHH described herein). In some embodiments, the vector is a plasmid or a viral vector.

[0046] In one aspect, provided herein are viral particles comprising a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a VHH described herein).

[0047] In one aspect, provided herein are in vitro cell or population of cells comprising a VHH

described herein, a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a VHH described herein), or a vector described herein (e.g., a vector comprising a nucleic acid molecule encoding a VHH described herein).

[0048] In one aspect, provided herein are pharmaceutical compositions comprising a VHH described herein, a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a VHH described herein), or a vector described herein (e.g., a vector comprising a nucleic acid molecule encoding a VHH described herein) or a viral particle described herein (e.g., a viral particle comprising a nucleic acid molecule encoding a VHH described herein), and an excipient.

[0049] In one aspect, provided herein are methods of making a VHH polypeptides described herein, comprising introducing into an in vitro cell or population of cells a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a VHH described herein), or a vector described herein (e.g., a vector comprising a nucleic acid molecule encoding a VHH described herein) or a viral particle described herein (e.g., a viral particle comprising a nucleic acid molecule encoding a VHH described herein); culturing the cell or population of cells in a culture medium under conditions suitable for expression of the VHH, isolating the VHH from the culture medium, and optionally purifying the VHH.

[0050] In one aspect, provided herein are $(VHH)_2$s comprising a first VHH that specifically binds SYNGAP1 comprising three complementarity determining regions: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312, or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 comprising 1, 2, or 3 amino acid modifications; and a second VHH that specifically binds SYNGAP1 comprising three complementarity determining regions: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or

the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312, or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 comprising 1, 2, or 3 amino acid modifications; wherein the first VHH and the second VHH are directly or indirectly operably connected.

[0051] In some embodiments, the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 comprising 1, 2, or 3 amino acid modifications; and the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 comprising 1, 2, or 3 amino acid modifications.

[0052] In some embodiments, the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 comprising 1, 2, or 3 amino acid modifications; and the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID

NO: 295, or the amino acid sequence of SEQ ID NO: 295 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 comprising 1, 2, or 3 amino acid modifications.

[0053] In some embodiments, the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 comprising 1, 2, or 3 amino acid modifications; and the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 comprising 1, 2, or 3 amino acid modifications.

[0054] In some embodiments, the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 comprising 1, 2, or 3 amino acid modifications; and the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 comprising 1, 2, or 3 amino acid

modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 comprising 1, 2, or 3 amino acid modifications.

[0055] In some embodiments, the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 comprising 1, 2, or 3 amino acid modifications; and the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 comprising 1, 2, or 3 amino acid modifications.

[0056] In some embodiments, the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 comprising 1, 2, or 3 amino acid modifications; and the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 comprising 1, 2, or 3 amino acid modifications; the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 comprising 1, 2, or 3 amino acid modifications; and/or the amino acid sequence of CDR3 comprises the amino acid sequence of

SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 comprising 1, 2, or 3 amino acid modifications.

[0057] In some embodiments, the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313.

[0100] In some embodiments, the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293; the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 297; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 297; the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 301; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 301; the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 305; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 305; the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 309; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 309; or the first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 313; and the second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%,

95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 313.

[0058] In some embodiments, the first VHH is operably connected to the second VHH via a peptide linker.

[0059] In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications.

[0060] In one aspect, provided herein are nucleic acid molecules encoding a $(VHH)_2$ described herein. In some embodiments, the nucleic acid molecule is a DNA molecule. In some embodiments, the nucleic acid molecule is an RNA molecule.

[0061] In one aspect, provided herein are vectors comprising a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a $(VHH)_2$ described herein). In some embodiments, the vector is a plasmid or a viral vector.

[0062] In one aspect, provided herein are viral particles comprising a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a $(VHH)_2$ described herein).

[0063] In one aspect, provided herein are in vitro cell or population of cells comprising a $(VHH)_2$ described herein, a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a $(VHH)_2$ described herein), or a vector described herein (e.g., a vector comprising a nucleic acid molecule encoding a $(VHH)_2$ described herein).

[0064] In one aspect, provided herein are pharmaceutical compositions comprising a $(VHH)_2$ described herein, a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a $(VHH)_2$ described herein), or a vector described herein (e.g., a vector comprising a nucleic acid molecule encoding a $(VHH)_2$ described herein) or a viral particle described herein (e.g., a viral particle comprising a nucleic acid molecule encoding a $(VHH)_2$ described herein), and an excipient.

[0065] In one aspect, provided herein are methods of making a $(VHH)_2$ polypeptides described herein, comprising introducing into an in vitro cell or population of cells a nucleic acid molecule described herein (e.g., a nucleic acid molecule encoding a $(VHH)_2$ described herein), or a vector described herein (e.g., a vector comprising a nucleic acid molecule encoding a $(VHH)_2$ described herein) or a viral particle described herein (e.g., a viral particle comprising a nucleic acid molecule encoding a $(VHH)_2$ described herein); culturing the cell or population of cells in a culture medium

under conditions suitable for expression of the $(VHH)_2$, isolating the $(VHH)_2$ from the culture medium, and optionally purifying the $(VHH)_2$.

[0066] In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications.

[0067] In one aspect, provided herein, are fusion proteins comprising: (a) an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof; and (b) a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein.

[0068] In some embodiments, the deubiquitinase is a cysteine protease or a metalloprotease.

[0069] In some embodiments, the deubiquitinase is a cysteine protease. In some embodiments, the cysteine protease is a ubiquitin-specific protease (USP), a ubiquitin C-terminal hydrolase (UCH), a Machado-Josephin domain protease (MJD), an ovarian tumour protease (OTU), a MINDY protease, or a ZUFSP protease.

[0070] In some embodiments, the cysteine protease is a USP. In some embodiments, the USP is selected from the group consisting of USP1, USP2, USP3, USP4, USP5, USP6, USP7, USP8, USP9X, USP9Y, USP10, USP11, USP12, USP13, USP14, USP15, USP16, USP17, USP17L2, USP17L3, USP17L4, USP17L5, USP17L7, USP17L8, USP18, USP19, USP20, USP21, USP22, USP23, USP24, USP25, USP26, USP27X, USP28, USP29, USP30, USP31, USP32, USP33, USP34, USP35, USP36, USP37, USP38, USP39, USP40, USP41, USP42, USP43, USP44, USP45, and USP46.

[0071] In some embodiments, the cysteine protease is a UCH. In some embodiments, the UCH is selected from the group consisting of BAP1, UCHL1, UCHL3, and UCHL5.

[0072] In some embodiments, the cysteine protease is a MJD. In some embodiments, the MJD is selected from the group consisting of ATXN3 and ATXN3L.

[0073] In some embodiments, the cysteine protease is a OTU. In some embodiments, the OTU is selected from the group consisting of OTUB1 and OTUB2.

[0074] In some embodiments, the cysteine protease is a MINDY. In some embodiments, the MINDY is selected from the group consisting of MINDY1, MINDY2, MINDY3, and MINDY4.

[0075] In some embodiments, the cysteine protease is a ZUFSP. In some embodiments, the ZUFSP is ZUP1.

[0076] In some embodiments, the deubiquitinase is a metalloprotease. In some embodiments, the metalloprotease is a Jab1/Mov34/Mpr1 Pad1 N-terminal+ (MPN+) (JAMM) domain protease.

[0077] In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1-112.

[0078] In some embodiments, the catalytic domain comprises a catalytic domain derived from a deubiquitinase at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1-112.

[0079] In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 113-220.

[0080] In some embodiments, the moiety that specifically binds a cytosolic protein comprises an antibody, or functional fragment or functional variant thereof. In some embodiments, the antibody, or functional fragment or functional variant thereof, comprises a full-length antibody, a single chain variable fragment (scFv), a scFv2, a scFv-Fc, a Fab, a Fab', a F(ab')2, a F(v), or a VHH. In some embodiments, the antibody, or functional fragment or functional variant thereof, comprises a VHH.

[0081] In some embodiments, the cytosolic protein is a transcription factor.

[0082] In some embodiments, the cytosolic protein is selected from the group consisting of cyclin-dependent kinase-like 5 (CDKL5), copper-transporting ATPase 2 (ATP7B), syntaxin-binding protein 1 (STXBP1), Ras/Rap GTPase-activating protein (SYNGAP1), progranulin (GRN), protein jagged-1 (JAG1), GATOR complex protein DEPDC5 (DEPDC5), tuberin (TSC2), hamartin (TSC1), kinesin-like protein KIF1A (KIF1A), dynamin-1 (DNM1), SH3 and multiple ankyrin repeat domains protein 3 (SHANK3), dystrophin (DMD), oxygen-regulated protein 1 (RP1), titin (TTN), cytoplasmic dynein 1 heavy chain 1 (DYNC1H1), TRIO and F-actin-binding protein (TRIO), and probable ubiquitin carboxyl-terminal hydrolase FAF-X (USP9X)

[0083] In some embodiments, the cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 221-328.

[0084] In some embodiments, the effector domain is directly fused to the targeting domain. In

some embodiments, the effector domain is indirectly fused to the targeting domain. In some embodiments, the effector domain is indirectly fused to the targeting domain via a peptide linker. In some embodiments, the effector domain is indirectly fused to the targeting domain via a peptide linker of sufficient length such that the effector domain and the targeting domain can simultaneous bind the respective target proteins.

[0085] In some embodiments, the effector domain is fused to the C terminus of the targeting domain. In some embodiments, the effector moiety is fused to the N terminus of the targeting domain.

[0086] In one aspect, provided herein are nucleic acid molecules encoding the fusion protein described herein. In some embodiments, the nucleic acid molecule is a DNA molecule. In some embodiments, the nucleic acid molecule is an RNA molecule.

[0087] In one aspect, provided herein are vectors comprising a nucleic acid molecule described herein. In some embodiments, the vector is a plasmid or a viral vector.

[0088] In one aspect, provided herein are viral particles comprising a nucleic acid described herein.

[0089] In one aspect, described herein is an in vitro cell or population of cells comprising a fusion protein described herein, a nucleic acid molecule described herein, or a vector described herein.

[0090] In one aspect, provided herein are pharmaceutical compositions comprising a fusion protein described herein, a nucleic acid molecule described herein, a vector described herein, or a viral particle described herein, and an excipient.

[0091] In one aspect, provided herein are methods of making a fusion protein described herein, comprising (a) introducing into an in vitro cell or population of cells a nucleic acid described herein, a vector described herein, or a viral particle described herein; (b) culturing the cell or population of cells in a culture medium under conditions suitable for expression of the fusion protein, (c) isolating the fusion protein from the culture medium, and (d) optionally purifying the fusion protein.

[0092] In one aspect, provided herein are methods of treating a disease in a subject comprising administering a fusion protein described herein, a nucleic acid described herein, a vector described herein, or a viral particle described herein, or a pharmaceutical composition described herein, to a subject in need thereof.

[0093] In some embodiments, the subject is human.

[0094] In some embodiments, the disease is associated with decreased expression of a functional version of the cytosolic protein relative to a non-diseased control.

[0095] In some embodiments, the disease is associated with decreased stability of a functional version of the cytosolic protein relative to a non-diseased control.

[0096] In some embodiments, the disease is associated with increased ubiquitination and degradation of the cytosolic protein relative to a non-diseased control.

[0097] In some embodiments, the disease is a genetic disease.

[0098] In some embodiments, the disease is a SYNGAP1 encephalopathy, CDKL5 deficiency disorder, STXBP1 encephalopathy early, infantile epileptic encephalopathy type 2, Wilson disease, early infantile epileptic encephalopathy type 4, mental retardation autosomal dominant 5, aphasia (e.g., Aphasia, primary progressive & FTD), alagille syndrome 1, epilepsy (e.g., Familial Focal Epilepsy), tuberous sclerosis-2, tuberous sclerosis-1, KIF1A-associated neurological disorder, encephalopathy, Phelan-McDermid syndrome, Becker Muscular Dystrophy, RP1, retinitis pigmentosa 1, dilated cardiomyopathy 1G, DYNC1H1 Syndrome, TRIO-Related intellectual disability (ID), and USP9X Development Disorder.

[0099] The method of any one of claims 43-48, wherein the disease is early infantile epileptic encephalopathy type 2, Wilson disease, early infantile epileptic encephalopathy type 4, mental retardation autosomal dominant 5, aphasia primary progressive & FTD (frontotemporal degeneration), alagille syndrome 1, epilepsy familial focal with variable foci 1, tuberous sclerosis-2, tuberous sclerosis-1, KIF1A-associated neurological disorder, encephalopathy, Phelan-McDermid syndrome, Becker Muscular Dystrophy, RP1, retinitis pigmentosa 1, dilated cardiomyopathy 1G, DYNC1H1 Syndrome, TRIO-Related intellectual disability (ID), and USP9X Development Disorder.

[00100] In some embodiments, the disease is a haploinsufficiency disease.

[00101] In some embodiments, the fusion protein is administered at a therapeutically effective dose.

[00102] In some embodiments, the fusion protein is administered systematically or locally.

[00103] In some embodiments, the fusion protein is administered intravenously, subcutaneously, or intramuscularly.

4. BRIEF DESCRIPTION OF THE FIGURES

[00104] **FIGS. 1A-1D** provides a schematic representation of exemplary fusion proteins described herein. **FIG. 1A** is a schematic of an engineered deubiquitinase comprising from N' to C' terminus a VHH that specifically binds a cytosolic target protein and the catalytic domain of a deubiquitinase. In this specific embodiment, the C-terminus of the VHH is directly connected to the N-terminus of the catalytic domain of the deubiquitinase. **FIG. 1B** is a schematic of an engineered deubiquitinase comprising from N' to C' terminus the catalytic domain of a deubiquitinase that specifically binds a cytosolic target protein and a VHH that specifically binds a cytosolic target protein. In this specific embodiment, the C-terminus of the catalytic domain of the deubiquitinase is directly connected to the N-terminus of the VHH. **FIG. 1C** is a schematic of an engineered deubiquitinase comprising from N' to C' terminus a VHH that specifically binds a cytosolic target protein and the catalytic domain of a deubiquitinase. In this specific embodiment, the C-terminus of the VHH is indirectly connected to the N-terminus of the catalytic domain of the deubiquitinase through a peptide linker. **FIG. 1D** is a schematic of an engineered deubiquitinase comprising from N' to C' terminus the catalytic domain of a deubiquitinase that specifically binds a cytosolic target protein and a VHH that specifically binds a cytosolic target protein. In this specific embodiment, the C-terminus of the catalytic domain of the deubiquitinase is indirectly connected to the N-terminus of the VHH through a peptide linker.

[00105] **FIG. 2** is a schematic representation of the assay utilized in Example 3, to screen the effect of targeted deubiquitination of different cytosolic proteins on target protein expression.

[00106] **FIG 3.** is a bar graph depicting the fold change in SHANK3 expression relative to control (as indicated).

[00107] **FIG. 4.** is a bar graph depicting the fold change in SYNGAP1 protein expression relative to control (as indicated).

[00108] **FIG. 5** is a bar graph depicting the fold change in PYDC2 protein expression relative to control (deubiquitinase without the nanobody targeting the alfa-tag).

[00109] **FIG. 6** is a bar graph depicting the fold change in CSTB protein expression relative to control (deubiquitinase without the nanobody targeting the alfa-tag).

[00110] **FIG. 7** is a bar graph depicting the fold change in PCBD1 protein expression relative to control (deubiquitinase without the nanobody targeting the alfa-tag).

[00111] **FIG. 8** is an image of a reduced SDS-PAGE gel stained with Coomassie blue. Two μg

of purified His-SynGAP-EC [1186-1277] obtained from E. coli was loaded in the right lane. The left lane labeled "MW" was loaded with a molecular weight marker. The arrow indicates the purified His-SynGAP-EC [1186-1277] protein with a molecular weight of 15.75 kDA.

[00112] **FIG. 9** is a bar graph showing the fold change in SYNGAP1 expression relative to control.

5. DETAILED DESCRIPTION

5.1 Overview

[00113] Ubiquitination is the process by which ubiquitin ligases mediate the addition of ubiquitin, a 76 amino acid regulatory protein, to a substrate protein. Ubiquitination generally starts by the attachment of a single ubiquitin molecule to a lysine amino acid residue of the substrate protein. Mevissen T. et al. Mechanisms of Deubiquitinase Specificity and Regulation Annual Review of Biochemistry 86:1, 159-192 (2017), the entire contents of which is incorporated by reference herein. These monoubiquitination events are abundant and serve various functions. Ubiquitin itself contains seven lysine residues, all of which can be ubiquitinated resulting in polyubiquitinated proteins. Komander, D. et al. Breaking the chains: structure and function of the deubiquitinases. Nat Rev Mol Cell Biol 10, 550–563 (2009), the entire contents of which is incorporated by reference herein. Mono and polyubiquitination can have multiple effects on the substrate protein, including marking the substrate protein for degradation via the proteasome, altering the protein's cellular location, altering the protein's activity, and/or promoting or preventing normal protein interactions. See e.g., Hershko A. et al. The ubiquitin system. Annu Rev Biochem. 67:425-79 (1998); Nandi D, et al. The ubiquitin-proteasome system. J Biosci. Mar;31(1):137-55 (2006), the entire contents of each of which is incorporated by reference herein. The effects of ubiquitination can be reversed or prevented by removing the ubiquitin protein(s) from the substrate protein. The removal of ubiquitin from a substrate protein is mediated by deubiquitinase (DUB) proteins. *Id.*

[00114] Numerous genetic diseases are associated with or caused by a decrease in the level of expression of a functional cytosolic protein or the stability of the cytosolic protein. For example, haploinsufficiency genetic diseases are caused by the presence a single copy of a wild-type allele in heterozygous combination with a loss of function variant allele, wherein the level of functional protein expressed is insufficient to produce the standard phenotype. See e.g., Johnson, A. et al,

Causes and effects of haploinsufficiency. Biol Rev, 94: 1774-1785 (2019), the entire contents of which is incorporated by reference herein. Haploinsufficiency can arise from a de novo or inherited loss-of-function mutation in the variant allele, such that it produces little or no functional protein. Other genetic disorders result from the ubiquitination and subsequent degradation of variant but functional proteins, resulting in a decrease in expression of the functional protein.

[00115] The present disclosure provides, *inter alia*, novel fusion proteins that comprise the catalytic domain (or functional fragment thereof) of a deubiquitinase and a targeting moiety, such as a VHH, that specifically binds to a target cytosolic protein. In some embodiments, decreased expression of a functional version of the target cytosolic protein or decreased stability of a functional version of the target cytosolic protein is associated with a disease phenotype. As such, the fusion proteins described herein are particularly useful in the treatment of genetic diseases characterized by a decrease in the level of expression of a functional target cytosolic protein or the stability of the target cytosolic protein. Upon expression of the fusion protein by host cells, the catalytic domain of the deubiquitinase will be specifically targeted to the target cytosolic protein and deubiquitinated, resulting in increased expression of the target cytosolic protein, e.g., to a level sufficient to alleviate the disease phenotype.

5.2 Definitions

[00116] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[00117] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. For example, the Concise Dictionary of Biomedicine and Molecular Biology, Juo, Pei-Show, 2nd ed., 2002, CRC Press; The Dictionary of Cell and Molecular Biology, 3rd ed., 1999, Academic Press; and the Oxford Dictionary Of Biochemistry And Molecular Biology, Revised, 2000, Oxford University Press, provide one of skill with a general dictionary of many of the terms used in this disclosure.

[00118] It is to be understood that the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of any subject matter claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise.

[00119] It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Furthermore, use of the term "including" as well as other forms, such as "include," "includes," and "included," is not limiting.

[00120] It is understood that wherever aspects are described herein with the language "comprising," otherwise analogous aspects described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[00121] The term "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term "and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following aspects: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[00122] Units, prefixes, and symbols are denoted in their Système International de Unites (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range. The headings provided herein are not limitations of the various aspects of the disclosure, which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification in its entirety.

[00123] As described herein, any concentration range, percentage range, ratio range or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated.

[00124] The terms "about" or "comprising essentially of" refer to a value or composition that is within an acceptable error range for the particular value or composition as determined by one of ordinary skill in the art, which will depend in part on how the value or composition is measured or determined, i.e., the limitations of the measurement system. For example, "about" or "comprising essentially of" can mean within 1 or more than 1 standard deviation per the practice in the art. Alternatively, "about" or "comprising essentially of" can mean a range of up to 20%. Furthermore, particularly with respect to biological systems or processes, the terms can mean up to an order of magnitude or up to 5-fold of a value. When particular values or compositions are provided in the application and claims, unless otherwise stated, the meaning of "about" or "comprising essentially

of" should be assumed to be within an acceptable error range for that particular value or composition.

[00125] As used herein, the term "catalytic domain" in reference to a deubiquitinase refers to an amino acid sequence, or a variant thereof, of a deubiquitinase that is capable of mediating deubiquitination of a target protein. The catalytic domain may comprise a naturally occurring amino acid sequence of a deubiquitinase or it may comprise a variant amino acid sequence of a naturally occurring deubiquitinase. The catalytic domain may comprise the minimum amino acid sequence of a deubiquitinase to mediate deubiquitination of a target protein. The catalytic domain may comprise more than the minimum amino acid sequence of a deubiquitinase to mediate deubiquitination of a target protein.

[00126] The terms "polynucleotide" and "nucleic acid sequence" are used interchangeably herein and refer to a polymer of DNA or RNA. The polynucleotide sequence can be single-stranded or double-stranded; contain natural, non-natural, or altered nucleotides; and contain a natural, non-natural, or altered internucleotide linkage, such as a phosphoroamidate linkage or a phosphorothioate linkage, instead of the phosphodiester found between the nucleotides of an unmodified polynucleotide sequence. Polynucleotide sequences include, but are not limited to, all polynucleotide sequences which are obtained by any means available in the art, including, without limitation, recombinant means, *e.g.,* the cloning of polynucleotide sequences from a recombinant library or a cell genome, using ordinary cloning technology and polymerase chain reaction, and the like, and by synthetic means.

[00127] The terms "amino acid sequence" and "polypeptide" are used interchangeably herein and refer to a polymer of amino acids connected by one or more peptide bonds.

[00128] The term "functional variant" as used herein in reference to a protein or polypeptide refers to a protein that comprises at least one amino acid modification (*e.g.,* a substitution, deletion, addition) compared to the amino acid sequence of a reference protein, that retains at least one particular function. In some embodiments, the reference protein is a wild type protein. For example, a functional variant of an IL-2 protein can refer to an IL-2 protein comprising an amino acid substitution as compared to a wild type IL-2 protein that retains the ability to bind the intermediate affinity IL-2 receptor but abrogates the ability of the protein to bind the high affinity IL-2 receptor. Not all functions of the reference wild type protein need be retained by the functional variant of the protein. In some instances, one or more functions are selectively reduced

or eliminated.

[00129] The term "functional fragment" as used herein in reference to a protein or polypeptide refers to a fragment of a reference protein that retains at least one particular function. For example, a functional fragment of an anti-HER2 antibody can refer to a fragment of the anti-HER2 antibody that retains the ability to specifically bind the HER2 antigen. Not all functions of the reference protein need be retained by a functional fragment of the protein. In some instances, one or more functions are selectively reduced or eliminated.

[00130] As used herein, the term "modification," with reference to a polynucleotide sequence, refers to a polynucleotide sequence that comprises at least one substitution, alteration, inversion, addition, or deletion of nucleotide compared to a reference polynucleotide sequence. Modifications can include non-naturally nucleotides. As used herein, the term "modification," with reference to an amino acid sequence refers to an amino acid sequence that comprises at least one substitution, alteration, inversion, addition, or deletion of an amino acid residue compared to a reference amino acid sequence. Modifications can include the inclusion of non-naturally occurring amino acid residues.

[00131] As used herein, the term "derived from" with reference to an amino acid sequence refers to an amino acid sequence that has at least 80% sequence identity to a reference naturally occurring amino acid sequence. For example, a catalytic domain derived from a naturally occurring deubiquitinase means that the catalytic domain has an amino acid sequence with at least 80% sequence identity to the sequence of the deubiquitinase catalytic domain from which it is derived. The term "derived from" as used herein does not denote any specific process or method for obtaining the amino acid sequence. For example, the amino acid sequence can be chemically or recombinantly synthesized.

[00132] The term "fusion protein" and grammatical equivalents as used herein refers to a protein that comprises an amino acid sequence derived from at least two separate proteins. The amino acid sequence of the at least two separate proteins can be directly connected through a peptide bond; or can be operably connected through an amino acid linker. Therefore, the term fusion protein encompasses embodiments, wherein the amino acid sequence of e.g., Protein A is directly connected to the amino acid sequence of Protein B through a peptide bond (Protein A – Protein B), and embodiments, wherein the amino acid sequence of e.g., Protein A is operably connected to the amino acid sequence of Protein B through an amino acid linker (Protein A – linker

– Protein B).

[00133] The term "fuse" and grammatical equivalents thereof as used herein refers to the operable connection of an amino acid sequence derived from one protein to the amino acid sequence derived from different protein. The term fuse encompasses both a direct connection of the two amino acid sequences through a peptide bond, and the indirect connection through an amino acid linker.

[00134] An "isolated antibody" refers to an antibody that is substantially free of other antibodies having different antigenic specificities (e.g., an isolated antibody that binds specifically to HER2 is substantially free of antibodies that bind specifically to antigens other than HER2). An isolated antibody that binds specifically to HER2 may, however, cross-react with other antigens, such as HER2 molecules from different species. Moreover, an isolated antibody may be substantially free of other cellular material and/or chemicals. By comparison, an "isolated" nucleic acid refers to a nucleic acid composition of matter that is markedly different, i.e., has a distinctive chemical identity, nature and utility, from nucleic acids as they exist in nature. For example, an isolated DNA, unlike native DNA, is a freestanding portion of a native DNA and not an integral part of a larger structural complex, the chromosome, found in nature. Further, an isolated DNA, unlike native DNA, can be used as a PCR primer or a hybridization probe for, among other things, measuring gene expression and detecting biomarker genes or mutations for diagnosing disease or predicting the efficacy of a therapeutic. An isolated nucleic acid may also be purified so as to be substantially free of other cellular components or other contaminants, e.g., other cellular nucleic acids or proteins, using standard techniques well known in the art.

[00135] As used herein, the term "antibody" or "antibodies" are used in the broadest sense and encompasses various antibody structures, including but not limited to monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments so long as they exhibit the desired antigen-binding activity (i.e. antigen binding fragments as defined herein). The term antibody thus includes, for example, include full-length antibodies, antigen-binding fragments of full-length antibodies, molecules comprising antibody CDRs, VH regions, and/or VL regions; and antibody-like scaffolds (e.g., fibronectins). Examples of antibodies include, without limitation, monoclonal antibodies, recombinantly produced antibodies, monospecific antibodies, multispecific antibodies (including bispecific antibodies), human antibodies, humanized antibodies, chimeric antibodies, immunoglobulins, synthetic

antibodies, tetrameric antibodies comprising two heavy chain and two light chain molecules, an antibody light chain monomer, an antibody heavy chain monomer, an antibody light chain dimer, an antibody heavy chain dimer, an antibody light chain- antibody heavy chain pair, intrabodies, heteroconjugate antibodies, antibody-drug conjugates, single domain antibodies (e.g.,VHH, $(VHH)_2$), monovalent antibodies, single chain antibodies, single-chain Fvs (scFv; $(scFv)_2$), camelized antibodies, affybodies, Fab fragments (e.g., Fab, single chain Fab (scFab), $F(ab')_2$ fragments, disulfide-linked Fvs (sdFv), anti-idiotypic (anti-Id) antibodies (including, *e.g.*, anti-anti-Id antibodies), diabodies, tribodies, and antibody-like scaffolds (e.g., fibronectins), Fc fusions (e.g., Fab-Fc, scFv-Fc, VHH-Fc, $(scFv)_2$-Fc, $(VHH)_2$-Fc, and antigen-binding fragments of any of the above, and conjugates or fusion proteins comprising any of the above. In certain embodiments, antibodies described herein refer to polyclonal antibody populations. In certain embodiments, antibodies described herein refer to monoclonal antibody populations. Antibodies can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA or IgY), any class (*e.g.*, IgG_1, IgG_2, IgG_3, IgG_4, IgA_1 or IgA_2), or any subclass (*e.g.*, IgG_{2a} or IgG_{2b}) of immunoglobulin (Ig) molecule. In certain embodiments, antibodies described herein are IgG antibodies, or a class (*e.g.*, human IgG_1 or IgG_4) or subclass thereof. In a specific embodiment, the antibody is a humanized monoclonal antibody. In another specific embodiment, the antibody is a human monoclonal antibody.

[00136] The term "full-length antibody," as used herein refers to an antibody having a structure substantially similar to a native antibody structure comprising two heavy chains and two light chains interconnected by disulfide bonds. In some embodiments, the two heavy chains comprise a substantially identical amino acid sequence; and the two light chains comprise a substantially identical amino acid sequence. Antibody chains may be substantially identical but not entirely identical if they differ due to post-translational modifications, such as C-terminal cleavage of lysine residues, alternative glycosylation patterns, etc.

[00137] The terms "antigen binding fragment" and "antigen binding domain" are used interchangeably herein and refer to one or more polypeptides, other than a full-length antibody, that is capable of specifically binding to antigen and comprises a portion of a full-length antibody (e.g., a VH, a VL). Exemplary antigen binding fragments include, but are not limited to, single domain antibodies (e.g.,VHH, $(VHH)_2$), single chain antibodies, single-chain Fvs (scFv; $(scFv)_2$), camelized antibodies, affybodies, Fab fragments (e.g., Fab, single chain Fab (scFab), $F(ab')_2$ fragments, and disulfide-linked Fvs (sdFv). The antigen binding domain can be part of a larger

protein, e.g., a full-length antibody.

[00138] The term "$(scFv)_2$" as used herein refers to an antibody that comprises a first and a second scFv operably connected (e.g., via a linker). The first and second scFv can specifically bind the same or different antigens. In some embodiments, the first and second scFv are operably connected by an amino via an amino acid linker.

[00139] The term "$(VHH)_2$" as used herein refers to an antibody that comprises a first and a second VHH operably connected (e.g., via a linker). The first and the second VHH can specifically bind the same or different antigens. In some embodiments, the first and second VHH are operably connected by an amino via an amino acid linker.

[00140] The term "Fab-Fc" as used herein refers to an antibody that comprises a Fab operably linked to an Fc domain or a subunit of an Fc domain. A full-length antibody described herein comprises two Fabs, one Fab operably connected to one Fc domain and the other Fab operably connected to a second Fc domain.

[00141] The term "scFv-Fc" as used herein refers to an antibody that comprises a scFv operably linked to an Fc domain or subunit of an Fc domain.

[00142] The term "VHH-Fc" as used herein refers to an antibody that comprises a VHH operably linked to an Fc domain or a subunit of an Fc domain.

[00143] The term "$(scFv)_2$-Fc" as used herein refers to a $(scFv)_2$ operably linked to an Fc domain or a subunit of an Fc domain.

[00144] The term "$(VHH)_2$-Fc" as used herein refers to $(VHH)_2$ operably linked to an Fc domain or a subunit of an Fc domain.

[00145] "Antibody-like scaffolds" are known in the art, for example, fibronectin and designed ankyrin repeat proteins (DARPins) have been used as alternative scaffolds for antigen-binding domains, *see, e.g.,* Gebauer and Skerra, Engineered protein scaffolds as next-generation antibody therapeutics. Curr Opin Chem Biol 13:245-255 (2009) and Stumpp et al., Darpins: A new generation of protein therapeutics. Drug Discovery Today 13: 695-701 (2008). Exemplary antibody-like scaffold proteins include, but are not limited to, lipocalins (Anticalin), Protein A-derived molecules such as Z-domains of Protein A (Affibody), an A-domain (Avimer/Maxibody), a serum transferrin (trans-body); a designed ankyrin repeat protein (DARPin), VNAR fragments, a fibronectin (AdNectin), a C-type lectin domain (Tetranectin); a variable domain of a new antigen receptor beta-lactamase (VNAR fragments), a human gamma-crystallin or ubiquitin (Affilin

molecules); a kunitz type domain of human protease inhibitors, microbodies such as the proteins from the knottin family, peptide aptamers and fibronectin (adnectin).

[00146] As used herein, the term "CDR" or "complementarity determining region" means the noncontiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. These particular regions have been described by Kabat *et al.*, J. Biol. Chem. 252, 6609-6616 (1977) and Kabat *et al.*, Sequences of protein of immunological interest. (1991), all of which are herein incorporated by reference in their entireties. Unless otherwise specified, the term "CDR" is a CDR as defined by Kabat *et al.*, J. Biol. Chem. 252, 6609-6616 (1977) and Kabat *et al.*, Sequences of protein of immunological interest. (1991).

[00147] As used herein, the term "framework (FR) amino acid residues" refers to those amino acids in the framework region of an antibody variable region. The term "framework region" or "FR region" as used herein, includes the amino acid residues that are part of the variable region, but are not part of the CDRs (*e.g.*, using the Kabat definition of CDRs).

[00148] As used herein, the term "heavy chain" when used in reference to an antibody can refer to any distinct type, *e.g.*, alpha (α), delta (δ), epsilon (ε), gamma (γ), and mu (μ), based on the amino acid sequence of the constant domain, which give rise to IgA, IgD, IgE, IgG, and IgM classes of antibodies, respectively, including subclasses of IgG, *e.g.*, IgG_1, IgG_2, IgG_3, and IgG_4.

[00149] As used herein, the term "light chain" when used in reference to an antibody can refer to any distinct type, *e.g.*, kappa (κ) or lambda (λ) based on the amino acid sequence of the constant domains. Light chain amino acid sequences are well known in the art. In specific embodiments, the light chain is a human light chain.

[00150] As used herein, the terms "variable region" refers to a portion of an antibody, generally, a portion of a light or heavy chain, typically about the amino-terminal 110 to 120 amino acids or 110 to 125 amino acids in the mature heavy chain and about 90 to 115 amino acids in the mature light chain, which differ extensively in sequence among antibodies and are used in the binding and specificity of a particular antibody for its particular antigen. The variability in sequence is concentrated in those regions called complementarity determining regions (CDRs) while the more highly conserved regions in the variable domain are called framework regions (FR). Without wishing to be bound by any particular mechanism or theory, it is believed that the CDRs of the light and heavy chains are primarily responsible for the interaction and specificity of the antibody with antigen. In certain embodiments, the variable region is a human variable region. In certain

embodiments, the variable region comprises rodent or murine CDRs and human framework regions (FRs). In particular embodiments, the variable region is a primate (*e.g.*, non-human primate) variable region. In certain embodiments, the variable region comprises rodent or murine CDRs and primate (*e.g.*, non-human primate) framework regions (FRs).

[00151] The terms "VL" and "VL domain" are used interchangeably to refer to the light chain variable region of an antibody.

[00152] The terms "VH" and "VH domain" are used interchangeably to refer to the heavy chain variable region of an antibody.

[00153] As used herein, the terms "constant region" and "constant domain" are interchangeable and are common in the art. The constant region is an antibody portion, *e.g.*, a carboxyl terminal portion of a light and/or heavy chain which is not directly involved in binding of an antibody to antigen but which can exhibit various effector functions, such as interaction with an Fc receptor (*e.g.*, Fc gamma receptor). The constant region of an immunoglobulin (Ig) molecule generally has a more conserved amino acid sequence relative to an immunoglobulin (Ig) variable domain.

[00154] The term "Fc region" as used herein refers to the C-terminal region of an immunoglobulin (Ig) heavy chain that comprises from N- to C-terminus at least a CH2 domain operably connected to a CH3 domain. In some embodiments, the Fc region comprises an immunoglobulin (Ig) hinge region operably connected to the N-terminus of the CH2 domain. Examples of proteins with engineered Fc regions can be found in Saunders 2019 (K. O. Saunders, "*Conceptual Approaches to Modulating Antibody Effector Functions and Circulation Half-Life*," 2019, Frontiers in Immunology, V. 10, Art. 1296, pp. 1-20, which is incorporated by reference herein).

[00155] As used herein, the term "EU numbering system" refers to the EU numbering convention for the constant regions of an antibody, as described in Edelman, G.M. *et al.*, Proc. Natl. Acad. USA, 63, 78-85 (1969) and Kabat *et al*, Sequences of Proteins of Immunological Interest, U.S. Dept. Health and Human Services, 5th edition, 1991, each of which is herein incorporated by reference in its entirety.

[00156] As used herein, the term "Kabat numbering system" refers to the Kabat numbering convention for variable regions of an antibody, see e.g., Kabat *et al*, Sequences of Proteins of Immunological Interest, U.S. Dept. Health and Human Services, 5th edition, 1991. Unless otherwise noted, numbering of the variable regions of an antibody are denoted according to the

Kabat numbering system.

[00157] As used herein, the terms "specifically binds," refers to molecules that bind to an antigen (*e.g.*, epitope or immune complex) as such binding is understood by one skilled in the art. For example, a molecule that specifically binds to an antigen can bind to other peptides or polypeptides, generally with lower affinity as determined by, *e.g.*, immunoassays, BIAcore®, KinExA 3000 instrument (Sapidyne Instruments, Boise, ID), or other assays known in the art. In a specific embodiment, molecules that specifically bind to an antigen bind to the antigen with a K_A that is at least 2 logs (*e.g.*, factors of 10), 2.5 logs, 3 logs, 4 logs or greater than the K_A when the molecules bind non-specifically to another antigen. The skilled worker will appreciate that an antibody, as described herein, can specifically bind to more than one antigen (*e.g.*, via different regions of the antibody molecule). The term specifically binds includes molecules that are cross reactive with the same antigen of a different species. For example, an antigen binding domain that specifically binds human CD20 may be cross reactive with CD20 of another species (e.g., cynomolgus monkey, or murine), and still be considered herein to specifically bind human CD20.

[00158] "Affinity" refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (e.g., a receptor) and its binding partner (e.g., a ligand). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity, which reflects a 1 : 1 interaction between members of a binding pair (e.g., an antigen binding moiety and an antigen, or a receptor and its ligand). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (KD), which is the ratio of dissociation and association rate constants (koff and kon, respectively). Thus, equivalent affinities may comprise different rate constants, as long as the ratio of the rate constants remains the same. Affinity can be measured by well-established methods known in the art, including those described herein. A particular method for measuring affinity is Surface Plasmon Resonance (SPR).

[00159] The determination of "percent identity" between two sequences (e.g., amino acid sequences or nucleic acid sequences) can be accomplished using a mathematical algorithm. Identity measures the percent of identical matches between the smaller of two or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (i.e., "algorithms"). A specific, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin S & Altschul SF (1990) PNAS 87: 2264-2268, modified as in Karlin S & Altschul SF (1993) PNAS 90: 5873-5877, each of which is herein

incorporated by reference in its entirety. Such an algorithm is incorporated into the BLASTN, BLASTP, BLASTX programs of Altschul SF et al., (1990) J Mol Biol 215: 403, which is herein incorporated by reference in its entirety. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, e.g., for score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecule described herein. BLAST protein searches can be performed with the BLASTP program parameters set, e.g., default settings; to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul SF et al., (1997) Nuc Acids Res 25: 3389-3402, which is herein incorporated by reference in its entirety. Alternatively, PSI BLAST can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI Blast programs, the default parameters of the respective programs (e.g., of BLASTP and BLASTN) can be used (see, e.g., National Center for Biotechnology Information (NCBI) on the worldwide web, ncbi.nlm.nih.gov). Another specific, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, CABIOS 4:11-17, which is herein incorporated by reference in its entirety. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted. As described above, the percent identity is based on the amino acid matches between the smaller of two proteins. Therefore, for example, using NCBI Basic Local Alignment Tool - BLASTP program on the default settings (Search Parameters: word size 3, expect value 0.05, hitlist 100, Gapcosts 11,1; Matrix BLOSUM62, Filter string: F; Genetic Code: 1; Window Size: 40; Threshold: 11; Composition Based Stats: 2; Karlin-Altschul Statistics: Lambda: 0.31293; 0.267; K: 0.132922; 0.041; H: 0.401809; 0.14; and Relative Statistics: Effective search space: 288906); the percent identity between SEQ ID NO: 80 and SEQ ID NO: 286 is 100% identity.

[00160] As used herein, the term “operably connected” refers to a linkage of polynucleotide sequence elements or amino acid sequence elements in a functional relationship. For example, a polynucleotide sequence is operably connected when it is placed into a functional relationship with

another polynucleotide sequence. In some embodiments, a transcription regulatory polynucleotide sequence *e.g.*, a promoter, enhancer, or other expression control element is operably-linked to a polynucleotide sequence that encodes a protein if it affects the transcription of the polynucleotide sequence that encodes the protein.

[00161] The terms "subject" and "patient" are used interchangeably herein and include any human or nonhuman animal. The term "nonhuman animal" includes, but is not limited to, vertebrates such as nonhuman primates, sheep, dogs, and rodents such as mice, rats and guinea pigs. In some embodiments, the subject is a human.

[00162] As used herein, the term "administering" refers to the physical introduction of a therapeutic agent (or a precursor of the therapeutic agent that is metabolized or altered within the body of the subject to produce the therapeutic agent in vivo) to a subject, using any of the various methods and delivery systems known to those skilled in the art. Exemplary routes of include intravenous, intramuscular, subcutaneous, intraperitoneal, spinal or other parenteral routes of administration, for example by injection or infusion. The term "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intralymphatic, intralesional, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion, as well as *in vivo* electroporation. A therapeutic agent may be administered via a non-parenteral route, or orally. Other non-parenteral routes include a topical, epidermal or mucosal route of administration, for example, intranasally, vaginally, rectally, sublingually or topically. Administering can also be performed, for example, once, a plurality of times, and/or over one or more extended periods.

[00163] A "therapeutically effective amount" or "therapeutically effective dose" of a drug or therapeutic agent is any amount of the drug that, when used alone or in combination with another therapeutic agent, protects a subject against the onset of a disease or promotes disease regression evidenced by a decrease in severity of disease symptoms, an increase in frequency and duration of disease symptom-free periods, or a prevention of impairment or disability due to the disease affliction. The ability of a therapeutic agent to promote disease regression can be evaluated using a variety of methods known to the skilled practitioner, such as in human subjects during clinical trials, in animal model systems predictive of efficacy in humans, or by assaying the activity of the

agent in in vitro assays.

[00164] The terms "disease," "disorder," and "syndrome" are used interchangeably herein.

[00165] As used herein, the terms "treat," treating," "treatment," and the like refer to reducing or ameliorating a disease and/or symptom(s) associated therewith or obtaining a desired pharmacologic and/or physiologic effect. It will be appreciated that, although not precluded, treating a disease does not require that the disease or symptoms associated therewith be completely eliminated. In some embodiments, the effect is therapeutic, i.e., without limitation, the effect partially or completely reduces, diminishes, abrogates, abates, alleviates, decreases the intensity of, or cures a disease and/or adverse symptom attributable to the disease. In some embodiments, the effect is preventative, i.e., the effect protects or prevents an occurrence or reoccurrence of a disease. To this end, the presently disclosed methods comprise administering a therapeutically effective amount of a compositions as described herein.

5.3 Fusion Proteins

[00166] In certain aspects, provided herein are fusion proteins that comprise an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof; and a targeting domain comprising a moiety that specifically binds a target cytosolic protein.

5.3.1 Effector Domain

[00167] In some embodiments, the effector domain comprises a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof. In some embodiments, the deubiquitinase is human. In some embodiments, the catalytic domain is derived from a naturally occurring deubiquitinase (e.g., a naturally occurring human deubiquitinase).

[00168] In some embodiments, the amino acid sequence of the effector domain comprises the amino acid sequence of a full length deubiquitinase. In some embodiments, the amino acid sequence of the effector domain comprises the amino acid sequence of a catalytic domain of a deubiquitinase and an additional amino acid sequence at the N-terminal, C-terminal, or N-terminal and C-terminal end of the catalytic domain.

[00169] In some embodiments, the catalytic domain comprises a naturally occurring amino acid sequence of a deubiquitinase. In some embodiments, the catalytic domain comprises a variant of

a naturally occurring deubiquitinase. In some embodiments, the amino acid sequence of the catalytic domain of the fusion protein is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of a naturally occurring deubiquitinase. In some embodiments, the amino acid sequence of the catalytic domain of the fusion protein comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 amino acid modifications compared to the amino acid sequence of the catalytic domain of a naturally occurring deubiquitinase.

[00170] In some embodiments, the catalytic domain comprises the minimum amino acid sequence of a naturally occurring deubiquitinase sufficient to mediate deubiquitination of a target protein. In some embodiments, the catalytic domain comprises more than the minimum amino acid sequence of a naturally occurring deubiquitinase sufficient to mediate deubiquitination of a target protein.

[00171] In some embodiments, the deubiquitinase is a cysteine protease or a metalloprotease. In some embodiments, the deubiquitinase is a cysteine protease. In some embodiments, the deubiquitinase is a metalloprotease. In some embodiments, the deubiquitinase is a ubiquitin-specific protease (USP), a ubiquitin C-terminal hydrolase (UCH), a Machado-Josephin domain protease (MJD), an ovarian tumor protease (OTU), a MINDY protease, or a ZUFSP protease.

[00172] Exemplary deubiquitinases include, but are not limited to, USP1, USP2, USP3, USP4, USP5, USP6, USP7, USP8, USP9X, USP9Y, USP10, USP11, USP12, USP13, USP14, USP15, USP16, USP17, USP17L2, USP17L3, USP17L4, USP17L5, USP17L7, USP17L8, USP18, USP19, USP20, USP21, USP22, USP23, USP24, USP25, USP26, USP27X, USP28, USP29, USP30, USP31, USP32, USP33, USP34, USP35, USP36, USP37, USP38, USP39, USP40, USP41, USP42, USP43, USP44, USP45, USP46, BAP1, UCHL1, UCHL3, UCHL5, ATXN3, ATXN3L, OTUB1, OTUB2, MINDY1, MINDY2, MINDY3, MINDY4, and ZUP1. Exemplary deubiquitinases for use in the present disclosure are also disclosed in Komander, D. et al. Breaking the chains: structure and function of the deubiquitinases. Nat Rev Mol Cell Biol 10, 550–563 (2009), the entire contents of which is incorporated by reference herein.

[00173] In some embodiments, the deubiquitinase is selected from the group consisting of USP1, USP2, USP3, USP4, USP5, USP6, USP7, USP8, USP9X, USP9Y, USP10, USP11, USP12, USP13, USP14, USP15, USP16, USP17, USP17L2, USP17L3, USP17L4, USP17L5, USP17L7, USP17L8, USP18, USP19, USP20, USP21, USP22, USP23, USP24, USP25, USP26, USP27X,

USP28, USP29, USP30, USP31, USP32, USP33, USP34, USP35, USP36, USP37, USP38, USP39, USP40, USP41, USP42, USP43, USP44, USP45, and USP46.

[00174] In some embodiments, the deubiquitinase is BAP1, UCHL1, UCHL3, or UCHL5. In some embodiments, the deubiquitinase is ATXN3 or ATXN3L. In some embodiments, the deubiquitinase is OTUB1 or OTUB2. In some embodiments, the deubiquitinase is MINDY1, MINDY2, MINDY3, or MINDY4. In some embodiments, the deubiquitinase is ZUP1. In some embodiments, the deubiquitinase is a Jab1/Mov34/Mpr1 Pad1 N-terminal+ (MPN+) (JAMM) domain protease.

[00175] In some embodiments, the deubiquitinase is a deubiquitinase described in Table 1. In some embodiments, the amino acid sequence of the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a deubiquitinase in Table 1. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a catalytic domain of a deubiquitinase in Table 1. In some embodiments, the effector domain comprises a functional fragment of a deubiquitinase in Table 1. In some embodiments, the effector domain deubiquitinase comprises a functional variant of deubiquitinase in Table 1. In some embodiments, the catalytic domain comprises a functional fragment of a catalytic domain of a deubiquitinase in Table 1. In some embodiments, the catalytic domain comprises a functional variant of a catalytic domain of a deubiquitinase in Table 1.

[00176] In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical any one of SEQ ID NOS: 1-112. In some embodiments, the deubiquitinase consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical any one of SEQ ID NOS: 1-112.

[00177] In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 2. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 3. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 4. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 5. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 6. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 7. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 8. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 9. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 10. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 11. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 12. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 13. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 14. In some

embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 15. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 16. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 17. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 18. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 19. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 20. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 21. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 22. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 23. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 24. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 25. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 26. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 27. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 28. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 29. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 30. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 31. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 32. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 33. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 34. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 35. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 36. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 37. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 38. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or

100% identical to SEQ ID NO: 39. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 40. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 41. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 42. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 43. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 44. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 45. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 46. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 47. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 48. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 49. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 50. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 51. In some embodiments, the deubiquitinase comprises an amino

acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 52. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 53. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 54. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 55. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 56. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 57. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 58. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 59. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 60. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 61. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 62. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 63. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 64. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 65. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 66. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 67. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 68. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 69. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 70. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 71. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 72. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 73. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 74. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 75. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 76. In some

embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 77. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 78. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 79. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 80. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 81. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 82. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 83. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 84. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 85. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 86. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 87. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 88. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 89. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 90. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 91. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 92. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 93. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 94. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 95. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 96. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 97. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 98. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 99. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 100. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or

100% identical to SEQ ID NO: 101. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 102. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 103. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 104. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 105. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 106. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 107. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 108. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 109. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 110. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 111. In some embodiments, the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 112.

[00178] In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the

catalytic domain of any one of SEQ ID NOS: 1-112. In some embodiments, the amino acid sequence of the effector domain consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of any one of SEQ ID NOS: 1-112.

[00179] In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 1. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 2. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 3. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 4. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 5. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 6. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 7. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino

acid sequence of the catalytic domain of SEQ ID NO: 8. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 9. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 10. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 11. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 12. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 13. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 14. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 15. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 16. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 17. In some embodiments, the amino acid

sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 18. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 19. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 20. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 21. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 22. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 23. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 24. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 25. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 26. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 27. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 28. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 29. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 30. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 31. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 32. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 33. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 34. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 35. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or

100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 36. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 37. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 38. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 39. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 40. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 41. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 42. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 43. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 44. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 45. In some

embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 46. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 47. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 48. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 49. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 50. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 51. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 52. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 53. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 54. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence

at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 55. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 56. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 57. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 58. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 59. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 60. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 61. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 62. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 63. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%,

95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 64. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 65. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 66. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 67. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 68. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 69. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 70. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 71. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 72. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain

of SEQ ID NO: 73. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 74. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 75. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 76. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 77. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 78. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 79. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 80. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 81. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 82. In some embodiments, the amino acid sequence of the effector domain

comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 83. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 84. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 85. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 86. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 87. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 88. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 89. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 90. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 91. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 92. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 93. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 94. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 95. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 96. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 97. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 98. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 99. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 100. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino

acid sequence of the catalytic domain of SEQ ID NO: 101. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 102. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 103. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 104. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 105. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 106. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 107. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 108. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 109. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 110. In some embodiments, the amino acid

sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 111. In some embodiments, the amino acid sequence of the effector domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of the catalytic domain of SEQ ID NO: 112.

[00180] In some embodiments, the catalytic domain is derived from a deubiquitinase that comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112.

[00181] In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 3. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 4. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 5. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an

amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 6. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 7. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 8. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 9. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 10. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 11. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 12. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 13. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 14. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 15. In some

embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 16. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 17. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 18. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 19. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 20. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 21. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 22. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 23. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 24. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 25. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 26. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 27. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 28. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 29. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 30. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 31. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 32. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 33. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 34. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%,

81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 35. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 36. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 37. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 38. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 39. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 40. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 41. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 42. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 43. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 44. In some embodiments, the catalytic

domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 45. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 46. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 47. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 48. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 49. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 50. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 51. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 52. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 53. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%

identical to the amino acid sequence of SEQ ID NO: 54. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 55. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 56. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 57. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 58. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 59. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 60. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 61. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 62. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 63. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%,

85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 64. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 65. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 66. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 67. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 68. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 69. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 70. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 71. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 72. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 73. In some embodiments, the catalytic domain is derived

from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 74. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 75. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 76. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 77. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 78. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 79. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 80. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 81. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 82. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the

amino acid sequence of SEQ ID NO: 83. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 84. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 85. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 86. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 87. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 88. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 89. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 90. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 91. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 92. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,

88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 93. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 94. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 95. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 96. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 97. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 98. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 99. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 100. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 101. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 102. In some embodiments, the catalytic domain is derived from a deubiquitinase

that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 102. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 104. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 105. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 106. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 107. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 108. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 109. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 110. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 111. In some embodiments, the catalytic domain is derived from a deubiquitinase that consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence

of SEQ ID NO: 112.

[00182] In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286. In some embodiments, the catalytic domain consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220.

[00183] In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 113. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 114. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 115. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 116. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 117. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 118. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 119. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 120. In some embodiments, the catalytic domain

comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 121. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 122. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 123. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 124. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 125. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 126. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 127. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 128. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 129. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 130. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 131. In some embodiments, the catalytic domain comprises an

amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 132. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 133. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 134. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 135. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 136. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 137. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 138. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 139. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 140. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 141. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 142. In some embodiments, the catalytic domain comprises an amino acid sequence

at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 143. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 144. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 145. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 146. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 147. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 148. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 149. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 150. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 151. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 152. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 153. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%,

82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 154. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 155. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 156. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 157. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 158. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 159. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 160. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 161. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 162. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 163. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 164. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%,

86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 165. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 166. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 167. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 168. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 169. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 170. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 171. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 172. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 173. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 174. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 175. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 176. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 177. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 178. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 179. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 180. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 181. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 182. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 183. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 184. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 185. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 186. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 187. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 188. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 189. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 190. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 191. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 192. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 193. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 194. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 195. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 196. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 197. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%,

95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 198. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 199. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 200. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 201. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 202. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 203. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 204. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 205. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 206. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 207. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 208. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%,

99%, or 100% identical to the amino acid sequence of SEQ ID NO: 209. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 210. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 211. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 212. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 213. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 214. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 215. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 216. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 217. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 218. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 219. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical

to the amino acid sequence of SEQ ID NO: 220. In some embodiments, the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286.

[00184] Table 1 below describes, the amino acid sequence of exemplary human deubiquitinases and exemplary catalytic domains of the exemplary human deubiquitinases. The catalytic domains are exemplary. A person of ordinary skill in the art could readily determine a sufficient amino acid sequence of a human deubiquitinase to mediate deubiquitination (e.g., a catalytic domain). Any of the human deubiquitinases (functional fragment or variants thereof) may be used to derive a catalytic domain for use in a fusion protein described herein.

Table 1. The amino acid sequence of exemplary human deubiquitinases and exemplary catalytic domains of the same

Description	SEQ ID NO	Amino Acid Sequence	SEQ ID NO	Exemplary Catalytic Domains (Amino Acid Sequence)
UBP27_HUMAN Ubiquitin carboxyl-terminal hydrolase 27	1	MCKDYVYDKDIEQIAKEEQGEALKLQASTSTEVSHQQCSVPGLGEKFPTWETTKPELELLGHNPRRRRITSSFTIGLRGLINLGNTCFMNCIVQALTHTPILRDFFLSDRHRCEMPSPELCLVCEMSSLFRELYSGNPSPHVPYKLLHLVWIHARHLAGYRQQDAHEFLIAALDVLHRHCKGDDVGKAANNPNHCNCIIDQIFTGGLQSDVTCQACHGVSTTIDPCWDISLDLPGSCTSFWPMSPGRESSVNGESHIPGITTLTDCLRRFTRPEHLGSSAKIKCGSCQSYQESTKQLTMNKLPVVACFHFKRFEHSAKQRRKITTYISFPLELDMTPFMASSKESRMNGQLQLPTNSGNNENKYSLFAVVNHQGTLESGHYTSFIRHHKDQWFKCDDAVITKASIKDVLDSEGYLLFYHKQVLEHESEKVKEMNTQAY	113	SSFTIGLRGLINLGNTCFMNCIVQALTHTPILRDFFLSDRHRCEMPSPELCLVCEMSSLFRELYSGNPSPHVPYKLLHLVWIHARHLAGYRQQDAHEFLIAALDVLHRHCKGDDVGKAANNPNHCNCIIDQIFTGGLQSDVTCQACHGVSTTIDPCWDISLDLPGSCTSFWPMSPGRESSVNGESHIPGITTLTDCLRRFTRPEHLGSSAKIKCGSCQSYQESTKQLTMNKLPVVACFHFKRFEHSAKQRRKITTYISFPLELDMTPFMASSKESRMNGQLQLPTNSGNNENKYSLFAVVNHQGTLESGHYTSFIRHHKDQWFKCDDAVITKASIKDVLDSEGYLLFYHKQVLEHESEKVKEMNTQAY
UBP48_HUMAN Ubiquitin carboxyl-terminal hydrolase 48	2	MAPRLQLEKAAWRWAETVRPEEVSQEHIETAYRIWLEPCIRGVCRRNCKGNPNCLVGIGEHIWLGEIDENSFHNIDDPNCERRKKNSFVGLTNLGATCYVNTFLQVWFLNLELRQALYLCPSTCSDYMLGDGIQEEKDYEPQTICEHLQYLFALLQNSNRRYIDPSGFVKALGLDTGQQQDAQEFSKLFMSLLEDTLSKQKNPDVRNIVQQQFCGEYAYV	114	NSFHNIDDPNCERRKKNSFVGLTNLGATCYVNTFLQVWFLNLELRQALYLCPSTCSDYMLGDGIQEEKDYEPQTICEHLQYLFALLQNSNRRYIDPSGFVKALGLDTGQQQDAQEFSKLFMSLLEDTLSKQKNPDVRNIVQQQFCGEYAYVTVCNQCGRESKLLSKFYELELNIQGHKQLTDCISEFLKEEKLEGDNRYF

		TVCNQCGRESKLLSKFYELELN IQGHKQLTDCISEFLKEEKLEG DNRYFCENCQSKQNATRKIRLL SLPCTLNLQLMRFVFDRQTGHK KKLNTYIGFSEILDMEPYVEHK GGSYVYELSAVLIHRGVSAYSG HYIAHVKDPQSGEWYKFNDEDI EKMEGKKLQLGIEEDLAEPSKS QTRKPKCGKGTHCSRNAYMLVY RLQTQEKPNTTVQVPAFLQELV DRDNSKFEEWCIEMAEMRKQSV DKGKAKHEEVKELYQRLPAGAE PYEFVSLEWLQKWLDESTPTKP IDNHACLCSHDKLHPDKISIMK RISEYAADIFYSRYGGGPRLTV KALCKECVVERCRILRLKNQLN EDYKTVNNLLKAAVKGSDGFWV GKSSLRSWRQLALEQLDEQDGD AEQSNGKMNGSTLNKDESKEER KEEEELNFNEDILCPHGELCIS ENERRLVSKEAWSKLQQYFPKA PEFPSYKECCSQCKILEREGEE NEALHKMIANEQKTSLPNLFQD KNRPCLSNWPEDTDVLYIVSQF FVEEWRKFVRKPTRCSPVSSVG NSALLCPHGGLMFTFASMTKED SKLIALIWPSEWQMIQKLFVVD HVIKITRIEVGDVNPSETQYIS EPKLCPECREGLLCQQQRDLRE YTQATIYVHKVVDNKKVMKDSA PELNVSSSETEEDKEEAKPDGE KDPDFNQSNGGTKRQKISHQNY IAYQKQVIRRSMRHRKVRGEKA LLVSANQTLKELKIQIMHAFSV APFDQNLSIDGKILSDDCATLG TLGVIPESVILLKADEPIADYA AMDDVMQVCMPEEGFKGTGLLG H		CENCQSKQNATRKIRLLSLP CTLNLQLMRFVFDRQTGHKK KLNTYIGFSEILDMEPYVEH KGGSYVYELSAVLIHRGVSA YSGHYIAHVKDPQSGEWYKF NDEDIEKMEGKKLQLGIEED LAEPSKSQTRKPKCGKGTHC SRNAYMLVYRLQT
UBP3_HUMAN Ubiquitin carboxyl-terminal hydrolase 3	3	MECPHLSSSVCIAPDSAKFPNG SPSSWCCSVCRSNKSPWVCLTC SSVHCGRYVNGHAKKHYEDAQV PLTNHKKSEKQDKVQHTVCMDC SSYSTYCYRCDDFVVNDTKLGL VQKVREHLQNLENSAFTADRHK KRKLLENSTLNSKLLKVNGSTT AICATGLRNLGNTCFMNAILQS LSNIEQFCCYFKELPAVELRNG KTAGRRTYHTRSQGDNNVSLVE EFRKTLCALWQGSQTAFSPESL FYVVWKIMPNFRGYQQQDAHEF MRYLLDHLHLELQGGFNGVSRS	115	TAICATGLRNLGNTCFMNAI LQSLSNIEQFCCYFKELPAV ELRNGKTAGRRTYHTRSQGD NNVSLVEEFRKTLCALWQGS QTAFSPESLFYVVWKIMPNF RGYQQQDAHEFMRYLLDHLH LELQGGFNGVSRSAILQENS TLSASNKCCINGASTVVTAI FGGILQNEVNCLICGTESRK FDPFLDLSLDIPSQFRSKRS KNQENGPVCSLRDCLRSFTD LEELDETELYMCHKCKKKQK STKKFWIQKLPKVLCLHLKR

		AILQENSTLSASNKCCINGAST VVTAIFGGILQNEVNCLICGTE SRKFDPFLDLSLDIPSQFRSKR SKNQENGPVCSLRDCLRSFTDL EELDETELYMCHKCKKKQKSTK KFWIQKLPKVLCLHLKRFHWTA YLRNKVDTYVEFPLRGLDMKCY LLEPENSGPESCLYDLAAVVVH HGSGVGSGHYTAYATHEGRWFH FNDSTVTLTDEETVVKAKAYIL FYVEHQAKAGSDKL		FHWTAYLRNKVDTYVEFPLR GLDMKCYLLEPENSGPESCL YDLAAVVVHHGSGVGSGHYT AYATHEGRWFHFNDSTVTLT DEETVVKAKAYILFYVEHQ
U17LB_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 11	4	QLAPREKLPLSSRRPAAVGAGL QNMGNTCYVNASLQCLTYTPPL ANYMLSREHSQTCHRHKGCMLC TMQAHITRALHNPGHVIQPSQA LAAGFHRGKQEDAHEFLMFTVD AMKKACLPGHKQVDHHSKDTTL IHQIFGGYWRSQIKCLHCHGIS DTFDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGVCL QRAPASKTLTLHTSAKVLILVL KRFSDVTGNKIAKNVQYPECLD MQPYMSQTNTGPLVYVLYAVLV HAGWSCHNGHYFSYVKAQEGQW YKMDDAEVTASSITSVLSQQAY VLFYIQKSEWERHSESVSRGRE PRALGAEDTDRRATQGELKRDH PCLQAPELDEHLVERATQESTL DHWKFLQEQNKTKPEFNVRKVE GTLPPDVLVIHQSKYKCGMKNH HPEQQSSLLNLSSTTPTHQESM NTGTLASLRGRARRSKGKNKHS KRALLVCQ	116	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQTNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS
UBP1_HUMAN Ubiquitin carboxyl-terminal hydrolase 1	5	MPGVIPSESNGLSRGSPSKKNR LSLKFFQKKETKRALDFTDSQE NEEKASEYRASEIDQVVPAAQS SPINCEKRENLLPFVGLNNLGN TCYLNSILQVLYFCPGFKSGVK HLFNIISRKKEALKDEANQKDK GNCKEDSLASYELICSLQSLII SVEQLQASFLLNPEKYTDELAT QPRRLLNTLRELNPMYEGYLQH DAQEVLQCILGNIQETCQLLKK EEVKNVAELPTKVEEIPHPKEE MNGINSIEMDSMRHSEDFKEKL PKGNGKRKSDTEFGNMKKKVKL SKEHQSLEENQRQTRSKRKATS DTLESPPKIIPKYISENESPRP SQKKSRVKINWLKSATKQPSIL SKFCSLGKITTNQGVKGQSKEN ECDPEEDLGKCESDNTTNGCGL	117	LPFVGLNNLGNTCYLNSILQ VLYFCPGFKSGVKHLFNIIS RKKEALKDEANQKDKGNCKE DSLASYELICSLQSLIISVE QLQASFLLNPEKYTDELATQ PRRLLNTLRELNPMYEGYLQ HDAQEVLQCILGNIQETCQL LKKEEVKNVAELPTKVEEIP HPKEEMNGINSIEMDSMRHS EDFKEKLPKGNGKRKSDTEF GNMKKKVKLSKEHQSLEENQ RQTRSKRKATSDTLESPPKI IPKYISENESPRPSQKKSRV KINWLKSATKQPSILSKFCS LGKITTNQGVKGQSKENECD PEEDLGKCESDNTTNGCGLE SPGNTVTPVNVNEVKPINKG EEQIGFELVEKLFQGQLVLR

		ESPGNTVTPVNVNEVKPINKGE EQIGFELVEKLFQGQLVLRTRC LECESLTERREDFQDISVPVQE DELSKVEESSEISPEPKTEMKT LRWAISQFASVERIVGEDKYFC ENCHHYTEAERSLLFDKMPEVI TIHLKCFAASGLEFDCYGGGLS KINTPLLTPLKLSLEEWSTKPT NDSYGLFAVVMHSGITISSGHY TASVKVTDLNSLELDKGNFVVD QMCEIGKPEPLNEEEARGVVEN YNDEEVSIRVGGNTQPSKVLNK KNVEAIGLLGGQKSKADYELYN KASNPDKVASTAFAENRNSETS DTTGTHESDRNKESSDQTGINI SGFENKISYVVQSLKEYEGKWL LFDDSEVKVTEEKDFLNSLSPS TSPTSTPYLLFYKKL		TRCLECESLTERREDFQDIS VPVQEDELSKVEESSEISPE PKTEMKTLRWAISQFASVER IVGEDKYFCENCHHYTEAER SLLFDKMPEVITIHLKCFAA SGLEFDCYGGGLSKINTPLL TPLKLSLEEWSTKPTNDSYG LFAVVMHSGITISSGHYTAS VKVTDLNSLELDKGNFVVDQ MCEIGKPEPLNEEEARGVVE NYNDEEVSIRVGGNTQPSKV LNKKNVEAIGLLGGQKSKAD YELYNKASNPDKVASTAFAE NRNSETSDTTGTHESDRNKE SSDQTGINISGFENKISYVV QSLKEYEGKWLLFDDSEVKV TEEKDFLNSLSPSTSPTSTP YLLFYKKL
UBP40_HUMAN Ubiquitin carboxyl-terminal hydrolase 40	6	MFGDLFEEEYSTVSNNQYGKGK KLKTKALEPPAPREFTNLSGIR NQGGTCYLNSLLQTLHFTPEFR EALFSLGPEELGLFEDKDKPDA KVRIIPLQLQRLFAQLLLLDQE AASTADLTDSFGWTSNEEMRQH DVQELNRILFSALETSLVGTSG HDLIYRLYHGTIVNQIVCKECK NVSERQEDFLDLTVAVKNVSGL EDALWNMYVEEEVFDCDNLYHC GTCDRLVKAAKSAKLRKLPPFL TVSLLRFNFDFVKCERYKETSC YTFPLRINLKPFCEQSELDDLE YIYDLFSVIIHKGGCYGGHYHV YIKDVDHLGNWQFQEEKSKPDV NLKDLQSEEEIDHPLMILKAIL LEENNLIPVDQLGQKLLKKIGI SWNKKYRKQHGPLRKFLQLHSQ IFLLSSDESTVRLLKNSSLQAE SDFQRNDQQIFKMLPPESPGLN NSISCPHWFDINDSKVQPIREK DIEQQFQGKESAYMLFYRKSQL QRPPEARANPRYGVPCHLLNEM DAANIELQTKRAECDSANNTFE LHLHLGPQYHFFNGALHPVVSQ TESVWDLTFDKRKTLGDLRQSI FQLLEFWEGDMVLSVAKLVPAG LHIYQSLGGDELTLCETEIADG EDIFVWNGVEVGGVHIQTGIDC EPLLLNVLHLDTSSDGEKCCQV IESPHVFPANAEVGTVLTALAI PAGVIFINSAGCPGGEGWTAIP KEDMRKTFREQGLRNGSSILIQ	118	FTNLSGIRNQGGTCYLNSLL QTLHFTPEFREALFSLGPEE LGLFEDKDKPDAKVRIIPLQ LQRLFAQLLLLDQEAASTAD LTDSFGWTSNEEMRQHDVQE LNRILFSALETSLVGTSGHD LIYRLYHGTIVNQIVCKECK NVSERQEDFLDLTVAVKNVS GLEDALWNMYVEEEVFDCDN LYHCGTCDRLVKAAKSAKLR KLPPFLTVSLLRFNFDFVKC ERYKETSCYTFPLRINLKPF CEQSELDDLEYIYDLFSVII HKGG CYGGHYHVYIKDVDHLGNWQ FQEEKSKPDVNLKDLQSEEE IDHPLMILKAILLEENNLIP VDQLGQKLLKKIGISWNKKY RKQHGPLRKFLQLHSQIFLL SSDESTVRLLKNSSLQAESD FQRNDQQIFKMLPPESPGLN NSISCPHWFDINDSKVQPIR EKDIEQQFQGKESAYMLFYR KSQLQRPPEARANPRYGVPC HLLNEMDAANIELQTKRAEC DSANNTFELHLHLGPQYHFF NGALHPVVSQTESVWDLTFD KRKTLGDLRQSIFQLLEFWE GDMVLSVAKLVPAGLHIYQS LGGDELTLCETEIADGEDIF VWNGVEVGGVHIQTGIDCEP LLLNVLHLDTSSDGEKCCQV IESPHVFPANAEVGTVLTAL

		DSHDDNSLLTKEEKWVTSMNEI DWLHVKNLCQLESEEKQVKISA TVNTMVFDIRIKAIKELKLMKE LADNSCLRPIDRNGKLLCPVPD SYTLKEAELKMGSSLGLCLGKA PSSSQLFLFFAMGSDVQPGTEM EIVVEETISVRDCLKLMLKKSG LQGDAWHLRKMDWCYEAGEPLC EEDATLKELLICSGDTLLLIEG QLPPLGFLKVPIWWYQLQGPSG HWESHQDQTNCTSSWGRVWRAT SSQGASGNEPAQVSLLYLGDIE ISEDATLAELKSQAMTLPPFLE FGVPSPAHLRAWTVERKRPGRL LRTDRQPLREYKLGRRIEICLE PLQKGENLGPQDVLLRTQVRIP GERTYAPALDLVWNAAQGGTAG SLRQRVADFYRLPVEKIEIAKY FPEKFEWLPISSWNQQITKRKK KKKQDYLQGAPYYLKDGDTIGV KNLLIDDDDDFSTIRDDTGKEK QKQRALGRRKSQEALHEQSSYI LSSAETPARPRAPETSLSIHVG SFR		AIPAGVIFINSAGCPGGEGW TAIPKEDMRKTFREQGLRNG SSILIQDSHDDNSLLTKEEK WVTSMNEIDWLHVKNLCQLE SEEKQVKISATVNTMVFDIR IKAIKELKLMKELADNSCLR PIDRNGKLLCPVPDSYTLKE AELKMGSSLGLCLGKAPSSS QLFLFFAMGSDVQPGTEMEI VVEETISVRDCLKLMLKKSG LQGDAWHLRKMDWCYEAGEP LCEEDATLKELLICSGDTLL LIEGQLPPLGFLKVPIWWYQ LQGPSGHWESHQDQTNCTSS WGRVWRATSSQGASGNEPAQ VSLLYLGDIEISEDATLAEL KSQAMTLPPFLEFGVPSPAH LRAWTVERKRPGRLLRTDRQ PLREYKLGRRIEICLEPLQK GENLGPQDVLLRTQVRIPGE RTYAPALDLVWNAAQGGTAG SLRQRVADFYRLPVEKIEIA KYFPEKFEWLPISSWNQQIT KRKKKKKQDYLQGAPYYLKD GDTIGVKNLLIDDDDDFSTI RDDTGKEKQKQRALGRRKSQ
UBP7_HUMAN Ubiquitin carboxyl-terminal hydrolase 7	7	MNHQQQQQQQKAGEQQLSEPED MEMEAGDTDDPPRITQNPVING NVALSDGHNTAEEDMEDDTSWR SEATFQFTVERFSRLSESVLSP PCFVRNLPWKIMVMPRFYPDRP HQKSVGFFLQCNAESDSTSWSC HAQAVLKIINYRDDEKSFSRRI SHLFFHKENDWGFSNFMAWSEV TDPEKGFIDDDKVTFEVFVQAD APHGVAWDSKKHTGYVGLKNQG ATCYMNSLLQTLFFTNQLRKAV YMMPTEGDDSSKSVPLALQRVF YELQHSDKPVGTKKLTKSFGWE TLDSFMQHDVQELCRVLLDNVE NKMKGTCVEGTIPKLFRGKMVS YIQCKEVDYRSDRREDYYDIQL SIKGKKNIFESFVDYVAVEQLD GDNKYDAGEHGLQEAEKGVKFL TLPPVLHLQLMRFMYDPQTDQN IKINDRFEFPEQLPLDEFLQKT DPKDPANYILHAVLVHSGDNHG GHYVVYLNPKGDGKWCKFDDDV VSRCTKEEAIEHNYGGHDDDLS VRHCTNAYMLVYIRESKLSEVL QAVTDHDIPQQLVERLQEEKRI	119	TGYVGLKNQGATCYMNSLLQ TLFFTNQLRKAVYMMPTEGD DSSKSVPLALQRVFYELQHS DKPVGTKKLTKSFGWETLDS FMQHDVQELCRVLLDNVENK MKGTCVEGTIPKLFRGKMVS YIQCKEVDYRSDRREDYYDI QLSIKGKKNIFESFVDYVAV EQLDGDNKYDAGEHGLQEAE KGVKFLTLPPVLHLQLMRFM YDPQTDQNIKINDRFEFPEQ LPLDEFLQKTDPKDPANYIL HAVLVHSGDNHGGHYVVYLN PKGDGKWCKFDDDVVSRCTK EEAIEHNYGGHDDDLSVRHC TNAYMLVYIRE

		EAQKRKERQEAHLYMQVQIVAE DQFCGHQGNDMYDEEKVKYTVF KVLKNSSLAEFVQSLSQTMGFP QDQIRLWPMQARSNGTKRPAML DNEADGNKTMIELSDNENPWTI FLETVDPELAASGATLPKFDKD HDVMLFLKMYDPKTRSLNYCGH IYTPISCKIRDLLPVMCDRAGF IQDTSLILYEEVKPNLTERIQD YDVSLDKALDELMDGDIIVFQK DDPENDNSELPTAKEYFRDLYH RVDVIFCDKTIPNDPGFVVTLS NRMNYFQVAKTVAQRLNTDPML LQFFKSQGYRDGPGNPLRHNYE GTLRDLLQFFKPRQPKKLYYQQ LKMKITDFENRRSFKCIWLNSQ FREEEITLYPDKHGCVRDLLEE CKKAVELGEKASGKLRLLEIVS YKIIGVHQEDELLECLSPATSR TFRIEEIPLDQVDIDKENEMLV TVAHFHKEVFGTFGIPFLLRIH QGEHFREVMKRIQSLLDIQEKE FEKFKFAIVMMGRHQYINEDEY EVNLKDFEPQPGNMSHPRPWLG LDHFNKAPKRSRYTYLEKAIKI HN		
U17L5_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 5	8	MEDDSLYLRGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLAK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPECLDMQPYMS QPNTGPLVYVLYAVLVHAGWSC HNGHYFSYVKAQEGQWYKMDDA EVTASSITSVLSQQAYVLFYIQ KSEWERHSESVSRGREPRALGA EDTDRRATQGELKRDHPCLQAP ELDEHLVERATQESTLDHWKFL QEQNKTKPEFNVRKVEGTLPPD VLVIHQSKYKCGMKNHHPEQQS SLLNLSSSTPTHQESMNTGTLA SLRGRARRSKGKNKHSKRALLV CQ	120	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLAKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQPNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS EWERHSESVSRGREPRALGA EDTDRRATQGELKRDHPCLQ APEL

U17LL_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 21	9	MEEDSLYLGGEWQFNHFSKLTSSRPDAAFAEIQRTSLPEKSPLSCETRVDLCDDLAPVARQLAPREKLPLSNRRPAAVGAGLQNMGNTCYVNASLQCLTYTPPLANYMLSREHSQTCHRHKGCMLCTMQAHITRALHNPGHVIQPSQALAAGFHRGKQEDAHEFLMFTVDAMKKACLPGHKQVDHHSKDTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAYHCGVCLQRAPASKMLTLLTSAKVLILVLKRFSDVTGNKIAKNVQYPECLDMQPYMSQPNTGPLVYVLYAVLVHAGWSCHNGHYFSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKSEWERHSESVSRGREPRALGAEDTDRRATQGELKRDHPCLQAPEL	121	AVGAGLQNMGNTCYVNASLQCLTYTPPLANYMLSREHSQTCHRHKGCMLCTMQAHITRALHNPGHVIQPSQALAAGFHRGKQEDAHEFLMFTVDAMKKACLPGHKQVDHHSKDTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAYHCGVCLQRAPASKMLTLLTSAKVLILVLKRFSDVTGNKIAKNVQYPECLDMQPYMSQPNTGPLVYVLYAVLVHAGWSCHNGHYFSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKSEWERHSESVSRGREPRALGAEDTDRRATQGELKRDHPCLQAPEL
U17LA_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 10	10	MEDDSLYLGGEWQFNHFSKLTSSRPDAAFAEIQRTSLPEKSPLSCETRVDLCDDLAPVARQLAPREKPPLSSRRPAAVGAGLQNMGNTCYVNASLQCLTYKPPLANYMLFREHSQTCHRHKGCMLCTMQAHITRALHIPGHVIQPSQALAAGFHRGRGKQEDAHEFLMFTVDAMRKACLPGHKQVDRHSKDTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAYHCGVCLQRAPASKTLTLHNSAKVLILVLKRFPDVTGNKIAKNVQYPECLDMQPYMSQQNTGPLVYVLYAVLVHAGWSCHNGHYSSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKSEWERHSESVSRGREPRALGVEDTDRRATQGELKRDHPCLQAPELDEHLVERATQESTLDHWKFLQEQNKTKPEFNVRKVEGTLPPDVLVIHQSKYKCGMKNHHPEQQSSLLNLSSSTPTHQESMNTGTLASLRGRARRSKGKNKHSKRALLVCQ	122	AVGAGLQNMGNTCYVNASLQCLTYKPPLANYMLFREHSQTCHRHKGCMLCTMQAHITRALHIPGHVIQPSQALAAGFHRGKQEDAHEFLMFTVDAMRKACLPGHKQVDRHSKDTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAYHCGVCLQRAPASKTLTLHNSAKVLILVLKRFPDVTGNKIAKNVQYPECLDMQPYMSQQNTGPLVYVLYAVLVHAGWSCHNGHYSSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKSEWERHSESVSRGREPRALGVEDTDRRATQGELKRDHPCLQAPEL
U17LA_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 10	10	MEDDSLYLGGEWQFNHFSKLTSSRPDAAFAEIQRTSLPEKSPLSCETRVDLCDDLAPVARQLAPREKPPLSSRRPAAVGAGLQNMGNTCYVNASLQCLTYKPPLANYMLFREHSQTCHRHKGCMLCTMQAHITRALHIPGHVIQPSQALAAGFHRGKQEDAHEFLMFTVDAMRKACLPGHKQVDRHSKDTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAYHCGVCLQRAPASKTLTLHNSAKVLILVLKRFPDVTGNKIAKNVQYPECLDMQPYMSQQNTGPLVYVLYAVLVHAGWSCHNGHYSSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKSEWERHSESVSRGREPRALGVEDTDRRATQGELKRDHPCLQAPELDEHLVERATQESTLDHWKFLQEQNKTKPEFNVRRVEGTVPPDVLVIHQSKYKCRMKNHHPEQQSSLLNLSSTTPTDQESMNTGTLASLRGRTRRSKGKNKHSKRALLVCQ	122	AVGAGLQNMGNTCYVNASLQCLTYKPPLANYMLFREHSQTCHRHKGCMLCTMQAHITRALHIPGHVIQPSQALAAGFHRGKQEDAHEFLMFTVDAMRKACLPGHKQVDRHSKDTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAYHCGVCLQRAPASKTLTLHNSAKVLILVLKRFPDVTGNKIAKNVQYPECLDMQPYMSQQNTGPLVYVLYAVLVHAGWSCHNGHYSSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKSEWERHSESVSRGREPRALGVEDTDRRATQGELKRDHPCLQAPEL

UBP41_HUMAN Putative ubiquitin carboxyl-terminal hydrolase 41	11	MDGVLFRAHQCQYVHPCVHVYV TVGLMDPLCERKEKASKQEREN PLAHLAAWGLVGLHNIGQTCCL NSLIQVFVMNVDFARILKRITV PRGADEQRRSVPFQMLLLLEKM QDSRQKAVWPLELAYCLQKYNV PLFVQHDAAQLYLKLWNLIKDQ IADVHLVERLQALYMIRMKDSL ICLDCAMESSRNSSMLTLRLSF FDVDSKPLKTLEDALHCFFQPR ELSSKSKCFCENCGKKTRGKQV LKLTHLPQTLTIHLMRFSIRNS QTRKICHSLYFPQSLDFSQILP MKRESCDAEEQSGGQYELFAVI AHVGMADSGHYCVYIRNAVDGK WFCFNDSNICLVSWEDIQCTYG NPNYHW	123	WGLVGLHNIGQTCCLNSLIQ VFVMNVDFARILKRITVPRG ADEQRRSVPFQMLLLLEKMQ DSRQKAVWPLELAYCLQKYN VPLFVQHDAAQLYLKLWNLI KDQIADVHLVERLQALYMIR MKDSLICLDCAMESSRNSSM LTLRLSFFDVDSKPLKTLED ALHCFFQPRELSSKSKCFCE NCGKKTRGKQVLKLTHLPQT LTIHLMRFSIRNSQTRKICH SLYFPQSLDFSQILPMKRES CDAEEQSGGQYELFAVIAHV GMADSGHYCVYIRNAVDGKW FCFNDSNICLVSWEDIQCTY GNPNYHW
UBP38_HUMAN Ubiquitin carboxyl-terminal hydrolase 38	12	MDKILEGLVSSSHPLPLKRVIV RKVVESAEHWLDEAQCEAMFDL TTRLILEGQDPFQRQVGHQVLE AYARYHRPEFESFFNKTFVLGL LHQGYHSLDRKDVAILDYIHNG LKLIMSCPSVLDLFSLLQVEVL RMVCERPEPQLCARLSDLLTDF VQCIPKGKLSITFCQQLVRTIG HFQCVSTQERELREYVSQVTKV SNLLQNIWKAEPATLLPSLQEV FASISSTDASFEPSVALASLVQ HIPLQMITVLIRSLTTDPNVKD ASMTQALCRMIDWLSWPLAQHV DTWVIALLKGLAAVQKFTILID VTLLKIELVFNRLWFPLVRPGA LAVLSHMLLSFQHSPEAFHLIV PHVVNLVHSFKNDGLPSSTAFL VQLTELIHCMMYHYSGFPDLYE PILEAIKDFPKPSEEKIKLILN QSAWTSQSNSLASCLSRLSGKS ETGKTGLINLGNTCYMNSVIQA LFMATDFRRQVLSLNLNGCNSL MKKLQHLFAFLAHTQREAYAPR IFFEASRPPWFTPRSQQDCSEY LRFLLDRLHEEEKILKVQASHK PSEILECSETSLQEVASKAAVL TETPRTSDGEKTLIEKMFGGKL RTHIRCLNCRSTSQKVEAFTDL SLAFCPSSSLENMSVQDPASSP SIQDGGLMQASVPGPSEEPVVY NPTTAAFICDSLVNEKTIGSPP NEFYCSENTSVPNESNKILVNK DVPQKPGGETTPSVTDLLNYFL APEILTGDNQYYCENCASLQNA	124	SETGKTGLINLGNTCYMNSV IQALFMATDFRRQVLSLNLN GCNSLMKKLQHLFAFLAHTQ REAYAPRIFFEASRPPWFTP RSQQDCSEYLRFLLDRLHEE EKILKVQASHKPSEILECSE TSLQEVASKAAVLTETPRTS DGEKTLIEKMFGGKLRTHIR CLNCRSTSQKVEAFTDLSLA FCPSSSLENMSVQDPASSPS IQDGGLMQASVPGPSEEPVV YNPTTAAFICDSLVNEKTIG SPPNEFYCSENTSVPNESNK ILVNKDVPQKPGGETTPSVT DLLNYFLAPEILTGDNQYYC ENCASLQNAEKTMQITEEPE YLILTLLRFSYDQKYHVRRK ILDNVSLPLVLELPVKRITS FSSLSESWSVDVDFTDLSEN LAKKLKPSGTDEASCTKLVP YLLSSVVVHSGISSESGHYY SYARNITSTDSSYQMYHQSE ALALASSQSHLLGRDSPSAV FEQDLENKEMSKEWFLFNDS RVTFTSFQSVQKITSRFPKD TAYVLLYKKQH

		EKTMQITEEPEYLILTLLRFSY DQKYHVRRKILDNVSLPLVLEL PVKRITSFSSLSESWSVDVDFT DLSENLAKKLKPSGTDEASCTK LVPYLLSSVVVHSGISSESGHY YSYARNITSTDSSYQMYHQSEA LALASSQSHLLGRDSPSAVFEQ DLENKEMSKEWFLFNDSRVTFT SFQSVQKITSRFPKDTAYVLLY KKQHSTNGLSGNNPTSGLWING DPPLQKELMDAITKDNKLYLQE QELNARARALQAASASCSFRPN GFDDNDPPGSCGPTGGGGGGGF NTVGRLVF		
UBP43_HUMAN Ubiquitin carboxyl-terminal hydrolase 43	13	MDLGPGDAAGGGPLAPRPRRRR SLRRLFSRFLLALGSRSRPGDS PPRPQPGHCDGDGEGGFACAPG PVPAAPGSPGEERPPGPQPQLQ LPAGDGARPPGAQGLKNHGNTC FMNAVVQCLSNTDLLAEFLALG RYRAAPGRAEVTEQLAALVRAL WTREYTPQLSAEFKNAVSKYGS QFQGNSQHDALEFLLWLLDRVH EDLEGSSRGPVSEKLPPEATKT SENCLSPSAQLPLGQSFVQSHF QAQYRSSLTCPHCLKQSNTFDP FLCVSLPIPLRQTRFLSVTLVF PSKSQRFLRVGLAVPILSTVAA LRKMVAEEGGVPADEVILVELY PSGFQRSFFDEEDLNTIAEGDN VYAFQVPPSPSQGTLSAHPLGL SASPRLAAREGQRFSLSLHSES KVLILFCNLVGSGQQASRFGPP FLIREDRAVSWAQLQQSILSKV RHLMKSEAPVQNLGSLFSIRVV GLSVACSYLSPKDSRPLCHWAV DRVLHLRRPGGPPHVKLAVEWD SSVKERLFGSLQEERAQDADSV WQQQQAHQQHSCTLDECFQFYT KEEQLAQDDAWKCPHCQVLQQG MVKLSLWTLPDILIIHLKRFCQ VGERRNKLSTLVKFPLSGLNMA PHVAQRSTSPEAGLGPWPSWKQ PDCLPTSYPLDFLYDLYAVCNH HGNLQGGHYTAYCRNSLDGQWY SYDDSTVEPLREDEVNTRGAYI LFYQKRNSIPPWSASSSMRGST SSSLSDHWLLRLGSHAGSTRGS LLSWSSAPCPSLPQVPDSPIFT NSLCNQEKGGLEPRRLVRGVKG RSISMKAPTTSRAKQGPFKTMP	125	RPPGAQGLKNHGNTCFMNAV VQCLSNTDLLAEFLALGRYR AAPGRAEVTEQLAALVRALW TREYTPQLSAEFKNAVSKYG SQFQGNSQHDALEFLLWLLD RVHEDLEGSSRGPVSEKLPP EATKTSENCLSPSAQLPLGQ SFVQSHFQAQYRSSLTCPHC LKQSNTFDPFLCVSLPIPLR QTRFLSVTLVFPSKSQRFLR VGLAVPILSTVAALRKMVAE EGGVPADEVILVELYPSGFQ RSFFDEEDLNTIAEGDNVYA FQVPPSPSQGTLSAHPLGLS ASPRLAAREGQRFSLSLHSE SKVLILFCNLVGSGQQASRF GPPFLIREDRAVSWAQLQQS ILSKVRHLMKSEAPVQNLGS LFSIRVVGLSVACSYLSPKD SRPLCHWAVDRVLHLRRPGG PPHVKLAVEWDSSVKERLFG SLQEERAQDADSVWQQQQAH QQHSCTLDECFQFYTKEEQL AQDDAWKCPHCQVLQQGMVK LSLWTLPDILIIHLKRFCQV GERRNKLSTLVKFPLSGLNM APHVAQRSTSPEAGLGPWPS WKQPDCLPTSYPLDFLYDLY AVCNHHGNLQGGHYTAYCRN SLDGQWYSYDDSTVEPLRED EVNTRGAYILFYQKRN

		LRWSFGSKEKPPGASVELVEYL ESRRRPRSTSQSIVSLLTGTAG EDEKSASPRSNVALPANSEDGG RAIERGPAGVPCPSAQPNHCLA PGNSDGPNTARKLKENAGQDIK LPRKFDLPLTVMPSVEHEKPAR PEGQKAMNWKESFQMGSKSSPP SPYMGFSGNSKDSRRGTSELDR PLQGTLTLLRSVFRKKENRRNE RAEVSPQVPPVSLVSGGLSPAM DGQAPGSPPALRIPEGLARGLG SRLERDVWSAPSSLRLPRKASR APRGSALGMSQRTVPGEQASYG TFQRVKYHTLSLGRKKTLPESS F		
UBP2_HUMAN Ubiquitin carboxyl-terminal hydrolase 2	14	MSQLSSTLKRYTESARYTDAHY AKSGYGAYTPSSYGANLAASLL EKEKLGFKPVPTSSFLTRPRTY GPSSLLDYDRGRPLLRPDITGG GKRAESQTRGTERPLGSGLSGG SGFPYGVTNNCLSYLPINAYDQ GVTLTQKLDSQSDLARDFSSLR TSDSYRIDPRNLGRSPMLARTR KELCTLQGLYQTASCPEYLVDY LENYGRKGSASQVPSQAPPSRV PEIISPTYRPIGRYTLWETGKG QAPGPSRSSSPGRDGMNSKSAQ GLAGLRNLGNTCFMNSILQCLS NTRELRDYCLQRLYMRDLHHGS NAHTALVEEFAKLIQTIWTSSP NDVVSPSEFKTQIQRYAPRFVG YNQQDAQEFLRFLLDGLHNEVN RVTLRPKSNPENLDHLPDDEKG RQMWRKYLEREDSRIGDLFVGQ LKSSLTCTDCGYCSTVFDPFWD LSLPIAKRGYPEVTLMDCMRLF TKEDVLDGDEKPTCCRCRGRKR CIKKFSIQRFPKILVLHLKRFS ESRIRTSKLTTFVNFPLRDLDL REFASENTNHAVYNLYAVSNHS GTTMGGHYTAYCRSPGTGEWHT FNDSSVTPMSSSQVRTSDAYLL FYELASPPSRM	126	SAQGLAGLRNLGNTCFMNSI LQCLSNTRELRDYCLQRLYM RDLHHGSNAHTALVEEFAKL IQTIWTSSPNDVVSPSEFKT QIQRYAPRFVGYNQQDAQEF LRFLLDGLHNEVNRVTLRPK SNPENLDHLPDDEKGRQMWR KYLEREDSRIGDLFVGQLKS SLTCTDCGYCSTVFDPFWDL SLPIAKRGYPEVTLMDCMRL FTKEDVLDGDEKPTCCRCRG RKRCIKKFSIQRFPKILVLH LKRFSESRIRTSKLTTFVNF PLRDLDLREFASENTNHAVY NLYAVSNHSGTTMGGHYTAY CRSPGTGEWHTFNDSSVTPM SSSQVRTSDAYLLFYELAS
UBP45_HUMAN Ubiquitin carboxyl-terminal hydrolase 45	15	MRVKDPTKALPEKAKRSKRPTV PHDEDSSDDIAVGLTCQHVSHA ISVNHVKRAIAENLWSVCSECL KERRFYDGQLVLTSDIWLCLKC GFQGCGKNSESQHSLKHFKSSR TEPHCIIINLSTWIIWCYECDE KLSTHCNKKVLAQIVDFLQKHA SKTQTSAFSRIMKLCEEKCETD	127	LSVRGITNLGNTCFFNAVMQ NLAQTYTLTDLMNEIKESST KLKIFPSSDSQLDPLVVELS RPGPLTSALFLFLHSMKETE KGPLSPKVLFNQLCQKAPRF KDFQQQDSQELLHYLLDAVR TEETKRIQASILKAFNNPTT KTADDETRKKVKAYGKEGVK

		EIQKGGKCRNLSVRGITNLGNT CFFNAVMQNLAQTYTLTDLMNE IKESSTKLKIFPSSDSQLDPLV VELSRPGPLTSALFLFLHSMKE TEKGPLSPKVLFNQLCQKAPRF KDFQQQDSQELLHYLLDAVRTE ETKRIQASILKAFNNPTTKTAD DETRKKVKAYGKEGVKMNFIDR IFIGELTSTVMCEECANISTVK DPFIDISLPIIEERVSKPLLWG RMNKYRSLRETDHDRYSGNVTI ENIHQPRAAKKHSSSKDKSQLI HDRKCIRKLSSGETVTYQKNEN LEMNGDSLMFASLMNSESRLNE SPTDDSEKEASHSESNVDADSE PSESESASKQTGLFRSSSGSGV QPDGPLYPLSAGKLLYTKETDS GDKEMAEAISELRLSSTVTGDQ DFDRENQPLNISNNLCFLEGKH LRSYSPQNAFQTLSQSYITTSK ECSIQSCLYQFTSMELLMGNNK LLCENCTKNKQKYQEETSFAEK KVEGVYTNARKQLLISAVPAVL ILHLKRFHQAGLSLRKVNRHVD FPLMLDLAPFCSATCKNASVGD KVLYGLYGIVEHSGSMREGHYT AYVKVRTPSRKLSEHNTKKKNV PGLKAADNESAGQWVHVSDTYL QVVPESRALSAQAYLLFYERVL		MNFIDRIFIGELTSTVMCEE CANISTVKDPFIDISLPIIE ERVSKPLLWGRMNKYRSLRE TDHDRYSGNVTIENIHQPRA AKKHSSSKDKSQLIHDRKCI RKLSSGETVTYQKNENLEMN GDSLMFASLMNSESRLNESP TDDSEKEASHSESNVDADSE PSESESASKQTGLFRSSSGS GVQPDGPLYPLSAGKLLYTK ETDSGDKEMAEAISELRLSS TVTGDQDFDRENQPLNISNN LCFLEGKHLRSYSPQNAFQT LSQSYITTSKECSIQSCLYQ FTSMELLMGNNKLLCENCTK NKQKYQEETSFAEKKVEGVY TNARKQLLISAVPAVLILHL KRFHQAGLSLRKVNRHVDFP LMLDLAPFCSATCKNASVGD KVLYGLYGIVEHSGSMREGH YTAYVKVRTPSRKLSEHNTK KKNVPGLKAADNESAGQWVH VSDTYLQVVPESRALSAQAY LLFYERVL
UBP32_HUMAN Ubiquitin carboxyl-terminal hydrolase 32	16	MGAKESRIGFLSYEEALRRVTD VELKRLKDAFKRTCGLSYYMGQ HCFIREVLGDGVPPKVAEVIYC SFGGTSKGLHFNNLIVGLVLLT RGKDEEKAKYIFSLFSSESGNY VIREEMERMLHVVDGKVPDTLR KCFSEGEKVNYEKFRNWLFLNK DAFTFSRWLLSGGVYVTLTDDS DTPTFYQTLAGVTHLEESDIID LEKRYWLLKAQSRTGRFDLETF GPLVSPPIRPSLSEGLFNAFDE NRDNHIDFKEISCGLSACCRGP LAERQKFCFKVFDVDRDGVLSR VELRDMVVALLEVWKDNRTDDI PELHMDLSDIVEGILNAHDTTK MGHLTLEDYQIWSVKNVLANEF LNLLFQVCHIVLGLRPATPEEE GQIIRGWLERESRYGLQAGHNW FIISMQWWQQWKEYVKYDANPV VIEPSSVLNGGKYSFGTAAHPM EQVEDRIGSSLSYVNTTEEKFS DNISTASEASETAGSGFLYSAT	128	TEKGATGLSNLGNTCFMNSS IQCVSNTQPLTQYFISGRHL YELNRTNPIGMKGHMAKCYG DLVQELWSGTQKNVAPLKLR WTIAKYAPRFNGFQQQDSQE LLAFLLDGLHEDLNRVHEKP YVELKDSDGRPDWEVAAEAW DNHLRRNRSIVVDLFHGQLR SQVKCKTCGHISVRFDPFNF LSLPLPMDSYMHLEITVIKL DGTTPVRYGLRLNMDEKYTG LKKQLSDLCGLNSEQILLAE VHGSNIKNFPQDNQKVRLSV SGFLCAFEIPVPVSPISASS PTQTDFSSSPSTNEMFTLTT NGDLPRPIFIPNGMPNTVVP CGTEKNFTNGMVNGHMPSLP DSPFTGYIIAVHRKMMRTEL YFLSSQKNRPSLFGMPLIVP CTVHTRKKDLYDAVWIQVSR LASPLPPQEASNHAQDCDDS MGYQYPFTLRVVQKDGNSCA

		PGADVCFARQHNTSDNNNQCLL GANGNILLHLNPQKPGAIDNQP LVTQEPVKATSLTLEGGRLKRT PQLIHGRDYEMVPEPVWRALYH WYGANLALPRPVIKNSKTDIPE LELFPRYLLFLRQQPATRTQQS NIWVNMGNVPSPNAPLKRVLAY TGCFSRMQTIKEIHEYLSQRLR IKEEDMRLWLYNSENYLTLLDD EDHKLEYLKIQDEQHLVIEVRN KDMSWPEEMSFIANSSKIDRHK VPTEKGATGLSNLGNTCFMNSS IQCVSNTQPLTQYFISGRHLYE LNRTNPIGMKGHMAKCYGDLVQ ELWSGTQKNVAPLKLRWTIAKY APRFNGFQQQDSQELLAFLLDG LHEDLNRVHEKPYVELKDSDGR PDWEVAAEAWDNHLRRNRSIVV DLFHGQLRSQVKCKTCGHISVR FDPFNFLSLPLPMDSYMHLEIT VIKLDGTTPVRYGLRLNMDEKY TGLKKQLSDLCGLNSEQILLAE VHGSNIKNFPQDNQKVRLSVSG FLCAFEIPVPVSPISASSPTQT DFSSSPSTNEMFTLTTNGDLPR PIFIPNGMPNTVVPCGTEKNFT NGMVNGHMPSLPDSPFTGYIIA VHRKMMRTELYFLSSQKNRPSL FGMPLIVPCTVHTRKKDLYDAV WIQVSRLASPLPPQEASNHAQD CDDSMGYQYPFTLRVVQKDGNS CAWCPWYRFCRGCKIDCGEDRA FIGNAYIAVDWDPTALHLRYQT SQERVVDEHESVEQSRRAQAEP INLDSCLRAFTSEEELGENEMY YCSKCKTHCLATKKLDLWRLPP ILIIHLKRFQFVNGRWIKSQKI VKFPRESFDPSAFLVPRDPALC QHKPLTPQGDELSEPRILAREV KKVDAQSSAGEEDVLLSKSPSS LSANIISSPKGSPSSSRKSGTS CPSSKNSSPNSSPRTLGRSKGR LRLPQIGSKNKLSSSKENLDAS KENGAGQICELADALSRGHVLG GSQPELVTPQDHEVALANGFLY EHEACGNGYSNGQLGNHSEEDS TDDQREDTRIKPIYNLYAISCH SGILGGGHYVTYAKNPNCKWYC YNDSSCKELHPDEIDTDSAYIL FYEQQGIDYAQFLPKTDGKKMA DTSSMDEDFESDYKKYCVLQ		WCPWYRFCRGCKIDCGEDRA FIGNAYIAVDWDPTALHLRY QTSQERVVDEHESVEQSRRA QAEPINLDSCLRAFTSEEEL GENEMYYCSKCKTHCLATKK LDLWRLPPILIIHLKRFQFV NGRWIKSQKIVKFPRESFDP SAFLVPRDPALCQHKPLTPQ GDELSEPRILAREVKKVDAQ SSAGEEDVLLSKSPSSLSAN IISSPKGSPSSSRKSGTSCP SSKNSSPNSSPRTLGRSKGR LRLPQIGSKNKLSSSKENLD ASKENGAGQICELADALSRG HVLGGSQPELVTPQDHEVAL ANGFLYEHEACGNGYSNGQL GNHSEEDSTDDQREDTRIKP IYNLYAISCHSGILGGGHYV TYAKNPNCKWYCYNDSSCKE LHPDEIDTDSAYILFYEQQG IDYAQFLPKTDGKKMADTSS MDEDFESDYKKYCVLQ

U17L6_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 6	17	MEDDSLYLRGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPECLDMQPYMS QQNTGPLVYVLYAVLVHAGWSC HNGHYFSYVKAQEGQWYKMDDA EVTASSITSVLSQQAYVLFYIQ KSEWERHSESVSRGREPRALGS ED	129	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS
UBP42_HUMAN Ubiquitin carboxyl-terminal hydrolase 42	18	MTIVDKASESSDPSAYQNQPGS SEAVSPGDMDAGSASWGAVSSL NDVSNHTLSLGPVPGAVVYSSS SVPDKSKPSPQKDQALGDGIAP PQKVLFPSEKICLKWQQTHRVG AGLQNLGNTCFANAALQCLTYT PPLANYMLSHEHSKTCHAEGFC MMCTMQAHITQALSNPGDVIKP MFVINEMRRIARHFRFGNQEDA HEFLQYTVDAMQKACLNGSNKL DRHTQATTLVCQIFGGYLRSRV KCLNCKGVSDTFDPYLDITLEI KAAQSVNKALEQFVKPEQLDGE NSYKCSKCKKMVPASKRFTIHR SSNVLTLSLKRFANFTGGKIAK DVKYPEYLDIRPYMSQPNGEPI VYVLYAVLVHTGFNCHAGHYFC YIKASNGLWYQMNDSIVSTSDI RSVLSQQAYVLFYIRSHDVKNG GELTHPTHSPGQSSPRPVISQR VVTNKQAAPGFIGPQLPSHMIK NPPHLNGTGPLKDTPSSSMSSP NGNSSVNRASPVNASASVQNWS VNRSSVIPEHPKKQKITISIHN KLPVRQCQSQPNLHSNSLENPT KPVPSSTITNSAVQSTSNASTM SVSSKVTKPIPRSESCSQPVMN GKSKLNSSVLVPYGAESSEDSD EESKGLGKENGIGTIVSSHSPG QDAEDEEATPHELQEPMTLNGA NSADSDSDPKENGLAPDGASCQ GQPALHSENPFAKANGLPGKLM	130	RVGAGLQNLGNTCFANAALQ CLTYTPPLANYMLSHEHSKT CHAEGFCMMCTMQAHITQAL SNPGDVIKPMFVINEMRRIA RHFRFGNQEDAHEFLQYTVD AMQKACLNGSNKLDRHTQAT TLVCQIFGGYLRSRVKCLNC KGVSDTFDPYLDITLEIKAA QSVNKALEQFVKPEQLDGEN SYKCSKCKKMVPASKRFTIH RSSNVLTLSLKRFANFTGGK IAKDVKYPEYLDIRPYMSQP NGEPIVYVLYAVLVHTGFNC HAGHYFCYIKASNGLWYQMN DSIVSTSDIRSVLSQQAYVL FYIRSHDVKNGGE

		PAPLLSLPEDKILETFRLSNKL KGSTDEMSAPGAERGPPEDRDA EPQPGSPAAESLEEPDAAAGLS STKKAPPPRDPGTPATKEGAWE AMAVAPEEPPPSAGEDIVGDTA PPDLCDPGSLTGDASPLSQDAK GMIAEGPRDSALAEAPEGLSPA PPARSEEPCEQPLLVHPSGDHA RDAQDPSQSLGAPEAAERPPAP VLDMAPAGHPEGDAEPSPGERV EDAAAPKAPGPSPAKEKIGSLR KVDRGHYRSRRERSSSGEPARE SRSKTEGHRHRRRRTCPRERDR QDRHAPEHHPGHGDRLSPGERR SLGRCSHHHSRHRSGVELDWVR HHYTEGERGWGREKFYPDRPRW DRCRYYHDRYALYAARDWKPFH GGREHERAGLHERPHKDHNRGR RGCEPARERERHRPSSPRAGAP HALAPHPDRFSHDRTALVAGDN CNLSDRFHEHENGKSRKRRHDS VENSDSHVEKKARRSEQKDPLE EPKAKKHKKSKKKKKSKDKHRD RDSRHQQDSDLSAACSDADLHR HKKKKKKKKRHSRKSEDFVKDS ELHLPRVTSLETVAQFRRAQGG FPLSGGPPLEGVGPFREKTKHL RMESRDDRCRLFEYGQGKRRYL ELGR		
U17L7_HUMAN Inactive ubiquitin carboxyl-terminal hydrolase 17-like protein 7	19	MEDDSLYLGGDWQFNHFSKLTS SRLDAAFAEIQRTSLSEKSPLS SETRFDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQKIGNT FYVNVSLQCLTYTLPLSNYMLS REDSQTCHLHKCCMFCTMQAHI TWALHSPGHVIQPSQVLAAGFH RGEQEDAHEFLMFTVDAMKKAC LPGHKQLDHHSKDTTLIHQIFG AYWRSQIKYLHCHGVSDTFDPY LDIALDIQAAQSVKQALEQLVK PKELNGENAYHCGLCLQKAPAS KTLTLPTSAKVLILVLKRFSDV TGNKLAKNVQYPKCRDMQPYMS QQNTGPLVYVLYAVLVHAGWSC HNGHYFSYVKAQEGQWYKMDDA EVTASGITSVLSQQAYVLFYIQ KSEWERHSESVSRGREPRALGA EDTDRPATQGELKRDHPCLQVP ELDEHLVERATQESTLDHWKFP QEQNKTKPEFNVRKVEGTLPPN VLVIHQSKYKCGMKNHHPEQQS	131	AVGAGLQKIGNTFYVNVSLQ CLTYTLPLSNYMLSREDSQT CHLHKCCMFCTMQAHITWAL HSPGHVIQPSQVLAAGFHRG EQEDAHEFLMFTVDAMKKAC LPGHKQLDHHSKDTTLIHQI FGAYWRSQIKYLHCHGVSDT FDPYLDIALDIQAAQSVKQA LEQLVKPKELNGENAYHCGL CLQKAPASKTLTLPTSAKVL ILVLKRFSDVTGNKLAKNVQ YPKCRDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SGITSVLSQQAYVLFYIQKS EWERHSESVSRGREPRALGA EDTDRPATQGELKRDHPCLQ VPEL

		SLLNLSSTKPTDQESMNTGTLA SLQGSTRRSKGNNKHSKRSLLV CQ		
U17LH_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 17	20	MEDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPECLDMQPYMS QQNTGPLVYVLYAVLVHAGWSC HNGHYFSYVKAQEGQWYKMDDA EVTAASITSVLSQQAYVLFYIQ KSEWERHSESVSRGREPRALGA EDTDRRATQGELKRDHPCLQAP ELDEHLVERATQESTLDHWKFL QEQNKTKPEFNVRKVEGTLPPD VLVIHQSKYKCGMKNHHPEQQS SLLNLSSSTPTHQESMNTGTLA SLRGRARRSKGKNKHSKRALLV CQ	132	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA ASITSVLSQQAYVLFYIQKS EWERHSESVSRGREPRALGA EDTDRRATQGELKRDHPCLQ APEL
UBP13_HUMAN Ubiquitin carboxyl-terminal hydrolase 13	21	MQRRGALFGMPGGSGGRKMAAG DIGELLVPHMPTIRVPRSGDRV YKNECAFSYDSPNSEGGLYVCM NTFLAFGREHVERHFRKTGQSV YMHLKRHVREKVRGASGGALPK RRNSKIFLDLDTDDDLNSDDYE YEDEAKLVIFPDHYEIALPNIE ELPALVTIACDAVLSSKSPYRK QDPDTWENELPVSKYANNLTQL DNGVRIPPSGWKCARCDLRENL WLNLTDGSVLCGKWFFDSSGGN GHALEHYRDMGYPLAVKLGTIT PDGADVYSFQEEEPVLDPHLAK HLAHFGIDMLHMHGTENGLQDN DIKLRVSEWEVIQESGTKLKPM YGPGYTGLKNLGNSCYLSSVMQ AIFSIPEFQRAYVGNLPRIFDY SPLDPTQDFNTQMTKLGHGLLS GQYSKPPVKSELIEQVMKEEHK PQQNGISPRMFKAFVSKSHPEF SSNRQQDAQEFFLHLVNLVERN RIGSENPSDVFRFLVEERIQCC QTRKVRYTERVDYLMQLPVAME	133	YGPGYTGLKNLGNSCYLSSV MQAIFSIPEFQRAYVGNLPR IFDYSPLDPTQDFNTQMTKL GHGLLSGQYSKPPVKSELIE QVMKEEHKPQQNGISPRMFK AFVSKSHPEFSSNRQQDAQE FFLHLVNLVERNRIGSENPS DVFRFLVEERIQCCQTRKVR YTERVDYLMQLPVAMEAATN KDELIAYELTRREAEANRRP LPELVRAKIPFSACLQAFSE PENVDDFWSSALQAKSAGVK TSRFASFPEYLVVQIKKFTF GLDWVPKKFDVSIDMPDLLD INHLRARGLQPGEEELPDIS PPIVIPDDSKDRLMNQLIDP SDIDESSVMQLAEMGFPLEA CRKAVYFTGNMGAEVAFNWI IVHMEEPDFAEPLTMPGYGG AASAGASVFGASGLDNQPPE EIVAIITSMGFQRNQAIQAL RATNNNLERALDWIFSHPEF EEDSDFVIEMENNANANIIS

		AATNKDELIAYELTRREAEANR RPLPELVRAKIPFSACLQAFSE PENVDDFWSSALQAKSAGVKTS RFASFPEYLVVQIKKFTFGLDW VPKKFDVSIDMPDLLDINHLRA RGLQPGEEELPDISPPIVIPDD SKDRLMNQLIDPSDIDESSVMQ LAEMGFPLEACRKAVYFTGNMG AEVAFNWIIVHMEEPDFAEPLT MPGYGGAASAGASVFGASGLDN QPPEEIVAIITSMGFQRNQAIQ ALRATNNNLERALDWIFSHPEF EEDSDFVIEMENNANANIISEA KPEGPRVKDGSGTYELFAFISH MGTSTMSGHYICHIKKEGRWVI YNDHKVCASERPPKDLGYMYFY RRIPS		EAKPEGPRVKDGSGTYELFA FISHMGTSTMSGHYICHIKK EGRWVIYNDHKVCASERPPK DLGYMYFYRRIPS
UBP11_HUMAN Ubiquitin carboxyl-terminal hydrolase 11	22	MAVAPRLFGGLCFRFRDQNPEV AVEGRLPISHSCVGCRRERTAM ATVAANPAAAAAAVAAAAAVTE DREPQHEELPGLDSQWRQIENG ESGRERPLRAGESWFLVEKHWY KQWEAYVQGGDQDSSTFPGCIN NATLFQDEINWRLKEGLVEGED YVLLPAAAWHYLVSWYGLEHGQ PPIERKVIELPNIQKVEVYPVE LLLVRHNDLGKSHTVQFSHTDS IGLVLRTARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDA ALETGQLIIMETRKKDGTWPSA QLHVMNNNMSEEDEDFKGQPGI CGLTNLGNTCFMNSALQCLSNV PQLTEYFLNNCYLEELNFRNPL GMKGEIAEAYADLVKQAWSGHH RSIVPHVFKNKVGHFASQFLGY QQHDSQELLSFLLDGLHEDLNR VKKKEYVELCDAAGRPDQEVAQ EAWQNHKRRNDSVIVDTFHGLF KSTLVCPDCGNVSVTFDPFCYL SVPLPISHKRVLEVFFIPMDPR RKPEQHRLVVPKKGKISDLCVA LSKHTGISPERMMVADVFSHRF YKLYQLEEPLSSILDRDDIFVY EVSGRIEAIEGSREDIVVPVYL RERTPARDYNNSYYGLMLFGHP LLVSVPRDRFTWEGLYNVLMYR LSRYVTKPNSDDEDDGDEKEDD EEDKDDVPGPSTGGSLRDPEPE QAGPSSGVTNRCPFLLDNCLGT SQWPPRRRRKQLFTLQTVNSNG TSDRTTSPEEVHAQPYIAIDWE	134	KGQPGICGLTNLGNTCFMNS ALQCLSNVPQLTEYFLNNCY LEELNFRNPLGMKGEIAEAY ADLVKQAWSGHHRSIVPHVF KNKVGHFASQFLGYQQHDSQ ELLSFLLDGLHEDLNRVKKK EYVELCDAAGRPDQEVAQEA WQNHKRRNDSVIVDTFHGLF KSTLVCPDCGNVSVTFDPFC YLSVPLPISHKRVLEVFFIP MDPRRKPEQHRLVVPKKGKI SDLCVALSKHTGISPERMMV ADVFSHRFYKLYQLEEPLSS ILDRDDIFVYEVSGRIEAIE GSREDIVVPVYLRERTPARD YNNSYYGLMLFGHPLLVSVP RDRFTWEGLYNVLMYRLSRY VTKPNSDDEDDGDEKEDDEE DKDDVPGPSTGGSLRDPEPE QAGPSSGVTNRCPFLLDNCL GTSQWPPRRRRKQLFTLQTV NSNGTSDRTTSPEEVHAQPY IAIDWEPEMKKRYYDEVEAE GYVKHDCVGYVMKKAPVRLQ ECIELFTTVETLEKENPWYC PSCKQHQLATKKLDLWMLPE ILIIHLKRFSYTKFSREKLD TLVEFPIRDLDFSEFVIQPQ NESNPELYKYDLIAVSNHYG GMRDGHYTTFACNKDSGQWH YFDDNSVSPVNENQIESKAA YVLFYQRQD

		PEMKKRYYDEVEAEGYVKHDCV GYVMKKAPVRLQECIELFTTVE TLEKENPWYCPSCKQHQLATKK LDLWMLPEILIIHLKRFSYTKF SREKLDTLVEFPIRDLDFSEFV IQPQNESNPELYKYDLIAVSNH YGGMRDGHYTTFACNKDSGQWH YFDDNSVSPVNENQIESKAAYV LFYQRQDVARRLLSPAGSSGAP ASPACSSPPSSEFMDVN		
U17L1_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 1	23	MGDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS SETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYENASLQCLTYTLPLANYMLS REHSQTCQRPKCCMLCTMQAHI TWALHSPGHVIQPSQALAAGFH RGKQEDVHEFLMFTVDAMKKAC LPGHKQVDHHCKDTTLIHQIFG GCWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVKQALEQLVK PEELNGENAYHCGLCLQRAPAS NTLTLHTSAKVLILVLKRFSDV AGNKLAKNVQYPECLDMQPYMS QQNTGPLVYVLYAVLVHAGWSC HDGHYFSYVKAQEVQWYKMDDA EVTVCSIISVLSQQAYVLFYIQ KSEWERHSESVSRGREPRALGA EDTDRRAKQGELKRDHPCLQAP ELDEHLVERATQESTLDHWKFL QEQNKTKPEFNVGKVEGTLPPN ALVIHQSKYKCGMKNHHPEQQS SLLNLSSTTRTDQESMNTGTLA SLQGRTRRAKGKNKHSKRALLV CQ	135	AVGAGLQNMGNTCYENASLQ CLTYTLPLANYMLSREHSQT CQRPKCCMLCTMQAHITWAL HSPGHVIQPSQALAAGFHRG KQEDVHEFLMFTVDAMKKAC LPGHKQVDHHCKDTTLIHQI FGGCWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVKQA LEQLVKPEELNGENAYHCGL CLQRAPASNTLTLHTSAKVL ILVLKRFSDVAGNKLAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHDGHYF SYVKAQEVQWYKMDDAEVTV CSIISVLSQQAYVLFYIQKS
UBP14_HUMAN Ubiquitin carboxyl-terminal hydrolase 14	24	MPLYSVTVKWGKEKFEGVELNT DEPPMVFKAQLFALTGVQPARQ KVMVKGGTLKDDDWGNIKIKNG MTLLMMGSADALPEEPSAKTVF VEDMTEEQLASAMELPCGLTNL GNTCYMNATVQCIRSVPELKDA LKRYAGALRASGEMASAQYITA ALRDLFDSMDKTSSSIPPIILL QFLHMAFPQFAEKGEQGQYLQQ DANECWIQMMRVLQQKLEAIED DSVKETDSSSASAATPSKKKSL IDQFFGVEFETTMKCTESEEEE VTKGKENQLQLSCFINQEVKYL FTGLKLRLQEEITKQSPTLQRN ALYIKSSKISRLPAYLTIQMVR FFYKEKESVNAKVLKDVKFPLM	136	ASAMELPCGLTNLGNTCYMN ATVQCIRSVPELKDALKRYA GALRASGEMASAQYITAALR DLFDSMDKTSSSIPPIILLQ FLHMAFPQFAEKGEQGQYLQ QDANECWIQMMRVLQQKLEA IEDDSVKETDSSSASAATPS KKKSLIDQFFGVEFETTMKC TESEEEEVTKGKENQLQLSC FINQEVKYLFTGLKLRLQEE ITKQSPTLQRNALYIKSSKI SRLPAYLTIQMVRFFYKEKE SVNAKVLKDVKFPLMLDMYE LCTPELQEKMVSFRSKFKDL EDKKVNQQPNTSDKKSSPQK EVKYEPFSFADDIGSNNCGY

		LDMYELCTPELQEKMVSFRSKF KDLEDKKVNQQPNTSDKKSSPQ KEVKYEPFSFADDIGSNNCGYY DLQAVLTHQGRSSSSGHYVSWV KRKQDEWIKFDDDKVSIVTPED ILRLSGGGDWHIAYVLLYGPRR VEIMEEESEQ		YDLQAVLTHQGRSSSSGHYV SWVKRKQDEWIKFDDDKVSI VTPEDILRLSGGGDWHIAYV LLYGPRR
Q13107|UBP4_HUMAN Ubiquitin carboxyl-terminal hydrolase 4	25	MAEGGGCRERPDAETQKSELGP LMRTTLQRGAQWYLIDSRWFKQ WKKYVGFDSWDMYNVGEHNLFP GPIDNSGLFSDPESQTLKEHLI DELDYVLVPTEAWNKLLNWYGC VEGQQPIVRKVVEHGLFVKHCK VEVYLLELKLCENSDPTNVLSC HFSKADTIATIEKEMRKLFNIP AERETRLWNKYMSNTYEQLSKL DNTVQDAGLYQGQVLVIEPQNE DGTWPRQTLQSKSSTAPSRNFT TSPKSSASPYSSVSASLIANGD STSTCGMHSSGVSRGGSGFSAS YNCQEPPSSHIQPGLCGLGNLG NTCFMNSALQCLSNTAPLTDYF LKDEYEAEINRDNPLGMKGEIA EAYAELIKQMWSGRDAHVAPRM FKTQVGRFAPQFSGYQQQDSQE LLAFLLDGLHEDLNRVKKKPYL ELKDANGRPDAVVAKEAWENHR LRNDSVIVDTFHGLFKSTLVCP ECAKVSVTFDPFCYLTLPLPLK KDRVMEVFLVPADPHCRPTQYR VTVPLMGAVSDLCEALSRLSGI AAENMVVADVYNHRFHKIFQMD EGLNHIMPRDDIFVYEVCSTSV DGSECVTLPVYFRERKSRPSST SSASALYGQPLLLSVPKHKLTL ESLYQAVCDRISRYVKQPLPDE FGSSPLEPGACNGSRNSCEGED EEEMEHQEEGKEQLSETEGSGE DEPGNDPSETTQKKIKGQPCPK RLFTFSLVNSYGTADINSLAAD GKLLKLNSRSTLAMDWDSETRR LYYDEQESEAYEKHVSMLQPQK KKKTTVALRDCIELFTTMETLG EHDPWYCPNCKKHQQATKKFDL WSLPKILVVHLKRFSYNRYWRD KLDTVVEFPIRGLNMSEFVCNL SARPYVYDLIAVSNHYGAMGVG HYTAYAKNKLNGKWYYFDDSNV SLASEDQIVTKAAYVLFYQRRD DEFYKTPSLSSSGSSDGGTRPS SSQQGFGDDEACSMDTN	137	SHIQPGLCGLGNLGNTCFMN SALQCLSNTAPLTDYFLKDE YEAEINRDNPLGMKGEIAEA YAELIKQMWSGRDAHVAPRM FKTQVGRFAPQFSGYQQQDS QELLAFLLDGLHEDLNRVKK KPYLELKDANGRPDAVVAKE AWENHRLRNDSVIVDTFHGL FKSTLVCPECAKVSVTFDPF CYLTLPLPLKKDRVMEVFLV PADPHCRPTQYRVTVPLMGA VSDLCEALSRLSGIAAENMV VADVYNHRFHKIFQMDEGLN HIMPRDDIFVYEVCSTSVDG SECVTLPVYFRERKSRPSST SSASALYGQPLLLSVPKHKL TLESLYQAVCDRISRYVKQP LPDEFGSSPLEPGACNGSRN SCEGEDEEEMEHQEEGKEQL SETEGSGEDEPGNDPSETTQ KKIKGQPCPKRLFTFSLVNS YGTADINSLAADGKLLKLNS RSTLAMDWDSETRRLYYDEQ ESEAYEKHVSMLQPQKKKKT TVALRDCIELFTTMETLGEH DPWYCPNCKKHQQATKKFDL WSLPKILVVHLKRFSYNRYW RDKLDTVVEFPIRGLNMSEF VCNLSARPYVYDLIAVSNHY GAMGVGHYTAYAKNKLNGKW YYFDDSNVSLASEDQIVTKA AYVLFYQRRD

UBP26_HUMAN Ubiquitin carboxyl-terminal hydrolase 26	26	MAALFLRGFVQIGNCKTGISKS KEAFIEAVERKKKDRLVLYFKS GKYSTFRLSDNIQNVVLKSYRG NQNHLHLTLQNNNGLFIEGLSS TDAEQLKIFLDRVHQNEVQPPV RPGKGGSVFSSTTQKEINKTSF HKVDEKSSSKSFEIAKGSGTGV LQRMPLLTSKLTLTCGELSENQ HKKRKRMLSSSSEMNEEFLKEN NSVEYKKSKADCSRCVSYNREK QLKLKELEENKKLECESSCIMN ATGNPYLDDIGLLQALTEKMVL VFLLQQGYSDGYTKWDKLKLFF ELFPEKICHGLPNLGNTCYMNA VLQSLLSIPSFADDLLNQSFPW GKIPLNALTMCLARLLFFKDTY NIEIKEMLLLNLKKAISAAAEI FHGNAQNDAHEFLAHCLDQLKD NMEKLNTIWKPKSEFGEDNFPK QVFADDPDTSGFSCPVITNFEL ELLHSIACKACGQVILKTELNN YLSINLPQRIKAHPSSIQSTFD LFFGAEELEYKCAKCEHKTSVG VHSFSRLPRILIVHLKRYSLNE FCALKKNDQEVIISKYLKVSSH CNEGTRPPLPLSEDGEITDFQL LKVIRKMTSGNISVSWPATKES KDILAPHIGSDKESEQKKGQTV FKGASRRQQQKYLGKNSKPNEL ESVYSGDRAFIEKEPLAHLMTY LEDTSLCQFHKAGGKPASSPGT PLSKVDFQTVPENPKRKKYVKT SKFVAFDRIINPTKDLYEDKNI RIPERFQKVSEQTQQCDGMRIC EQAPQQALPQSFPKPGTQGHTK NLLRPTKLNLQKSNRNSLLALG SNKNPRNKDILDKIKSKAKETK RNDDKGDHTYRLISVVSHLGKT LKSGHYICDAYDFEKQIWFTYD DMRVLGIQEAQMQEDRRCTGYI FFYMHNEIFEEMLKREENAQLN SKEVEETLQKE	138	KICHGLPNLGNTCYMNAVLQ SLLSIPSFADDLLNQSFPWG KIPLNALTMCLARLLFFKDT YNIEIKEMLLLNLKKAISAA AEIFHGNAQNDAHEFLAHCL DQLKDNMEKLNTIWKPKSEF GEDNFPKQVFADDPDTSGFS CPVITNFELELLHSIACKAC GQVILKTELNNYLSINLPQR IKAHPSSIQSTFDLFFGAEE LEYKCAKCEHKTSVGVHSFS RLPRILIVHLKRYSLNEFCA LKKNDQEVIISKYLKVSSHC NEGTRPPLPLSEDGEITDFQ LLKVIRKMTSGNISVSWPAT KESKDILAPHIGSDKESEQK KGQTVFKGASRRQQQKYLGK NSKPNELESVYSGDRAFIEK EPLAHLMTYLEDTSLCQFHK AGGKPASSPGTPLSKVDFQT VPENPKRKKYVKTSKFVAFD RIINPTKDLYEDKNIRIPER FQKVSEQTQQCDGMRICEQA PQQALPQSFPKPGTQGHTKN LLRPTKLNLQKSNRNSLLAL GSNKNPRNKDILDKIKSKAK ETKRNDDKGDHTYRLISVVS HLGKTLKSGHYICDAYDFEK QIWFTYDDMRVLGIQEAQMQ EDRRCTGYIFFYMHN
UBP19_HUMAN Ubiquitin carboxyl-terminal hydrolase 19	27	MSGGASATGPRRGPPGLEDTTS KKKQKDRANQESKDGDPRKETG SRYVAQAGLEPLASGDPSASAS HAAGITGSRHRTRLFFPSSSGS ASTPQEEQTKEGACEDPHDLLA TPTPELLLDWRQSAEEVIVKLR VGVGPLQLEDVDAAFTDTDCVV RFAGGQQWGGVFYAEIKSSCAK VQTRKGSLLHLTLPKKVPMLTW	139	LPGFTGLVNLGNTCFMNSVI QSLSNTRELRDFFHDRSFEA EINYNNPLGTGGRLAIGFAV LLRALWKGTHHAFQPSKLKA IVASKASQFTGYAQHDAQEF MAFLLDGLHEDLNRIQNKPY TETVDSDGRPDEVVAEEAWQ RHKMRNDSFIVDLFQGQYKS KLVCPVCAKVSITFDPFLYL

		PSLLVEADEQLCIPPLNSQTCL LGSEENLAPLAGEKAVPPGNDP VSPAMVRSRNPGKDDCAKEEMA VAADAATLVDEPESMVNLAFVK NDSYEKGPDSVVVHVYVKEICR DTSRVLFREQDFTLIFQTRDGN FLRLHPGCGPHTTFRWQVKLRN LIEPEQCTFCFTASRIDICLRK RQSQRWGGLEAPAARVGGAKVA VPTGPTPLDSTPPGGAPHPLTG QEEARAVEKDKSKARSEDTGLD SVATRTPMEHVTPKPETHLASP KPTCMVPPMPHSPVSGDSVEEE EEEEKKVCLPGFTGLVNLGNTC FMNSVIQSLSNTRELRDFFHDR SFEAEINYNNPLGTGGRLAIGF AVLLRALWKGTHHAFQPSKLKA IVASKASQFTGYAQHDAQEFMA FLLDGLHEDLNRIQNKPYTETV DSDGRPDEVVAEEAWQRHKMRN DSFIVDLFQGQYKSKLVCPVCA KVSITFDPFLYLPVPLPQKQKV LPVFYFAREPHSKPIKFLVSVS KENSTASEVLDSLSQSVHVKPE NLRLAEVIKNRFHRVFLPSHSL DTVSPSDTLLCFELLSSELAKE RVVVLEVQQRPQVPSVPISKCA ACQRKQQSEDEKLKRCTRCYRV GYCNQLCQKTHWPDHKGLCRPE NIGYPFLVSVPASRLTYARLAQ LLEGYARYSVSVFQPPFQPGRM ALESQSPGCTTLLSTGSLEAGD SERDPIQPPELQLVTPMAEGDT GLPRVWAAPDRGPVPSTSGISS EMLASGPIEVGSLPAGERVSRP EAAVPGYQHPSEAMNAHTPQFF IYKIDSSNREQRLEDKGDTPLE LGDDCSLALVWRNNERLQEFVL VASKELECAEDPGSAGEAARAG HFTLDQCLNLFTRPEVLAPEEA WYCPQCKQHREASKQLLLWRLP NVLIVQLKRFSFRSFIWRDKIN DLVEFPVRNLDLSKFCIGQKEE QLPSYDLYAVINHYGGMIGGHY TACARLPNDRSSQRSDVGWRLF DDSTVTTVDESQVVTRYAYVLF YRRRNSPVERPPRAGHSEHHPD LGPAAEAAASQASRIWQELEAE EEPVPEGSGPLGPWGPQDWVGP LPRGPTTPDEGCLRYFVLGTVA ALVALVLNVFYPLVSQSRWR		PVPLPQKQKVLPVFYFAREP HSKPIKFLVSVSKENSTASE VLDSLSQSVHVKPENLRLAE VIKNRFHRVFLPSHSLDTVS PSDTLLCFELLSSELAKERV VVLEVQQRPQVPSVPISKCA ACQRKQQSEDEKLKRCTRCY RVGYCNQLCQKTHWPDHKGL CRPENIGYPFLVSVPASRLT YARLAQLLEGYARYSVSVFQ PPFQPGRMALESQSPGCTTL LSTGSLEAGDSERDPIQPPE LQLVTPMAEGDTGLPRVWAA PDRGPVPSTSGISSEMLASG PIEVGSLPAGERVSRPEAAV PGYQHPSEAMNAHTPQFFIY KIDSSNREQRLEDKGDTPLE LGDDCSLA LVWRNNERLQEFVLVASKEL ECAEDPGSAGEAARAGHFTL DQCLNLFTRPEVLAPEEAWY CPQCKQHREASKQLLLWRLP NVLIVQLKRFSFRSFIWRDK INDLVEFPVRNLDLSKFCIG QKEEQLPSYDLYAVINHYGG MIGGHYTACARLPNDRSSQR SDVGWRLFDDSTVTTVDESQ VVTRYAYVLFYRRRN	

UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10	28	MALHSPQYIFGDFSPDEFNQFF VTPRSSVELPPYSGTVLCGTQA VDKLPDGQEYQRIEFGVDEVIE PSDTLPRTPSYSISSTLNPQAP EFILGCTASKITPDGITKEASY GSIDCQYPGSALALDGSSNVEA EVLENDGVSGGLGQRERKKKKK RPPGYYSYLKDGGDDSISTEAL VNGHANSAVPNSVSAEDAEFMG DMPPSVTPRTCNSPQNSTDSVS DIVPDSPFPGALGSDTRTAGQP EGGPGADFGQSCFPAEAGRDTL SRTAGAQPCVGTDTTENLGVAN GQILESSGEGTATN GVELHTTESIDLDPTKPESASP PADGTGSASGTLPVSQPKSWAS LFHDSKPSSSSPVAYVETKYSP PAISPLVSEKQVEVKEGLVPVS EDPVAIKIAELLENVTLIHKPV SLQPRGLINKGNWCYINATLQA LVACPPMYHLMKFIPLYSKVQR PCTSTPMIDSFVRLMNEFTNMP VPPKPRQALGDKIVRDIRPGAA FEPTYIYRLLTVNKSSLSEKGR QEDAEEYLGFILNGLHEEMLNL KKLLSPSNEKLTISNGPKNHSV NEEEQEEQGEGSEDEWEQVGPR NKTSVTRQADFVQT PITGIFGGHIRSVVYQQSSKES ATLQPFFTLQLDIQSDKIRTVQ DALESLVARESVQGYTTKTKQE VEISRRVTLEKLPPVLVLHLKR FVYEKTGGCQKLIKNIEYPVDL EISKELLSPGVKNKNFKCHRTY RLFAVVYHHGNSATGGHYTTDV FQIGLNGWLRIDDQTVKVINQY QVVKPTAERTAYLLYYRRVDLL	140	SLQPRGLINKGNWCYINATL QALVACPPMYHLMKFIPLYS KVQRPCTSTPMIDSFVRLMN EFTNMPVPPKPRQALGDKIV RDIRPGAAFEPTYIYRLLTV NKSSLSEKGRQEDAEEYLGF ILNGLHEEMLNLKKLLSPSN EKLTISNGPKNHSVNEEEQE EQGEGSEDEWEQVGPRNKTS VTRQADFVQTPITGIFGGHI RSVVYQQSSKESATLQPFFT LQLDIQSDKIRTVQDALESL VARESVQGYTTKTKQEVEIS RRVTLEKLPPVLVLHLKRFV YEKTGGCQKLIKNIEYPVDL EISKELLSPGVKNKNFKCHR TYRLFAVVYHHGNSATGGHY TTDVFQIGLNGWLRIDDQTV KVINQYQVVKPTAERTAYLL YYRRVD
UBP49_HUMAN Ubiquitin carboxyl-terminal hydrolase 49	29	MDRCKHVGRLRLAQDHSILNPQ KWCCLECATTESVWACLKCSHV ACGRYIEDHALKHFEETGHPLA MEVRDLYVFCYLCKDYVLNDNP EGDLKLLRSSLLAVRGQKQDTP VRRGRTLRSMASGEDVVLPQRA PQGQPQMLTALWYRRQRLLART LRLWFEKSSRGQAKLEQRRQEE ALERKKEEARRRRREVKRRLLE ELASTPPRKSARLLLHTPRDAG PAASRPAALPTSRRVPAATLKL RRQPAMAPGVTGLRNLGNTCYM NSILQVLSHLQKFRECFLNLDP SKTEHLFPKATNGK	141	MDRCKHVGRLRLAQDHSILN PQKWCCLECATTESVWACLK CSHVACGRYIEDHALKHFEE TGHPLAMEVRDLYVFCYLCK DYVLNDNPEGDLKLLRSSLL AVRGQKQDTPVRRGRTLRSM ASGEDVVLPQRAPQGQPQML TALWYRRQRLLARTLRLWFE KSSRGQAKLEQRRQEEALER KKEEARRRRREVKRRLLEEL ASTPPRKSARLLLHTPRDAG PAASRPAALPTSRRVPAATL KLRRQPAMAPGVTGLRNLGN TCYMNSILQVLSHLQKFREC

		TQLSGKPTNSSATELSLRNDRA EACEREGFCWNGRASISRSLEL IQNKEPSSKHISLCRELHTLFR VMWSGKWALVSPFAMLHSVWSL IPAFRGYDQQDAQEFLCELLHK VQQELESEGTTRRILIPFSQRK LTKQVLKVVNTIFHGQLLSQVT CISCNYKSNTIEPFWDLSLEFP ERYHCIEKGFVPLNQTECLLTE MLAKFTETEALEGRIYACDQCN SKRRKSNPKPLVLSEARKQLMI YRLPQVLRLHLKRFRWSGRNHR EKIGVHVVFDQVLTMEPYCCRD MLSSLDKETFAYDL SAVVMHHGKGFGSGHYTAYCYN TEGGFWVHCNDSKLNVCSVEEV CKTQAYILFYTQRTVQGNARIS ETHLQAQVQSSNNDEGRPQTFS		FLNLDPSKTEHLFPKATNGK TQLSGKPTNSSATELSLRND RAEACEREGFCWNGRASISR SLELIQNKEPSSKHISLCRE LHTLFRVMWSGKWALVSPFA MLHSVWSLIPAFRGYDQQDA QEFLCELLHKVQQELESEGT TRRILIPFSQRKLTKQVLKV VNTIFHGQLLSQVTCISCNY KSNTIEPFWDLSLEFPERYH CIEKGFVPLNQTECLLTEML AKFTETEALEGRIYACDQCN SKRRKSNPKPLVLSEARKQL MIYRLPQVLRLHLKRFRWSG RNHREKIGVHVVFDQVLTME PYCCRDMLSSLDKETFAYDL SAVVMHHGKGFGSGHYTAYC YNTEGGFWVHCNDSKLNVCS VEEVCKTQAYILFYTQRT
U17L8_HUMAN Inactive ubiquitin carboxyl-terminal hydrolase 17-like protein 8	30	MEDDSLYLGGEWQFNHFSKLTS PRPDAAFAEIQRTSLPEKSPLS SETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYLNASLQCLTYTPPLANYMLS REHSQTCQRPKCCMLCTMQAHI TWALHSPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GCWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVKQALEQLVK PEELNGENAYPCGLCLQRAPAS NTLTLHTSAKVLILVLKRFCDV TGNKLAKNVQYPEC LDMQPYMSQQNTGPLVYVLYAV LVHAGWSCHNGYYFSYVKAQEG QWYKMDDAEVTACSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRPATQGELKR DHPCLQVPELDEHLVERATEES TLDHWKFPQEQNKMKPEFNVRK VEGTLPPNVLVIHQSKYKCGMK NHHPEQQSSLLNLSSMNSTDQE SMNTGTLASLQGRTRRSKGKNK HSKRSLLVCQ	142	AVGAGLQNMGNTCYLNASLQ CLTYTPPLANYMLSREHSQT CQRPKCCMLCTMQAHITWAL HSPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGCWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVKQA LEQLVKPEELNGENAYPCGL CLQRAPASNTLTLHTSAKVL ILVLKRFCDVTGNKLAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHNGYYF SYVKAQEGQWYKMDDAEVTA CSITSVLSQQAYVLFYIQKS
6VN6_1	31	GSKKHTGYVGLKNQGATCYMNS LLQTLFFTNQLRKAVYMMPTEG DDSSKSVPLALQRVFYELQHSD KPVGTKKLTKSFGWETLDSFMQ HDVQELCRVLLDNVENKMKGTC VEGTIPKLFRGKMVSYIQCKEV DYRSDRREDYYDIQLSIKGKKN	143	TGYVGLKNQGATCYMNSLLQ TLFFTNQLRKAVYMMPTEGD DSSKSVPLALQRVFYELQHS DKPVGTKKLTKSFGWETLDS FMQHDVQELCRVLLDNVENK MKGTCVEGTIPKLFRGKMVS YIQCKEVDYRSDRREDYYDI

		IFESFVDYVAVEQLDGDNKYDA GEHGLQEAEKGVKFLTLPPVLH LQLMRFMYDPQTDQNIKINDRF EFPEQLPLDEFLQKTDPKDPAN YILHAVLVHSGDNHGGHYVVYL NPKGDGKWCKFDDDVVSRCTKE EAIEHNYGGHDDDLSVRHCTNA YMLVYIRESKLSEVLQAVTDHD IPQQLVERLQEEKRIEAQKR		QLSIKGKKNIFESFVDYVAV EQLDGDNKYDAGEHGLQEAE KGVKFLTLPPVLHLQLMRFM YDPQTDQNIKINDRFEFPEQ LPLDEFLQKTDPKDPANYIL HAVLVHSGDNHGGHYVVYLN PKGDGKWCKFDDDVVSRCTK EEAIEHNYGGHDDDLSVRHC TNAYMLVYIRE
6DGF_1	32	AQGLAGLRNLGNTCFMNSILQC LSNTRELRDYCLQRLYMRDLHH GSNAHTALVEEFAKLIQTIWTS SPNDVVSPSEFKTQIQRYAPRF VGYNQQDAQEFLRFLLDGLHNE VNRVTLRPKSNPENLDHLPDDE KGRQMWRKYLEREDSRIGDLFV GQLKSSLTCTDCGYCSTVFDPF WDLSLPIAKRGYPEVTLMDCMR LFTKEDVLDGDEKPTCCRCRGR KRCIKKFSIQRFPKILVLHLKR FSESRIRTSKLTTFVNFPLRDL DLREFASENTNHAVYNLYAVSN HSGTTMGGHYTAYCRSPGTGEW HTFNDSSVTPMSSSQVRTSDAY LLFYELASPPSRM	144	AQGLAGLRNLGNTCFMNSIL QCLSNTRELRDYCLQRLYMR DLHHGSNAHTALVEEFAKLI QTIWTSSPNDVVSPSEFKTQ IQRYAPRFVGYNQQDAQEFL RFLLDGLHNEVNRVTLRPKS NPENLDHLPDDEKGRQMWRK YLEREDSRIGDLFVGQLKSS LTCTDCGYCSTVFDPFWDLS LPIAKRGYPEVTLMDCMRLF TKEDVLDGDEKPTCCRCRGR KRCIKKFSIQRFPKILVLHL KRFSESRIRTSKLTTFVNFP LRDLDLREFASENTNHAVYN LYAVSNHSGTTMGGHYTAYC RSPGTGEWHTFNDSSVTPMS SSQVRTSDAYLLFYELAS
2VHF_1	33	GLEIMIGKKKGIQGHYNSCYLD STLFCLFAFSSVLDTVLLRPKE KNDVEYYSETQELLRTEIVNPL RIYGYVCATKIMKLRKILEKVE AASGFTSEEKDPEEFLNILFHH ILRVEPLLKIRSAGQKVQDCYF YQIFMEKNEKVGVPTIQQLLEW SFINSNLKFAEAPSCLIIQMPR FGKDFKLFKKIFPSLELNITDL LEDTPRQCRICGGLAMYECREC YDDPDISAGKIKQFCKTCNTQV HLHPKRLNHKYNPVSLPKDLPD WDWRHGCIPCQNMELFAVLCIE TSHYVAFVKYGKDDSAWLFFDS MADRDGGQNGFNIPQVTPCPEV GEYLKMSLEDLHSLDSRRIQGC ARRLLCDAYMCMYQSPTMSLYK	145	MIGKKKGIQGHYNSCYLDST LFCLFAFSSVLDTVLLRPKE KNDVEYYSETQELLRTEIVN PLRIYGYVCATKIMKLRKIL EKVEAASGFTSEEKDPEEFL NILFHHILRVEPLLKIRSAG QKVQDCYFYQIFMEKNEKVG VPTIQQLLEWSFINSNLKFA EAPSCLIIQMPRFGKDFKLF KKIFPSLELNITDLLEDTPR QCRICGGLAMYECRECYDDP DISAGKIKQFCKTCNTQVHL HPKRLNHKYNPVSLPKDLPD WDWRHGCIPCQNMELFAVLC IETSHYVAFVKYGKDDSAWL FFDSMADRDGGQNGFNIPQV TPCPEVGEYLKMSLEDLHSL DSRRIQGCARRLLCDAYMCM YQS
U17LI_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 18	34	MEDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI	146	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI

		TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPEC LDMQPYMSQTNTGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTASSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRAKQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK NHHPEQQSSLLNLSSTTPTHQE SMNTGTLASLRGRARRSKGKNK HSKRALLVCQ		FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQTNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS
UBP22_HUMAN Ubiquitin carboxyl-terminal hydrolase 22	35	MVSRPEPEGEAMDAELAVAPPG CSHLGSFKVDNWKQNLRAIYQC FVWSGTAEARKRKAKSCICHVC GVHLNRLHSCLYCVFFGCFTKK HIHEHAKAKRHNLAIDLMYGGI YCFLCQDYIYDKDMEIIAKEEQ RKAWKMQGVGEKFSTWEPTKRE LELLKHNPKRRKITSNCTIGLR GLINLGNTCFMNCIVQALTHTP LLRDFFLSDRHRCEMQSPSSCL VCEMSSLFQEFYSGHRSPHIPY KLLHLVWTHARHLAGYEQQDAH EFLIAALDVLHRHCKGDDNGKK ANNPNHCNCIIDQIFTGGLQSD VTCQVCHGVSTTIDPFWDISLD LPGSSTPFWPLSPGSEGNVVNG ESHVSGTTTLTDCLRRFTRPEH LGSSAKIKCSGCHSYQESTKQL TMKKLPIVACFHLKRFEHSAKL RRKITTYVSFPLELDMTPFMAS SKESRMNGQYQQPTDSLNNDNK YSLFAVVNHQGTLESGHYTSFI RQHKDQWFKCDDAIITKASIKD VLDSEGYLLFYHKQFLEYE	147	LGNTCFMNCIVQALTHTPLL RDFFLSDRHRCEMQSPSSCL VCEMSSLFQEFYSGHRSPHI PYKLLHLVWTHARHLAGYEQ QDAHEFLIAALDVLHRHCKG DDNGKKANNPNHCNCIIDQI FTGGLQSDVTCQVCHGVSTT IDPFWDISLDLPGSSTPFWP LSPGSEGNVVNGESHVSGTT TLTDCLRRFTRPEHLGSSAK IKCSGCHSYQESTKQLTMKK LPIVACFHLKRFEHSAKLRR KITTYVSFPLELDMTPFMAS SKESRMNGQYQQPTDSLNND NKYSLFAVVNHQGTLESGHY TSFIRQHKDQWFKCDDAIIT KASIKDVLDSEGYLLFYHKQ F
UBP18_HUMAN Ubl carboxyl-terminal hydrolase 18	36	MSKAFGLLRQICQSILAESSQS PADLEEKKEEDSNMKREQPRER PRAWDYPHGLVGLHNIGQTCCL NSLIQVFVMNVDFTRILKRITV PRGADEQRRSVPFQMLLLLEKM QDSRQKAVRPLELAYCLQKCNV PLFVQHDAAQLYLKLWNLIKDQ ITDVHLVERLQALYTIRVKDSL	148	KGLVPGLVNLGNTCFMNSLL QGLSACPAFIRWLEEFTSQY SRDQKEPPSHQYLSLTLLHL LKALSCQEVTDDEVLDASCL LDVLRMYRWQISSFEEQDAH ELFHVITSSLEDERDRQPRV THLFDVHSLEQQSEITPKQI TCRTRGSPHPTSNHWKSQHP

		ICVDCAMESSRNSSMLTLPLSL FDVDSKPLKTLEDALHCFFQPR ELSSKSKCFCENCGKKTRGKQV LKLTHLPQTLTIHLMRFSIRNS QTRKICHSLYFPQSLDFSQILP MKRESCDAEEQSGG QYELFAVIAHVGMADSGHYCVY IRNAVDGKWFCFNDSNICLVSW EDIQCTYGNPNYHWQETAYLLV YMKMEC		FHGRLTSNMVCKHCEHQSPV RFDTFDSLSLSIPAATWGHP LTLDHCLHHFISSESVRDVV CDNCTKIEAKGTLNGEKVEH QRTTFVKQLKLGKLPQCLCI HLQRLSWSSHGTPLKRHEHV QFNEFLMMDIYKYHLLGHKP SQHNPKLNKNPGPTLELQDG PGAPTPVLNQPGAPKTQIFM NGACSPSLLPTLSAPMPFPL PVVPDYSSSTYLFRLMAVVV HHGDMHSGHFVTYRRSPPSA RNPLSTSNQWLWVSDDTVRK ASLQEVLSSSAYLLFYERVL
UBP28_HUMAN Ubiquitin carboxyl-terminal hydrolase 28	37	MTAELQQDDAAGAADGHGSSCQ MLLNQLREITGIQDPSFLHEAL KASNGDITQAVSLLTDERVKEP SQDTVATEPSEVEGSAANKEVL AKVIDLTHDNKDDLQAAIALSL LESPKIQADGRDLNRMHEATSA ETKRSKRKRCEVWGENPNPNDW RRVDGWPVGLKNVGNTCWFSAV IQSLFQLPEFRRLVLSYSLPQN VLENCRSHTEKRNIMFMQELQY LFALMMGSNRKFVDPSAALDLL KGAFRSSEEQQQDVSEFTHKLL DWLEDAFQLAVNVNSPRNKSEN PMVQLFYGTFLTEG VREGKPFCNNETFGQYPLQVNG YRNLDECLEGAMVEGDVELLPS DHSVKYGQERWFTKLPPVLTFE LSRFEFNQSLGQPEKIHNKLEF PQIIYMDRYMYRSKELIRNKRE CIRKLKEEIKILQQKLERYVKY GSGPARFPLPDMLKYVIEFAST KPASESCPPESDTHMTLPLSSV HCSVSDQTSKESTSTESSSQDV ESTFSSPEDSLPKSKPLTSSRS SMEMPSQPAPRTVTDEEINFVK TCLQRWRSEIEQDIQDLKTCIA STTQTIEQMYCDPLLRQVPYRL HAVLVHEGQANAGHYWAYIYNQ PRQSWLKYNDISVTESSWEEVE RDSYGGLRNVSAYCLMYINDKL PYFNAEAAPTESDQMSEVEALS VELKHYIQEDNWRFEQEVEEWE EEQSCKIPQMESSTNSSSQDYS TSQEPSVASSHGVRCLSSEHAV IVKEQTAQAIANTARAYEKSGV EAALSEVMLSPAMQGVILAIAK ARQTFDRDGSEAGLIKAFHEEY	149	GWPVGLKNVGNTCWFSAVIQ SLFQLPEFRRLVLSYSLPQN VLENCRSHTEKRNIMFMQEL QYLFALMMGSNRKFVDPSAA LDLLKGAFRSSEEQQQDVSE FTHKLLDWLEDAFQLAVNVN SPRNKSENPMVQLFYGTFLT EGVREGKPFCNNETFGQYPL QVNGYRNLDECLEGAMVEGD VELLPSDHSVKYGQERWFTK LPPVLTFELSRFEFNQSLGQ PEKIHNKLEFPQIIYMDRYM YRSKELIRNKRECIRKLKEE IKILQQKLERYVKYGSGPAR FPLPDMLKYVIEFASTKPAS ESCPPESDTHMTLPLSSVHC SVSDQTSKESTSTESSSQDV ESTFSSPEDSLPKSKPLTSS RSSMEMPSQPAPRTVTDEEI NFVKTCLQRWRSEIEQDIQD LKTCIASTTQTIEQMYCDPL LRQVPYRLHAVLVHEGQANA GHYWAYIYNQPRQSWLKYND ISVTESSWEEVERDSYGGLR NVSAYCLMYINDKLPY

		SRLYQLAKETPTSHSDPRLQHV LVYFFQNEAPKRVVERTLLEQF ADKNLSYDERSISIMKVAQAKL KEIGPDDMNMEEYKKWHEDYSL FRKVSVYLLTGLELYQKGKYQE ALSYLVYAYQSNAALLMKGPRR GVKESVIALYRRKCLLELNAKA ASLFETNDDHSVTEGINVMNEL IIPCIHLIINNDISKDDLDAIE VMRNHWCSYLGQDIAENLQLCL GEFLPRLLDPSAEIIVLKEPPT IRPNSPYDLCSRFAAVMESIQG VSTVTVK		
U17L2_HUMAN Ubiquitin carboxyl-terminal hydrolase 17	38	MEDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS SEARVDLCDDLAPVARQLAPRK KLPLSSRRPAAVGAGLQNMGNT CYENASLQCLTYTPPLANYMLS REHSQTCQRPKCCMLCTMQAHI TWALHSPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GCWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVKQALEQLVK PEELNGENAYHCGLCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKLAKNVQYPEC LDMQPYMSQQNTGPLVYVLYAV LVHAGWSCHDGHYFSYVKAQEG QWYKMDDAKVTACSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDERLVERATQES TLDHWKFPQEQNKTKPEFNVRK VEGTLPPNVLVIHQSKYKCGMK NHHPEQQSSLLNLSSTTRTDQE SVNTGTLASLQGRTRRSKGKNK HSKRALLVCQ	150	AVGAGLQNMGNTCYENASLQ CLTYTPPLANYMLSREHSQT CQRPKCCMLCTMQAHITWAL HSPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGCWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVKQA LEQLVKPEELNGENAYHCGL CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKLAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHDGHYF SYVKAQEGQWYKMDDAKVTA CSITSVLSQQAYVLFYIQKS
UBP31_HUMAN Ubiquitin carboxyl-terminal hydrolase 31	39	MSKVTAPGSGPPAAASGKEKRS FSKRLFRSGRAGGGAGGPGAS GPAAPSSPSSPSSARSVGSFMS RVLKTLSTLSHLSSEGAAPDRG GLRSCFPPGPAAAPTPPPCPPP PASPAPPACAAEPVPGVAGLRN HGNTCFMNATLQCLSNTELFAE YLALGQYRAGRPEPSPDPEQPA GRGAQGQGEVTEQLAHLVRALW TLEYTPQHSRDFKTIVSKNALQ YRGNSQHDAQEFLLWLLDRVHE DLNHSVKQSGQPPLKPPSETDM	151	PVPGVAGLRNHGNTCFMNAT LQCLSNTELFAEYLALGQYR AGRPEPSPDPEQPAGRGAQG QGEVTEQLAHLVRALWTLEY TPQHSRDFKTIVSKNALQYR GNSQHDAQEFLLWLLDRVHE DLNHSVKQSGQPPLKPPSET DMMPEGPSFPVCSTFVQELF QAQYRSSLTCPHCQKQSNTF DPFLCISLPIPLPHTRPLYV TVVYQGKCSHCMRIGVAVPL SGTVARLREAVSMETKIPTD QIVLTEMYYDGFHRSFCDTD

		MPEGPSFPVCSTFVQELFQAQY RSSLTCPHCQKQSN TFDPFLCISLPIPLPHTRPLYV TVVYQGKCSHCMRIGVAVPLSG TVARLREAVSMETKIPTDQIVL TEMYYDGFHRSFCDTDDLETVH ESDCIFAFETPEIFRPEGILSQ RGIHLNNNLNHLKFGLDYHRLS SPTQTAAKQGKMDSPTSRAGSD KIVLLVCNRACTGQQGKRFGLP FVLHLEKTIAWDLLQKEILEKM KYFLRPTVCIQVCPFSLRVVSV VGITYLLPQEEQPLCHPIVERA LKSCGPGGTAHVKLVVEWDKET RDFLFVNTEDEYIPDAESVRLQ RERHHQPQTCTLSQ CFQLYTKEERLAPDDAWRCPHC KQLQQGSITLSLWTLPDVLIIH LKRFRQEGDRRMKLQNMVKFPL TGLDMTPHVVKRSQSSWSLPSH WSPWRRPYGLGRDPEDYIYDLY AVCNHHGTMQGGHYTAYCKNSV DGLWYCFDDSDVQQLSEDEVCT QTAYILFYQRRTAIPSWSANSS VAGSTSSSLCEHWVSRLPGSKP ASVTSAASSRRTSLASLSESVE MTGERSEDDGGFSTRPFVRSVQ RQSLSSRSSVTSPLAVNENCMR PSWSLSAKLQMRSNSPSRFSGD SPIHSSASTLEKIG EAADDKVSISCFGSLRNLSSSY QEPSDSHSRREHKAVGRAPLAV MEGVFKDESDTRRLNSSVVDTQ SKHSAQGDRLPPLSGPFDNNNQ IAYVDQSDSVDSSPVKEVKAPS HPGSLAKKPESTTKRSPSSKGT SEPEKSLRKGRPALASQESSLS STSPSSPLPVKVSLKPSRSRSK ADSSSRGSGRHSSPAPAQPKKE SSPKSQDSVSSPSPQKQKSASA LTYTASSTSAKKASGPATRSPF PPGKSRTSDHSLSREGSRQSLG SDRASATSTSKPNSPRVSQARA GEGRGAGKHVRSSS MASLRSPSTSIKSGLKRDSKSE DKGLSFFKSALRQKETRRSTDL GKTALLSKKAGGSSVKSVCKNT GDDEAERGHQPPASQQPNANTT GKEQLVTKDPASAKHSLLSARK SKSSQLDSGVPSSPGGRQSAEK SSKKLSSSMQTSARPSQKPQ		DLETVHESDCIFAFETPEIF RPEGILSQRGIHLNNNLNHL KFGLDYHRLSSPTQTAAKQG KMDSPTSRAGSDKIVLLVCN RACTGQQGKRFGLPFVLHLE KTIAWDLLQKEILEKMKYFL RPTVCIQVCPFSLRVVSVVG ITYLLPQEEQPLCHPIVE RALKSCGPGGTAHVKLVVEW DKETRDFLFVNTEDEYIPDA ESVRLQRERHHQPQTCTLSQ CFQLYTKEERLAPDDAWRCP HCKQLQQGSITLSLWTLPDV LIIHLKRFRQEGDRRMKLQN MVKFPLTGLDMTPHVVKRSQ SSWSLPSHWSPWRRPYGLGR DPEDYIYDLYAVCNHHGTMQ GGHYTAYCKNSVDGLWYCFD DSDVQQLSEDEVCTQTAYIL FYQRRT

U17LJ_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 19	40	MEEDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPEC LDMQPYMSQTNTGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTASSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK NHHPEQQSSLLKLSSTTPTHQE SMNTGTLASLRGRARRSKGKNK HSKRALLVCQ	152	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQTNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS EWERHSESVSRGREPRALGA EDTDRRATQGELKRDHPCLQ APEL
U17LF_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 15	41	MEDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIDKNVQYPEC LDMKLYMSQTNSGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTASSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK NHHPEQQSSLLNLSSTTPTHQE SMNTGTLASLRGRARRSKGKNK HSKRALLVCQWSQWKYRPTRRG AHTHAHTQTHT	153	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIDKNVQ YPECLDMKLYMSQTNSGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS

UBP47_HUMAN Ubiquitin carboxyl-terminal hydrolase 47	42	MVPGEENQLVPKEDVFWRCRQN IFDEMKKKFLQIENAAEEPRVL CIIQDTTNSKTVNERITLNLPA STPVRKLFEDVANKVGYINGTF DLVWGNGINTADMAPLDHTSDK SLLDANFEPGKKNFLHLTDKDG EQPQILLEDSSAGEDSVHDRFI GPLPREGSGGSTSDYVSQSYSY SSILNKSETGYVGLVNQAMTCY LNSLLQTLFMTPEFRNALYKWE FEESEEDPVTSIPYQLQRLFVL LQTSKKRAIETTDVTRSFGWDS SEAWQQHDVQELCRVMFDALEQ KWKQTEQADLINEL YQGKLKDYVRCLECGYEGWRID TYLDIPLVIRPYGSSQAFASVE EALHAFIQPEILDGPNQYFCER CKKKCDARKGLRFLHFPYLLTL QLKRFDFDYTTMHRIKLNDRMT FPEELDMSTFIDVEDEKSPQTE SCTDSGAENEGSCHSDQMSNDF SNDDGVDEGICLETNSGTEKIS KSGLEKNSLIYELFSVMVHSGS AAGGHYYACIKSFSDEQWYSFN DQHVSRITQEDIKKTHGGSSGS RGYYSSAFASSTNAYMLIYRLK DPARNAKFLEVDEYPEHIKNLV QKERELEEQEKRQR EIERNTCKIKLFCLHPTKQVMM ENKLEVHKDKTLKEAVEMAYKM MDLEEVIPLDCCRLVKYDEFHD YLERSYEGEEDTPMGLLLGGVK STYMFDLLLETRKPDQVFQSYK PGEVMVKVHVVDLKAESVAAPI TVRAYLNQTVTEFKQLISKAIH LPAETMRIVLERCYNDLRLLSV SSKTLKAEGFFRSNKVFVESSE TLDYQMAFADSHLWKLLDRHAN TIRLFVLLPEQSPVSYSKRTAY QKAGGDSGNVDDDCERVKGPVG SLKSVEAILEESTEKLKSLSLQ QQQDGDNGDSSKST ETSDFENIESPLNERDSSASVD NRELEQHIQTSDPENFQSEERS DSDVNNDRSTSSVDSDILSSSH SSDTLCNADNAQIPLANGLDSH SITSSRRTKANEGKKETWDTAE EDSGTDSEYDESGKSRGEMQYM YFKAEPYAADEGSGEGHKWLMV HVDKRITLAAFKQHLEPFVGVL SSHFKVFRVYASNQEFESVRLN	154	ETGYVGLVNQAMTCYLNSLL QTLFMTPEFRNALYKWEFEE SEEDPVTSIPYQLQRLFVLL QTSKKRAIETTDVTRSFGWD SSEAWQQHDVQELCRVMFDA LEQKWKQTEQADLINELYQG KLKDYVRCLECGYEGWRIDT YLDIPLVIRPYGSSQAFASV EEALHAFIQPEILDGPNQYF CERCKKKCDARKGLRFLHFP YLLTLQLKRFDFDYTTMHRI KLNDRMTFPEELDMSTFIDV EDEKSPQTESCTDSGAENEG SCHSDQMSNDFSNDDGVDEG ICLETNSGTEKISKSGLEKN SLIYELFSVMVHSGSAAGGH YYACIKSFSDEQWYSFNDQH VSRITQEDIKKTHGGSSGSR GYYSSAFASSTNAYMLIYRL KD

		ETLSSFSDDNKITIRLGRALKK GEYRVKVYQLLVNEQEPCKFLL DAVFAKGMTVRQSKEELIPQLR EQCGLELSIDRFRLRKKTWKNP GTVFLDYHIYEEDI NISSNWEVFLEVLDGVEKMKSM SQLAVLSRRWKPSEMKLDPFQE VVLESSSVDELREKLSEISGIP LDDIEFAKGRGTFPCDISVLDI HQDLDWNPKVSTLNVWPLYICD DGAVIFYRDKTEELMELTDEQR NELMKKESSRLQKTGHRVTYSP RKEKALKIYLDGAPNKDLTQD		
UBP51_HUMAN Ubiquitin carboxyl-terminal hydrolase 51	43	MAQVRETSLPSGSGVRWISGGG GGASPEEAVEKAGKMEEAAAGA TKASSRREAEEMKLEPLQEREP APEENLTWSSSGGDEKVLPSIP LRCHSSSSPVCPRRKPRPRPQP RARSRSQPGLSAPPPPPARPPP PPPPPPPPAPRPRAWRGSRRRS RPGSRPQTRRSCSGDLDGSGDP GGLGDWLLEVEFGQGPTGCSHV ESFKVGKNWQKNLRLIYQRFVW SGTPETRKRKAKSCICHVCSTH MNRLHSCLSCVFFGCFTEKHIH KHAETKQHHLAVDLYHGVIYCF MCKDYVYDKDIEQI AKETKEKILRLLTSTSTDVSHQ QFMTSGFEDKQSTCETKEQEPK LVKPKKKRRKKSVYTVGLRGLI NLGNTCFMNCIVQALTHIPLLK DFFLSDKHKCIMTSPSLCLVCE MSSLFHAMYSGSRTPHIPYKLL HLIWIHAEHLAGYRQQDAHEFL IAILDVLHRHSKDDSGGQEANN PNCCNCIIDQIFTGGLQSDVTC QACHSVSTTIDPCWDISLDLPG SCATFDSQNPERADSTVSRDDH IPGIPSLTDCLQWFTRPEHLGS SAKIKCNSCQSYQESTKQLTMK KLPIVACFHLKRFE HVGKQRRKINTFISFPLELDMT PFLASTKESRMKEGQPPTDCVP NENKYSLFAVINHHGTLESGHY TSFIRQQKDQWFSCDDAIITKA TIEDLLYSEGYLLFYHKQGLEK D	155	YTVGLRGLINLGNTCFMNCI VQALTHIPLLKDFFLSDKHK CIMTSPSLCLVCEMSSLFHA MYSGSRTPHIPYKLLHLIWI HAEHLAGYRQQDAHEFLIAI LDVLHRHSKDDSGGQEANNP NCCNCIIDQIFTGGLQSDVT CQACHSVSTTIDPCWDISLD LPGSCATFDSQNPERADSTV SRDDHIPGIPSLTDCLQWFT RPEHLGSSAKIKCNSCQSYQ ESTKQLTMKKLPIVACFHLK RFEHVGKQRRKINTFISFPL ELDMTPFLASTKESRMKEGQ PPTDCVPNENKYSLFAVINH HGTLESGHYTSFIRQQKDQW FSCDDAIITKATIEDLLYSE GYLLFYHKQG
UBP36_HUMAN Ubiquitin carboxyl-	44	MPIVDKLKEALKPGRKDSADDG ELGKLLASSAKKVLLQKIEFEP ASKSFSYQLEALKSKYVLLNPK TEGASRHKSGDDPPARRQGSEH	156	RVGAGLHNLGNTCFLNATIQ CLTYTPPLANYLLSKEHARS CHQGSFCMLCVMQNHIVQAF ANSGNAIKPVSFIRDLKKIA

terminal hydrolase 36		TYESCGDGVPAPQKVLFPTERL SLRWERVFRVGAGLHNLGNTCF LNATIQCLTYTPPLANYLLSKE HARSCHQGSFCMLCVMQNHIVQ AFANSGNAIKPVSFIRDLKKIA RHFRFGNQEDAHEFLRYTIDAM QKACLNGCAKLDRQTQATTLVH QIFGGYLRSRVKCSVCKSVSDT YDPYLDVALEIRQAANIVRALE LFVKADVLSGENAY MCAKCKKKVPASKRFTIHRTSN VLTLSLKRFANFSGGKITKDVG YPEFLNIRPYMSQNNGDPVMYG LYAVLVHSGYSCHAGHYYCYVK ASNGQWYQMNDSLVHSSNVKVV LNQQAYVLFYLRIPGSKKSPEG LISRTGSSSLPGRPSVIPDHSK KNIGNGIISSPLTGKRQDSGTM KKPHTTEEIGVPISRNGSTLGL KSQNGCIPPKLPSGSPSPKLSQ TPTHMPTILDDPGKKVKKPAPP QHFSPRTAQGLPGTSNSNSSRS GSQRQGSWDSRDVVLSTSPKLL ATATANGHGLKGND ESAGLDRRGSSSSSPEHSASSD STKAPQTPRSGAAHLCDSQETN CSTAGHSKTPPSGADSKTVKLK SPVLSNTTTEPASTMSPPPAKK LALSAKKASTLWRATGNDLRPP PPSPSSDLTHPMKTSHPVVAST WPVHRARAVSPAPQSSSRLQPP FSPHPTLLSSTPKPPGTSEPRS CSSISTALPQVNEDLVSLPHQL PEASEPPQSPSEKRKKTFVGEP QRLGSETRLPQHIREATAAPHG KRKRKKKKRPEDTAASALQEGQ TQRQPGSPMYRREGQAQLPAVR RQEDGTQPQVNGQQ VGCVTDGHHASSRKRRRKGAEG LGEEGGLHQDPLRHSCSPMGDG DPEAMEESPRKKKKKRKQETQ RAVEEDGHLKCPRSAKPQDAVV PESSSCAPSANGWCPGDRMGLS QAPPVSWNGERESDVVQELLKY SSDKAYGRKVLTWDGKMSAVSQ DAIEDSRQARTETVVDDWDEEF DRGKEKKIKKFKREKRRNFNAF QKLQTRRNFWSVTHPAKAASLS YRR		RHFRFGNQEDAHEFLRYTID AMQKACLNGCAKLDRQTQAT TLVHQIFGGYLRSRVKCSVC KSVSDTYDPYLDVALEIRQA ANIVRALELFVKADVLSGEN AYMCAKCKKKVPASKRFTIH RTSNVLTLSLKRFANFSGGK ITKDVGYPEFLNIRPYMSQN NG DPVMYGLYAVLVHSGYSCHA GHYYCYVKASNGQWYQMNDS LVHSSNVKVVLNQQAYVLFY LRIP
UBP44_HUMAN Ubiquitin	45	MLAMDTCKHVGQLQLAQDHSSL NPQKWHCVDCNTTESIWACLSC	157	TPGVTGLRNLGNTCYMNSVL QVLSHLLIFRQCFLKLDLNQ

carboxyl-terminal hydrolase 44		SHVACGRYIEEHALKHFQESSH PVALEVNEMYVFCYLCDDYVLN DNTTGDLKLLRRTLSAIKSQNY HCTTRSGRFLRSMGTGDDSYFL HDGAQSLLQSEDQLYTALWHRR RILMGKIFRTWFEQSPIGRKKQ EEPFQEKIVVKREVKKRRQELE YQVKAELESMPPRKSLRLQGLA QSTIIEIVSVQVPAQTPASPAK DKVLSTSENEISQKVSDSSVKR RPIVTPGVTGLRNLGNTCYMNS VLQVLSHLLIFRQC FLKLDLNQWLAMTASEKTRSCK HPPVTDTVVYQMNECQEKDTGF VCSRQSSLSSGLSGGASKGRKM ELIQPKEPTSQYISLCHELHTL FQVMWSGKWALVSPFAMLHSVW RLIPAFRGYAQQDAQEFLCELL DKIQRELETTGTSLPALIPTSQ RKLIKQVLNVVNNIFHGQLLSQ VTCLACDNKSNTIEPFWDLSLE FPERYQCSGKDIASQPCLVTEM LAKFTETEALEGKIYVCDQCNS KRRRFSSKPVVLTEAQKQLMIC HLPQVLRLHLKRFRWSGRNNRE KIGVHVGFEEILNM EPYCCRETLKSLRPECFIYDLS AVVMHHGKGFGSGHYTAYCYNS EGGFWVHCNDSKLSMCTMDEVC KAQAYILFYTQRVTENGHSKLL PPELLLGSQHPNEDADTSSNEI LS		WLAMTASEKTRSCKHPPVTD TVVYQMNECQEKDTGFVCSR QSSLSSGLSGGASKGRKMEL IQPKEPTSQYISLCHELHTL FQVMWSGKWALVSPFAMLHS VWRLIPAFRGYAQQDAQEFL CELLDKIQRELETTGTSLPA LIPTSQRKLIKQVLNVVNNI FHGQLLSQVTCLACDNKSNT IEPFWDLSLEFPERYQCSGK DIASQPCLVTEMLAKFTETE ALEGKIYVCDQCNSKRRRFS SKPVVLTEAQKQLMICHLPQ VLRLHLKRFRWSGRNNREKI GVHVGFEEILNMEPYCCRET LKSLRPECFIYDLSAVVMHH GKGFGSGHYTAYCYNSEGGF WVHCNDSKLSMCTMDEVCKA QAYILFYTQRV
UBP8_HUMAN Ubiquitin carboxyl-terminal hydrolase 8	46	MPAVASVPKELYLSSSLKDLNK KTEVKPEKISTKSYVHSALKIF KTAEECRLDRDEERAYVLYMKY VTVYNLIKKRPDFKQQQDYFHS ILGPGNIKKAVEEAERLSESLK LRYEEAEVRKKLEEKDRQEEAQ RLQQKRQETGREDGGTLAKGSL ENVLDSKDKTQKSNGEKNEKCE TKEKGAITAKELYTMMTDKNIS LIIMDARRMQDYQDSCILHSLS VPEEAISPGVTASWIEAHLPDD SKDTWKKRGNVEYVVLLDWFSS AKDLQIGTTLRSLKDALFKWES KTVLRNEPLVLEGG YENWLLCYPQYTTNAKVTPPPR RQNEEVSISLDFTYPSLEESIP SKPAAQTPPASIEVDENIELIS GQNERMGPLNISTPVEPVAASK SDVSPIIQPVPSIKNVPQIDRT	158	PALTGLRNLGNTCYMNSILQ CLCNAPHLADYFNRNCYQDD INRSNLLGHKGEVAEEFGII MKALWTGQYRYISPKDFKIT IGKINDQFAGYSQQDSQELL LFLMDGLHEDLNKADNRKRY KEENNDHLDDFKAAEHAWQK HKQLNESIIVALFQGQFKST VQCLTCHKKSRTFEAFMYLS LPLASTSKCTLQDCLRLFSK EEKLTDNNRFYCSHCRARRD SLKKIEIWKLPPVLLVHLKR FSYDGRWKQKLQTSVDFPLE NLDLSQYVIGPKNNLKKYNL FSVSNHYGGLDGGHYTAYCK NAARQRWFKFDDHEVSDISV SSVKSSAAYILFYTSLG

		KKPAVKLPEEHRIKSESTNHEQ QSPQSGKVIPDRSTKPVVFSPT LMLTDEEKARIHAETALLMEKN KQEKELRERQQEEQKEKLRKEE QEQKAKKKQEAEENEITEKQQK AKEEMEKKESEQAKKEDKETSA KRGKEITGVKRQSKSEHETSDA KKSVEDRGKRCPTPEIQKKSTG DVPHTSVTGDSGSG KPFKIKGQPESGILRTGTFRED TDDTERNKAQREPLTRARSEEM GRIVPGLPSGWAKFLDPITGTF RYYHSPTNTVHMYPPEMAPSSA PPSTPPTHKAKPQIPAERDREP SKLKRSYSSPDITQAIQEEEKR KPTVTPTVNRENKPTCYPKAEI SRLSASQIRNLNPVFGGSGPAL TGLRNLGNTCYMNSILQCLCNA PHLADYFNRNCYQDDINRSNLL GHKGEVAEEFGIIMKALWTGQY RYISPKDFKITIGKINDQFAGY SQQDSQELLLFLMDGLHEDLNK ADNRKRYKEENNDH LDDFKAAEHAWQKHKQLNESII VALFQGQFKSTVQCLTCHKKSR TFEAFMYLSLPLASTSKCTLQD CLRLFSKEEKLTDNNRFYCSHC RARRDSLKKIEIWKLPPVLLVH LKRFSYDGRWKQKLQTSVDFPL ENLDLSQYVIGPKNNLKKYNLF SVSNHYGGLDGGHYTAYCKNAA RQRWFKFDDHEVSDISVSSVKS SAAYILFYTSLGPRVTDVAT		
UBP37_HUMAN Ubiquitin carboxyl-terminal hydrolase 37	47	MSPLKIHGPIRIRSMQTGITKW KEGSFEIVEKENKVSLVVHYNT GGIPRIFQLSHNIKNVVLRPSG AKQSRLMLTLQDNSFLSIDKVP SKDAEEMRLFLDAVHQNRLPAA MKPSQGSGSFGAILGSRTSQKE TSRQLSYSDNQASAKRGSLETK DDIPFRKVLGNPGRGSIKTVAG SGIARTIPSLTSTSTPLRSGLL ENRTEKRKRMISTGSELNEDYP KENDSSSNNKAMTDPSRKYLTS SREKQLSLKQSEENRTSGLLPL QSSSFYGSRAGSKEHSSGGTNL DRTNVSSQTPSAKR SLGFLPQPVPLSVKKLRCNQDY TGWNKPRVPLSSHQQQQLQGFS NLGNTCYMNAILQSLFSLQSFA NDLLKQGIPWKKIPLNALIRRF	159	QQLQGFSNLGNTCYMNAILQ SLFSLQSFANDLLKQGIPWK KIPLNALIRRFAHLLVKKDI CNSETKKDLLKKVKNAISAT AERFSGYMQNDAHEFLSQCL DQLKEDMEKLNKTWKTEPVS GEENSPDISATRAYTCPVIT NLEFEVQHSIICKACGEIIP KREQFNDLSIDLPRRKKPLP PRSIQDSLDLFFRAEELEYS CEKCGGKCALVRHKFNRLPR VLILHLKRYSFNVALSLNNK IGQQVIIPRYLTLSSHCTEN TKP PFTLGWSAHMAISRPLKASQ MVNSCITSPSTPSKKFTFKS KSSLALCLDSDSEDELKRSV ALSQRLCEMLGNEQQQEDLE

		AHLLVKKDICNSETKKDLLKKV KNAISATAERFSGYMQNDAHEF LSQCLDQLKEDMEKLNKTWKTE PVSGEENSPDISATRAYTCPVI TNLEFEVQHSIICKACGEIIPK REQFNDLSIDLPRRKKPLPPRS IQDSLDLFFRAEELEYSCEKCG GKCALVRHKFNRLPRVLILHLK RYSFNVALSLNNKIGQQVIIPR YLTLSSHCTENTKP PFTLGWSAHMAISRPLKASQMV NSCITSPSTPSKKFTFKSKSSL ALCLDSDSEDELKRSVALSQRL CEMLGNEQQQEDLEKDSKLCPI EPDKSELENSGFDRMSEEELLA AVLEISKRDASPSLSHEDDDKP TSSPDTGFAEDDIQEMPENPDT METEKPKTITELDPASFTEITK DCDENKENKTPEGSQGEVDWLQ QYDMEREREEQELQQALAQSLQ EQEAWEQKEDDDLKRATELSLQ EFNNSFVDALGSDEDSGNEDVF DMEYTEAEAEELKRNAETGNLP HSYRLISVVSHIGS TSSSGHYISDVYDIKKQAWFTY NDLEVSKIQEAAVQSDRDRSGY IFFYMHKEIFDELLETEKNSQS LSTEVGKTTRQAL		KDSKLCPIEPDKSELENSGF DRMSEEELLAAVLEISKRDA SPSLSHEDDDKPTSSPDTGF AEDDIQEMPENPDTMETEKP KTITELDPASFTEITKDCDE NKENKTPEGSQGEVDWLQQY DMEREREEQELQQALAQSLQ EQEAWEQKEDDDLKRATELS LQEFNNSFVDALGSDEDSGN EDVFDMEYTEAEAEELKRNA ETGNLPHSYRLISVVSHIGS TSSSGHYISDVYDIKKQAWF TYNDLEVSKIQEAAVQSDRD RSGYIFFYMHK
U17LD_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 13	48	MEEDSLYLGGEWQFNHFSKLTS SRLDAAFAEIQRTSLPEKSPLS CETRVDLCDDLVPEARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHPSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPEC LDMQPYMSQQNTGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTAASITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDEHLVERATQES TLDRWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK NHHPEQQSSLLNLSSSTPTHQE	160	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHPSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA ASITSVLSQQAYVLFYIQKS

		SMNTGTLASLRGRARRSKGKNK HSKRALLVCQ		
U17L3_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 3	49	MGDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS SETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYENASLQCLTYTLPLANYMLS REHSQTCQRPKCCMLCTMQAHI TWALHSPGHVIQPSQALASGFH RGKQEDVHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GCWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVKQALEQLVK PEELNGENAYHCGLCLQRAPAS NTLTLHTSAKVLILVLKRFSDV AGNKLAKNVQYPEC LDMQPYMSQQNTGPLVYVLYAV LVHAGWSCHDGHYFSYVKAQEG QWYKMDDAEVTVCSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRAKQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVGK VEGTLPPNALVIHQSKYKCGMK NHHPEQQSSLLNLSSTTRTDQE SMNTGTLASLQGRTRRAKGKNK HSKRALLVCQ	161	AVGAGLQNMGNTCYENASLQ CLTYTLPLANYMLSREHSQT CQRPKCCMLCTMQAHITWAL HSPGHVIQPSQALASGFHRG KQEDVHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGCWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVKQA LEQLVKPEELNGENAYHCGL CLQRAPASNTLTLHTSAKVL ILVLKRFSDVAGNKLAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHDGHYF SYVKAQEGQWYKMDDAEVTV CSITSVLSQQAYVLFYIQKS
UBP54_HUMAN Inactive ubiquitin carboxyl-terminal hydrolase 54	50	MSWKRNYFSGGRGSVQGMFAPR SSTSIAPSKGLSNEPGQNSCFL NSALQVLWHLDIFRRSFRQLTT HKCMGDSCIFCALKGIFNQFQC SSEKVLPSDTLRSALAKTFQDE QRFQLGIMDDAAECFENLLMRI HFHIADETKEDICTAQHCISHQ KFAMTLFEQCVCTSCGATSDPL PFIQMVHYISTTSLCNQAICML ERREKPSPSMFGELLQNASTMG DLRNCPSNCGERIRIRRVLMNA PQIITIGLVWDSDHSDLAEDVI HSLGTCLKLGDLFFRVTDDRAK QSELYLVGMICYYG KHYSTFFFQTKIRKWMYFDDAH VKEIGPKWKDVVTKCIKGHYQP LLLLYADPQGTPVSTQDLPPQA EFQSYSRTCYDSEDSGREPSIS SDTRTDSSTESYPYKHSHHESV VSHFSSDSQGTVIYNVENDSMS QSSRDTGHLTDSECNQKHTSKK GSLIERKRSSGRVRRKGDEPQA SGYHSEGETLKEKQAPRNASKP SSSTNRLRDFKETVSNMIHNRP	162	APSKGLSNEPGQNSCFLNSA LQVLWHLDIFRRSFRQLTTH KCMGDSCIFCALKGIFNQFQ CSSEKVLPSDTLRSALAKTF QDEQRFQLGIMDDAAECFEN LLMRIHFHIADETKEDICTA QHCISHQKFAMTLFEQCVCT SCGATSDPLPFIQ MVHYISTTSLCNQAICMLER REKPSPSMFGELLQNASTMG DLRNCPSNCGERIRIRRVLM NAPQIITIGLVWDSDHSDLA EDVIHSLGTCLKLGDLFFRV TDDRAKQSELYLVGMICYYG KHYSTFFFQTKIRKWMYFDD AHVKEIGPKWKDVVTKCIKG HYQPLLLLYADPQGTPVSTQ DLPPQAEFQSYSRTCYDSED SGREPSISSDTRTDSSTESY PYKHSHHESVVSHFSSDSQG TVIYNVEND

		SLASQTNVGSHCRGRGGDQPDK KPPRTLPLHSRDWEIESTSSES KSSSSSKYRPTWRPKRESLNID SIFSKDKRKHCGYT QLSPFSEDSAKEFIPDEPSKPP SYDIKFGGPSPQYKRWGPARPG SHLLEQHPRLIQRMESGYESSE RNSSSPVSLDAALPESSNVYRD PSAKRSAGLVPSWRHIPKSHSS SILEVDSTASMGGWTKSQPFSG EEISSKSELDELQEEVARRAQE QELRRKREKELEAAKGFNPHPS RFMDLDELQNQGRSDGFERSLQ EAESVFEESLHLEQKGDCAAAL ALCNEAISKLRLALHGASCSTH SRALVDKKLQISIRKARSLQDR MQQQQSPQQPSQPSACLPTQAG TLSQPTSEQPIPLQ VLLSQEAQLESGMDTEFGASSF FHSPASCHESHSSLSPESSAPQ HSSPSRSALKLLTSVEVDNIEP SAFHRQGLPKAPGWTEKNSHHS WEPLDAPEGKLQGSRCDNSSCS KLPPQEGRGIAQEQLFQEKKDP ANPSPVMPGIATSERGDEHSLG CSPSNSSAQPSLPLYRTCHPIM PVASSFVLHCPDPVQKTNQCLQ GQSLKTSLTLKVDRGSEETYRP EFPSTKGLVRSLAEQFQRMQGV SMRDSTGFKDRSLSGSLRKNSS PSDSKPPFSQGQEKGHWPWAKQ QSSLEGGDRPLSWE ESTEHSSLALNSGLPNGETSSG GQPRLAEPDIYQEKLSQVRDVR SKDLGSSTDLGTSLPLDSWVNI TRFCDSQLKHGAPRPGMKSSPH DSHTCVTYPERNHILLHPHWNQ DTEQETSELESLYQASLQASQA GCSGWGQQDTAWHPLSQTGSAD GMGRRLHSAHDPGLSKTSTAEM EHGLHEARTVRTSQATPCRGLS RECGEDEQYSAENLRRISRSLS GTVVSEREEAPVSSHSFDSSNV RKPLETGHRCSSSSSLPVIHDP SVFLLGPQLYLPQPQFLSPDVL MPTMAGEPNRLPGT SRSVQQFLAMCDRGETSQGAKY TGRTLNYQSLPHRSRTDNSWAP WSETNQHIGTRFLTTPGCNPQL TYTATLPERSKGLQVPHTQSWS DLFHSPSHPPIVHPVYPPSSSL		

		HVPLRSAWNSDPVPGSRTPGPR RVDMPPDDDWRQSSYASHSGHR RTVGEGFLFVLSDAPRREQIRA RVLQHSQW		
SNUT2_HUMAN U4/U6.U5 tri-snRNP-associated protein 2	51	MSGRSKRESRGSTRGKRESESR GSSGRVKRERDREREPEAASSR GSPVRVKREFEPASAREAPASV VPFVRVKREREVDEDSEPEREV RAKNGRVDSEDRRSRHCPYLDT INRSVLDFDFEKLCSISLSHIN AYACLVCGKYFQGRGLKSHAYI HSVQFSHHVFLNLHTLKFYCLP DNYEIIDSSLEDITYVLKPTFT KQQIANLDKQAKLSRAYDGTTY LPGIVGLNNIKANDYANAVLQA LSNVPPLRNYFLEEDNYKNIKR PPGDIMFLLVQRFGELMRKLWN PRNFKAHVSPHEML QAVVLCSKKTFQITKQGDGVDF LSWFLNALHSALGGTKKKKKTI VTDVFQGSMRIFTKKLPHPDLP AEEKEQLLHNDEYQETMVESTF MYLTLDLPTAPLYKDEKEQLII PQVPLFNILAKFNGITEKEYKT YKENFLKRFQLTKLPPYLIFCI KRFTKNNFFVEKNPTIVNFPIT NVDLREYLSEEVQAVHKNTTYD LIANIVHDGKPSEGSYRIHVLH HGTGKWYELQDLQVTDILPQMI TLSEAYIQIWKRRDNDETNQQG A	163	LPGIVGLNNIKANDYANAVL QALSNVPPLRNYFLEEDNYK NIKRPPGDIMFLLVQRFGEL MRKLWNPRNFKAHVSPHEML QAVVLCSKKTFQITKQGDGV DFLSWFLNALHSALGGTKKK KKTIVTDVFQGSMRIFTKKL PHPDLPAEEKEQLLHNDEYQ ETMVESTFMYLTLDLPTAPL YKDEKEQLIIPQVPLFNILA KFNGITEKEYKTYKENFLKR FQLTKLPPYLIFCIKRFTKN NFFVEKNPTIVNFPITNVDL REYLSEEVQAVHKNTTYDLI ANIVHDGKPSEGSYRIHVLH HGTGKWYELQDLQVTDILPQ MITLSEAYIQIWKRRD
UBP35_HUMAN Ubiquitin carboxyl-terminal hydrolase 35	52	MDKILEAVVTSSYPVSVKQGLV RRVLEAARQPLEREQCLALLAL GARLYVGGAEELPRRVGCQLLH VAGRHHPDVFAEFFSARRVLRL LQGGAGPPGPRALACVQLGLQL LPEGPAADEVFALLRREVLRTV CERPGPAACAQVARLLARHPRC VPDGPHRLLFCQQLVRCLGRFR CPAEGEEGAVEFLEQAQQVSGL LAQLWRAQPAAILPCLKELFAV ISCAEEEPPSSALASVVQHLPL ELMDGVVRNLSNDDSVTDSQML TAISRMIDWVSWPLGKNIDKWI IALLKGLAAVKKFS ILIEVSLTKIEKVFSKLLYPIV RGAALSVLKYMLLTFQHSHEAF HLLLPHIPPMVASLVKEDSNSG TSCLEQLAELVHCMVFRFPGFP DLYEPVMEAIKDLHVPNEDRIK QLLGQDAWTSQKSELAGFYPRL	164	SDTGKIGLINLGNTCYVNSI LQALFMASDFRHCVLRLTEN NSQPLMTKLQWLFGFLEHSQ RPAISPENFLSASWTPWFSP GTQQDCSEYLKYLLDRLHEE EKTGTRICQKLKQSSSPSPP EEPPAPSSTSVEKMFGGKIV TRICCLCCLNVSSREEAFTD LSLAFPPPERCRRRRLGSVM RPTEDITARELPPPTSAQGP GRVGPRRQRKHCITEDTPPT SLYIEGLDSKEAGGQSSQEE RIEREEEGKEERTEKEEVGE EEESTRGEGEREKEEEVEEE EEKVE KETEKEAEQEKEEDSLGAGT HPDAAIPSGERTCGSEGSRS VLDLVNYFLSPEKLTAENRY YCESCASLQDAEKVVELSQG PCYLILTLLRFSFDLRTMRR

		MAKSDTGKIGLINLGNTCYVNS ILQALFMASDFRHCVLRLTENN SQPLMTKLQWLFGFLEHSQRPA ISPENFLSASWTPWFSPGTQQD CSEYLKYLLDRLHEEEKTGTRI CQKLKQSSSPSPPEEPPAPSST SVEKMFGGKIVTRICCLCCLNV SSREEAFTDLSLAF PPPERCRRRRLGSVMRPTEDIT ARELPPPTSAQGPGRVGPRRQR KHCITEDTPPTSLYIEGLDSKE AGGQSSQEERIEREEEGKEERT EKEEVGEEEESTRGEGEREKEE EVEEEEEKVEKETEKEAEQEKE EDSLGAGTHPDAAIPSGERTCG SEGSRSVLDLVNYFLSPEKLTA ENRYYCESCASLQDAEKVVELS QGPCYLILTLLRFSFDLRTMRR RKILDDVSIPLLLRLPLAGGRG QAYDLCSVVVHSGVSSESGHYY CYAREGAARPAASLGTADRPEP ENQWYLFNDTRVSF SSFESVSNVTSFFPKDTAYVLF YRQRPREGPEAELGSSRVRTEP TLHKDLMEAISKDNILYLQEQE KEARSRAAYISALPTSPHWGRG FDEDKDEDEGSPGGCNPAGGNG GDFHRLVF		RKILDDVSIPLLLRLPLAGG RGQAYDLCSVVVHSGVSSES GHYYCYAREGAARPAASLGT ADRPEPENQWYLFNDTRVSF SSFESVSNVTSFFPKDTAYV LFYRQRP
UBP15_HUMAN Ubiquitin carboxyl-terminal hydrolase 15	53	MAEGGAADLDTQRSDIATLLKT SLRKGDTWYLVDSRWFKQWKKY VGFDSWDKYQMGDQNVYPGPID NSGLLKDGDAQSLKEHLIDELD YILLPTEGWNKLVSWYTLMEGQ EPIARKVVEQGMFVKHCKVEVY LTELKLCENGNMNNVVTRRFSK ADTIDTIEKEIRKIFSIPDEKE TRLWNKYMSNTFEPLNKPDSTI QDAGLYQGQVLVIEQKNEDGTW PRGPSTPKSPGASNFSTLPKIS PSSLSNNYNNMNNRNVKNSNYC LPSYTAYKNYDYSEPGRNNEQP GLCGLSNLGNTCFM NSAIQCLSNTPPLTEYFLNDKY QEELNFDNPLGMRGEIAKSYAE LIKQMWSGKFSYVTPRAFKTQV GRFAPQFSGYQQQDCQELLAFL LDGLHEDLNRIRKKPYIQLKDA DGRPDKVVAEEAWENHLKRNDS IIVDIFHGLFKSTLVCPECAKI SVTFDPFCYLTLPLPMKKERTL EVYLVRMDPLTKPMQYKVVVPK	165	EQPGLCGLSNLGNTCFMNSA IQCLSNTPPLTEYFLNDKYQ EELNFDNPLGMRGEIAKSYA ELIKQMWSGKFSYVTPRAFK TQVGRFAPQFSGYQQQDCQE LLAFLLDGLHEDLNRIRKKP YIQLKDADGRPDKVVAEEAW ENHLKRNDSIIVDIFHGLFK STLVCPECAKISVTFDPFCY LTLPLPMKKERTLEVYLVRM DPLTKPMQYKVVVPKIGNIL DLCTALSALSGIPADKMIVT DIYNHRFHRIFAMDENLSSI MERDDIYVFEININRTEDTE HVIIPVCLREKFRHSSYTHH TGSSLFGQPFLMAVPRNNTE DKLYNLLLLRMCRYVKISTE TEETEGSLHCCKDQNINGNG PNGIHEEGSPSEMETDEPDD ESSQDQELPSENENSQSEDS VGGDNDSENGLCTEDTCKGQ LTGHKKRLFTFQFNNLGNTD INYIKDDTRHIRFDDRQLRL

		IGNILDLCTALSALSGIPADKM IVTDIYNHRFHRIFAMDENLSS IMERDDIYVFEININRTEDTEH VIIPVCLREKFRHSSYTHHTGS SLFGQPFLMAVPRN NTEDKLYNLLLLRMCRYVKIST ETEETEGSLHCCKDQNINGNGP NGIHEEGSPSEMETDEPDDESS QDQELPSENENSQSEDSVGGDN DSENGLCTEDTCKGQLTGHKKR LFTFQFNNLGNTDINYIKDDTR HIRFDDRQLRLDERSFLALDWD PDLKKRYFDENAAEDFEKHESV EYKPPKKPFVKLKDCIELFTTK EKLGAEDPWYCPNCKEHQQATK KLDLWSLPPVLVVHLKRFSYSR YMRDKLDTLVDFPINDLDMSEF LINPNAGPCRYNLIAVSNHYGG MGGGHYTAFAKNKD DGKWYYFDDSSVSTASEDQIVS KAAYVLFYQRQDTFSGTGFFPL DRETKGASAATGIPLESDEDSN DNDNDIENENCMHTN		DERSFLALDWDPDLKKRYFD ENAAEDFEKHESVEYKPPKK PFVKLKDCIELFTTKEKLGA EDPWYCPNCKEHQQATKKLD LWSLPPVLVVHLKRFSYSRY MRDKLDTLVDFPINDLDMSE FLINPNAGPCRYNLIAVSNH YGGMGGGHYTAFAKNKDDGK WYYFDDSSVSTASEDQIVSK AAYVLFYQRQD
UBP29_HUMAN Ubiquitin carboxyl-terminal hydrolase 29	54	MISLKVCGFIQIWSQKTGMTKL KEALIETVQRQKEIKLVVTFKS GKFIRIFQLSNNIRSVVLRHCK KRQSHLRLTLKNNVFLFIDKLS YRDAKQLNMFLDIIHQNKSQQP MKSDDDWSVFESRNMLKEIDKT SFYSICNKPSYQKMPLFMSKSP THVKKGILENQGGKGQNTLSSD VQTNEDILKEDNPVPNKKYKTD SLKYIQSNRKNPSSLEDLEKDR DLKLGPSFNTNCNGNPNLDETV LATQTLNAKNGLTSPLEPEHSQ GDPRCNKAQVPLDSHSQQLQQG FPNLGNTCYMNAVL QSLFAIPSFADDLLTQGVPWEY IPFEALIMTLTQLLALKDFCST KIKRELLGNVKKVISAVAEIFS GNMQNDAHEFLGQCLDQLKEDM EKLNATLNTGKECGDENSSPQM HVGSAATKVFVCPVVANFEFEL QLSLICKACGHAVLKVEPNNYL SINLHQETKPLPLSIQNSLDLF FKEEELEYNCQMCKQKSCVARH TFSRLSRVLIIHLKRYSFNNAW LLVKNNEQVYIPKSLSLSSYCN ESTKPPLPLSSSAPVGKCEVLE VSQEMISEINSPLTPSMKLTSE SSDSLVLPVEPDKN	166	QLQQGFPNLGNTCYMNAVLQ SLFAIPSFADDLLTQGVPWE YIPFEALIMTLTQLLALKDF CSTKIKRELLGNVKKVISAV AEIFSGNMQNDAHEFLGQCL DQLKEDMEKLNATLNTGKEC GDENSSPQMHVGSAATKVFV CPVVANFEFELQLSLICKAC GHAVLKVEPNNYLSINLHQE TKPLPLSIQNSLDLFFKEEE LEYNCQMCKQKSCVARHTFS RLSRVLIIHLKRYSFNNAWL LVKNNEQVYIPKSLSLSSYC NESTKPPLPLSSSAPVGKCE VLEVSQEMISEINSPLTPSM KLTSESSDSLVLPVEPDKNA DLQRFQRDCGDASQEQHQRD LENGSALESELVHFRDRAIG EKELPVADSLMDQGDISLPV MYEDGGKLISSPDTRLVEVH LQEVPQHPELQKYEKTNTFV EFNFDSVTESTNGFYDCKEN RIPEGSQGMAEQLQQCIEES IIDEFLQQAPPPGVRKLDAQ EHTEETLNQSTELRLQKADL NHLGALGSDNPGNKNILDAE NTRGEAKELTRNVKMGDPLQ AYRLISVVSHIGSSPNSGHY

		ADLQRFQRDCGDASQEQHQRDL ENGSALESELVHFRDRAIGEKE LPVADSLMDQGDISLPVMYEDG GKLISSPDTRLVEVHLQEVPQH PELQKYEKTNTFVEEFNFDSVTE STNGFYDCKENRIPEGSQGMAE QLQQCIEESIIDEFLQQAPPPG VRKLDAQEHTEETLNQSTELRL QKADLNHLGALGSDNPGNKNIL DAENTRGEAKELTRNVKMGDPL QAYRLISVVSHIGSSPNSGHYI SDVYDFQKQAWFTYNDLCVSEI SETKMQEARLHSGYIFFYMHNG IFEELLRKAENSRLPSTQAGVI PQGEYEGDSLYRPA		ISDVYDFQKQAWFTYNDLCV SEISETKMQEARLHSGYIFF YMHN
UBP6_HUMAN Ubiquitin carboxyl-terminal hydrolase 6	55	MDMVENADSLQAQERKDILMKY DKGHRAGLPEDKGPEPVGINSS IDRFGILHETELPPVTAREAKK IRREMTRTSKWMEMLGEWETYK HSSKLIDRVYKGIPMNIRGPVW SVLLNIQEIKLKNPGRYQIMKE RGKRSSEHIHHIDLDVRTTLRN HVFFRDRYGAKQRELFYILLAY SEYNPEVGYCRDLSHITALFLL YLPEEDAFWALVQLLASERHSL PGFHSPNGGTVQGLQDQQEHVV PKSQPKTMWHQDKEGLCGQCAS LGCLLRNLIDGISLGLTLRLWD VYLVEGEQVLMPIT SIALKVQQKRLMKTSRCGLWAR LRNQFFDTWAMNDDTVLKHLRA STKKLTRKQGDLPPPAKREQGS LAPRPVPASRGGKTLCKGYRQA PPGPPAQFQRPICSASPPWASR FSTPCPGGAVREDTYPVGTQGV PSLALAQGGPQGSWRFLEWKSM PRLPTDLDIGGPWFPHYDFEWS CWVRAISQEDQLATCWQAEHCG EVHNKDMSWPEEMSFTANSSKI DRQKVPTEKGATGLSNLGNTCF MNSSIQCVSNTQPLTQYFISGR HLYELNRTNPIGMKGHMAKCYG DLVQELWSGTQKSV APLKLRRTIAKYAPKFDGFQQQ DSQELLAFLLDGLHEDLNRVHE KPYVELKDSDGRPDWEVAAEAW DNHLRRNRSIIVDLFHGQLRSQ VKCKTCGHISVRFDPFNFLSLP LPMDSYMDLEITVIKLDGTTPV RYGLRLNMDEKYTGLKKQLRDL CGLNSEQILLAEVHDSNIKNFP	167	KGATGLSNLGNTCFMNSSIQ CVSNTQPLTQYFISGRHLYE LNRTNPIGMKGHMAKCYGDL VQELWSGTQKSVAPLKLRRT IAKYAPKFDGFQQQDSQELL AFLLDGLHEDLNRVHEKPYV ELKDSDGRPDWE VAAEAWDNHLRRNRSIIVDL FHGQLRSQVKCKTCGHISVR FDPNFLSLPLPMDSYMDLEI TVIKLDGTTPVRYGLRLNMD EKYTGLKKQLRDLCGLNSEQ ILLAEVHDSNIKNFPQDNQK VQLSVSGFLCAFEIPVPSSP ISASSPTQIDFSSSPSTNGM FTLTTNGDLPKPIFIPNGMP NTVVPCGTEKNFTNGMVNGH MPSLPDSPFTGYIIAVHRKM MRTELYFLSPQENRPSLFGM PLIVPCTVHTRKKDLYDAVW IQVSWLARPLPPQEASIHAQ DRDNCMGYQYPFTLRVVQKD GNSCAWCPQYRFCRGCKIDC GEDRAFIGNAYIAVDWHPTA LHLRYQTSQERVVDKHESVE QSRRAQAEPINLDSCLRAFT SEEELGESEMYYCSKCKTHC LATKKLDLWRLPPFLIIHLK RFQFVNDQWIKSQKIVRFLR ESFDPSAFLVPRDPALCQHK PLTPQGDELSKPRILAREVK KVDAQSSAGKEDMLLSKSPS SLSANISSSPKGSPSSSRKS GTSCPSSKNSSPNSSPRTLG RSKGRLRLPQIGSKNKPSSS KKNLDASKENGAGQICELAD

		QDNQKVQLSVSGFLCAFEIPVP SSPISASSPTQIDFSSSPSTNG MFTLTTNGDLPKPIFIPNGMPN TVVPCGTEKNFTNGMVNGHMPS LPDSPFTGYIIAVHRKMMRTEL YFLSPQENRPSLFG MPLIVPCTVHTRKKDLYDAVWI QVSWLARPLPPQEASIHAQDRD NCMGYQYPFTLRVVQKDGNSCA WCPQYRFCRGCKIDCGEDRAFI GNAYIAVDWHPTALHLRYQTSQ ERVVDKHESVEQSRRAQAEPIN LDSCLRAFTSEEELGESEMYYC SKCKTHCLATKKLDLWRLPPFL IIHLKRFQFVNDQWIKSQKIVR FLRESFDPSAFLVPRDPALCQH KPLTPQGDELSKPRILAREVKK VDAQSSAGKEDMLLSKSPSSLS ANISSSPKGSPSSSRKSGTSCP SSKNSSPNSSPRTL GRSKGRLRLPQIGSKNKPSSSK KNLDASKENGAGQICELADALS RGHMRGGSQPELVTPQDHEVAL ANGFLYEHEACGNGCGDGYSNG QLGNHSEEDSTDDQREDTHIKP IYNLYAISCHSGILSGGHYITY AKNPNCKWYCYNDSSCEELHPD EIDTDSAYILFYEQQGIDYAQF LPKIDGKKMADTSSTDEDSESD YEKYSMLQ		ALSRGHMRGGSQPELVTPQD HEVALANGFLYEHEACGNGC GDGYSNGQLGNHSEEDSTDD QREDTHIKPIYNLYAISCHS GILSGGHYITYAKNPNCKWY CYNDSSCEELHPDEIDTDSA YILFYEQQG
UBP53_HUMAN Inactive ubiquitin carboxyl-terminal hydrolase 53	56	MAWVKFLRKPGGNLGKVYQPGS MLSLAPTKGLLNEPGQNSCFLN SAVQVLWQLDIFRRSLRVLTGH VCQGDACIFCALKTIFAQFQHS REKALPSDNIRHALAESFKDEQ RFQLGLMDDAAECFENMLERIH FHIVPSRDADMCTSKSCITHQK FAMTLYEQCVCRSCGASSDPLP FTEFVRYISTTALCNEVERMLE RHERFKPEMFAELLQAANTTDD YRKCPSNCGQKIKIRRVLMNCP EIVTIGLVWDSEHSDLTEAVVR NLATHLYLPGLFYRVTDENAKN SELNLVGMICYTSQ HYCAFAFHTKSSKWVFFDDANV KEIGTRWKDVVSKCIRCHFQPL LLFYANPDGTAVSTEDALRQVI SWSHYKSVAENMGCEKPVIHKS DNLKENGFGDQAKQRENQKFPT DNISSSNRSHSHTGVGKGPAKL SHIDQREKIKDISRECALKAIE	168	APTKGLLNEPGQNSCFLNSA VQVLWQLDIFRRSLRVLTGH VCQGDACIFCALKTIFAQFQ HSREKALPSDNIRHALAESF KDEQRFQLGLMDDAAECFEN MLERIHFHIVPSRDADMCTS KSCITHQKFAMTLYEQCVCR SCGASSDPLPFTEFVRYIST TALCNEVERMLERHERFKPE MFAELLQAANTTDDYRKCPS NCGQKIKIRRVLMNCPEIVT IGLVWDSEHSDLTEAVVRNL ATHLYLPGLFYRVTDENAKN SELNLVGMICYTSQHYCAFA FHTKSSKWVFFDDANVKEIG TRWKDVVSKCIRCHFQPLLL FYANPDGTAVSTEDALRQVI SWSHYKSVAENMGCEKPVIH KSDNLKENGFGDQAKQRENQ KFPTDNISSSNRSHSHTGVG KGPAKLSHIDQREKIKDISR

		QKNLLSSQRKDLEKGQRKDLGR HRDLVDEDLSHFQSGSPPAPNG FKQHGNPHLYHSQGKGSYKHDR VVPQSRASAQIISSSKSQILAP GEKITGKVKSDNGTGYDTDSSQ DSRDRGNSCDSSSKSRNRGWKP MRETLNVDSIFSES EKRQHSPRHKPNISNKPKSSKD PSFSNWPKENPKQKGLMTIYED EMKQEIGSRSSLESNGKGAEKN KGLVEGKVHGDNWQMQRTESGY ESSDHISNGSTNLDSPVIDGNG TVMDISGVKETVCFSDQITTSN LNKERGDCTSLQSQHHLEGFRK ELRNLEAGYKSHEFHPESHLQI KNHLIKRSHVHEDNGKLFPSSS LQIPKDHNAREHIHQSDEQKLE KPNECKFSEWLNIENSERTGLP FHVDNSASGKRVNSNEPSSLWS SHLRTVGLKPETAPLIQQQNIM DQCYFENSLSTECI IRSASRSDGCQMPKLFCQNLPP PLPPKKYAITSVPQSEKSESTP DVKLTEVFKATSHLPKHSLSTA SEPSLEVSTHMNDERHKETFQV RECFGNTPNCPSSSSTNDFQAN SGAIDAFCQPELDSISTCPNET VSLTTYFSVDSCMTDTYRLKYH QRPKLSFPESSGFCNNSLS		ECALKAIEQKNLLSSQRKDL EKGQRK
U17LO_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 24	57	MEDDSLYLRGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPEC LDMQPYMSQPNTGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTASSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK	169	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQPNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS

		NHHPEQQSSLLNLSSSTPTHQE SMNTGTLASLRGRARRSKGKNK HSKRALLVCQ		
U17LM_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 22		MEDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPEC LDMQPYMSQQNTGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTASSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK NHHPEQQSSLLKLSSTTPTHQE SMNTGTLASLRGRARRSKGKNK HSKRALLVCQ		AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS
UBP5_HUMAN Ubiquitin carboxyl-terminal hydrolase 5	58	MAELSEEALLSVLPTIRVPKAG DRVHKDECAFSFDTPESEGGLY ICMNTFLGFGKQYVERHFNKTG QRVYLHLRRTRRPKEEDPATGT GDPPRKKPTRLAIGVEGGFDLS EEKFELDEDVKIVILPDYLEIA RDGLGGLPDIVRDRVTSAVEAL LSADSASRKQEVQAWDGEVRQV SKHAFSLKQLDNPARIPPCGWK CSKCDMRENLWLNLTDGSILCG RRYFDGSGGNNHAVEHYRETGY PLAVKLGTITPDGADVYSYDED DMVLDPSLAEHLSHFGIDMLKM QKTDKTMTELEIDM NQRIGEWELIQESGVPLKPLFG PGYTGIRNLGNSCYLNSVVQVL FSIPDFQRKYVDKLEKIFQNAP TDPTQDFSTQVAKLGHGLLSGE YSKPVPESGDGERVPEQKEVQD GIAPRMFKALIGKGHPEFSTNR QQDAQEFFLHLINMVERNCRSS ENPNEVFRFLVEEKIKCLATEK VKYTQRVDYIMQLPVPMDAALN	170	FGPGYTGIRNLGNSCYLNSV VQVLFSIPDFQRKYVDKLEK IFQNAPTDPTQDFSTQVAKL GHGLLSGEYSKPVPESGDGE RVPEQKEVQDGIAPRMFKAL IGKGHPEFSTNRQQDAQEFF LHLINMVERNCRSSENPNEV FRFLVEEKIKCLATEKVKYT QRVDYIMQLPVPMDAALNKE ELLEYEEKKRQAEEEKMALP ELVRAQVPFSSCLEAYGAPE QVDDFWSTALQAKSVAVKTT RFASFPDYLVIQIKKFTFGL DWVPKKLDVSIEMPEELDIS QLRGTGLQPGEEELPDIAPP LVTPDEPKGSLGFYGNEDED SFCSPHFSSPTSPMLDESVI IQLVEMGFPMDACRKAVYYT GNSGAEAAMNWVMSHMDDPD FANPLILPGSSGPGSTSAAA DPPPEDCVTTIVSMGFSRDQ ALKALRATNNSLERAVDWIF SHIDDLDAEAAMDISEGRSA

		KEELLEYEEKKRQAEEEKMALP ELVRAQVPFSSCLEAYGAPEQV DDFWSTALQAKSVAVKTTRFAS FPDYLVIQIKKFTFGLDWVPKK LDVSIEMPEELDIS QLRGTGLQPGEEELPDIAPPLV TPDEPKGSLGFYGNEDEDSFCS PHFSSPTSPMLDESVIIQLVEM GFPMDACRKAVYYTGNSGAEAA MNWVMSHMDDPDFANPLILPGS SGPGSTSAAADPPPEDCVTTIV SMGFSRDQALKALRATNNSLER AVDWIFSHIDDLDAEAAMDISE GRSAADSISESVPVGPKVRDGP GKYQLFAFISHMGTSTMCGHYV CHIKKEGRWVIYNDQKVCASEK PPKDLGYIYFYQRVAS		ADSISESVPVGPKVRDGPGK YQLFAFISHMGTSTMCGHYV CHIKKEGRWVIYNDQKVCAS EKPPKDLGYIYFYQRVA
UBP25_HUMAN Ubiquitin carboxyl-terminal hydrolase 25	59	MTVEQNVLQQSAAQKHQQTFLN QLREITGINDTQILQQALKDSN GNLELAVAFLTAKNAKTPQQEE TTYYQTALPGNDRYISVGSQAD TNVIDLTGDDKDDLQRAIALSL AESNRAFRETGITDEEQAISRV LEASIAENKACLKRTPTEVWRD SRNPYDRKRQDKAPVGLKNVGN TCWFSAVIQSLFNLLEFRRLVL NYKPPSNAQDLPRNQKEHRNLP FMRELRYLFALLVGTKRKYVDP SRAVEILKDAFKSNDSQQQDVS EFTHKLLDWLEDAFQMKAEEET DEEKPKNPMVELFY GRFLAVGVLEGKKFENTEMFGQ YPLQVNGFKDLHECLEAAMIEG EIESLHSENSGKSGQEHWFTEL PPVLTFELSRFEFNQALGRPEK IHNKLEFPQVLYLDRYMHRNRE ITRIKREEIKRLKDYLTVLQQR LERYLSYGSGPKRFPLVDVLQY ALEFASSKPVCTSPVDDIDASS PPSGSIPSQTLPSTTEQQGALS SELPSTSPSSVAAISSRSVIHK PFTQSRIPPDLPMHPAPRHITE EELSVLESCLHRWRTEIENDTR DLQESISRIHRTIELMYSDKSM IQVPYRLHAVLVHE GQANAGHYWAYIFDHRESRWMK YNDIAVTKSSWEELVRDSFGGY RNASAYCLMYINDKAQFLIQEE FNKETGQPLVGIETLPPDLRDF VEEDNQRFEKELEEWDAQLAQK ALQEKLLASQKLRESETSVTTA		KAPVGLKNVGNTCWFSAVIQ SLFNLLEFRRLVLNYKPPSN AQDLPRNQKEHRNLPFMREL RYLFALLVGTKRKYVDPSRA VEILKDAFKSNDSQQQDVSE FTHKLLDWLEDAFQMKAEEE TDEEKPKNPMVELFYGRFLA VGVLEGKKFENTEMFGQYPL QVNGFKDLHECLEAAMIEGE IESLHSENSGKSGQEHWFTE LPPVLTFELSRFEFNQALGR PEKIHNKLEFPQVLYLDRYM HRNREITRIKREEIKRLKDY LTVLQQRLERYLSYGSGPKR FPLVDVLQYALEFASSKPVC TSPVDDIDASSPPSGSIPSQ TLPSTTEQQGALSSELPSTS PSSVAAISSRSVIHKPFTQS RIPPDLPMHPAPRHITEEEL SVLESCLHRWRTEIENDTRD LQESISRIHRTIELMYSDKS MIQVPYRLHAVLVHEGQANA GHYWAYIFDHRESRWMKYND IAVTKSSWEELVRDSFGGYR NAS

		QAAGDPEYLEQPSRSDFSKHLK EETIQIITKASHEHEDKSPETV LQSAIKLEYARLVKLAQEDTPP ETDYRLHHVVVYFIQNQAPKKI IEKTLLEQFGDRNLSFDERCHN IMKVAQAKLEMIKPEEVNLEEY EEWHQDYRKFRETTMYLIIGLE NFQRESYIDSLLFL ICAYQNNKELLSKGLYRGHDEE LISHYRRECLLKLNEQAAELFE SGEDREVNNGLIIMNEFIVPFL PLLLVDEMEEKDILAVEDMRNR WCSYLGQEMEPHLQEKLTDFLP KLLDCSMEIKSFHEPPKLPSYS THELCERFARIMLSLSRTPADG R		
UBP33_HUMAN Ubiquitin carboxyl-terminal hydrolase 33	60	MTGSNSHITILTLKVLPHFESL GKQEKIPNKMSAFRNHCPHLDS VGEITKEDLIQKSLGTCQDCKV QGPNLWACLENRCSYVGCGESQ VDHSTIHSQETKHYLTVNLTTL RVWCYACSKEVFLDRKLGTQPS LPHVRQPHQIQENSVQDFKIPS NTTLKTPLVAVFDDLDIEADEE DELRARGLTGLKNIGNTCYMNA ALQALSNCPPLTQFFLDCGGLA RTDKKPAICKSYLKLMTELWHK SRPGSVVPTTLFQGIKTVNPTF RGYSQQDAQEFLRCLMDLLHEE LKEQVMEVEEDPQT ITTEETMEEDKSQSDVDFQSCE SCSNSDRAENENGSRCFSEDNN ETTMLIQDDENNSEMSKDWQKE KMCNKINKVNSEGEFDKDRDSI SETVDLNNQETVKVQIHSRASE YITDVHSNDLSTPQILPSNEGV NPRLSASPPKSGNLWPGLAPPH KKAQSASPKRKKQHKKYRSVIS DIFDGTIISSVQCLTCDRVSVT LETFQDLSLPIPGKEDLAKLHS SSHPTSIVKAGSCGEAYAPQGW IAFFMEYVKRFVVSCVPSWFWG PVVTLQDCLAAFFARDELKGDN MYSCEKCKKLRNGV KFCKVQNFPEILCIHLKRFRHE LMFSTKISTHVSFPLEGLDLQP FLAKDSPAQIVTYDLLSVICHH GTASSGHYIAYCRNNLNNLWYE FDDQSVTEVSESTVQNAEAYVL FYRKSSEEAQKERRRISNLLNI MEPSLLQFYISRQWLNKFKTFA	171	ARGLTGLKNIGNTCYMNAAL QALSNCPPLTQFFLDCGGLA RTDKKPAICKSYLKLMTELW HKSRPGSVVPTTLFQGIKTV NPTFRGYSQQDAQEFLRCLM DLLHEELKEQVMEVEEDPQT ITTEETMEEDKSQSDVDFQS CESCSNSDRAENENGSRCFS EDNNETTMLIQDDENNSEMS KDWQKEKMCNKINKVNSEGE FDKDRDSISETVDLNNQETV KVQIHSRASEYITDVHSNDL STPQILPSNEGVNPRLSASP PKSGNLWPGLAPPHKKAQSA SPKRKKQHKKYRSVISDIFD GTIISSVQCLTCDRVSVTLE TFQDLSLPIPGKEDLAKLHS SSHPTSIVKAGSCGEAYAPQ GWIAFFMEYVKRFVVSCVPS WFWGPVVTLQDCLAAFFARD ELKGDNMYSCEKCKKLRNGV KFCKVQNFPEILCIHLKRFR HELMFSTKISTHVSFPLEGL DLQPFLAKDSPAQIVTYDLL SVICHHGTASSGHYIAYCRN NLNNLWYEFDDQSVTEVSES TVQNAEAYVLFYRKSS

		EPGPISNNDFLCIHGGVPPRKA GYIEDLVLMLPQNIWDNLYSRY GGGPAVNHLYICHTCQIEAEKI EKRRKTELEIFIRLNRAFQKED SPATFYCISMQWFREWESFVKG KDGDPPGPIDNTKIAVTKCGNV MLRQGADSGQISEETWNFLQSI YGGGPEVILRPPVVHVDPDILQ AEEKIEVETRSL		
UBP21_HUMAN Ubiquitin carboxyl-terminal hydrolase 21	61	MPQASEHRLGRTREPPVNIQPR VGSKLPFAPRARSKERRNPASG PNPMLRPLPPRPGLPDERLKKL ELGRGRTSGPRPRGPLRADHGV PLPGSPPPTVALPLPSRTNLAR SKSVSSGDLRPMGIALGGHRGT GELGAALSRLALRPEPPTLRRS TSLRRLGGFPGPPTLFSIRTEP PASHGSFHMISARSSEPFYSDD KMAHHTLLLGSGHVGLRNLGNT CFLNAVLQCLSSTRPLRDFCLR RDFRQEVPGGGRAQELTEAFAD VIGALWHPDSCEAVNPTRFRAV FQKYVPSFSGYSQQ DAQEFLKLLMERLHLEINRRGR RAPPILANGPVPSPPRRGGALL EEPELSDDDRANLMWKRYLERE DSKIVDLFVGQLKSCLKCQACG YRSTTFEVFCDLSLPIPKKGFA GGKVSLRDCFNLFTKEEELESE NAPVCDRCRQKTRSTKKLTVQR FPRILVLHLNRFSASRGSIKKS SVGVDFPLQRLSLGDFASDKAG SPVYQLYALCNHSGSVHYGHYT ALCRCQTGWHVYNDSRVSPVSE NQVASSEGYVLFYQLMQEPPRC L	172	LGSGHVGLRNLGNTCFLNAV LQCLSSTRPLRDFCLRRDFR QEVPGGGRAQELTEAFADVI GALWHPDSCEAVNPTRFRAV FQKYVPSFSGYSQQDAQEFL KLLMERLHLEINRRGRRAPP ILANGPVPSPPRRGGALLEE PELSDDDRANLMWK RYLEREDSKIVDLFVGQLKS CLKCQACGYRSTTFEVFCDL SLPIPKKGFAGGKVSLRDCF NLFTKEEELESENAPVCDRC RQKTRSTKKLTVQRFPRILV LHLNRFSASRGSIKKSSVGV DFPLQRLSLGDFASDKAGSP VYQLYALCNHSGSVHYGHYT ALCRCQTGWHVYNDSRVSPV SENQVASSEGYVLFYQLMQ
U17L4_HUMAN Inactive ubiquitin carboxyl-terminal hydrolase 17-like protein 4	62	MGDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS SETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYENASLQCLTYTLPLANYMLS REHSQTCQRPKCCMLCTMQAHI TWALHSPGHVIQPSQALAAGFH RGKQEDVHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GCWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVKQALEQLVK PEELNGENAYHCGLCLQRAPAS NTLTLHTSAKVLILVLKRFSDV AGNKLAKNVQYPEC	173	AVGAGLQNMGNTCYENASLQ CLTYTLPLANYMLSREHSQT CQRPKCCMLCTMQAHITWAL HSPGHVIQPSQALAAGFHRG KQEDVHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGCWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVKQA LEQLVKPEELNGENAYHCGL CLQRAPASNTLTLHTSAKVL ILVLKRFSDVAGNKLAKNVQ YPECLDMQPYMSQQNTGPLV YVLYAVLVHAGWSCHDGYYF SYVKAQEGQWYKMDDAEVTV CSITSVLSQQAYVLFYIQKS

		LDMQPYMSQQNTGPLVYVLYAV LVHAGWSCHDGYYFSYVKAQEG QWYKMDDAEVTVCSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRPATQGELKR DHPCLQVPELDEHLVERATEES TLDHWKFPQEQNKMKPEFNVRK VEGTLPPNVLVIHQSKYKCGMK NHHPEQQSSLLNLSSMNSTDQE SMNTGTLASLQGRTRRSKGKNK HSKRSLLVCQ		
U17LK_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 20	63	MEDDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSSRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KTLTLHTSAKVLILVLKRFSDV TGNKIAKNVQYPECLDMQPYMS QPNTGPLVYVLYAVLVHAGWSC HNGHYFSYVKAQEGQWYKMDDA EVTASSITSVLSQQAYVLFYIQ KSEWERHSESVSRGREPRALGA EDTDRRATQGELKRDHPCLQAP ELDEHLVERATQESTLDHWKFL QEQNKTKPEFNVRKVEGTLPPD VLVIHQSKYKCGMKNHHPEQQS SLLNLSSTTPTHQESMNTGTLA SLRGRARRSKGKNKHSKRALLV CQ	174	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKTLTLHTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQPNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS
UBP12_HUMAN Ubiquitin carboxyl-terminal hydrolase 12	64	MEILMTVSKFASICTMGANASA LEKEIGPEQFPVNEHYFGLVNF GNTCYCNSVLQALYFCRPFREK VLAYKSQPRKKESLLTCLADLF HSIATQKKKVGVIPPKKFITRL RKENELFDNYMQQDAHEFLNYL LNTIADILQEERKQEKQNGRLP NGNIDNENNNSTPDPTWVHEIF QGTLTNETRCLTCETISSKDED FLDLSVDVEQNTSITHCLRGFS NTETLCSEYKYYCEECRSKQEA HKRMKVKKLPMILALHLKRFKY MDQLHRYTKLSYRVVFPLELRL FNTSGDATNPDRMY	175	EHYFGLVNFGNTCYCNSVLQ ALYFCRPFREKVLAYKSQPR KKESLLTCLADLFHSIATQK KKVGVIPPKKFITRLRKENE LFDNYMQQDAHEFLNYLLNT IADILQEERKQEKQNGRLPN GNIDNENNNSTPDPTWVHEI FQGTLTNETRCLTCETISSK DEDFLDLSVDVEQNTSITHC LRGFSNTETLCSEYKYYCEE CRSKQEAHKRMKVKKLPMIL ALHLKRFKYMDQLHRYTKLS YRVVFPLELRLFNTSGDATN PDRMYDLVAVVVHCGSGPNR GHYIAIVKSHDFWLLFDDDI

		DLVAVVVHCGSGPNRGHYIAIV KSHDFWLLFDDDIVEKIDAQAI EEFYGLTSDISKNSESGYILFY QSRD		VEKIDAQAIEEFYGLTSDIS KNSESGYILFYQSR
UL17C_HUMAN Ubiquitin carboxyl-terminal hydrolase 17-like protein 12	65	MEEDSLYLGGEWQFNHFSKLTS SRPDAAFAEIQRTSLPEKSPLS CETRVDLCDDLAPVARQLAPRE KLPLSNRRPAAVGAGLQNMGNT CYVNASLQCLTYTPPLANYMLS REHSQTCHRHKGCMLCTMQAHI TRALHNPGHVIQPSQALAAGFH RGKQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQIFG GYWRSQIKCLHCHGISDTFDPY LDIALDIQAAQSVQQALEQLVK PEELNGENAYHCGVCLQRAPAS KMLTLLTSAKVLILVLKRFSDV TGNKIAKNVQYPEC LDMQPYMSQPNTGPLVYVLYAV LVHAGWSCHNGHYFSYVKAQEG QWYKMDDAEVTASSITSVLSQQ AYVLFYIQKSEWERHSESVSRG REPRALGAEDTDRRATQGELKR DHPCLQAPELDEHLVERATQES TLDHWKFLQEQNKTKPEFNVRK VEGTLPPDVLVIHQSKYKCGMK NHHPEQQSSLLKLSSTTPTHQE SMNTGTLASLRGRARRSKGKNK HSKRALLVCQ	176	AVGAGLQNMGNTCYVNASLQ CLTYTPPLANYMLSREHSQT CHRHKGCMLCTMQAHITRAL HNPGHVIQPSQALAAGFHRG KQEDAHEFLMFTVDAMKKAC LPGHKQVDHHSKDTTLIHQI FGGYWRSQIKCLHCHGISDT FDPYLDIALDIQAAQSVQQA LEQLVKPEELNGENAYHCGV CLQRAPASKMLTLLTSAKVL ILVLKRFSDVTGNKIAKNVQ YPECLDMQPYMSQPNTGPLV YVLYAVLVHAGWSCHNGHYF SYVKAQEGQWYKMDDAEVTA SSITSVLSQQAYVLFYIQKS
UBP20_HUMAN Ubiquitin carboxyl-terminal hydrolase	66	MGDSRDLCPHLDSIGEVTKEDL LLKSKGTCQSCGVTGPNLWACL QVACPYVGCGESFADHSTIHAQ AKKHNLTVNLTTFRLWCYACEK EVFLEQRLAAPLLGSSSKFSEQ DSPPPSHPLKAVPIAVADEGES ESEDDDLKPRGLTGMKNLGNSC YMNAALQALSNCPPLTQFFLEC GGLVRTDKKPALCKSYQKLVSE VWHKKRPSYVVPTSLSHGIKLV NPMFRGYAQQDTQEFLRCLMDQ LHEELKEPVVATVALTEARDSD SSDTDEKREGDRSPSEDEFLSC DSSSDRGEGDGQGR GGGSSQAETELLIPDEAGRAIS EKERMKDRKFSWGQQRTNSEQV DEDADVDTAMAALDDQPAEAQP PSPRSSSPCRTPEPDNDAHLRS SSRPCSPVHHHEGHAKLSSSPP RASPVRMAPSYVLKKAQVLSAG SRRRKEQRYRSVISDIFDGSIL SLVQCLTCDRVSTTVETFQDLS	177	PRGLTGMKNLGNSCYMNAAL QALSNCPPLTQFFLECGGLV RTDKKPALCKSYQKLVSEVW HKKRPSYVVPTSLSHGIKLV NPMFRGYAQQDTQEFLRCLM DQLHEELKEPVVATVALTEA RDSDSSDTDEKREGDRSPSE DEFLSCDSSSDRGEGDGQGR GGGSSQAETELLIPDEAGRA ISEKERMKDRKFSWGQQRTN SEQVDEDADVDTAMAALDDQ PAEAQPPSPRSSSPCRTPEP DNDAHLRSSSRPCSPVHHHE GHAKLSSSPPRASPVRMAPS YVLKKAQVLSAGSRRRKEQR YRSVISDIFDGSILSLVQCL TCDRVSTTVETFQDLSLPIP GKEDLAKLHSAIYQNVPAKP GACGDSYAAQGWLAFIVEYI RRFVVSCTPSWFWGPVVTLE DCLAAFFAADELKGDNMYSC ERCKKLRNGVKYCKVLRLPE

		LPIPGKEDLAKLHSAIYQNVPA KPGACGDSYAAQGWLAFIVEYI RRFVVSCTPSWFWGPVVTLEDC LAAFFAADELKGDNMYSCERCK KLRNGVKYCKVLRLPEILCIHL KRFRHEVMYSFKIN SHVSFPLEGLDLRPFLAKECTS QITTYDLLSVICHHGTAGSGHY IAYCQNVINGQWYEFDDQYVTE VHETVVQNAEGYVLFYRKSSEE AMRERQQVVSLAAMREPSLLRF YVSREWLNKFNTFAEPGPITNQ TFLCSHGGIPPHKYHYIDDLVV ILPQNVWEHLYNRFGGGPAVNH LYVCSICQVEIEALAKRRRIEI DTFIKLNKAFQAEESPGVIYCI SMQWFREWEAFVKGKDNEPPGP IDNSRIAQVKGSGHVQLKQGAD YGQISEETWTYLNSLYGGGPEI AIRQSVAQPLGPENLHGEQKIE AETRAV		ILCIHLKRFRHEVMYSFKIN SHVSFPLEGLDLRPFLAKEC TSQITTYDLLSVICHHGTAG SGHYIAYCQNVINGQWYEFD DQYVTEVHETVVQNAEGYVL FYRKSS
UBP46_HUMAN Ubiquitin carboxyl-terminal hydrolase 46	67	MTVRNIASICNMGTNASALEKD IGPEQFPINEHYFGLVNFGNTC YCNSVLQALYFCRPFRENVLAY KAQQKKKENLLTCLADLFHSIA TQKKKVGVIPPKKFISRLRKEN DLFDNYMQQDAHEFLNYLLNTI ADILQEEKKQEKQNGKLKNGNM NEPAENNKPELTWVHEIFQGTL TNETRCLNCETVSSKDEDFLDL SVDVEQNTSITHCLRDFSNTET LCSEQKYYCETCCSKQEAQKRM RVKKLPMILALHLKRFKYMEQL HRYTKLSYRVVFPLELRLFNTS SDAVNLDRMYDLVA VVVHCGSGPNRGHYITIVKSHG FWLLFDDDIVEKIDAQAIEEFY GLTSDISKNSESGYILFYQSRE	178	EHYFGLVNFGNTCYCNSVLQ ALYFCRPFRENVLAYKAQQK KKENLLTCLADLFHSIATQK KKVGVIPPKKFISRLRKEND LFDNYMQQDAHEFLNYLLNT IADILQEEKKQEKQNGKLKN GNMNEPAENNKPELTWVHEI FQGTLTNETRCLNCETVSSK DEDFLDLSVDVEQNTSITHC LRDFSNTETLCSEQKYYCET CCSKQEAQKRMRVKKLPMIL ALHLKRFKYMEQLHRYTKLS YRVVFPLELRLFNTSSDAVN LDRMYDLVAVVVHCGSGPNR GHYITIVKSHGFWLLFDDDI VEKIDAQAIEEFYGLTSDIS KNSESGYILFYQSR
CYLD_HUMAN Ubiquitin carboxyl-terminal hydrolase CYLD	68	MSSGLWSQEKVTSPYWEERIFY LLLQECSVTDKQTQKLLKVPKG SIGQYIQDRSVGHSRIPSAKGK KNQIGLKILEQPHAVLFVDEKD VVEINEKFTELLLAITNCEERF SLFKNRNRLSKGLQIDVGCPVK VQLRSGEEKFPGVVRFRGPLLA ERTVSGIFFGVELLEEGRGQGF TDGVYQGKQLFQCDEDCGVFVA LDKLELIEDDDTALESDYAGPG DTMQVELPPLEINSRVSLKVGE TIESGTVIFCDVLPGKESLGYF	179	GKKKGIQGHYNSCYLDSTLF CLFAFSSVLDTVLLRPKEKN DVEYYSETQELLRTEIVNPL RIYGYVCATKIMKLRKILEK VEAASGFTSEEKDPEEFLNI LFHHILRVEPLLKIRSAGQK VQDCYFYQIFME KNEKVGVPTIQQLLEWSFIN SNLKFAEAPSCLIIQMPRFG KDFKLFKKIFPSLELNITDL LEDTPRQCRICGGLAMYECR ECYDDPDISAGKIKQFCKTC NTQVHLHPKRLNHKYNPVSL

		VGVDMDNPIGNWDGRFDGVQLC SFACVESTILLHIN DIIPALSESVTQERRPPKLAFM SRGVGDKGSSSHNKPKATGSTS DPGNRNRSELFYTLNGSSVDSQ PQSKSKNTWYIDEVAEDPAKSL TEISTDFDRSSPPLQPPPVNSL TTENRFHSLPFSLTKMPNTNGS IGHSPLSLSAQSVMEELNTAPV QESPPLAMPPGNSHGLEVGSLA EVKENPPFYGVIRWIGQPPGLN EVLAGLELEDECAGCTDGTFRG TRYFTCALKKALFVKLKSCRPD SRFASLQPVSNQIERCNSLAFG GYLSEVVEENTPPKMEKEGLEI MIGKKKGIQGHYNS CYLDSTLFCLFAFSSVLDTVLL RPKEKNDVEYYSETQELLRTEI VNPLRIYGYVCATKIMKLRKIL EKVEAASGFTSEEKDPEEFLNI LFHHILRVEPLLKIRSAGQKVQ DCYFYQIFMEKNEKVGVPTIQQ LLEWSFINSNLKFAEAPSCLII QMPRFGKDFKLFKKIFPSLELN ITDLLEDTPRQCRICGGLAMYE CRECYDDPDISAGKIKQFCKTC NTQVHLHPKRLNHKYNPVSLPK DLPDWDWRHGCIPCQNMELFAV LCIETSHYVAFVKYGKDDSAWL FFDSMADRDGGQNGFNIPQVTP CPEVGEYLKMSLEDLHSLDSRR IQGCARRLLCDAYMCMYQSPTM SLYK		PKDLPDWDWRHGCIPCQNME LFAVLCIETSHYVAFVKYGK DDSAWLFFDSMADRDGGQNG FNIPQVTPCPEVGEYLKMSL EDLHSLDSRRIQGCARRLLC DAYMCMYQSPT
UBP16_HUMAN Ubiquitin carboxyl-terminal hydrolase 16	69	MGKKRTKGKTVPIDDSSETLEP VCRHIRKGLEQGNLKKALVNVE WNICQDCKTDNKVKDKAEEETE EKPSVWLCLKCGHQGCGRNSQE QHALKHYLTPRSEPHCLVLSLD NWSVWCYVCDNEVQYCSSNQLG QVVDYVRKQASITTPKPAEKDN GNIELENKKLEKESKNEQEREK KENMAKENPPMNSPCQITVKGL SNLGNTCFFNAVMQNLSQTPVL RELLKEVKMSGTIVKIEPPDLA LTEPLEINLEPPGPLTLAMSQF LNEMQETKKGVVTPKELFSQVC KKAVRFKGYQQQDS QELLRYLLDGMRAEEHQRVSKG ILKAFGNSTEKLDEELKNKVKD YEKKKSMPSFVDRIFGGELTSM IMCDQCRTVSLVHESFLDLSLP	180	ITVKGLSNLGNTCFFNAVMQ NLSQTPVLRELLKEVKMSGT IVKIEPPDLALTEPLEINLE PPGPLTLAMSQFLNEMQETK KGVVTPKELFSQVCKKAVRF KGYQQQDSQELLRYLLDGMR AEEHQRVSKGILKAFGNSTE KLDEELKNKVKDYEKKKSMP SFVDRIFGGELTSMIMCDQC RTVSLVHESFLDLSLPVLDD QSGKKSVNDKNLKKTVEDED QDSEEEKDNDSYIKERSDIP SGTSKHLQKKAKKQAKKQAK NQRRQQKIQGKVLHLNDICT IDHPEDSEYEAEMSLQGEVN IKSNHISQEGVMHKEYCVNQ KDLNGQAKMIESVTDNQKST EEVDMKNINMDNDLEVLTSS

		VLDDQSGKKSVNDKNLKKTVED EDQDSEEEKDNDSYIKERSDIP SGTSKHLQKKAKKQAKKQAKNQ RRQQKIQGKVLHLNDICTIDHP EDSEYEAEMSLQGEVNIKSNHI SQEGVMHKEYCVNQKDLNGQAK MIESVTDNQKSTEEVDMKNINM DNDLEVLTSSPTRNLNGAYLTE GSNGEVDISNGFKNLNLNAALH PDEINIEILNDSHT PGTKVYEVVNEDPETAFCTLAN REVFNTDECSIQHCLYQFTRNE KLRDANKLLCEVCTRRQCNGPK ANIKGERKHVYTNAKKQMLISL APPVLTLHLKRFQQAGFNLRKV NKHIKFPEILDLAPFCTLKCKN VAEENTRVLYSLYGVVEHSGTM RSGHYTAYAKARTANSHLSNLV LHGDIPQDFEMESKGQWFHISD THVQAVPTTKVLNSQAYLLFYE RIL		PTRNLNGAYLTEGSNGEVDI SNGFKNLNLNAALHPDEINI EILNDSHTPGTKVYEVVNED PETAFCTLANREVFNTDECS IQHCLYQFTRNEKLRDANKL LCEVCTRRQCNGPKANIKGE RKHVYTNAKKQMLISLAPPV LTLHLKRFQQAGFNLRKVNK HIKFPEIL DLAPFCTLKCKNVAEENTRV LYSLYGVVEHSGTMRSGHYT AYAKARTANSHLSNLVLHGD IPQDFEMESKGQWFHISDTH VQAVPTTKVLNSQAYLLFYE RIL
ALG13_HUMAN Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13	70	MKCVFVTVGTTSFDDLIACVSA PDSLQKIESLGYNRLILQIGRG TVVPEPFSTESFTLDVYRYKDS LKEDIQKADLVISHAGAGSCLE TLEKGKPLVVVINEKLMNNHQL ELAKQLHKEGHLFYCTCRVLTC PGQAKSIASAPGKCQDSAALTS TAFSGLDFGLLSGYLHKQALVT ATHPTCTLLFPSCHAFFPLPLT PTLYKMHKGWKNYCSQKSLNEA SMDEYLGSLGLFRKLTAKDASC LFRAISEQLFCSQVHHLEIRKA CVSYMRENQQTFESYVEGSFEK YLERLGDPKESAGQ LEIRALSLIYNRDFILYRFPGK PPTYVTDNGYEDKILLCYSSSG HYDSVYSKQFQSSAAVCQAVLY EILYKDVFVVDEEELKTAIKLF RSGSKKNRNNAVTGSEDAHTDY KSSNQNRMEEWGACYNAENIPE GYNKGTEETKSPENPSKMPFPY KVLKALDPEIYRNVEFDVWLDS RKELQKSDYMEYAGRQYYLGDK CQVCLESEGRYYNAHIQEVGNE NNSVTVFIEELAEKHVVPLANL KPVTQVMSVPAWNAMPSRKGRG YQKMPGGYVPEIVISEMDIKQQ KKMFKKIRGKEVYM TMAYGKGDPLLPPRLQHSMHYG HDPPMHYSQTAGNVMSNEHFHP	181	YRYKDSLKEDIQKADLVISH AGAGSCLETLEKGKPLVVVI NEKLMNNHQLELAKQLHKEG HLFYCTCRVLTCPGQAKSIA SAPGKCQDSAALTSTAFSGL DFGLLSGYLHKQALVTATHP TCTLLFPSCHAFFPLPLTPT LYKMHKGWKNYCSQKSLNEA SMDEYLGSLGLFRKLTAKDA SCLFRAISEQLFCSQVHHLE IRKACVSYMRENQQTFESYV EGSFEKYLERLGDPKESAGQ LEIRALSLIYNRDFILYRFP GKPPTYVTDNGYEDKILLCY SSSGHYDSVYS

		QHPSPRQGRGYGMPRNSSRFIN RHNMPGPKVDFYPGPGKRCCQS YDNFSYRSRSFRRSHRQMSCVN KESQYGFTPGNGQMPRGLEETI TFYEVEEGDETAYPTLPNHGGP STMVPATSGYCVGRRGHSSGKQ TLNLEEGNGQSENGRYHEEYLY RAEPDYETSGVYSTTASTANLS LQDRKSCSMSPQDTVTSYNYPQ KMMGNIAAVAASCANNVPAPVL SNGAAANQAISTTSVSSQNAIQ PLFVSPPTHGRPVI ASPSYPCHSAIPHAGASLPPPP PPPPPPPPPPPPPPPPPPPPP PALDVGETSNLQPPPPLPPPPY SCDPSGSDLPQDTKVLQYYFNL GLQCYYHSYWHSMVYVPQMQQQ LHVENYPVYTEPPLVDQTVPQC YSEVRREDGIQAEASANDTFPN ADSSSVPHGAVYYPVMSDPYGQ PPLPGFDSCLPVVPDYSCVPPW HPVGTAYGGSSQIHGAINPGPI GCIAPSPPASHYVPQGM		
OTU1_HUMAN Ubiquitin thioesterase OTU1	71	MFGPAKGRHFGVHPAPGFPGGV SQQAAGTKAGPAGAWPVGSRTD TMWRLRCKAKDGTHVLQGLSSR TRVRELQGQIAAITGIAPGGQR ILVGYPPECLDLSNGDTILEDL PIQSGDMLIIEEDQTRPRSSPA FTKRGASSYVRETLPVLTRTVV PADNSCLFTSVYYVVEGGVLNP ACAPEMRRLIAQIVASDPDFYS EAILGKTNQEYCDWIKRDDTWG GAIEISILSKFYQCEICVVDTQ TVRIDRFGEDAGYTKRVLLIYD GIHYDPLQRNFPDPDTPPLTIF SSNDDIVLVQALELADEARRRR QFTDVNRFTLRCMVCQKGLTGQ AEAREHAKETGHTNFGEV	182	QGLSSRTRVRELQGQIAAIT GIAPGGQRILVGYPPECLDL SNGDTILEDLPIQSGDMLII EEDQTRPRSSPAFTKRGASS YVRETLPVLTRTVVPADNSC LFTSVYYVVEGGVLNPACAP EMRRLIAQIVASDPDFYSEA ILGKTNQEYCDWIKRDDTWG GAIEISILSKFYQCEICVVD TQTVRIDRFGEDAGYTKRVL LIYDGIHYDPLQ
OTUD1_HUMAN OTU domain-containing protein 1	72	MQLYSSVCTHYPAGAPGPTAAA PAPPAAATPFKVSLQPPGAAGA APEPETGECQPAAAAEHREAAA VPAAKMPAFSSCFEVVSGAAAP ASAAAGPPGASCKPPLPPHYTS TAQITVRALGADRLLLHGPDPV PGAAGSAAAPRGRCLLLAPAPA APVPPRRGSSAWLLEELLRPDC PEPAGLDATREGPDRNFRLSEH RQALAAAKHRGPAATPGSPDPG PGPWGEEHLAERGPRGWERGGD RCDAPGGDAARRPDPEAEAPPA	183	HREAAAVPAAKMPAFSSCFE VVSGAAAPASAAAGPPGASC KPPLPPHYTSTAQITVRALG ADRLLLHGPDPVPGAAGSAA APRGRCLLLAPAPAAPVPPR RGSSAWLLEELLRPDCPEPA GLDATREGPDRNFRLSEHRQ ALAAAKHRGPAATPGSPDPG PGPWGEEHLAERGPRGWERG GDRCDAPGGDAARRPDPEAE APPAGSIEAAPSSAAEPVIV SRSDPRDEKLALYLAEVEKQ

		GSIEAAPSSAAEPVIVSRSDPR DEKLALYLAEVEKQ DKYLRQRNKYRFHIIPDGNCLY RAVSKTVYGDQSLHRELREQTV HYIADHLDHFSPLIEGDVGEFI IAAAQDGAWAGYPELLAMGQML NVNIHLTTGGRLESPTVSTMIH YLGPEDSLRPSIWLSWLSNGHY DAVFDHSYPNPEYDNWCKQTQV QRKRDEELAKSMAISLSKMYIE QNACS		DKYLRQRNKYRFHIIPDGNC LYRAVSKTVYGDQSLHRELR EQTVHYIADHLDHFSPLIEG DVGEFIIAAAQDGAWAGYPE LLAMGQMLNVNIHLTTGGRL ESPTVSTMIHYLGPEDSLRP SIWLSWLSNGHYDAV
OTU6B_HUMAN Deubiquitinase OTUD6B	73	MEAVLTEELDEEEQLLRRHRKE KKELQAKIQGMKNAVPKNDKKR RKQLTEDVAKLEKEMEQKHREE LEQLKLTTKENKIDSVAVNISN LVLENQPPRISKAQKRREKKAA LEKEREERIAEAEIENLTGARH MESEKLAQILAARQLEIKQIPS DGHCMYKAIEDQLKEKDCALTV VALRSQTAEYMQSHVEDFLPFL TNPNTGDMYTPEEFQKYCEDIV NTAAWGGQLELRALSHILQTPI EIIQADSPPIIVGEEYSKKPLI LVYMRHAYGLGEHYNSVTRLVN IVTENCS	184	QKHREELEQLKLTTKENKID SVAVNISNLVLENQPPRISK AQKRREKKAALEKEREERIA EAEIENLTGARHMESEKLAQ ILAARQLEIKQIPSDGHCMY KAIEDQLKEKDCALTVVALR SQTAEYMQSHVEDFLPFLTN PNTGDMYTPEEFQKYCEDIV NTAAWGGQLELRALSHILQT PIEIIQADSPPIIVGEEYSK KPLILVYMRHAYG
OTU6A_HUMAN OTU domain-containing protein 6A	74	MDDPKSEQQRILRRHQRERQEL QAQIRSLKNSVPKTDKTKRKQL LQDVARMEAEMAQKHRQELEKF QDDSSIESVVEDLAKMNLENRP PRSSKAHRKRERMESEERERQE SIFQAEMSEHLAGFKREEEEKL AAILGARGLEMKAIPADGHCMY RAIQDQLVFSVSVEMLRCRTAS YMKKHVDEFLPFFSNPETSDSF GYDDFMIYCDNIVRTTAWGGQL ELRALSHVLKTPIEVIQADSPT LIIGEEYVKKPIILVYLRYAYS LGEHYNSVTPLEAGAAGGVLPR LL	185	QELEKFQDDSSIESVVEDLA KMNLENRPPRSSKAHRKRER MESEERERQESIFQAEMSEH LAGFKREEEEKLAAILGARG LEMKAIPADGHCMYRAIQDQ LVFSVSVEMLRCRTASYMKK HVDEFLPFFSNPETSDSFGY DDFMIYCDNIVRTTAWGGQL ELRALSHVLKTPIEVIQADS PTLIIGEEYVKKPIILVYLR YAYS
OTUB1_HUMAN Ubiquitin thioesterase OTUB1	75	MAAEEPQQQKQEPLGSDSEGVN CLAYDEAIMAQQDRIQQEIAVQ NPLVSERLELSVLYKEYAEDDN IYQQKIKDLHKKYSYIRKTRPD GNCFYRAFGFSHLEALLDDSKE LQRFKAVSAKSKEDLVSQGFTE FTIEDFHNTFMDLIEQVEKQTS VADLLASFNDQSTSDYLVVYLR LLTSGYLQRESKFFEHFIEGGR TVKEFCQQEVEPMCKESDHIHI IALAQALSVSIQVEYMDRGEGG	75	MAAEEPQQQKQEPLGSDSEG VNCLAYDEAIMAQQDRIQQE IAVQNPLVSERLELSVLYKE YAEDDNIYQQKIKDLHKKYS YIRKTRPDGNCFYRAFGFSH LEALLDDSKELQRFKAVSAK SKEDLVSQGFTEFTIEDFHN TFMDLIEQVEKQTSVADLLA SFNDQSTSDYLVVYLRLLTS GYLQRESKFFEHFIEGGRTV KEFCQQEVEPMCKESDHIHI IALAQALSVSIQVEYMDRGE

		TTNPHIFPEGSEPKVYLLYRPGHYDILYK		GGTTNPHIFPEGSEPKVYLLYRPGHYDILYK
OTU7A_HUMAN OTU domain-containing protein 7A	76	MVSSVLPNPTSAECWAALLHDPMTLDMDAVLSDFVRSTGAEPGLARDLLEGKNWDLTAALSDYEQLRQVHTANLPHVFNEGRGPKQPEREPQPGHKVERPCLQRQDDIAQEKRLSRGISHASSAIVSLARSHVASECNNEQFPLEMPIYTFQLPDLSVYSEDFRSFIERDLIEQATMVALEQAGRLNWWSTVCTSCKRLLPLATTGDGNCLLHAASLGMWGFHDRDLVLRKALYTMMRTGAEREALKRRWRWQQTQQNKEEEWEREWTELLKLASSEPRTHFSKNGGTGGGVDNSEDPVYESLEEFHVFVLAHILRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPPNRCHCSPLVLAYDQAHFSALVSMEQRDQQREQAVIPLTDSEHKLLPLHFAVDPGKDWEWGKDDNDNARLAHLILSLEAKLNLLHSYMNVTWIRIPSETRAPLAQPESPTASAGEDVQSLADSLDSDRDSVCSNSNSNNGKNGKDKEKEKQRKEKDKTRADSVANKLGSFSKTLGIKLKKNMGGLGGLVHGKMGRANSANGKNGDSAERGKEKKAKSRKGSKEESGASASTSPSEKTTPSPTDKAAGASPAEKGGGPRGDAWKYSTDVKLSLNILRAAMQGERKFIFAGLLLTSHRHQFHEEMIGYYLTSAQERFSAEQEQRRRDAATAAAAAAAAAATAKRPPRRPETEGVPVPERASPGPPTQLVLKLKERPSPGPAAGRAARAAAGGTASPGGGARRASASGPVPGRSPPAPARQSVIHVQASGARDEACAPAVGALRPCATYPQQNRSLSSQSYSPARAAALRTVNTVESLARAVPGALPGAAGTAGAAEHKSQTYTNGFGALRDGLEFADADAPTARSNGECGRGGPGPVQRRCQRENCAFYGRAETEHYCSYCYREELRRRREARGARP	186	SDYEQLRQVHTANLPHVFNEGRGPKQPEREPQPGHKVERPCLQRQDDIAQEKRLSRGISHASSAIVSLARSHVASECNNEQFPLEMPIYTFQLPDLSVYSEDFRSFIERDLIEQATMVALEQAGRLNWWSTVCTSCKRLLPLATTGDGNCLLHAASLGMWGFHDRDLVLRKALYTMMRTGAEREALKRRWRWQQTQQNKEEEWEREWTELLKLASSEPRTHFSKNGGTGGGVDNSEDPVYESLEEFHVFVLAHILRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPPNRCHCSPLVLAYDQAHFSAL
OTUD4_HUMAN OTU domain-containing protein 4	77	MEAAVGVPDGGDQGGAGPREDATPMDAYLRKLGLYRKLVAKDGSCLFRAVAEQVLHSQSRHVEVRMACIHYLRENREKFEAFIEGSFEEYLKRLENPQEWVGQVEISALSLMYRKDFIIYREPNVSPSQVTE	187	MEAAVGVPDGGDQGGAGPREDATPMDAYLRKLGLYRKLVAKDGSCLFRAVAEQVLHSQSRHVEVRMACIHYLRENREKFEAFIEGSFEEYLKRLENPQEWVGQVEISALSLMYRKDFIIY

		NNFPEKVLLCFSNGNHYDIVYP IKYKESSAMCQSLLYELLYEKV FKTDVSKIVMELDTLEVADEDN SEISDSEDDSCKSKTAAAAADV NGFKPLSGNEQLKNNGNSTSLP LSRKVLKSLNPAVYRNVEYEIW LKSKQAQQKRDYSIAAGLQYEV GDKCQVRLDHNGKF LNADVQGIHSENGPVLVEELGK KHTSKNLKAPPPESWNTVSGKK MKKPSTSGQNFHSDVDYRGPKN PSKPIKAPSALPPRLQHPSGVR QHAFSSHSSGSQSQKFSSEHKN LSRTPSQIIRKPDRERVEDFDH TSRESNYFGLSPEERREKQAIE ESRLLYEIQNRDEQAFPALSSS SVNQSASQSSNPCVQRKSSHVG DRKGSRRRMDTEERKDKDSIHG HSQLDKRPEPSTLENITDDKYA TVSSPSKSKKLECPSPAEQKPA EHVSLSNPAPLLVSPEVHLTPA VPSLPATVPAWPSE PTTFGPTGVPAPIPVLSVTQTL TTGPDSAVSQAHLTPSPVPVSI QAVNQPLMPLPQTLSLYQDPLY PGFPCNEKGDRAIVPPYSLCQT GEDLPKDKNILRFFFNLGVKAY SCPMWAPHSYLYPLHQAYLAAC RMYPKVPVPVYPHNPWFQEAPA AQNESDCTCTDAHFPMQTEASV NGQMPQPEIGPPTFSSPLVIPP SQVSESHGQLSYQADLESETPG QLLHADYEESLSGKNMFPQSFG PNPFLGPVPIAPPFFPHVWYGY PFQGFIENPVMRQNIVLPSDEK GELDLSLENLDLS KDCGSVSTVDEFPEARGEHVHS LPEASVSSKPDEGRTEQSSQTR KADTALASIPPVAEGKAHPPTQ ILNRERETVPVELEPKRTIQSL KEKTEKVKDPKTAADVVSPGAN SVDSRVQRPKEESSEDENEVSN ILRSGRSKQFYNQTYGSRKYKS DWGYSGRGGYQHVRSEESWKGQ PSRSRDEGYQYHRNVRGRPFRG DRRRSGMGDGHRGQHT		REPNVSPSQVTENNFPEKVL LCFSNGNHYDIVYP
OTUB2_HUMAN Ubiquitin thioesterase OTUB2	78	MSETSFNLISEKCDILSILRDH PENRIYRRKIEELSKRFTAIRK TKGDGNCFYRALGYSYLESLLG KSREIFKFKERVLQTPNDLLAA GFEEHKFRNFFNAFYSVVELVE	78	MSETSFNLISEKCDILSILR DHPENRIYRRKIEELSKRFT AIRKTKGDGNCFYRALGYSY LESLLGKSREIFKFKERVLQ TPNDLLAAGFEEHKFRNFFN

		KDGSVSSLLKVFNDQSASDHIV QFLRLLTSAFIRNRADFFRHFI DEEMDIKDFCTHEVEPMATECD HIQITALSQALSIALQVEYVDE MDTALNHHVFPEAATPSVYLLY KTSHYNILYAADKH		AFYSVVELVEKDGSVSSLLK VFNDQSASDHIVQFLRLLTS AFIRNRADFFRHFIDEEMDI KDFCTHEVEPMATECDHIQI TALSQALSIALQVEYVDEMD TALNHHVFPEAATPSVYLLY KTSHYNILYAADKH
OTUD3_HUMAN OTU domain-containing protein 3	79	MSRKQAAKSRPGSGSRKAEAER KRDERAARRALAKERRNRPESG GGGGCEEEFVSFANQLQALGLK LREVPGDGNCLFRALGDQLEGH SRNHLKHRQETVDYMIKQREDF EPFVEDDIPFEKHVASLAKPGT FAGNDAIVAFARNHQLNVVIHQ LNAPLWQIRGTEKSSVRELHIA YRYGEHYDSVRRINDNSEAPAH LQTDFQMLHQDESNKREKIKTK GMDSEDDLRDEVEDAVQKVCNA TGCSDFNLIVQNLEAENYNIES AIIAVLRMNQGKRNNAEENLEP SGRVLKQCGPLWEE GGSGARIFGNQGLNEGRTENNK AQASPSEENKANKNQLAKVTNK QRREQQWMEKKKRQEERHRHKA LESRGSHRDNNRSEAEANTQVT LVKTFAALNI	188	MSRKQAAKSRPGSGSRKAEA ERKRDERAARRALAKERRNR PESGGGGGCEEEFVSFANQL QALGLKLREVPGDGNCLFRA LGDQLEGHSRNHLKHRQETV DYMIKQREDFEPFVEDDIPF EKHVASLAKPGTFAGNDAIV AFARNHQLNVVIHQLNAPLW QIRGTEKSSVRELHIAYRYG EHYDSVRR
OTU7B_HUMAN OTU domain-containing protein 7B (Also referred to herein as Cezanne)	80	MTLDMDAVLSDFVRSTGAEPGL ARDLLEGKNWDVNAALSDFEQL RQVHAGNLPPSFSEGSGGSRTP EKGFSDREPTRPPRPILQRQDD IVQEKRLSRGISHASSSIVSLA RSHVSSNGGGGGSNEHPLEMPI CAFQLPDLTVYNEDFRSFIERD LIEQSMLVALEQAGRLNWWVSV DPTSQRLLPLATTGDGNCLLHA ASLGMWGFHDRDLMLRKALYAL MEKGVEKEALKRRWRWQQTQQN KESGLVYTEDEWQKEWNELIKL ASSEPRMHLGTNGANCGGVESS EEPVYESLEEFHVFVLAHVLRR PIVVVADTMLRDSGGEAFAPIP FGGIYLPLEVPASQCHRSPLVL AYDQAHFSALVSMEQKENTKEQ AVIPLTDSEYKLLPLHFAVDPG KGWEWGKDDSDNVRLASVILSL EVKLHLLHSYMNVKWIPLSSDA QAPLAQPESPTASAGDEPRSTP ESGDSDKESVGSSSTSNEGGRR KEKSKRDREKDKKRADSVANKL GSFGKTLGSKLKKNMGGLMHSK GSKPGGVGTGLGGSSGTETLEK	189	MTLDMDAVLSDFVRSTGAEP GLARDLLEGKNWDVNAALSD FEQLRQVHAGNLPPSFSEGS GGSRTPEKGFSDREPTRPPR PILQRQDDIVQEKRLSRGIS HASSSIVSLARSHVSSNGGG GGSNEHPLEMPICAFQLPDL TVYNEDFRSFIERDLIEQSM LVALEQAGRLNWWVSVDPTS QRLLPLATTGDGNCLLHAAS LGMWGFHDRDLMLRKALYAL MEKGVEKEALKRRWRWQQTQ QNKESGLVYTEDEWQKEWNE LIKLASSEPRMHLGTNGANC GGVESSEEPVYESLEEFHVF VLAHVLRRPIVVVADTMLRD SGGEAFAPIPFGGIYLPLEV PASQCHRSPLVLAYDQAHFS AL
			286	PPSFSEGSGGSRTPEKGFSD REPTRPPRPILQRQDDIVQE KRLSRGISHASSSIVSLARS HVSSNGGGGGSNEHPLEMPI CAFQLPDLTVYNEDFRSFIE RDLIEQSMLVALEQAGRLNW

		KKKNSLKSWKGGKEEAAGDGPV SEKPPAESVGNGGSKYSQEVMQ SLSILRTAMQGEGKFIFVGTLK MGHRHQYQEEMIQRYLSDAEER FLAEQKQKEAERKIMNGGIGGG PPPAKKPEPDAREEQPTGPPAE SRAMAFSTGYPGDFTIPRPSGG GVHCQEPRRQLAGGPCVGGLPP YATFPRQCPPGRPYPHQDSIPS LEPGSHSKDGLHRGALLPPPYR VADSYSNGYREPPEPDGWAGGL RGLPPTQTKCKQPNCSFYGHPE TNNFCSCCYREELRRREREPDG ELLVHRF		WVSVDPTSQRLLPLATTGDG NCLLHAASLGMWGFHDRDLM LRKALYALMEKGVEKEALKR RWRWQQTQQNKESGLVYTED EWQKEWNELIKLASSEPRMH LGTNGANCGGVESSEEPVYE SLEEFHVFVLAHVLRRPIVV VADTMLRDSGGEAFAPIPFG GIYLPLEVPASQCHRSPLVL AYDQAHFSALVSMEQKENTK EQAVIPLTDSEYKLLPLHFA VDPGKGWEWGKDDSDNVRLA SVILSLEVKLHLLHSYMNVK WIPLSSDAQAPLAQ
OTUD5_HUMAN OTU domain-containing protein 5	81	MTILPKKKPPPPDADPANEPPP PGPMPPAPRRGGGVGVGGGGTG VGGGDRDRDSGVVGARPRASPP PQGPLPGPPGALHRWALAVPPG AVAGPRPQQASPPPCGGPGGPG GGPGDALGAAAAGVGAAGVVVG VGGAVGVGGCCSGPGHSKRRRQ APGVGAVGGGSPEREEVGAGYN SEDEYEAAAARIEAMDPATVEQ QEHWFEKALRDKKGFIIKQMKE DGACLFRAVADQVYGDQDMHEV VRKHCMDYLMKNADYFSNYVTE DFTTYINRKRKNNCHGNHIEMQ AMAEMYNRPVEVYQ YSTGTSAVEPINTFHGIHQNED EPIRVSYHRNIHYNSVVNPNKA TIGVGLGLPSFKPGFAEQSLMK NAIKTSEESWIEQQMLEDKKRA TDWEATNEAIEEQVARESYLQW LRDQEKQARQVRGPSQPRKASA TCSSATAAASSGLEEWTSRSPR QRSSASSPEHPELHAELGMKPP SPGTVLALAKPPSPCAPGTSSQ FSAGADRATSPLVSLYPALECR ALIQQMSPSAFGLNDWDDDEIL ASVLAVSQQEYLDSMKKNKVHR DPPPDKS	190	MTILPKKKPPPPDADPANEP PPPGPMPPAPRRGGGVGVGG GGTGVGGGDRDRDSGVVGAR PRASPPPQGPLPGPPGALHR WALAVPPGAVAGPRPQQASP PPCGGPGGPGGGPGDALGAA AAGVGAAGVVVGVGGAVGVG GCCSGPGHSKRRRQAPGVGA VGGGSPEREEVGAGYNSEDE YEAAAARIEAMDPATVEQQE HWFEKALRDKKGFIIKQMKE DGACLFRAVADQVYGDQDMH EVVRKHCMDYLMKNADYFSN YVTEDFTTYINRKRKNNCHG NHIEMQAMAEMYNRPVEVYQ YSTGTSAVEPINTFHGIHQN EDEPIRVSYHRNIHYNSV
TNAP3_HUMAN Tumor necrosis factor alpha-induced protein 3	82	MAEQVLPQALYLSNMRKAVKIR ERTPEDIFKPTNGIIHHFKTMH RYTLEMFRTCQFCPQFREIIHK ALIDRNIQATLESQKKLNWCRE VRKLVALKTNGDGNCLMHATSQ YMWGVQDTDLVLRKALFSTLKE TDTRNFKFRWQLESLKSQEFVE TGLCYDTRNWNDEWDNLIKMAS TDTPMARSGLQYNSLEEIHIFV LCNILRRPIIVISDKMLRSLES	191	MAEQVLPQALYLSNMRKAVK IRERTPEDIFKPTNGIIHHF KTMHRYTLEMFRTCQFCPQF REIIHKALIDRNIQATLESQ KKLNWCREVRKLVALKTNGD GNCLMHATSQYMWGVQDTDL VLRKALFSTLKETDTRNFKF RWQLESLKSQEFVETGLCYD TRNWNDEWDNLIKMASTDTP MARSGLQYNSLEEIHIFVLC

		GSNFAPLKVGGIYLPLHWPAQE CYRYPIVLGYDSHHFVPLVTLK DSGPEIRAVPLVNRDRGRFEDL KVHFLTDPENEMKE KLLKEYLMVIEIPVQGWDHGTT HLINAAKLDEANLPKEINLVDD YFELVQHEYKKWQENSEQGRRE GHAQNPMEPSVPQLSLMDVKCE TPNCPFFMSVNTQPLCHECSER RQKNQNKLPKLNSKPGPEGLPG MALGASRGEAYEPLAWNPEEST GGPHSAPPTAPSPFLFSETTAM KCRSPGCPFTLNVQHNGFCERC HNARQLHASHAPDHTRHLDPGK CQACLQDVTRTFNGICSTCFKR TTAEASSSLSTSLPPSCHQRSK SDPSRLVRSPSPHSCHRAGNDA PAGCLSQAARTPGD RTGTSKCRKAGCVYFGTPENKG FCTLCFIEYRENKHFAAASGKV SPTASRFQNTIPCLGRECGTLG STMFEGYCQKCFIEAQNQRFHE AKRTEEQLRSSQRRDVPRTTQS TSRPKCARASCKNILACRSEEL CMECQHPNQRMGPGAHRGEPAP EDPPKQRCRAPACDHFGNAKCN GYCNECFQFKQMYG		NILRRPIIVISDKMLRSLES GSNFAPLKVGGIYLPLHWPA QECYRYPIVLGYDSHHFVPL
ZRAN1_HUMAN Ubiquitin thioesterase ZRANB1	83	MSERGIKWACEYCTYENWPSAI KCTMCRAQRPSGTIITEDPFKS GSSDVGRDWDPSSTEGGSSPLI CPDSSARPRVKSSYSMENANKW SCHMCTYLNWPRAIRCTQCLSQ RRTRSPTESPQSSGSGSRPVAF SVDPCEEYNDRNKLNTRTQHWT CSVCTYENWAKAKRCVVCDHPR PNNIEAIELAETEEASSIINEQ DRARWRGSCSSGNSQRRSPPAT KRDSEVKMDFQRIELAGAVGSK EELEVDFKKLKQIKNRMKKTDW LFLNACVGVVEGDLAAIEAYKS SGGDIARQLTADEV RLLNRPSAFDVGYTLVHLAIRF QRQDMLAILLTEVSQQAAKCIP AMVCPELTEQIRREIAASLHQR KGDFACYFLTDLVTFTLPADIE DLPPTVQEKLFDEVLDRDVQKE LEEESPIINWSLELATRLDSRL YALWNRTAGDCLLDSVLQATWG IYDKDSVLRKALHDSLHDCSHW FYTRWKDWESWYSQSFGLHFSL REEQWQEDWAFILSLASQPGAS	192	MSERGIKWACEYCTYENWPS AIKCTMCRAQRPSGTIITED PFKSGSSDVGRDWDPSSTEG GSSPLICPDSSARPRVKSSY SMENANKWSCHMCTYLNWPR AIRCTQCLSQRRTRSPTESP QSSGSGSRPVAFSVDPCEEY NDRNKLNTRTQHWTCSVCTY ENWAKAKRCVVCDHPRPNNI EAIELAETEEASSIINEQDR ARWRGSCSSGNSQRRSPPAT KRDSEVKMDFQRIELAGAVG SKEELEVDFKKLKQIKNRMK KTDWLFLNACVGVVEGDLAA IEAYKSSGGDIARQLTADEV RLLNRPSAFDVGYTLVHLAI RFQRQDMLAILLTEVSQQAA KCIPAMVCPELTEQIRREIA ASLHQRKGDFACYFLTDLVT FTLPADIEDLPPTVQEKLFD EVLDRDVQKELEEESPIINW SLELATRLDSRLYALWNRTA GDCLLDSVLQATWGIYDKDS VLRKALHDSLHDCSHWFYTR

		LEQTHIFVLAHILRRPIIVYGV KYYKSFRGETLGYTRFQGVYLP LLWEQSFCWKSPIALGYTRGHF SALVAMENDGYGNR GAGANLNTDDDVTITFLPLVDS ERKLLHVHFLSAQELGNEEQQE KLLREWLDCCVTEGGVLVAMQK SSRRRNHPLVTQMVEKWLDRYR QIRPCTSLSDGEEDEDDEDE		WKDWESWYSQSFGLHFSLRE EQWQEDWAFILSLASQPGAS LEQTHIFVLAHILRRPIIVY GVKYYKSFRGETLGYTRFQG VYLPLLWEQSFCWKSPIALG YTRGHFSAL
VCIP1_HUMAN Deubiquitinating protein VCIP135	84	MSQPPPPPPPLPPPPPPPEAPQ TPSSLASAAASGGLLKRRDRRI LSGSCPDPKCQARLFFPASGSV SIECTECGQRHEQQQLLGVEEV TDPDVVLHNLLRNALLGVTGAP KKNTELVKVMGLSNYHCKLLSP ILARYGMDKQTGRAKLLRDMNQ GELFDCALLGDRAFLIEPEHVN TVGYGKDRSGSLLYLHDTLEDI KRANKSQECLIPVHVDGDGHCL VHAVSRALVGRELFWHALRENL KQHFQQHLARYQALFHDFIDAA EWEDIINECDPLFVPPEGVPLG LRNIHIFGLANVLH RPIILLDSLSGMRSSGDYSATF LPGLIPAEKCTGKDGHLNKPIC IAWSSSGRNHYIPLVGIKGAAL PKLPMNLLPKAWGVPQDLIKKY IKLEEDGGCVIGGDRSLQDKYL LRLVAAMEEVFMDKHGIHPSLV ADVHQYFYRRTGVIGVQPEEVT AAAKKAVMDNRLHKCLLCGALS ELHVPPEWLAPGGKLYNLAKST HGQLRTDKNYSFPLNNLVCSYD SVKDVLVPDYGMSNLTACNWCH GTSVRKVRGDGSIVYLDGDRTN SRSTGGKCGCGFKHFWDGKEYD NLPEAFPITLEWGG RVVRETVYWFQYESDSSLNSNV YDVAMKLVTKHFPGEFGSEILV QKVVHTILHQTAKKNPDDYTPV NIDGAHAQRVGDVQGQESESQL PTKIILTGQKTKTLHKEELNMS KTERTIQQNITEQASVMQKRKT EKLKQEQKGQPRTVSPSTIRDG PSSAPATPTKAPYSPTTSKEKK IRITTNDGRQSMVTLKSSTTFF ELQESIAREFNIPPYLQCIRYG FPPKELMPPQAGMEKEPVPLQH GDRITIEILKSKAEGGQSAAAH SAHTVKQEDIAVTGKLSSKELQ EQAEKEMYSLCLLA	193	PASGSVSIECTECGQRHEQQ QLLGVEEVTDPDVVLHNLLR NALLGVTGAPKKNTELVKVM GLSNYHCKLLSPILARYGMD KQTGRAKLLRDMNQGELFDC ALLGDRAFLIEPEHVNTVGY GKDRSGSLLYLHDTLEDIKR ANKSQECLIPVHVDGDGHCL VHAVSRALVGRELFWHALRE NLKQHFQQHLARYQALFHDF IDAAEWEDIINECDPLFVPP EGVPLGLRNIHIFGLANVLH RPIILLDSLSGMRSSGDYSA TFLPGLIPAEKCTGKDGHLN KPICIAWSSSGRNHYIPL

		TLMGEDVWSYAKGLPHMFQQGG VFYSIMKKTMGMADGKHCTFPH LPGKTFVYNASEDRLELCVDAA GHFPIGPDVEDLVKEAVSQVRA EATTRSRESSPSHGLLKLGSGG VVKKKSEQLHNVTAFQGKGHSL GTASGNPHLDPRARETSVVRKH NTGTDFSNSSTKTEPSVFTASS SNSELIRIAPGVVTMRDGRQLD PDLVEAQRKKLQEMVSSIQASM DRHLRDQSTEQSPSDLPQRKTE VVSSSAKSGSLQTGLPESFPLT GGTENLNTETTDGCVADALGAA FATRSKAQRGNSVEELEEMDSQ DAEMTNTTEPMDHS		
UCHL3_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L3	85	MEGQRWLPLEANPEVTNQFLKQ LGLHPNWQFVDVYGMDPELLSM VPRPVCAVLLLFPITEKYEVFR TEEEEKIKSQGQDVTSSVYFMK QTISNACGTIGLIHAIANNKDK MHFESGSTLKKFLEESVSMSPE ERARYLENYDAIRVTHETSAHE GQTEAPSIDEKVDLHFIALVHV DGHLYELDGRKPFPINHGETSD ETLLEDAIEVCKKFMERDPDEL RFNAIALSAA	194	QRWLPLEANPEVTNQFLKQL GLHPNWQFVDVYGMDPELLS MVPRPVCAVLLLFPITEKYE VFRTEEEEKIKSQGQDVTSS VYFMKQTISNACGTIGLIHA IANNKDKMHFESGSTLKKFL EESVSMSPEERARYLENYDA IRVTHETSAHEGQTEAPSID EKVDLHFIALVHVDGHLYEL DGRKPFPINHGETSDETLLE DAIEVCKKFMERDPDELRFN AIALSAA
UCHL1_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L1	86	MQLKPMEINPEMLNKVLSRLGV AGQWRFVDVLGLEEESLGSVPA PACALLLLFPLTAQHENFRKKQ IEELKGQEVSPKVYFMKQTIGN SCGTIGLIHAVANNQDKLGFED GSVLKQFLSETEKMSPEDRAKC FEKNEAIQAAHDAVAQEGQCRV DDKVNFHFILFNNVDGHLYELD GRMPFPVNHGASSEDTLLKDAA KVCREFTEREQGEVRFSAVALC KAA	86	MQLKPMEINPEMLNKVLSRL GVAGQWRFVDVLGLEEESLG SVPAPACALLLLFPLTAQHE NFRKKQIEELKGQEVSPKVY FMKQTIGNSCGTIGLIHAVA NNQDKLGFEDGSVLKQFLSE TEKMSPEDRAKCFEKNEAIQ AAHDAVAQEGQCRVDDKVNF HFILFNNVDGHLYELDGRMP FPVNHGASSEDTLLKDAAKV CREFTEREQGEVRFSAVALC KAA
UCHL5_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L5	87	MTGNAGEWCLMESDPGVFTELI KGFGCRGAQVEEIWSLEPENFE KLKPVHGLIFLFKWQPGEEPAG SVVQDSRLDTIFFAKQVINNAC ATQAIVSVLLNCTHQDVHLGET LSEFKEFSQSFDAAMKGLALSN SDVIRQVHNSFARQQMFEFDTK TSAKEEDAFHFVSYVPVNGRLY ELDGLREGPIDLGACNQDDWIS AVRPVIEKRIQKYSEGEIRFNL MAIVSDRKMIYEQKIAELQRQL AEEEPMDTDQGNSMLSAIQSEV	195	GEWCLMESDPGVFTELIKGF GCRGAQVEEIWSLEPENFEK LKPVHGLIFLFKWQPGEEPA GSVVQDSRLDTIFFAKQVIN NACATQAIVSVLLNCTHQDV HLGETLSEFKEFSQSFDAAM KGLALSNSDVIRQVHNSFAR QQMFEFDTKTSAKEEDAFHF VSYVPVNGRLYELDGLREGP IDLGACNQDDWISAVRPVIE KRIQKYSEGEIRFNLMAIVS DRK

		AKNQMLIEEEVQKLKRYKIENI RRKHNYLPFIMELLKTLAEHQQ LIPLVEKAKEKQNAKKAQETK		
ATX3_HUMAN Ataxin-3	88	MESIFHEKQEGSLCAQHCLNNL LQGEYFSPVELSSIAHQLDEEE RMRMAEGGVTSEDYRTFLQQPS GNMDDSGFFSIQVISNALKVWG LELILFNSPEYQRLRIDPINER SFICNYKEHWFTVRKLGKQWFN LNSLLTGPELISDTYLALFLAQ LQQEGYSIFVVKGDLPDCEADQ LLQMIRVQQMHRPKLIGEELAQ LKEQRVHKTDLERVLEANDGSG MLDEDEEDLQRALALSRQEIDM EDEEADLRRAIQLSMQGSSRNI SQDMTQTSGTNLTSEELRKRRE AYFEKQQQKQQQQQQQQQQGDL SGQSSHPCERPATSSGALGSDL GDAMSEEDMLQAAVTMSLETVR NDLKTEGKK	196	ESIFHEKQEGSLCAQHCLNN LLQGEYFSPVELSSIAHQLD EEERMRMAEGGVTSEDYRTF LQQPSGNMDDSGFFSIQVIS NALKVWGLELILFNSPEYQR LRIDPINERSFICNYKEHWF TVRKLGKQWFNLNSLLTGPE LISDTYLALFLAQLQQEGYS IFVVK
JOS2_HUMAN Josephin-2	89	MSQAPGAQPSPPTVYHERQRLE LCAVHALNNVLQQQLFSQEAAD EICKRLAPDSRLNPHRSLLGTG NYDVNVIMAALQGLGLAAVWWD RRRPLSQLALPQVLGLILNLPS PVSLGLLSLPLRRRHWVALRQV DGVYYNLDSKLRAPEALGDEDG VRAFLAAALAQGLCEVLLVVTK EVEEKGSWLRTD	197	PTVYHERQRLELCAVHALNN VLQQQLFSQEAADEICKRLA PDSRLNPHRSLLGTGNYDVN VIMAALQGLGLAAVWWDRRR PLSQLALPQVLGLILNLPSP VSLGLLSLPLRRRHWVALRQ VDGVYYNLDSKLRAPEALGD EDGVRAFLAAALAQGLCEVL LVV
JOS1_HUMAN Josephin-1	90	MSCVPWKGDKAKSESLELPQAA PPQIYHEKQRRELCALHALNNV FQDSNAFTRDTLQEIFQRLSPN TMVTPHKKSMLGNGNYDVNVIM AALQTKGYEAVWWDKRRDVGVI ALTNVMGFIMNLPSSLCWGPLK LPLKRQHWICVREVGGAYYNLD SKLKMPEWIGGESELRKFLKHH LRGKNCELLLVVPEEVEAHQSW RTDV	198	PQAAPPQIYHEKQRRELCAL HALNNVFQDSNAFTRDTLQE IFQRLSPNTMVTPHKKSMLG NGNYDVNVIMAALQTKGYEA VWWDKRRDVGVIALTNVMGF IMNLPSSLCWGPLKLPLKRQ HWICVREVGGAYYNLDSKLK MPEWIGGESELRKFLKHHLR GKNCELLLVV
ATX3L_HUMAN Ataxin-3-like protein	91	MDFIFHEKQEGFLCAQHCLNNL LQGEYFSPVELASIAHQLDEEE RMRMAEGGVTSEEYLAFLQQPS ENMDDTGFFSIQVISNALKFWG LEIIHFNNPEYQKLGIDPINER SFICNYKQHWFTIRKFGKHWFN LNSLLAGPELISDTCLANFLAR LQQQAYSVFVVKGDLPDCEADQ LLQIISVEEMDTPKLNGKKLVK QKEHRVYKTVLEKVSEESDESG TSDQDEEDFQRALELSRQETNR EDEHLRSTIELSMQGSSGNTSQ	199	DFIFHEKQEGFLCAQHCLNN LLQGEYFSPVELASIAHQLD EEERMRMAEGGVTSEEYLAF LQQPSENMDDTGFFSIQVIS NALKFWGLEIIHFNNPEYQK LGIDPINERSFICNYKQHWF TIRKFGKHWFNLNSLLAGPE LISDTCLANFLARLQQQAYS VFVVK

		DLPKTSCVTPASEQPKKIKEDY FEKHQQEQKQQQQQSDLPGHSS YLHERPTTSSRAIESDLSDDIS EGTVQAAVDTILEIMRKNLKIK GEK		
MINY3_HUMAN Ubiquitin carboxyl-terminal hydrolase MINDY-3	92	MSELTKELMELVWGTKSSPGLS DTIFCRWTQGFVFSESEGSALE QFEGGPCAVIAPVQAFLLKKLL FSSEKSSWRDCSEEEQKELLCH TLCDILESACCDHSGSYCLVSW LRGKTTEETASISGSPAESSCQ VEHSSALAVEELGFERFHALIQ KRSFRSLPELKDAVLDQYSMWG NKFGVLLFLYSVLLTKGIENIK NEIEDASEPLIDPVYGHGSQSL INLLLTGHAVSNVWDGDRECSG MKLLGIHEQAAVGFLTLMEALR YCKVGSYLKSPKFPIWIVGSET HLTVFFAKDMALVA PEAPSEQARRVFQTYDPEDNGF IPDSLLEDVMKALDLVSDPEYI NLMKNKLDPEGLGIILLGPFLQ EFFPDQGSSGPESFTVYHYNGL KQSNYNEKVMYVEGTAVVMGFE DPMLQTDDTPIKRCLQTKWPYI ELLWTTDRSPSLN	200	CRWTQGFVFSESEGSALEQF EGGPCAVIAPVQAFLLKKLL FSSEKSSWRDCSEEEQKELL CHTLCDILESACCDHSGSYC LVSWLRGKTTEETASISGSP AESSCQVEHSSALAVEELGF ERFHALIQKRSFRSLPELKD AVLDQYSMWGNKFG VLLFLYSVLLTKGIENIKNE IEDASEPLIDPVYGHGSQSL INLLLTGHAVSNVWDGDREC SGMKLLGIHEQAAVGFLTLM EALRYCKVGSYLKSPKFPIW IVGSETHLTVFFAKDMALVA PEAPSEQARRVFQTYDPEDN GFIPDSLLEDVMKALDLVSD PEYINLMKNKLDPEGLGIIL LGPFLQEFFPDQGSSGPESF TVYHYNGLKQSNYNEKVMYV EGTAVVMGFEDPMLQTDDTP IKRCLQTKWPYIELLWTTDR SPSLN
MINY1_HUMAN Ubiquitin carboxyl-terminal hydrolase MINDY-1	93	MEYHQPEDPAPGKAGTAEAVIP ENHEVLAGPDEHPQDTDARDAD GEARAREPADQALLPSQCGDNL ESPLPEASSAPPGPTLGTLPEV ETIRACSMPQELPQSPRTRQPE PDFYCVKWIPWKGEQTPIITQS TNGPCPLLAIMNILFLQWKVKL PPQKEVITSDELMAHLGNCLLS IKPQEKSEGLQLNFQQNVDDAM TVLPKLATGLDVNVRFTGVSDF EYTPECSVFDLLGIPLYHGWLV DPQSPEAVRAVGKLSYNQLVER IITCKHSSDTNLVTEGLIAEQF LETTAAQLTYHGLC ELTAAAKEGELSVFFRNNHFST MTKHKSHLYLLVTDQGFLQEEQ VVWESLHNVDGDSCFCDSDFHL SHSLGKGPGAEGGSGSPETQLQ VDQDYLIALSLQQQQPRGPLGL TDLELAQQLQQEEYQQQQAAQP VRMRTRVLSLQGRGATSGRPAG ERRQRPKHESDCILL	201	YCVKWIPWKGEQTPIITQST NGPCPLLAIMNILFLQWKVK LPPQKEVITSDELMAHLGNC LLSIKPQEKSEGLQLNFQQN VDDAMTVLPKLATGLDVNVR FTGVSDFEYTPECSVFDLLG IPLYHGWLVDPQSPEAVRAV GKLSYNQLVERIITCKHSSD TNLVTEGLIAEQFLETTAAQ LTYHGLCELTAAAKEGELSV FFRNNHFSTMTKHKSHLYLL VTDQGFLQEEQVVWESLHNV DGDSCFCDSDFHLSHSLGKG PGAEGGSGSPETQLQVDQDY LIALSLQQQQPRGPLGLTDL ELAQQLQQEEYQQQQAAQPV RMRTRVLSLQGRGATSGRPA GERRQRPKHESDCILL
MINY2_HUMAN	94	MESSPESLQPLEHGVAAGPASG TGSSQEGLQETRLAAGDGPGVW	202	YHIKWIQWKEENTPIITQNE NGPCPLLAILNVLLLAWKVK

Ubiquitin carboxyl-terminal hydrolase MINDY-2		AAETSGGNGLGAAAARRSLPDS ASPAGSPEVPGPCSSSAGLDLK DSGLESPAAAEAPLRGQYKVTA SPETAVAGVGHELGTAGDAGAR PDLAGTCQAELTAAGSEEPSSA GGLSSSCSDPSPPGESPSLDSL ESFSNLHSFPSSCEFNSEEGAE NRVPEEEEGAAVLPGAVPLCKE EEGEETAQVLAASKERFPGQSV YHIKWIQWKEENTPIITQNENG PCPLLAILNVLLLAWKVKLPPM MEIITAEQLMEYLG DYMLDAKPKEISEIQRLNYEQN MSDAMAILHKLQTGLDVNVRFT GVRVFEYTPECIVFDLLDIPLY HGWLVDPQIDDIVKAVGNCSYN QLVEKIISCKQSDNSELVSEGF VAEQFLNNTATQLTYHGLCELT STVQEGELCVFFRNNHFSTMTK YKGQLYLLVTDQGFLTEEKVVW ESLHNVDGDGNFCDSEFHLRPP SDPETVYKGQQDQIDQDYLMAL SLQQEQQSQEINWEQIPEGISD LELAKKLQEEEDRRASQYYQEQ EQAAAAAAAASTQAQQGQPAQA SPSSGRQSGNSERKRKEPREKD KEKEKEKNSCVIL		LPPMMEIITAEQLMEYLGDY MLDAKPKEISEIQRLNYEQN MSDAMAILHKLQTGLDVNVR FTGVRVFEYTPECIVFDLLD IPLYHGWLVDPQIDDIVKAV GNCSYNQLVEKIISCKQSDN SELVSEGFVAEQFLNNTATQ LTYHGLCELTSTVQEGELCV FFRNNHFSTMTKYKGQLYLL VTDQGFLTEEKVVWESLHNV DGDGNFCDSEFHLRPPSDPE TVYKGQQDQIDQDYLMALSL QQEQQSQEINWEQIPEGISD LELAKKLQEEEDRRASQYYQ EQEQAAAAAAAASTQAQQGQ PAQASPSSGRQSGNSERKRK EPREKDKEKEKEKNSCVIL
MINY4_HUMAN Probable ubiquitin carboxyl-terminal hydrolase MINDY-4	95	MDSLFVEEVAASLVREFLSRKG LKKTCVTMDQERPRSDLSINNR NDLRKVLHLEFLYKENKAKENP LKTSLELITRYFLDHFGNTANN FTQDTPIPALSVPKKNNKVPSR CSETTLVNIYDLSDEDAGWRTS LSETSKARHDNLDGDVLGNFVS SKRPPHKSKPMQTVPGETPVLT SAWEKIDKLHSEPSLDVKRMGE NSRPKSGLIVRGMMSGPIASSP QDSFHRHYLRRSSPSSSSTQPQ EESRKVPELFVCTQQDILASSN SSPSRTSLGQLSELTVERQKTT ASSPPHLPSKRLPP WDRARPRDPSEDTPAVDGSTDT DRMPLKLYLPGGNSRMTQERLE RAFKRQGSQPAPVRKNQLLPSD KVDGELGALRLEDVEDELIREE VILSPVPSVLKLQTASKPIDLS VAKEIKTLLFGSSFCCFNEEWK LQSFSFSNTASLKYGIVQNKGG PCGVLAAVQGCVLQKLLFEGDS KADCAQGLQPSDAHRTRCLVLA LADIVWRAGGRERAVVALASRT	203	FCCFNEEWKLQSFSFSNTAS LKYGIVQNKGGPCGVLAAVQ GCVLQKLLFEGDSKADCAQG LQPSDAHRTRCLVLALADIV WRAGGRERAVVALASRTQQF SPTGKYKADGVLETLTLHSL TCYEDLVTFLQQSIHQFEVG PYGCILLTLSAILSRSTELI RQDFDVPTSHLIGAHGYCTQ ELVNLLLTGKAVSNVFNDVV ELDSGDGNITLLRGIAARSD IGFLSLFEHYNMCQVGCFLK TPRFPIWVVCSESHFSILFS LQPGLLRDWRTERLFDLYYY DGLANQQEQIRLTIDTTQTI SEDTDNDLVPPLELCIRTKW KGASVNWNGSDPIL

		QQFSPTGKYKADGVLETLTLHS LTCYEDLVTFLQQSIHQFEVGP YGCILLTLSAILSRSTELIRQD FDVPTSHLIGAHGY CTQELVNLLLTGKAVSNVFNDV VELDSGDGNITLLRGIAARSDI GFLSLFEHYNMCQVGCFLKTPR FPIWVVCSESHFSILFSLQPGL LRDWRTERLFDLYYYDGLANQQ EQIRLTIDTTQTISEDTDNDLV PPLELCIRTKWKGASVNWNGSD PIL		
STABP_HUMAN STAM-binding protein	96	MSDHGDVSLPPEDRVRALSQLG SAVEVNEDIPPRRYFRSGVEII RMASIYSEEGNIEHAFILYNKY ITLFIEKLPKHRDYKSAVIPEK KDTVKKLKEIAFPKAEELKAEL LKRYTKEYTEYNEEKKKEAEEL ARNMAIQQELEKEKQRVAQQKQ QQLEQEQFHAFEEMIRNQELEK ERLKIVQEFGKVDPGLGGPLVP DLEKPSLDVFPTLTVSSIQPSD CHTTVRPAKPPVVDRSLKPGAL SNSESIPTIDGLRHVVVPGRLC PQFLQLASANTARGVETCGILC GKLMRNEFTITHVL IPKQSAGSDYCNTENEEELFLI QDQQGLITLGWIHTHPTQTAFL SSVDLHTHCSYQMMLPESVAIV CSPKFQETGFFKLTDHGLEEIS SCRQKGFHPHSKDPPLFCSCSH VTVVDRAVTITDLR	204	VVPGRLCPQFLQLASANTAR GVETCGILCGKLMRNEFTIT HVLIPKQSAGSDYCNTENEE ELFLIQDQQGLITLGWIHTH PTQTAFLSSVDLHTHCSYQM MLPESVAIVCSPKFQETGFF KLTDHGLEEISSCRQKGFHP HSKDPPLFCSCSHVTVVDRA VTITDLR
MPND_HUMAN MPN domain-containing protein	97	MAAPEPLSPAGGAGEEAPEEDE DEAEAEDPERPNAGAGGGRSGG GGSSVSGGGGGGGAGAGGCGGP GGALTRRAVTLRVLLKDALLEP GAGVLSIYYLGKKFLGDLQPDG RIMWQETGQTFNSPSAWATHCK KLVNPAKKSGCGWASVKYKGQK LDKYKATWLRLHQLHTPATAAD ESPASEGEEEELLMEEEEEDVL AGVSAEDKSRRPLGKSPSEPAH PEATTPGKRVDSKIRVPVRYCM LGSRDLARNPHTLVEVTSFAAI NKFQPFNVAVSSNVLFLLDFHS HLTRSEVVGYLGGR WDVNSQMLTVLRAFPCRSRLGD AETAAAIEEEIYQSLFLRGLSL VGWYHSHPHSPALPSLQDIDAQ MDYQLRLQGSSNGFQPCLALLC SPYYSGNPGPESKISPFWVMPP	205	VAVSSNVLFLLDFHSHLTRS EVVGYLGGRWDVNSQMLTVL RAFPCRSRLGDAETAAAIEE EIYQSLFLRGLSLVGWYHSH PHSPALPSLQDIDAQMDYQL RLQGSSNGFQPCLALLCSPY YSGNPGPESKISPFWVMPPP EMLLVEFYKGSPDLVRLQEP WSQEHTYLDKLKISLASRTP KDQSLCHVLEQVCGVLKQGS

		PEMLLVEFYKGSPDLVRLQEPW SQEHTYLDKLKISLASRTPKDQ SLCHVLEQVCGVLKQGS		
EMC9_HUMAN ER membrane protein complex subunit 9	98	MGEVEISALAYVKMCLHAARYP HAAVNGLFLAPAPRSGECLCLT DCVPLFHSHLALSVMLEVALNQ VDVWGAQAGLVVAGYYHANAAV NDQSPGPLALKIAGRIAEFFPD AVLIMLDNQKLVPQPRVPPVIV LENQGLRWVPKDKNLVMWRDWE ESRQMVGALLEDRAHQHLVDFD CHLDDIRQDWTNQRLNTQITQW VGPTNGNGNA	206	ALAYVKMCLHAARYPHAAVN GLFLAPAPRSGECLCLTDCV PLFHSHLALSVMLEVALNQV DVWGAQAGLVVAGYYHANAA VNDQSPGPLALKIAGRIAEF FPDAVLIMLDNQKLVPQPRV PPVIVLENQGLRWVPKDKNL VMWRDWEESRQMVGALLEDR AHQHLVDFDCHLDDIRQDWT NQRLNTQITQWVGPTNGNGN A
PSDE_HUMAN 26S proteasome non-ATPase regulatory subunit 14	99	MDRLLRLGGGMPGLGQGPPTDA PAVDTAEQVYISSLALLKMLKH GRAGVPMEVMGLMLGEFVDDYT VRVIDVFAMPQSGTGVSVEAVD PVFQAKMLDMLKQTGRPEMVVG WYHSHPGFGCWLSGVDINTQQS FEALSERAVAVVVDPIQSVKGK VVIDAFRLINANMMVLGHEPRQ TTSNLGHLNKPSIQALIHGLNR HYYSITINYRKNELEQKMLLNL HKKSWMEGLTLQDYSEHCKHNE SVVKEMLELAKNYNKAVEEEDK MTPEQLAIKNVGKQDPKRHLEE HVDVLMTSNIVQCLAAMLDTVV FK	207	QVYISSLALLKMLKHGRAGV PMEVMGLMLGEFVDDYTVRV IDVFAMPQSGTGVSVEAVDP VFQAKMLDMLKQTGRPEMVV GWYHSHPGFGCWLSGVDINT QQSFEALSERAVAVVVDPIQ SVKGKVVIDAFRLINANMMV LGHEPRQTTSNLGHLNKPSI QALIHGLNRHYYSITINYRK NELEQKMLLNLHKKSWMEGL TLQDYSEHCKHNESVVKEML ELAKNYNKAVEEEDKMTPEQ LAIKNVGKQDPKRHLEEHVD VLMTSNIVQCLAAMLDTVVF K
MYSM1_HUMAN Histone H2A deubiquitinase MYSM1	100	MAAEEADVDIEGDVVAAAGAQP GSGENTASVLQKDHYLDSSWRT ENGLIPWTLDNTISEENRAVIE KMLLEEEYYLSKKSQPEKVWLD QKEDDKKYMKSLQKTAKIMVHS PTKPASYSVKWTIEEKELFEQG LAKFGRRWTKISKLIGSRTVLQ VKSYARQYFKNKVKCGLDKETP NQKTGHNLQVKNEDKGTKAWTP SCLRGRADPNLNAVKIEKLSDD EEVDITDEVDELSSQTPQKNSS SDLLLDFPNSKMHETNQGEFIT SDSQEALFSKSSRGCLQNEKQD ETLSSSEITLWTEK QSNGDKKSIELNDQKFNELIKN CNKHDGRGIIVDARQLPSPEPC EIQKNLNDNEMLFHSCQMVEES HEEEELKPPEQEIEIDRNIIQE EEKQAIPEFFEGRQAKTPERYL KIRNYILDQWEICKPKYLNKTS VRPGLKNCGDVNCIGRIHTYLE LIGAINFGCEQAVYNRPQTVDK	208	QVKVASEALLIMDLHAHVSM AEVIGLLGGRYSEVDKVVEV CAAEPCNSLSTGLQCEMDPV SQTQASETLAVRGFSVIGWY HSHPAFDPNPSLRDIDTQAK YQSYFSRGGAKFIGMIVSPY NRNNPLPYSQITCLVISEEI SPDGSYRLPYKFEVQQMLEE PQWGLVFEKTRWIIEKYRLS HSSVPMDKIFRRDSDLTCLQ KLLECMRKTLSKVTNCFMAE EFLTEIENLFLSNYKSNQEN GVTEENCTKELLM

		VRIRDRKDAVEAYQLAQRLQSM RTRRRRVRDPWGNWCDAKDLEG QTFEHLSAEELAKRREEEKGRP VKSLKVPRPTKSSFDPFQLIPC NFFSEEKQEPFQVKVASEALLI MDLHAHVSMAEVIG LLGGRYSEVDKVVEVCAAEPCN SLSTGLQCEMDPVSQTQASETL AVRGFSVIGWYHSHPAFDPNPS LRDIDTQAKYQSYFSRGGAKFI GMIVSPYNRNNPLPYSQITCLV ISEEISPDGSYRLPYKFEVQQM LEEPQWGLVFEKTRWIIEKYRL SHSSVPMDKIFRRDSDLTCLQK LLECMRKTLSKVTNCFMAEEFL TEIENLFLSNYKSNQENGVTEE NCTKELLM		
ABRX2_HUMAN BRISC complex subunit Abraxas 2	101	MAASISGYTFSAVCFHSANSNA DHEGFLLGEVRQEETFSISDSQ ISNTEFLQVIEIHNHQPCSKLF SFYDYASKVNEESLDRILKDRR KKVIGWYRFRRNTQQQMSYREQ VLHKQLTRILGVPDLVFLLFSF ISTANNSTHALEYVLFRPNRRY NQRISLAIPNLGNTSQQEYKVS SVPNTSQSYAKVIKEHGTDFFD KDGVMKDIRAIYQVYNALQEKV QAVCADVEKSERVVESCQAEVN KLRRQITQRKNEKEQERRLQQA VLSRQMPSESLDPAFSPRMPSS GFAAEGRSTLGDAE ASDPPPPYSDFHPNNQESTLSH SRMERSVFMPRPQAVGSSNYAS TSAGLKYPGSGADLPPPQRAAG DSGEDSDDSDYENLIDPTEPSN SEYSHSKDSRPMAHPDEDPRNT QTSQI	209	AVCFHSANSNADHEGFLLGE VRQEETFSISDSQISNTEFL QVIEIHNHQPCSKLFSFYDY ASKVNEESLDRILKDRRKKV IGWYRFRRNTQQQMSYREQV LHKQLTRIL GVPDLVFLLFSFISTANNST HALEYVLFRPNRRYNQRISL AIPNLGNTSQQEYKVSSVPN TSQSYAKVIKEHGTDFFDKD GVMKDIRAIYQVYNALQEKV QAVCADVEKSERVVESCQAE VNKLRRQITQRKNEKEQERR LQQAVLSRQMPSESLDPAFS PRMPSSGFAAEGRSTLGDAE ASDPPPPYSDFHPNNQESTL SHSRMERSVFMPRPQAVGSS NYASTSAGLKYPGSGADLPP PQRAAGDSGEDSDDSDYENL IDPTEPSNSEYSHSKDSRPM AHPDEDPRNTQTSQI
PRP8_HUMAN Pre-mRNA-processing-splicing factor 8	102	MAGVFPYRGPGNPVPGPLAPLP DYMSEEKLQEKARKWQQLQAKR YAEKRKFGFVDAQKEDMPPEHV RKIIRDHGDMTNRKFRHDKRVY LGALKYMPHAVLKLLENMPMPW EQIRDVPVLYHITGAISFVNEI PWVIEPVYISQWGSMWIMMRRE KRDRRHFKRMRFPPFDDEEPPL DYADNILDVEPLEAIQLELDPE EDAPVLDWFYDHQPLRDSRKYV NGSTYQRWQFTLPMMSTLYRLA NQLLTDLVDDNYFYLFDLKAFF	210	FNPRTGQLFLKIIHTSVWAG QKRLGQLAKWKTAEEVAALI RSLPVEEQPKQIIVTRKGML DPLEVHLLDFPNIVIKGSEL QLPFQACLKVEKFGDLILKA TEPQMVLFNLYDDWLKTISS YTAFSRLILILRALHVNNDR AKVILKPDKTTITEPHHIWP TLTDEEWIKVEVQLKDLILA DYGKKNNVNVASLTQSEIRD IILGMEISAPSQQRQQIAEI EKQTKEQSQLTATQTRTVNK HGDEIITSTTSNYETQTFSS

		TSKALNMAIPGGPKFEPLVRDI NLQDEDWNEFNDIN KIIIRQPIRTEYKIAFPYLYNN LPHHVHLTWYHTPNVVFIKTED PDLPAFYFDPLINPISHRHSVK SQEPLPDDDEEFELPEFVEPFL KDTPLYTDNTANGIALLWAPRP FNLRSGRTRRALDIPLVKNWYR EHCPAGQPVKVRVSYQKLLKYY VLNALKHRPPKAQKKRYLFRSF KATKFFQSTKLDWVEVGLQVCR QGYNMLNLLIHRKNLNYLHLDY NFNLKPVKTLTTKERKKSRFGN AFHLCREVLRLTKLVVDSHVQY RLGNVDAFQLADGLQYIFAHVG QLTGMYRYKYKLMR QIRMCKDLKHLIYYRFNTGPVG KGPGCGFWAAGWRVWLFFMRGI TPLLERWLGNLLARQFEGRHSK GVAKTVTKQRVESHFDLELRAA VMHDILDMMPEGIKQNKARTIL QHLSEAWRCWKANIPWKVPGLP TPIENMILRYVKAKADWWTNTA HYNRERIRRGATVDKTVCKKNL GRLTRLYLKAEQERQHNYLKDG PYITAEEAVAVYTTTVHWLESR RFSPIPFPPLSYKHDTKLLILA LERLKEAYSVKSRLNQSQREEL GLIEQAYDNPHEALSRIKRHLL TQRAFKEVGIEFMD LYSHLVPVYDVEPLEKITDAYL DQYLWYEADKRRLFPPWIKPAD TEPPPLLVYKWCQGINNLQDVW ETSEGECNVMLESRFEKMYEKI DLTLLNRLLRLIVDHNIADYMT AKNNVVINYKDMNHTNSYGIIR GLQFASFIVQYYGLVMDLLVLG LHRASEMAGPPQMPNDFLSFQD IATEAAHPIRLFCRYIDRIHIF FRFTADEARDLIQRYLTEHPDP NNENIVGYNNKKCWPRDARMRL MKHDVNLGRAVFWDIKNRLPRS VTTVQWENSFVSVYSKDNPNLL FNMCGFECRILPKC RTSYEEFTHKDGVWNLQNEVTK ERTAQCFLRVDDESMQRFHNRV RQILMASGSTTFTKIVNKWNTA LIGLMTYFREAVVNTQELLDLL VKCENKIQTRIKIGLNSKMPSR FPPVVFYTPKELGGLGMLSMGH VLIPQSDLRWSKQTDVGITHFR		KTEWRVRAISAANLHLRTNH IYVSSDDIKETGYTYILPKN VLKKFICISDLRAQIAGYLY GVSPPDNPQVKEIRCIVMVP QWGTHQTVHLPGQLPQHEYL KEMEPLGWIHTQPNESPQLS PQDVTTHAKIMADNPSWDGE KTIIITCSFTPGSCTLTAYK LTPSGYEWGRQNTDKGNNPK GYLPSHYERVQMLLSDRFLG FFMVPAQSSWNYNFMGVRHD PNMKYELQLANPKEFYHEVH RPSHFLNFALLQEGEVYSAD REDLYA

		SGMSHEEDQLIPNLYRYIQPWE SEFIDSQRVWAEYALKRQEAIA QNRRLTLEDLEDSWDRGIPRIN TLFQKDRHTLAYDKGWRVRTDF KQYQVLKQNPFWWTHQRHDGKL WNLNNYRTDMIQALGGVEGILE HTLFKGTYFPTWEG LFWEKASGFEESMKWKKLTNAQ RSGLNQIPNRRFTLWWSPTINR ANVYVGFQVQLDLTGIFMHGKI PTLKISLIQIFRAHLWQKIHES IVMDLCQVFDQELDALEIETVQ KETIHPRKSYKMNSSCADILLF ASYKWNVSRPSLLADSKDVMDS TTTQKYWIDIQLRWGDYDSHDI ERYARAKFLDYTTDNMSIYPSP TGVLIAIDLAYNLHSAYGNWFP GSKPLIQQAMAKIMKANPALYV LRERIRKGLQLYSSEPTEPYLS SQNYGELFSNQIIWFVDDTNVY RVTIHKTFEGNLTT KPINGAIFIFNPRTGQLFLKII HTSVWAGQKRLGQLAKWKTAEE VAALIRSLPVEEQPKQIIVTRK GMLDPLEVHLLDFPNIVIKGSE LQLPFQACLKVEKFGDLILKAT EPQMVLFNLYDDWLKTISSYTA FSRLILILRALHVNNDRAKVIL KPDKTTITEPHHIWPTLTDEEW IKVEVQLKDLILADYGKKNNVN VASLTQSEIRDIILGMEISAPS QQRQQIAEIEKQTKEQSQLTAT QTRTVNKHGDEIITSTTSNYET QTFSSKTEWRVRAISAANLHLR TNHIYVSSDDIKET GYTYILPKNVLKKFICISDLRA QIAGYLYGVSPPDNPQVKEIRC IVMVPQWGTHQTVHLPGQLPQH EYLKEMEPLGWIHTQPNESPQL SPQDVTTHAKIMADNPSWDGEK TIIITCSFTPGSCTLTAYKLTP SGYEWGRQNTDKGNNPKGYLPS HYERVQMLLSDRFLGFFMVPAQ SSWNYNFMGVRHDPNMKYELQL ANPKEFYHEVHRPSHFLNFALL QEGEVYSADREDLYA		
NPL4_HUMAN Nuclear protein localization	103	MAESIIIRVQSPDGVKRITATK RETAATFLKKVAKEFGFQNNGF SVYINRNKTGEITASSNKSLNL LKIKHGDLLFLFPSSLAGPSSE METSVPPGFKVFGAPNVVEDEI	211	QPSAITLNRQKYRHVDNIMF ENHTVADRFLDFWRKTGNQH FGYLYGRYTEHKDIPLGIRA EVAAIYEPPQIGTQNSLELL EDPKAEVVDEIAAKLGLRKV

protein 4 homolog		DQYLSKQDGKIYRSRDPQLCRH GPLGKCVHCVPLEPFDEDYLNH LEPPVKHMSFHAYIRKLTGGAD KGKFVALENISCKIKSGCEGHL PWPNGICTKCQPSAITLNRQKY RHVDNIMFENHTVADRFLDFWR KTGNQHFGYLYGRYTEHKDIPL GIRAEVAAIYEPPQIGTQNSLE LLEDPKAEVVDEIA AKLGLRKVGWIFTDLVSEDTRK GTVRYSRNKDTYFLSSEECITA GDFQNKHPNMCRLSPDGHFGSK FVTAVATGGPDNQVHFEGYQVS NQCMALVRDECLLPCKDAPELG YAKESSSEQYVPDVFYKDVDKF GNEITQLARPLPVEYLIIDITT TFPKDPVYTFSISQNPFPIENR DVLGETQDFHSLATYLSQNTSS VFLDTISDFHLLLFLVTNEVMP LQDSISLLLEAVRTRNEELAQT WKRSEQWATIEQLCSTVGGQLP GLHEYGAVGGSTHTATAAMWAC QHCTFMNQPGTGHCEMCSLPRT		GWIFTDLVSEDTRKGTVRYS RNKDTYFLSSEECITAGDFQ NKHPNMCRLSPDGHFGSKFV TAVATGGPDNQVHFEGYQVS NQCMALVRDECLLPCKDAPE LGYAKESSSEQYVPDVFYKD VDKFGNEITQLARPLPVEYL IIDITTTFPKDPVYTFSISQ NPFPIENRDVLGETQDFHSL ATYLSQNTSSVFLDTISDFH LLLFLVTNEVMPLQDSISLL LEAVRTRNEELAQTWKRSEQ WATIEQLCSTVGGQLPGLHE YGAVGGSTHTATAAMWACQH CTFMNQPGTGHCEMCSLPRT
EMC8_HUMAN ER membrane protein complex subunit 8	104	MPGVKLTTQAYCKMVLHGAKYP HCAVNGLLVAEKQKPRKEHLPL GGPGAHHTLFVDCIPLFHGTLA LAPMLEVALTLIDSWCKDHSYV IAGYYQANERVKDASPNQVAEK VASRIAEGFSDTALIMVDNTKF TMDCVAPTIHVYEHHENRWRCR DPHHDYCEDWPEAQRISASLLD SRSYETLVDFDNHLDDIRNDWT NPEINKAVLHLC	212	TQAYCKMVLHGAKYPHCAVN GLLVAEKQKPRKEHLPLGGP GAHHTLFVDCIPLFHGTLAL APMLEVALTLIDSWCKDHSY VIAGYYQANERVKDASPNQV AEKVASRIAEGFSDTALIMV DNTKFTMDCVAPTIHVYEHH ENRWRCRDPHHDYCEDWPEA QRISASLLDSRSYETLVDFD NHLDDIRNDWTNPEINKAVL HLC
ABRX1_HUMAN BRCA1-A complex subunit Abraxas 1	105	MEGESTSAVLSGFVLGALAFQH LNTDSDTEGFLLGEVKGEAKNS ITDSQMDDVEVVYTIDIQKYIP CYQLFSFYNSSGEVNEQALKKI LSNVKKNVVGWYKFRRHSDQIM TFRERLLHKNLQEHFSNQDLVF LLLTPSIITESCSTHRLEHSLY KPQKGLFHRVPLVVANLGMSEQ LGYKTVSGSCMSTGFSRAVQTH SSKFFEEDGSLKEVHKINEMYA SLQEELKSICKKVEDSEQAVDK LVKDVNRLKREIEKRRGAQIQA AREKNIQKDPQENIFLCQALRT FFPNSEFLHSCVMS LKNRHVSKSSCNYNHHLDVVDN LTLMVEHTDIPEASPASTPQII KHKALDLDDRWQFKRSRLLDTQ	213	GFVLGALAFQHLNTDSDTEG FLLGEVKGEAKNSITDSQMD DVEVVYTIDIQKYIPCYQLF SFYNSSGEVNEQALKKILSN VKKNVVGWYKFRRHSDQIMT FRERLLHKNLQEHFSNQDLV FLLLTPSIITESCSTHRLEH SLYKPQKGLFHRVPLVVANL GMSEQLGYKTVSGSCMSTGF SRAVQTHSSKFFEEDGSLKE VHKINEMYASLQEELKSICK KVEDSEQAVDKLVKDVNRLK REIEKRRGAQIQAAREKNIQ KDPQENIFLCQALRTFFPNS EFLHSCVMSLKNRHVSKSSC NYNHHLDVVDNLTLMVEHTD IPEASPASTPQIIKHKALDL

		DKRSKADTGSSNQDKASKMSSP ETDEEIEKMKGFGEYSRSPTF		DDRWQFKRSRLLDTQDKRSK ADTGSSNQDKASKMSSPETD EEIEKMKGFGEYSRSPTF
STALP_HUMAN AMSH-like protease	106	MDQPFTVNSLKKLAAMPDHTDV SLSPEERVRALSKLGCNITISE DITPRRYFRSGVEMERMASVYL EEGNLENAFVLYNKFITLFVEK LPNHRDYQQCAVPEKQDIMKKL KEIAFPRTDELKNDLLKKYNVE YQEYLQSKNKYKAEILKKLEHQ RLIEAERKRIAQMRQQQLESEQ FLFFEDQLKKQELARGQMRSQQ TSGLSEQIDGSALSCFSTHQNN SLLNVFADQPNKSDATNYASHS PPVNRALTPAATLSAVQNLVVE GLRCVVLPEDLCHKFLQLAESN TVRGIETCGILCGK LTHNEFTITHVIVPKQSAGPDY CDMENVEELFNVQDQHDLLTLG WIHTHPTQTAFLSSVDLHTHCS YQLMLPEAIAIVCSPKHKDTGI FRLTNAGMLEVSACKKKGFHPH TKEPRLFSICKHVLVKDIKIIV LDLR	214	VVLPEDLCHKFLQLAESNTV RGIETCGILCGKLTHNEFTI THVIVPKQSAGPDYCDMENV EELFNVQDQHDLLTLGWIHT HPTQTAFLSSVDLHTHCSYQ LMLPEAIAIVCSPKHKDTGI FRLTNAGMLEVSACKKKGFH PHTKEPRLFSICKHVLVKDI KIIVLDLR
CSN6_HUMAN COP9 signalosome complex subunit 6	107	MAAAAAAAAATNGTGGSSGMEV DAAVVPSVMACGVTGSVSVALH PLVILNISDHWIRMRSQEGRPV QVIGALIGKQEGRNIEVMNSFE LLSHTVEEKIIIDKEYYYTKEE QFKQVFKELEFLGWYTTGGPPD PSDIHVHKQVCEIIESPLFLKL NPMTKHTDLPVSVFESVIDIIN GEATMLFAELTYTLATEEAERI GVDHVARMTATGSGENSTVAEH LIAQHSAIKMLHSRVKLILEYV KASEAGEVPFNHEILREAYALC HCLPVLSTDKFKTDFYDQCNDV GLMAYLGTITKTCNTMNQFVNK FNVLYDRQGIGRRMRGLFF	215	VALHPLVILNISDHWIRMRS QEGRPVQVIGALIGKQEGRN IEVMNSFELLSHTVEEKIII DKEYYYTKEEQFKQVFKELE FLGWYTTGGPPDPSDIHVHK QVCEIIESPLFLKLNPMTKH TDLPVSVFESVIDIINGEAT MLFAELTYTLATEEAERIGV DHVARMTATGSGENSTVAEH LIAQHSAIKMLHSRVKLILE YVKASEAGEVPFNHEILREA YALCHCLPVLSTDKFKTDFY DQCNDVGLMAYLGTITKTCN TMNQFVNKFNVLYDRQGIGR RMRGLFF
EIF3F_HUMAN Eukaryotic translation initiation factor 3 subunit F	108	MATPAVPVSAPPATPTPVPAAA PASVPAPTPAPAAAPVPAAAPA SSSDPAAAAAATAAPGQTPASA QAPAQTPAPALPGPALPGPFPG GRVVRLHPVILASIVDSYERRN EGAARVIGTLLGTVDKHSVEVT NCFSVPHNESEDEVAVDMEFAK NMYELHKKVSPNELILGWYATG HDITEHSVLIHEYYSREAPNPI HLTVDTSLQNGRMSIKAYVSTL MGVPGRTMGVMFTPLTVKYAYY DTERIGVDLIMKTCFSPNRVIG	216	VRLHPVILASIVDSYERRNE GAARVIGTLLGTVDKHSVEV TNCFSVPHNESEDEVAVDME FAKNMYELHKKVSPNELILG WYATGHDITEHSVLIHEYYS REAPNPIHLTVDTSLQNGRM SIKAYVSTLMGVPGRTMGVM FTPLTVKYAYYDTERIGVDL IMKTCFSPNRVIGLSSDLQQ VGGASARIQDALSTVLQYAE DVLSGKVSADNTVGRFLMSL VNQVPKIVPDDFETMLNSNI

		LSSDLQQVGGASARIQDALSTV LQYAEDVLSGKVSADNTVGRFL MSLVNQVPKIVPDDFETMLNSN INDLLMVTYLANLTQSQIALNE KLVNL		NDLLMVTYLANLTQSQIALN EKLVNL
PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7	109	MPELAVQKVVVHPLVLLSVVDH FNRIGKVGNQKRVVGVLLGSWQ KKVLDVSNSFAVPFDEDDKDDS VWFLDHDYLENMYGMFKKVNAR ERIVGWYHTGPKLHKNDIAINE LMKRYCPNSVLVIIDVKPKDLG LPTEAYISVEEVHDDGTPTSKT FEHVTSEIGAEEAEEVGVEHLL RDIKDTTVGTLSQRITNQVHGL KGLNSKLLDIRSYLEKVATGKL PINHQIIYQLQDVFNLLPDVSL QEFVKAFYLKTNDQMVVVYLAS LIRSVVALHNLINNKIANRDAE KKEGQEKEESKKDRKEDKEKDK DKEKSDVKKEEKKEKK	217	VVVHPLVLLSVVDHFNRIGK VGNQKRVVGVLLGSWQKKVL DVSNSFAVPFDEDDKDDSVW FLDHDYLENMYGMFKKVNAR ERIVGWYHTGPKLHKNDIAI NELMKRYCPNSVLVIIDVKP KDLGLPTEAYISVEEVHDDG TPTSKTFEHVTSEIGAEEAE EVGVEHLLRDIKDTTVGTLS QRITNQVHGLKGLNSKLLDI RSYLEKVATGKLPINHQIIY QLQDVFNLLPDVSLQEFVKA FYLKTNDQMVVVYLASLIRS VVALHNLINNKIANRDAEKK EGQEKEESKKDRKEDKEKDK DKEKSDVKKEEKKEKK
EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H	110	MASRKEGTGSTATSSSSTAGAA GKGKGKGGSGDSAVKQVQIDGL VVLKIIKHYQEEGQGTEVVQGV LLGLVVEDRLEITNCFPFPQHT EDDADFDEVQYQMEMMRSLRHV NIDHLHVGWYQSTYYGSFVTRA LLDSQFSYQHAIEESVVLIYDP IKTAQGSLSLKAYRLTPKLMEV CKEKDFSPEALKKANITFEYMF EEVPIVIKNSHLINVLMWELEK KSAVADKHELLSLASSNHLG KNLQLLMDRVDEMSQDIVKYNT YMRNTSKQQQQKHQYQQRRQQE NMQRQSRGEPPLPEEDLSKLFK PPQPPARMDSLLIAGQINTYCQ NIKEFTAQNLGKLFMAQALQEY NN	218	VQIDGLVVLKIIKHYQEEGQ GTEVVQGVLLGLVVEDRLEI TNCFPFPQHTEDDADFDEVQ YQMEMMRSLRHVNIDHLHVG WYQSTYYGSFVTRALLDSQF SYQHAIEESVVLIYDPIKTA QGSLSLKAYRLTPKLMEVCK EKDFSPEALKKANITFEYMF EEVPIVIKNSHLINVLMWEL EKKSAVADKHELLSLASSNH LGKNLQLLMDRVDEMSQDIV KYNTYMRNTSKQQQQKHQYQ QRRQQENMQRQSRGEPPLPE EDLSKLFKPPQPPARMDSLL IAGQINTYCQNIKEFTAQNL GKLFMAQALQEYNN
CSN5_HUMAN COP9 signalosome complex subunit 5	111	MAASGSGMAQKTWELANNMQEA QSIDEIYKYDKKQQQEILAAKP WTKDHHYFKYCKISALALLKMV MHARSGGNLEVMGLMLGKVDGE TMIIMDSFALPVEGTETRVNAQ AAAYEYMAAYIENAKQVGRLEN AIGWYHSHPGYGCWLSGIDVST QMLNQQFQEPFVAVVIDPTRTI SAGKVNLGAFRTYPKGYKPPDE GPSEYQTIPLNKIEDFGVHCKQ YYALEVSYFKSSLDRKLLELLW NKYWVNTLSSSSLLTNADYTTG QVFDLSEKLEQSEAQLGRGSFM	219	YCKISALALLKMVMHARSGG NLEVMGLMLGKVDGETMIIM DSFALPVEGTETRVNAQAAA YEYMAAYIENAKQVGRLENA IGWYHSHPGYGCWLSGIDVS TQMLNQQFQEPFVAVVIDPT RTISAGKVNLGAFRTYPKGY KPPDEGPSEYQTIPLNKIED FGVHCKQYYALEVSYFKSSL DRKLLELLWNKYWVNTLSSS SLLTNADYTTGQVFDLSEKL EQSEAQLGRGSFMLGLETHD RKSEDKLAKATRDSCKTTIE

		LGLETHDRKSEDKLAKATRDSCKTTIEAIHGLMSQVIKDKLFNQINIS		AIHGLMSQVIKDKLFNQINIS
BRCC3_HUMAN Lys-63-specific deubiquitinase BRCC36	112	MAVQVVQAVQAVHLESDAFLVCLNHALSTEKEEVMGLCIGELNDDTRSDSKFAYTGTEMRTVAEKVDAVRIVHIHSVIILRRSDKRKDRVEISPEQLSAASTEAERLAELTGRPMRVVGWYHSHPHITVWPSHVDVRTQAMYQMMDQGFVGLIFSCFIEDKNTKTGRVLYTCFQSIQAQKSSESLHGPRDFWSSSQHISIEGQKEEERYERIEIPIHIVPHVTIGKVCLESAVELPKILCQEEQDAYRRIHSLTHLDSVTKIHNGSVFTKNLCSQMSAVSGPLLQWLEDRLEQNQQHLQELQQEKEELMQELSSLE	220	VHLESDAFLVCLNHALSTEKEEVMGLCIGELNDDTRSDSKFAYTGTEMRTVAEKVDAVRIVHIHSVIILRRSDKRKDRVEISPEQLSAASTEAERLAELTGRPMRVVGWYHSHPHITVWPSHVDVRTQAMYQMMDQGFVGLIFSCFIEDKNTKTGRVLYTCFQSIQAQKSSESLHGPRDFWSSSQHISIEGQKEEERYERIEIPIHIVPHVTIGKVCLESAVELPKILCQEEQDAYRRIHSLTHLDSVTKIHNGSVFTKNLCSQMSAVSGPLLQWLEDRLEQNQQHLQELQQEKEELMQELSSLE

5.3.2 Targeting Domain

[00185] In some embodiments, the targeting domain comprises a targeting moiety that specifically binds to a target cytosolic protein. In some embodiments, the targeting moiety comprises an antibody (or antigen binding fragment thereof). In some embodiments, the antibody is a full-length antibody, a single chain variable fragment (scFv), a $(scFv)_2$, a scFv-Fc, a Fab, a Fab', a $(Fab')_2$, a F(v), a single domain antibody, a single chain antibody, a VHH, or a $(VHH)_2$.. In some embodiments the targeting moiety comprises a VHH. In some embodiments the targeting moiety comprises a $(VHH)_2$.

[00186] In some embodiments, the targeting moiety specifically binds to a wild type target cytosolic protein. In some embodiments, the targeting moiety specifically binds to a wild type target cytosolic protein, but does not specifically binds to a variant of the target cytosolic protein associated with a genetic disease. In some embodiments, the targeting moiety specifically binds to a naturally occurring variant of a target cytosolic protein. In some embodiments, the targeting moiety specifically binds to a naturally occurring variant of a target cytosolic protein that is associated with a genetic disease (e.g., a genetic disease described herein). In some embodiments, the targeting moiety specifically binds to a naturally occurring variant of a target cytosolic protein that is a cause of a genetic disease (e.g., a genetic disease described herein). In some embodiments, the targeting moiety specifically binds a naturally occurring variant of a target cytosolic protein that is a loss of a function variant. In some embodiments, the targeting moiety specifically binds a

naturally occurring variant of a target cytosolic protein that is a loss of a function variant associated with a genetic disease (e.g., a genetic disease described herein). In some embodiments, the targeting moiety specifically binds a naturally occurring variant of a target cytosolic protein that is a loss of a function variant that causes a genetic disease (e.g., a genetic disease described herein).

5.3.2.1 Exemplary Target Cytosolic Proteins

[00187] In some embodiments, targeting moiety specifically binds a target cytosolic protein (e.g., a cytosolic protein described herein). Exemplary target cytosolic proteins include, but are not limited to, Ras/Rap GTPase-activating protein (SYNGAP1), cyclin-dependent kinase-like 5 (CDKL5), copper-transporting ATPase 2 (ATP7B), syntaxin-binding protein 1 (STXBP1), progranulin (GRN), protein jagged-1 (JAG1), GATOR complex protein DEPDC5 (DEPDC5), tuberin (TSC2), hamartin (TSC1), kinesin-like protein KIF1A (KIF1A), dynamin-1 (DNM1), SH3 and multiple ankyrin repeat domains protein 3 (SHANK3), dystrophin (DMD), oxygen-regulated protein 1 (RP1), titin (TTN), cytoplasmic dynein 1 heavy chain 1 (DYNC1H1), TRIO and F-actin-binding protein (TRIO), probable ubiquitin carboxyl-terminal hydrolase FAF-X (USP9X), Cystatin-B (CSTB), and Pterin-4-alpha-carbinolamine dehydratase (PCBD1).

[00188] In some embodiments, the target cytosolic protein is SYNGAP1. In some embodiments, the target cytosolic protein is CDKL5. In some embodiments, the target cytosolic protein is ATP7B. In some embodiments, the target cytosolic protein is STXBP1. In some embodiments, the target cytosolic protein is GRN. In some embodiments, the target cytosolic protein is JAG1. In some embodiments, the target cytosolic protein is DEPDC5. In some embodiments, the target cytosolic protein is TSC2. In some embodiments, the target cytosolic protein is TSC1. In some embodiments, the target cytosolic protein is KIF1A. In some embodiments, the target cytosolic protein is DNM1. In some embodiments, the target cytosolic protein is SHANK3. In some embodiments, the target cytosolic protein is DMD. In some embodiments, the target cytosolic protein is TNT. In some embodiments, the target cytosolic protein is DYNC1H1. In some embodiments, the target cytosolic protein is TRIO. In some embodiments, the target cytosolic protein is USP9X. In some embodiments, the target cytosolic protein is TRIO. In some embodiments, the target cytosolic protein is USP9X. In some embodiments, the target cytosolic protein is CSTB. In some embodiments, the target cytosolic protein is USP9X. In some embodiments, the target cytosolic protein is PCBD1.

[00189] In some embodiments, the target cytosolic protein comprises an amino acid sequence

at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 221. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 222. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 223. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 224. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 225. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 226. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 227. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 228. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 229. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 230. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 231. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 232. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 233. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 234. In some embodiments,

the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 235. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 236. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 237. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 238. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 287. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 288. In some embodiments, the target cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 289.

[00190] Table 2 below, provides the wild type amino acid sequence of exemplary proteins to target for deubiquitination utilizing the fusion proteins described herein.

Table 2. The amino acid sequence of exemplary cytosolic proteins to target for deubiquitination utilizing the fusion proteins described herein and exemplary disease associations

Description	Disease Associations	SEQ ID NO	Wild Type Amino Acid Sequence
Cyclin-dependent kinase-like 5 (CDKL5)	CDKL5 Deficiency Disorder; Epileptic encephalopathy, early infantile Type 2	221	MKIPNIGNVMNKFEILGVVGEGAYGVVLKCRHKETHE IVAIKKFKDSEENEEVKETTLRELKMLRTLKQENIVE LKEAFRRRGKLYLVFEYVEKNMLELLEEMPNGVPPEK VKSYIYQLIKAIHWCHKNDIVHRDIKPENLLISHNDV LKLCDFGFARNLSEGNNANYTEYVATRWYRSPELLLG APYGKSVDMWSVGCILGELSDGQPLFPGESEIDQLFT IQKVLGPLPSEQMKLFYSNPRFHGLRFPAVNHPQSLE RRYLGILNSVLLDLMKNLLKLDPADRYLTEQCLNHPT FQTQRLLDRSPSRSAKRKPYHVESSTLSNRNQAGKST ALQSHHRSNSKDIQNLSVGLPRADEGLPANESFLNGN LAGASLSPLHTKTYQASSQPGSTSKDLTNNNIPHLLS PKEAKSKTEFDFNIDPKPSEGPGTKYLKSNSRSQQNR HSFMESSQSKAGTLQPNEKQSRHSYIDTIPQSSRSPS YRTKAKSHGALSDSKSVSNLSEARAQIAEPSTSRYFP SSCLDLNSPTSPTPTRHSDTRTLLSPSGRNNRNEGTL DSRRTTTRHSKTMEELKLPEHMDSSHSHSLSAPHESF

			SYGLGYTSPFSSQQRPHRHSMYVTRDKVRAKGLDGSL SIGQGMAARANSLQLLSPQPGEQLPPEMTVARSSVKE TSREGTSSFHTRQKSEGGVYHDPHSDDGTAPKENRHL YNDPVPRRVGSFYRVPSPRPDNSFHENNVSTRVSSLP SESSSGTNHSKRQPAFDPWKSPENISHSEQLKEKEKQ GFFRSMKKKKKKSQTVPNSDSPDLLTLQKSIHSASTP SSRPKEWRPEKISDLQTQSQPLKSLRKLLHLSSASNH PASSDPRFQPLTAQQTKNSFSEIRIHPLSQASGGSSN IRQEPAPKGRPALQLPGQMDPGWHVSSVTRSATEGPS YSEQLGAKSGPNGHPYNRTNRSRMPNLNDLKETAL
Copper-transporting ATPase 2 (ATP7B)	Wilson disease	222	MPEQERQITAREGASRKILSKLSLPTRAWEPAMKKSF AFDNVGYEGGLDGLGPSSQVATSTVRILGMTCQSCVK SIEDRISNLKGIISMKVSLEQGSATVKYVPSVVCLQQ VCHQIGDMGFEASIAEGKAASWPSRSLPAQEAVVKLR VEGMTCQSCVSSIEGKVRKLQGVVRVKVSLSNQEAVI TYQPYLIQPEDLRDHVNDMGFEAAIKSKVAPLSLGPI DIERLQSTNPKRPLSSANQNFNNSETLGHQGSHVVTL QLRIDGMHCKSCVLNIEENIGQLLGVQSIQVSLENKT AQVKYDPSCTSPVALQRAIEALPPGNFKVSLPDGAEG SGTDHRSSSSHSPGSPPRNQVQGTCSTTLIAIAGMTC ASCVHSIEGMISQLEGVQQISVSLAEGTATVLYNPSV ISPEELRAAIEDMGFEASVVSESCSTNPLGNHSAGNS MVQTTDGTPTSVQEVAPHTGRLPANHAPDILAKSPQS TRAVAPQKCFLQIKGMTCASCVSNIERNLQKEAGVLS VLVALMAGKAEIKYDPEVIQPLEIAQFIQDLGFEAAV MEDYAGSDGNIELTITGMTCASCVHNIESKLTRTNGI TYASVALATSKALVKFDPEIIGPRDIIKIIEEIGFHA SLAQRNPNAHHLDHKMEIKQWKKSFLCSLVFGIPVMA LMIYMLIPSNEPHQSMVLDHNIIPGLSILNLIFFILC TFVQLLGGWYFYVQAYKSLRHRSANMDVLIVLATSIA YVYSLVILVVAVAEKAERSPVTFFDTPPMLFVFIALG RWLEHLAKSKTSEALAKLMSLQATEATVVTLGEDNLI IREEQVPMELVQRGDIVKVVPGGKFPVDGKVLEGNTM ADESLITGEAMPVTKKPGSTVIAGSINAHGSVLIKAT HVGNDTTLAQIVKLVEEAQMSKAPIQQLADRFSGYFV PFIIIMSTLTLVVWIVIGFIDFGVVQRYFPNPNKHIS QTEVIIRFAFQTSITVLCIACPCSLGLATPTAVMVGT GVAAQNGILIKGGKPLEMAHKIKTVMFDKTGTITHGV PRVMRVLLLGDVATLPLRKVLAVVGTAEASSEHPLGV AVTKYCKEELGTETLGYCTDFQAVPGCGIGCKVSNVE GILAHSERPLSAPASHLNEAGSLPAEKDAVPQTFSVL IGNREWLRRNGLTISSDVSDAMTDHEMKGQTAILVAI DGVLCGMIAIADAVKQEAALAVHTLQSMGVDVVLITG DNRKTARAIATQVGINKVFAEVLPSHKVAKVQELQNK GKKVAMVGDGVNDSPALAQADMGVAIGTGTDVAIEAA DVVLIRNDLLDVVASIHLSKRTVRRIRINLVLALIYN LVGIPIAAGVFMPIGIVLQPWMGSAAMAASSVSVVLS SLQLKCYKKPDLERYEAQAHGHMKPLTASQVSVHIGM DDRWRDSPRATPWDQVSYVSQVSLSSLTSDKPSRHSA AADDDGDKWSLLLNGRDEEQYI

Syntaxin-binding protein 1 (STXBP1)	STXBP1 Encephalopathy; Epileptic encephalopathy, early infantile, Type 4	223	MAPIGLKAVVGEKIMHDVIKKVKKKGEWKVLVVDQLS MRMLSSCCKMTDIMTEGITIVEDINKRREPLPSLEAV YLITPSEKSVHSLISDFKDPPTAKYRAAHVFFTDSCP DALFNELVKSRAAKVIKTLTEINIAFLPYESQVYSLD SADSFQSFYSPHKAQMKNPILERLAEQIATLCATLKE YPAVRYRGEYKDNALLAQLIQDKLDAYKADDPTMGEG PDKARSQLLILDRGFDPSSPVLHELTFQAMSYDLLPI ENDVYKYETSGIGEARVKEVLLDEDDDLWIALRHKHI AEVSQEVTRSLKDFSSSKRMNTGEKTTMRDLSQMLKK MPQYQKELSKYSTHLHLAEDCMKHYQGTVDKLCRVEQ DLAMGTDAEGEKIKDPMRAIVPILLDANVSTYDKIRI ILLYIFLKNGITEENLNKLIQHAQIPPEDSEIITNMA HLGVPIVTDSTLRRRSKPERKERISEQTYQLSRWTPI IKDIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSAR YGHWHKNKAPGEYRSGPRLIIFILGGVSLNEMRCAYE VTQANGKWEVLIGSTHILTPQKLLDTLKKLNKTDEEI SS
Ras/Rap GTPase-activating protein (SYNGAP1)	SYNGAP1 Encephalopathy; Mental retardation, autosomal dominant 5	224	MSRSRASIHRGSIPAMSYAPFRDVRGPSMHRTQYVHS PYDRPGWNPRFCIISGNQLLMLDEDEIHPLLIRDRRS ESSRNKLLRRTVSVPVEGRPHGEHEYHLGRSRRKSVP GGKQYSMEGAPAAPFRPSQGFLSRRLKSSIKRTKSQP KLDRTSSFRQILPRFRSADHDRARLMQSFKESHSHES LLSPSSAAEALELNLDEDSIIKPVHSSILGQEFCFEV TTSSGTKCFACRSAAERDKWIENLQRAVKPNKDNSRR VDNVLKLWIIEARELPPKKRYYCELCLDDMLYARTTS KPRSASGDTVFWGEHFEFNNLPAVRALRLHLYRDSDK KRKKDKAGYVGLVTVPVATLAGRHFTEQWYPVTLPTG SGGSGGMGSGGGGGSGGGSGGKGKGGCPAVRLKARYQ TMSILPMELYKEFAEYVTNHYRMLCAVLEPALNVKGK EEVASALVHILQSTGKAKDFLSDMAMSEVDRFMEREH LIFRENTLATKAIEEYMRLIGQKYLKDAIGEFIRALY ESEENCEVDPIKCTASSLAEHQANLRMCCELALCKVV NSHCVFPRELKEVFASWRLRCAERGREDIADRLISAS LFLRFLCPAIMSPSLFGLMQEYPDEQTSRTLTLIAKV IQNLANFSKFTSKEDFLGFMNEFLELEWGSMQQFLYE ISNLDTLTNSSSFEGYIDLGRELSTLHALLWEVLPQL SKEALLKLGPLPRLLNDISTALRNPNIQRQPSRQSER PRPQPVVLRGPSAEMQGYMMRDLNSSIDLQSFMARGL NSSMDMARLPSPTKEKPPPPPPGGGKDLFYVSRPPLA RSSPAYCTSSSDITEPEQKMLSVNKSVSMLDLQGDGP GGRLNSSSVSNLAAVGDLLHSSQASLTAALGLRPAPA GRLSQGSGSSITAAGMRLSQMGVTTDGVPAQQLRIPL SFQNPLFHMAADGPGPPGGHGGGGGHGPPSSHHHHHH HHHHRGGEPPGDTFAPFHGYSKSEDLSSGVPKPPAAS ILHSHSYSDEFGPSGTDFTRRQLSLQDNLQHMLSPPQ ITIGPQRPAPSGPGGGSGGGSGGGGGGQPPPLQRGKS QQLTVSAAQKPRPSSGNLLQSPEPSYGPARPRQQSLS KEGSIGGSGGSGGGGGGGLKPSITKQHSQTPSTLNPT MPASERTVAWVSNMPHLSADIESAHIEREEYKLKEYS KSMDESRLDRVKEYEEEIHSLKERLHMSNRKLEEYER RLLSQEEQTSKILMQYQARLEQSEKRLRQQQAEKDSQ

			IKSIIGRLMLVEEELRRDHPAMAEPLPEPKKRLLDAQ ERQLPPLGPTNPRVTLAPPWNGLAPPAPPPPRLQIT ENGEFRNTADH
Progranulin (GRN)	Aphasia, primary progressive & FTD	225	MWTLVSWVALTAGLVAGTRCPDGQFCPVACCLDPGGA SYSCCRPLLDKWPTTLSRHLGGPCQVDAHCSAGHSCI FTVSGTSSCCPFPEAVACGDGHHCCPRGFHCSADGRS CFQRSGNNSVGAIQCPDSQFECPDFSTCCVMVDGSWG CCPMPQASCCEDRVHCCPHGAFCDLVHTRCITPTGTH PLAKKLPAQRTNRAVALSSSVMCPDARSRCPDGSTCC ELPSGKYGCCPMPNATCCSDHLHCCPQDTVCDLIQSK CLSKENATTDLLTKLPAHTVGDVKCDMEVSCPDGYTC CRLQSGAWGCCPFTQAVCCEDHIHCCPAGFTCDTQKG TCEQGPHQVPWMEKAPAHLSLPDPQALKRDVPCDNVS SCPSSDTCCQLTSGEWGCCPIPEAVCCSDHQHCCPQG YTCVAEGQCQRGSEIVAGLEKMPARRASLSHPRDIGC DQHTSCPVGQTCCPSLGGSWACCQLPHAVCCEDRQHC CPAGYTCNVKARSCEKEVVSAQPATFLARSPHVGVKD VECGEGHFCHDNQTCCRDNRQGWACCPYRQGVCCADR RHCCPAGFRCAARGTKCLRREAPRWDAPLRDPALRQL L
Protein jagged-1 (JAG1)	Alagille syndrome 1	226	MRSPRTRGRSGRPLSLLLALLCALRAKVCGASGQFEL EILSMQNVNGELQNGNCCGGARNPGDRKCTRDECDTY FKVCLKEYQSRVTAGGPCSFGSGSTPVIGGNTFNLKA SRGNDRNRIVLPFSFAWPRSYTLLVEAWDSSNDTVQP DSIIEKASHSGMINPSRQWQTLKQNTGVAHFEYQIRV TCDDYYYGFGCNKFCRPRDDFFGHYACDQNGNKTCME GWMGPECNRAICRQGCSPKHGSCKLPGDCRCQYGWQG LYCDKCIPHPGCVHGICNEPWQCLCETNWGGQLCDKD LNYCGTHQPCLNGGTCSNTGPDKYQCSCPEGYSGPNC EIAEHACLSDPCHNRGSCKETSLGFECECSPGWTGPT CSTNIDDCSPNNCSHGGTCQDLVNGFKCVCPPQWTGK TCQLDANECEAKPCVNAKSCKNLIASYYCDCLPGWMG QNCDININDCLGQCQNDASCRDLVNGYRCICPPGYAG DHCERDIDECASNPCLNGGHCQNEINRFQCLCPTGFS GNLCQLDIDYCEPNPCQNGAQCYNRASDYFCKCPEDY EGKNCSHLKDHCRTTPCEVIDSCTVAMASNDTPEGVR YISSNVCGPHGKCKSQSGGKFTCDCNKGFTGTYCHEN INDCESNPCRNGGTCIDGVNSYKCICSDGWEGAYCET NINDCSQNPCHNGGTCRDLVNDFYCDCKNGWKGKTCH SRDSQCDEATCNNGGTCYDEGDAFKCMCPGGWEGTTC NIARNSSCLPNPCHNGGTCVVNGESFTCVCKEGWEGP ICAQNTNDCSPHPCYNSGTCVDGDNWYRCECAPGFAG PDCRININECQSSPCAFGATCVDEINGYRCVCPPGHS GAKCQEVSGRPCITMGSVIPDGAKWDDDCNTCQCLNG RIACSKVWCGPRPCLLHKGHSECPSGQSCIPILDDQC FVHPCTGVGECRSSSLQPVKTKCTSDSYYQDNCANIT FTFNKEMMSPGLTTEHICSELRNLNILKNVSAEYSIY IACEPSPSANNEIHVAISAEDIRDDGNPIKEITDKII DLVSKRDGNSSLIAAVAEVRVQRRPLKNRTDFLVPLL SSVLTVAWICCLVTAFYWCLRKRRKPGSHTHSASEDN TTNNVREQLNQIKNPIEKHGANTVPIKDYENKNSKMS

			KIRTHNSEVEEDDMDKHQQKARFAKQPAYTLVDREEK PPNGTPTKHPNWTNKQDNRDLESAQSLNRMEYIV
GATOR complex protein DEPDC5 (DEPDC5)	Epilepsy, familial focal, with variable foci 1	227	MRTTKVYKLVIHKKGFGGSDDELVVNPKVFPHIKLGD IVEIAHPNDEYSPLLLQVKSLKEDLQKETISVDQTVT QVFRLRPYQDVYVNVVDPKDVTLDLVELTFKDQYIGR GDMWRLKKSLVSTCAYITQKVEFAGIRAQAGELWVKN EKVMCGYISEDTRVVFRSTSAMVYIFIQMSCEMWDFD IYGDLYFEKAVNGFLADLFTKWKEKNCSHEVTVVLFS RTFYDAKSVDEFPEINRASIRQDHKGRFYEDFYKVVV QNERREEWTSLLVTIKKLFIQYPVLVRLEQAEGFPQG DNSTSAQGNYLEAINLSFNVFDKHYINRNFDRTGQMS VVITPGVGVFEVDRLLMILTKQRMIDNGIGVDLVCMG EQPLHAVPLFKLHNRSAPRDSRLGDDYNIPHWINHSF YTSKSQLFCNSFTPRIKLAGKKPASEKAKNGRDTSLG SPKESENALPIQVDYDAYDAQVFRLPGPSRAQCLTTC RSVRERESHSRKSASSCDVSSSPSLPSRTLPTEEVRS QASDDSSLGKSANILMIPHPHLHQYEVSSSLGYTSTR DVLENMMEPPQRDSSAPGRFHVGSAESMLHVRPGGYT PQRALINPFAPSRMPMKLTSNRRRWMHTFPVGPSGEA IQIHHQTRQNMAELQGSGQRDPTHSSAELLELAYHEA AGRHSNSRQPGDGMSFLNFSGTEELSVGLLSNSGAGM NPRTQNKDSLEDSVSTSPDPILTLSAPPVVPGFCCTV GVDWKSLTTPACLPLTTDYFPDRQGLQNDYTEGCYDL LPEADIDRRDEDGVQMTAQQVFEEFICQRLMQGYQII VQPKTQKPNPAVPPPLSSSPLYSRGLVSRNRPEEEDQ YWLSMGRTFHKVTLKDKMITVTRYLPKYPYESAQIHY TYSLCPSHSDSEFVSCWVEFSHERLEEYKWNYLDQYI CSAGSEDFSLIESLKFWRTRFLLLPACVTATKRITEG EAHCDIYGDRPRADEDEWQLLDGFVRFVEGLNRIRRR HRSDRMMRKGTAMKGLQMTGPISTHSLESTAPPVGKK GTSALSALLEMEASQKCLGEQQAAVHGGKSSAQSAES SSVAMTPTYMDSPRKDGAFFMEFVRSPRTASSAFYPQ VSVDQTATPMLDGTSLGICTGQSMDRGNSQTFGNSQN IGEQGYSSTNSSDSSSQQLVASSLTSSSTLTEILEAM KHPSTGVQLLSEQKGLSPYCFISAEVVHWLVNHVEGI QTQAMAIDIMQKMLEEQLITHASGEAWRTFIYGFYFY KIVTDKEPDRVAMQQPATTWHTAGVDDFASFQRKWFE VAFVAEELVHSEIPAFLLPWLPSRPASYASRHSSFSR SFGGRSQAAALLAATVPEQRTVTLDVDVNNRTDRLEW CSCYYHGNFSLNAAFEIKLHWMAVTAAVLFEMVQGWH RKATSCGFLLVPVLEGPFALPSYLYGDPLRAQLFIPL NISCLLKEGSEHLFDSFEPETYWDRMHLFQEAIAHRF GFVQDKYSASAFNFPAENKPQYIHVTGTVFLQLPYSK RKFSGQQRRRRNSTSSTNQNMFCEERVGYNWAYNTML TKTWRSSATGDEKFADRLLKDFTDFCINRDNRLVTFW TSCLEKMHASAP
Tuberin (TSC2)	Tuberous sclerosis-2	228	MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTE FIITAEILRELSMECGLNNRIRMIGQICEVAKTKKFE EHAVEALWKAVADLLQPERPLEARHAVLALLKAIVQG QGERLGVLRALFFKVIKDYPSNEDLHERLEVFKALTD NGRHITYLEEELADFVLQWMDVGLSSEFLLVLVNLVK

			FNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVL DAVVCYNCLPAESLPLFIVTLCRTINVKELCEPCWKL MRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAV FFVGMALWGAHRLYSLRNSPTSVLPSFYQAMACPNEV VSYEIVLSITRLIKKYRKELQVVAWDILLNIIERLLQ QLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERY FELVERCADQRPESSLLNLISYRAQSIHPAKDGWIQN LQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFYE EELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEG CHTHHFNSLLDIIEKVMARSLSPPPELEERDVAAYSA SLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVS HIQLHYKHSYTLPIASSIRLQAFDFLLLLRADSLHRL GLPNKDGVVRFSPYCVCDYMEPERGSEKKTSGPLSPP TGPPGPAPAGPAVRLGSVPYSLLFRVLLQCLKQESDW KVLKLVLGRLPESLRYKVLIFTSPCSVDQLCSALCSM LSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYH NYLDKTKQREMVYCLEQGLIHRCASQCVVALSICSVE MPDIIIKALPVLVVKLTHISATASMAVPLLEFLSTLA RLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCL AHHVIAMWFIRCRLPFRKDFVPFITKGLRSNVLLSFD DTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNSPP VKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSAS LGSADENSVAQADDSLKNLHLELTETCLDMMARYVFS NFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSV GTGTRSLLGLDSGELQSGPESSSSPGVHVRQTKEAPA KLESQAGQQVSRGARDRVRSMSGGHGLRVGALDVPAS QFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLA AYVPLLTQGWAEILVRRPTGNTSWLMSLENPLSPFSS DINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAA STAKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWAD SAVVMEEGSPGEVPVLVEPPGLEDVEAALGMDRRTDA YSRSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGGR PSVDLSFQPSQPLSKSSSSPELQTLQDILGDPGDKAD VGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQPEG PLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDAL KSRATASNAEKVPGINPSFVFLQLYHSPFFGDESNKP ILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQ SNSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDK VYLGGLDVCGEDGQFTYCWHDDIMQAVFHIATLMPTK DVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQ FNFVHVIVTPLDYECNLVSLQCRKDMEGLVDTSVAKI VSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSK WIARLRHIKRLRQRICEEAAYSNPSLPLVHPPSHSKA PAQTPAEPTPGYEVGQRKRLISSVEDFTEFV
Hamartin (TSC1)	Tuberous sclerosis-1	229	MAQQANVGELLAMLDSPMLGVRDDVTAVFKENLNSDR GPMLVNTLVDYYLETSSQPALHILTTLQEPHDKHLLD RINEYVGKAATRLSILSLLGHVIRLQPSWKHKLSQAP LLPSLLKCLKMDTDVVVLTTGVLVLITMLPMIPQSGK QHLLDFFDIFGRLSSWCLKKPGHVAEVYLVHLHASVY ALFHRLYGMYPCNFVSFLRSHYSMKENLETFEEVVKP MMEHVRIHPELVTGSKDHELDPRRWKRLETHDVVIEC

			AKISLDPTEASYEDGYSVSHQISARFPHRSADVTTSP YADTQNSYGCATSTPYSTSRLMLLNMPGQLPQTLSSP STRLITEPPQATLWSPSMVCGMTTPPTSPGNVPPDLS HPYSKVFGTTAGGKGTPLGTPATSPPPAPLCHSDDYV HISLPQATVTPPRKEERMDSARPCLHRQHHLLNDRGS EEPPGSKGSVTLSDLPGFLGDLASEEDSIEKDKEEAA ISRELSEITTAEAEPVVPRGGFDSPFYRDSLPGSQRK THSAASSSQGASVNPEPLHSSLDKLGPDTPKQAFTPI DLPCGSADESPAGDRECQTSLETSIFTPSPCKIPPPT RVGFGSGQPPPYDHLFEVALPKTAHHFVIRKTEELLK KAKGNTEEDGVPSTSPMEVLDRLIQQGADAHSKELNK LPLPSKSVDWTHFGGSPPSDEIRTLRDQLLLLHNQLL YERFKRQQHALRNRRLLRKVIKAAALEEHNAAMKDQL KLQEKDIQMWKVSLQKEQARYNQLQEQRDTMVTKLHS QIRQLQHDREEFYNQSQELQTKLEDCRNMIAELRIEL KKANNKVCHTELLLSQVSQKLSNSESVQQQMEFLNRQ LLVLGEVNELYLEQLQNKHSDTTKEVEMMKAAYRKEL EKNRSHVLQQTQRLDTSQKRILELESHLAKKDHLLLE QKKYLEDVKLQARGQLQAAESRYEAQKRITQVFELEI LDLYGRLEKDGLLKKLEEEKAEAAEAAEERLDCCNDG CSDSMVGHNEEASGHNGETKTPRPSSARGSSGSRGGG GSSSSSSELSTPEKPPHQRAGPFSSRWETTMGEASAS IPTTVGSLPSSKSFLGMKARELFRNKSESQCDEDGMT SSLSESLKTELGKDLGVEAKIPLNLDGPHPSPPTPDS VGQLHIMDYNETHHEHS
Kinesin-like protein KIF1A (KIF1A)	KIF1A-Associated Neurological Disorder	230	MAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTI VNPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVY RDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMGKQ EKDQQGIIPQLCEDLFSRINDTTNDNMSYSVEVSYME IYCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSKLA VTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFN IIFTQKRHDAETNITTEKVSKISLVDLAGSERADSTG AKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNK KKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSP ADINYDETLSTLRYADRAKQIRCNAVINEDPNNKLIR ELKDEVTRLRDLLYAQGLGDITDMTNALVGMSPSSSL SALSSRAASVSSLHERILFAPGSEEAIERLKETEKII AELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGG TLGVFSPKKTPHLVNLNEDPLMSECLLYYIKDGITRV GREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEAVV TLEPCEGADTYVNGKKVTEPSILRSGNRIIMGKSHVF RFNHPEQARQERERTPCAETPAEPVDWAFAQRELLEK QGIDMKQEMEQRLQELEDQYRREREEATYLLEQQRLD YESKLEALQKQMDSRYYPEVNEEEEEPEDEVQWTERE CELALWAFRKWKWYQFTSLRDLLWGNAIFLKEANAIS VELKKKVQFQFVLLTDTLYSPLPPDLLPPEAAKDRET RPFPRTIVAVEVQDQKNGATHYWTLEKLRQRLDLMRE MYDRAAEVPSSVIEDCDNVVTGGDPFYDRFPWFRLVG RAFVYLSNLLYPVPLVHRVAIVSEKGEVKGFLRVAVQ AISADEEAPDYGSGVRQSGTAKISFDDQHFEKFQSES CPVVGMSRSGTSQEELRIVEGQGQGADVGPSADEVNN

			NTCSAVPPEGLLLDSSEKAALDGPLDAALDHLRLGNT FTFRVTVLQASSISAEYADIFCQFNFIHRHDEAFSTE PLKNTGRGPPLGFYHVQNIAVEVTKSFIEYIKSQPIV FEVFGHYQQHPFPPLCKDVLSPLRPSRRHFPRVMPLS KPVPATKLSTLTRPCPGPCHCKYDLLVYFEICELEAN GDYIPAVVDHRGGMPCMGTFLLHQGIQRRITVTLLHE TGSHIRWKEVRELVVGRIRNTPETDESLIDPNILSLN ILSSGYIHPAQDDRTFYQFEAAWDSSMHNSLLLNRVT PYREKIYMTLSAYIEMENCTQPAVVTKDFCMVFYSRD AKLPASRSIRNLFGSGSLRASESNRVTGVYELSLCHV ADAGSPGMQRRRRRVLDTSVAYVRGEENLAGWRPRSD SLILDHQWELEKLSLLQEVEKTRHYLLLREKLETAQR PVPEALSPAFSEDSESHGSSSASSPLSAEGRPSPLEA PNERQRELAVKCLRLLTHTFNREYTHSHVCVSASESK LSEMSVTLLRDPSMSPLGVATLTPSSTCPSLVEGRYG ATDLRTPQPCSRPASPEPELLPEADSKKLPSPARATE TDKEPQRLLVPDIQEIRVSPIVSKKGYLHFLEPHTSG WARRFVVVRRPYAYMYNSDKDTVERFVLNLATAQVEY SEDQQAMLKTPNTFAVCTEHRGILLQAASDKDMHDWL YAFNPLLAGTIRSKLSRRRSAQMRV
Dynamin-1 (DNM1)	Encephalopathy	231	MGNRGMEDLIPLVNRLQDAFSAIGQNADLDLPQIAVV GGQSAGKSSVLENFVGRDFLPRGSGIVTRRPLVLQLV NATTEYAEFLHCKGKKFTDFEEVRLEIEAETDRVTGT NKGISPVPINLRVYSPHVLNLTLVDLPGMTKVPVGDQ PPDIEFQIRDMLMQFVTKENCLILAVSPANSDLANSD ALKVAKEVDPQGQRTIGVITKLDLMDEGTDARDVLEN KLLPLRRGYIGVVNRSQKDIDGKKDITAALAAERKFF LSHPSYRHLADRMGTPYLQKVLNQQLTNHIRDTLPGL RNKLQSQLLSIEKEVEEYKNFRPDDPARKTKALLQMV QQFAVDFEKRIEGSGDQIDTYELSGGARINRIFHERF PFELVKMEFDEKELRREISYAIKNIHGIRTGLFTPDM AFETIVKKQVKKIREPCLKCVDMVISELISTVRQCTK KLQQYPRLREEMERIVTTHIREREGRTKEQVMLLIDI ELAYMNTNHEDFIGFANAQQRSNQMNKKKTSGNQDEI LVIRKGWLTINNIGIMKGGSKEYWFVLTAENLSWYKD DEEKEKKYMLSVDNLKLRDVEKGFMSSKHIFALFNTE QRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPER VGDKEKASETEENGSDSFMHSMDPQLERQVETIRNLV DSYMAIVNKTVRDLMPKTIMHLMINNTKEFIFSELLA NLYSCGDQNTLMEESAEQAQRRDEMLRMYHALKEALS IIGDINTTTVSTPMPPPVDDSWLQVQSVPAGRRSPTS SPTPQRRAPAVPPARPGSRGPAPGPPPAGSALGGAPP VPSRPGASPDPFGPPPQVPSRPNRAPPGVPSRSGQAS PSRPESPRPPFDL
SH3 and multiple ankyrin repeat domains protein 3 (SHANK3)	Phelan-McDermid syndrome	232	MDGPGASAVVVRVGIPDLQQTKCLRLDPAAPVWAAKQ RVLCALNHSLQDALNYGLFQPPSRGRAGKFLDEERLL QEYPPNLDTPLPYLEFRYKRRVYAQNLIDDKQFAKLH TKANLKKFMDYVQLHSTDKVARLLDKGLDPNFHDPDS GECPLSLAAQLDNATDLLKVLKNGGAHLDFRTRDGLT AVHCATRQRNAAALTTLLDLGASPDYKDSRGLTPLYH SALGGGDALCCELLLHDHAQLGITDENGWQEIHQACR

			FGHVQHLEHLLFYGADMGAQNASGNTALHICALYNQE SCARVLLFRGANRDVRNYNSQTAFQVAIIAGNFELAE VIKTHKDSDVVPFRETPSYAKRRRLAGPSGLASPRPL QRSASDINLKGEAQPAASPGPSLRSLPHQLLLQRLQE EKDRDRDADQESNISGPLAGRAGQSKISPSGPGGPGP APGPGPAPPAPPAPPPRGPKRKLYSAVPGRKFIAVKA HSPQGEGEIPLHRGEAVKVLSIGEGGFWEGTVKGRTG WFPADCVEEVQMRQHDTRPETREDRTKRLFRHYTVGS YDSLTSHSDYVIDDKVAVLQKRDHEGFGFVLRGAKAE TPIEEFTPTPAFPALQYLESVDVEGVAWRAGLRTGDF LIEVNGVNVVKVGHKQVVALIRQGGNRLVMKVVSVTR KPEEDGARRRAPPPPKRAPSTTLTLRSKSMTAELEEL ASIRRRKGEKLDEMLAAAAEPTLRPDIADADSRAATV KQRPTSRRITPAEISSLFERQGLPGPEKLPGSLRKGI PRTKSVGEDEKLASLLEGRFPRSTSMQDPVREGRGIP PPPQTAPPPPPAPYYFDSGPPPAFSPPPPPGRAYDTV RSSFKPGLEARLGAGAAGLYEPGAALGPLPYPERQKR ARSMIILQDSAPESGDAPRPPPAATPPERPKRRPRPP GPDSPYANLGAFSASLFAPSKPQRRKSPLVKQLQVED AQERAALAVGSPGPGGGSFAREPSPTHRGPRPGGLDY GAGDGPGLAFGGPGPAKDRRLEERRRSTVFLSVGAIE GSAPGADLPSLQPSRSIDERLLGTGPTAGRDLLLPSP VSALKPLVSGPSLGPSGSTFIHPLTGKPLDPSSPLAL ALAARERALASQAPSRSPTPVHSPDADRPGPLFVDVQ ARDPERGSLASPAFSPRSPAWIPVPARREAEKVPREE RKSPEDKKSMILSVLDTSLQRPAGLIVVHATSNGQEP SRLGGAEEERPGTPELAPAPMQSAAVAEPLPSPRAQP PGGTPADAGPGQGSSEEEPELVFAVNLPPAQLSSSDE ETREELARIGLVPPPEEFANGVLLATPLAGPGPSPTT VPSPASGKPSSEPPPAPESAADSGVEEADTRSSSDPH LETTSTISTVSSMSTLSSESGELTDTHTSFADGHTFL LEKPPVPPKPKLKSPLGKGPVTFRDPLLKQSSDSELM AQQHHAASAGLASAAGPARPRYLFQRRSKLWGDPVES RGLPGPEDDKPTVISELSSRLQQLNKDTRSLGEEPVG GLGSLLDPAKKSPIAAARLFSSLGELSSISAQRSPGG PGGGASYSVRPSGRYPVARRAPSPVKPASLERVEGLG AGAGGAGRPFGLTPPTILKSSSLSIPHEPKEVRFVVR SVSARSRSPSPSPLPSPASGPGPGAPGPRRPFQQKPL QLWSKFDVGDWLESIHLGEHRDRFEDHEIEGAHLPAL TKDDFVELGVTRVGHRMNIERALRQLDGS
Dystrophin (DMD)	Becker Muscular Dystrophy	233	MLWWEEVEDCYEREDVQKKTFTKWVNAQFSKFGKQHI ENLFSDLQDGRRLLDLLEGLTGQKLPKEKGSTRVHAL NNVNKALRVLQNNNVDLVNIGSTDIVDGNHKLTLGLI WNIILHWQVKNVMKNIMAGLQQTNSEKILLSWVRQST RNYPQVNVINFTTSWSDGLALNALIHSHRPDLFDWNS VVCQQSATQRLEHAFNIARYQLGIEKLLDPEDVDTTY PDKKSILMYITSLFQVLPQQVSIEAIQEVEMLPRPPK VTKEEHFQLHHQMHYSQQITVSLAQGYERTSSPKPRF KSYAYTQAAYVTTSDPTRSPFPSQHLEAPEDKSFGSS LMESEVNLDRYQTALEEVLSWLLSAEDTLQAQGEISN DVEVVKDQFHTHEGYMMDLTAHQGRVGNILQLGSKLI

			GTGKLSEDEETEVQEQMNLLNSRWECLRVASMEKQSN LHRVLMDLQNQKLKELNDWLTKTEERTRKMEEEPLG PDLEDLKRQVQQHKVLQEDLEQEQVRVNSLTHMVVVV DESSGDHATAALEEQLKVLGDRWANICRWTEDRWVLL QDILLKWQRLTEEQCLFSAWLSEKEDAVNKIHTTGFK DQNEMLSSLQKLAVLKADLEKKKQSMGKLYSLKQDLL STLKNKSVTQKTEAWLDNFARCWDNLVQKLEKSTAQI SQAVTTTQPSLTQTTVMETVTTVTTREQILVKHAQEE LPPPPPQKKRQITVDSEIRKRLDVDITELHSWITRSE AVLQSPEFAIFRKEGNFSDLKEKVNAIEREKAEKFRK LQDASRSAQALVEQMVNEGVNADSIKQASEQLNSRWI EFCQLLSERLNWLEYQNNIIAFYNQLQQLEQMTTTAE NWLKIQPTTPSEPTAIKSQLKICKDEVNRLSDLQPQI ERLKIQSIALKEKGQGPMFLDADFVAFTNHFKQVFSD VQAREKELQTIFDTLPPMRYQETMSAIRTWVQQSETK LSIPQLSVTDYEIMEQRLGELQALQSSLQEQQSGLYY LSTTVKEMSKKAPSEISRKYQSEFEEIEGRWKKLSSQ LVEHCQKLEEQMNKLRKIQNHIQTLKKWMAEVDVFLK EEWPALGDSEILKKQLKQCRLLVSDIQTIQPSLNSVN EGGQKIKNEAEPEFASRLETELKELNTQWDHMCQQVY ARKEALKGGLEKTVSLQKDLSEMHEWMTQAEEEYLER DFEYKTPDELQKAVEEMKRAKEEAQQKEAKVKLLTES VNSVIAQAPPVAQEALKKELETLTTNYQWLCTRLNGK CKTLEEVWACWHELLSYLEKANKWLNEVEFKLKTTEN IPGGAEEISEVLDSLENLMRHSEDNPNQIRILAQTLT DGGVMDELINEELETFNSRWRELHEEAVRRQKLLEQS IQSAQETEKSLHLIQESLTFIDKQLAAYIADKVDAAQ MPQEAQKIQSDLTSHEISLEEMKKHNQGKEAAQRVLS QIDVAQKKLQDVSMKFRLFQKPANFEQRLQESKMILD EVKMHLPALETKSVEQEVVQSQLNHCVNLYKSLSEVK SEVEMVIKTGRQIVQKKQTENPKELDERVTALKLHYN ELGAKVTERKQQLEKCLKLSRKMRKEMNVLTEWLAAT DMELTKRSAVEGMPSNLDSEVAWGKATQKEIEKQKVH LKSITEVGEALKTVLGKKETLVEDKLSLLNSNWIAVT SRAEEWLNLLLEYQKHMETFDQNVDHITKWIIQADTL LDESEKKKPQQKEDVLKRLKAELNDIRPKVDSTRDQA ANLMANRGDHCRKLVEPQISELNHRFAAISHRIKTGK ASIPLKELEQFNSDIQKLLEPLEAEIQQGVNLKEEDF NKDMNEDNEGTVKELLQRGDNLQQRITDERKREEIKI KQQLLQTKHNALKDLRSQRRKKALEISHQWYQYKRQA DDLLKCLDDIEKKLASLPEPRDERKIKEIDRELQKKK EELNAVRRQAEGLSEDGAAMAVEPTQIQLSKRWREIE SKFAQFRRLNFAQIHTVREETMMVMTEDMPLEISYVP STYLTEITHVSQALLEVEQLLNAPDLCAKDFEDLFKQ EESLKNIKDSLQQSSGRIDIIHSKKTAALQSATPVER VKLQEALSQLDFQWEKVNKMYKDRQGRFDRSVEKWRR FHYDIKIFNQWLTEAEQFLRKTQIPENWEHAKYKWYL KELQDGIGQRQTVVRTLNATGEEIIQQSSKTDASILQ EKLGSLNLRWQEVCKQLSDRKKRLEEQKNILSEFQRD LNEFVLWLEEADNIASIPLEPGKEQQLKEKLEQVKLL VEELPLRQGILKQLNETGGPVLVSAPISPEEQDKLEN

			KLKQTNLQWIKVSRALPEKQGEIEAQIKDLGQLEKKL EDLEEQLNHLLLWLSPIRNQLEIYNQPNQEGPFDVKE TEIAVQAKQPDVEEILSKGQHLYKEKPATQPVKRKLE DLSSEWKAVNRLLQELRAKQPDLAPGLTTIGASPTQT VTLVTQPVVTKETAISKLEMPSSLMLEVPALADFNRA WTELTDWLSLLDQVIKSQRVMVGDLEDINEMIIKQKA TMQDLEQRRPQLEELITAAQNLKNKTSNQEARTIITD RIERIQNQWDEVQEHLQNRRQQLNEMLKDSTQWLEAK EEAEQVLGQARAKLESWKEGPYTVDAIQKKITETKQL AKDLRQWQTNVDVANDLALKLLRDYSADDTRKVHMIT ENINASWRSIHKRVSEREAALEETHRLLQQFPLDLEK FLAWLTEAETTANVLQDATRKERLLEDSKGVKELMKQ WQDLQGEIEAHTDVYHNLDENSQKILRSLEGSDDAVL LQRRLDNMNFKWSELRKKSLNIRSHLEASSDQWKRLH LSLQELLVWLQLKDDELSRQAPIGGDFPAVQKQNDVH RAFKRELKTKEPVIMSTLETVRIFLTEQPLEGLEKLY QEPRELPPEERAQNVTRLLRKQAEEVNTEWEKLNLHS ADWQRKIDETLERLQELQEATDELDLKLRQAEVIKGS WQPVGDLLIDSLQDHLEKVKALRGEIAPLKENVSHVN DLARQLTTLGIQLSPYNLSTLEDLNTRWKLLQVAVED RVRQLHEAHRDFGPASQHFLSTSVQGPWERAISPNKV PYYINHETQTTCWDHPKMTELYQSLADLNNVRFSAYR TAMKLRRLQKALCLDLLSLSAACDALDQHNLKQNDQP MDILQIINCLTTIYDRLEQEHNNLVNVPLCVDMCLNW LLNVYDTGRTGRIRVLSFKTGIISLCKAHLEDKYRYL FKQVASSTGFCDQRRLGLLLHDSIQIPRQLGEVASFG GSNIEPSVRSCFQFANNKPEIEAALFLDWMRLEPQSM VWLPVLHRVAAAETAKHQAKCNICKECPIIGFRYRSL KHFNYDICQSCFFSGRVAKGHKMHYPMVEYCTPTTSG EDVRDFAKVLKNKFRTKRYFAKHPRMGYLPVQTVLEG DNMETPVTLINFWPVDSAPASSPQLSHDDTHSRIEHY ASRLAEMENSNGSYLNDSISPNESIDDEHLLIQHYCQ SLNQDSPLSQPRSPAQILISLESEERGELERILADLE EENRNLQAEYDRLKQQHEHKGLSPLPSPPEMMPTSPQ SPRDAELIAEAKLLRQHKGRLEARMQILEDHNKQLES QLHRLRQLLEQPQAEAKVNGTTVSSPSTSLQRSDSSQ PMLLRVVGSQTSDSMGEEDLLSPPQDTSTGLEEVMEQ LNNSFPSSRGRNTPGKPMREDTM
Oxygen-regulated protein 1 (RP1)	Retinitis Pigmentosa 1	234	MSDTPSTGFSIIHPTSSEGQVPPPRHLSLTHPVVAKR ISFYKSGDPQFGGVRVVVNPRSFKSFDALLDNLSRKV PLPFGVRNISTPRGRHSITRLEELEDGESYLCSHGRK VQPVDLDKARRRPRPWLSSRAISAHSPPHPVAVAAPG MPRPPRSLVVFRNGDPKTRRAVLLSRRVTQSFEAFLQ HLTEVMQRPVVKLYATDGRRVPSLQAVILSSGAVVAA GREPFKPGNYDIQKYLLPARLPGISQRVYPKGNAKSE SRKISTHMSSSSRSQIYSVSSEKTHNNDCYLDYSFVP EKYLALEKNDSQNLPIYPSEDDIEKSIIFNQDGTMTV EMKVRFRIKEEETIKWTTTVSKTGPSNNDEKSEMSFP GRTESRSSGLKLAACSFSADVSPMERSSNQEGSLAEE INIQMTDQVAETCSSASWENATVDTDIIQGTQDQAKH RFYRPPTPGLRRVRQKKSVIGSVTLVSETEVQEKMIG

			QFSYSEERESGENKSEYHMFTHSCSKMSSVSNKPVLV QINNNDQMEESSLERKKENSLLKSSAISAGVIEITSQ KMLEMSHNNGLPSTISNNSIVEEDVVDCVVLDNKTGI KNFKTYGNTNDRFSPISADATHFSSNNSGTDKNISEA PASEASSTVTARIDRLINEFAQCGLTKLPKNEKKILS SVASKKKKKSRQQAINSRYQDGQLATKGILNKNERIN TKGRITKEMIVQDSDSPLKGGILCEEDLQKSDTVIES NTFCSKSNLNSTISKNFHRNKLNTTQNSKVQGLLTKR KSRSLNKISLGAPKKREIGQRDKVFPHNESKYCKSTF ENKSLFHVFNILEQKPKDFYAPQSQAEVASGYLRGMA KKSLVSKVTDSHITLKSQKKRKGDKVKASAILSKQHA TTRANSLASLKKPDFPEAIAHHSIQNYIQSWLQNINP YPTLKPIKSAPVCRNETSVVNCSNNSFSGNDPHTNSG KISNFVMESNKHITKIAGLTGDNLCKEGDKSFIANDT GEEDLHETQVGSLNDAYLVPLHEHCTLSQSAINDHNT KSHIAAEKSGPEKKLVYQEINLARKRQSVEAAIQVDP IEEETPKDLLPVLMLHQLQASVPGIHKTQNGVVQMPG SLAGVPFHSAICNSSTNLLLAWLLVLNLKGSMNSFCQ VDAHKATNKSSETLALLEILKHIAITEEADDLKAAVA NLVESTTSHFGLSEKEQDMVPIDLSANCSTVNIQSVP KCSENERTQGISSLDGGCSASEACAPEVCVLEVTCSP CEMCTVNKAYSPKETCNPSDTFFPSDGYGVDQTSMNK ACFLGEVCSLTDTVFSDKACAQKENHTYEGACPIDET YVPVNVCNTIDFLNSKENTYTDNLDSTEELERGDDIQ KDLNILTDPEYKNGFNTLVSHQNVSNLSSCGLCLSEK EAELDKKHSSLDDFENCSLRKFQDENAYTSFDMEEPR TSEEPGSITNSMTSSERNISELESFEELENHDTDIFN TVVNGGEQATEELIQEEVEASKTLELIDISSKNIMEE KRMNGIIYEIISKRLATPPSLDFCYDSKQNSEKETNE GETKMVKMMVKTMETGSYSESSPDLKKCIKSPVTSDW SDYRPDSDSEQPYKTSSDDPNDSGELTQEKEYNIGFV KRAIEKLYGKADIIKPSFFPGSTRKSQVCPYNSVEFQ CSRKASLYDSEGQSFGSSEQVSSSSSMLQEFQEERQD KCDVSAVRDNYCRGDIVEPGTKQNDDSRILTDIEEGV LIDKGKWLLKENHLLRMSSENPGMCGNADTTSVDTLL DNNSSEVPYSHFGNLAPGPTMDELSSSELEELTQPLE LKCNYFNMPHGSDSEPFHEDLLDVRNETCAKERIANH HTEEKGSHQSERVCTSVTHSFISAGNKVYPVSDDAIK NQPLPGSNMIHGTLQEADSLDKLYALCGQHCPILTVI IQPMNEEDRGFAYRKESDIENFLGFYLWMKIHPYLLQ TDKNVFREENNKASMRQNLIDNAIGDIFDQFYFSNTF DLMGKRRKQKRINFLGLEEEGNLKKFQPDLKERFCMN FLHTSLLVVGNVDSNTQDLSGQTNEIFKAVDENNNLL NNRFQGSRTNLNQVVRENINCHYFFEMLGQACLLDIC QVETSLNISNRNILELCMFEGENLFIWEEEDILNLTD LESSREQEDL
Titin (TTN)	Dilated Cardiomyopathy 1G	235	MTTQAPTFTQPLQSVVVLEGSTATFEAHISGFPVPEV SWFRDGQVISTSTLPGVQISFSDGRAKLTIPAVTKAN SGRYSLKATNGSGQATSTAELLVKAETAPPNFVQRLQ SMTVRQGSQVRLQVRVTGIPTPVVKFYRDGAEIQSSL DFQISQEGDLYSLLIAEAYPEDSGTYSVNATNSVGRA

			TSTAELLVQGEEEVPAKKTKTIVSTAQISESRQTRIE KKIEAHFDARSIATVEMVIDGAAGQQLPHKTPPRIPP KPKSRSPTPPSIAAKAQLARQQSPSPIRHSPSPVRHV RAPTPSPVRSVSPAARISTSPIRSVRSPLLMRKTQAS TVATGPEVPPPWKQEGYVASSSEAEMRETTLTTSTQI RTEERWEGRYGVQEQVTISGAAGAAASVSASASYAAE AVATGAKEVKQDADKSAAVATVVAAVDMARVREPVIS AVEQTAQRTTTTAVHIQPAQEQVRKEAEKTAVTKVVV AADKAKEQELKSRTKEVITTKQEQMHVTHEQIRKETE KTFVPKVVISAAKAKEQETRISEEITKKQKQVTQEAI RQETEITAASMVVVATAKSTKLETVPGAQEETTTQQD QMHLSYEKIMKETRKTVVPKVIVATPKVKEQDLVSRG REGITTKREQVQITQEKMRKEAEKTALSTIAVATAKA KEQETILRTRETMATRQEQIQVTHGKVDVGKKAEAVA TVVAAVDQARVREPREPGHLEESYAQQTTLEYGYKER ISAAKVAEPPQRPASEPHVVPKAVKPRVIQAPSETHI KTTDQKGMHISSQIKKTTDLTTERLVHVDKRPRTASP HFTVSKISVPKTEHGYEASIAGSAIATLQKELSATSS AQKITKSVKAPTVKPSETRVRAEPTPLPQFPFADTPD TYKSEAGVEVKKEVGVSITGTTVREERFEVLHGREAK VTETARVPAPVEIPVTPPTLVSGLKNVTVIEGESVTL ECHISGYPSPTVTWYREDYQIESSIDFQITFQSGIAR LMIREAFAEDSGRFTCSAVNEAGTVSTSCYLAVQVSE EFEKETTAVTEKFTTEEKRFVESRDVVMTDTSLTEEQ AGPGEPAAPYFITKPVVQKLVEGGSVVFGCQVGGNPK PHVYWKKSGVPLTTGYRYKVSYNKQTGECKLVISMTF ADDAGEYTIVVRNKHGETSASASLLEEADYELLMKSQ QEMLYQTQVTAFVQEPKVGETAPGFVYSEYEKEYEKE QALIRKKMAKDTVVVRTYVEDQEFHISSFEERLIKEI EYRIIKTTLEELLEEDGEEKMAVDISESEAVESGFDS RIKNYRILEGMGVTFHCKMSGYPLPKIAWYKDGKRIK HGERYQMDFLQDGRASLRIPVVLPEDEGIYTAFASNI KGNAICSGKLYVEPAAPLGAPTYIPTLEPVSRIRSLS PRSVSRSPIRMSPARMSPARMSPARMSPARMSPGRRL EETDESQLERLYKPVFVLKPVSFKCLEGQTARFDLKV VGRPMPETFWFHDGQQIVNDYTHKVVIKEDGTQSLII VPATPSDSGEWTVVAQNRAGRSSISVILTVEAVEHQV KPMFVEKLKNVNIKEGSRLEMKVRATGNPNPDIVWLK NSDIIVPHKYPKIRIEGTKGEAALKIDSTVSQDSAWY TATAINKAGRDTTRCKVNVEVEFAEPEPERKLIIPRG TYRAKEIAAPELEPLHLRYGQEQWEEGDLYDKEKQQK PFFKKKLTSLRLKRFGPAHFECRLTPIGDPTMVVEWL HDGKPLEAANRLRMINEFGYCSLDYGVAYSRDSGIIT CRATNKYGTDHTSATLIVKDEKSLVEESQLPEGRKGL QRIEELERMAHEGALTGVTTDQKEKQKPDIVLYPEPV RVLEGETARFRCRVTGYPQPKVNWYLNGQLIRKSKRF RVRYDGIHYLDIVDCKSYDTGEVKVTAENPEGVIEHK VKLEIQQREDFRSVLRRAPEPRPEFHVHEPGKLQFEV QKVDRPVDTTETKEVVKLKRAERITHEKVPEESEELR SKFKRRTEEGYYEAITAVELKSRKKDESYEELLRKTK DELLHWTKELTEEEKKALAEEGKITIPTFKPDKIELS

			PSMEAPKIFERIQSQTVGQGSDAHFRVRVVGKPDPEC EWYKNGVKIERSDRIYWYWPEDNVCELVIRDVTAEDS ASIMVKAINIAGETSSHAFLLVQAKQLITFTQELQDV VAKEKDTMATFECETSEPFVKVKWYKDGMEVHEGDKY RMHSDRKVHFLSILTIDTSDAEDYSCVLVEDENVKTT AKLIVEGAVVEFVKELQDIEVPESYSGELECIVSPEN IEGKWYHNDVELKSNGKYTITSRRGRQNLTVKDVTKE DQGEYSFVIDGKKTTCKLKMKPRPIAILQGLSDQKVC EGDIVQLEVKVSLESVEGVWMKDGQEVQPSDRVHIVI DKQSHMLLIEDMTKEDAGNYSFTIPALGLSTSGRVSV YSVDVITPLKDVNVIEGTKAVLECKVSVPDVTSVKWY LNDEQIKPDDRVQAIVKGTKQRLVINRTHASDEGPYK LIVGRVETNCNLSVEKIKIIRGLRDLTCTETQNVVFE VELSHSGIDVLWNFKDKEIKPSSKYKIEAHGKIYKLT VLNMMKDDEGKYTFYAGENMTSGKLTVAGGAISKPLT DQTVAESQEAVFECEVANPDSKGEWLRDGKHLPLTNN IRSESDGHKRRLIIAATKLDDIGEYTYKVATSKTSAK LKVEAVKIKKTLKNLTVTETQDAVFTVELTHPNVKGV QWIKNGVVLESNEKYAISVKGTIYSLRIKNCAIVDES VYGFRLGRLGASARLHVETVKIIKKPKDVTALENATV AFEVSVSHDTVPVKWFHKSVEIKPSDKHRLVSERKVH KLMLQNISPSDAGEYTAVVGQLECKAKLFVETLHITK TMKNIEVPETKTASFECEVSHFNVPSMWLKNGVEIEM SEKFKIVVQGKLHQLIIMNTSTEDSAEYTFVCGNDQV SATLTVTPIMITSMLKDINAEEKDTITFEVTVNYEGI SYKWLKNGVEIKSTDKCQMRTKKLTHSLNIRNVHFGD AADYTFVAGKATSTATLYVEARHIEFRKHIKDIKVLE KKRAMFECEVSEPDITVQWMKDDQELQITDRIKIQKE KYVHRLLIPSTRMSDAGKYTVVAGGNVSTAKLFVEGR DVRIRSIKKEVQVIEKQRAVVEFEVNEDDVDAHWYKD GIEINFQVQERHKYVVERRIHRMFISETRQSDAGEYT FVAGRNRSSVTLYVNAPEPPQVLQELQPVTVQSGKPA RFCAVISGRPQPKISWYKEEQLLSTGFKCKFLHDGQE YTLLLIEAFPEDAAVYTCEAKNDYGVATTSASLSVEV PEVVSPDQEMPVYPPAIITPLQDTVTSEGQPARFQCR VSGTDLKVSWYSKDKKIKPSRFFRMTQFEDTYQLEIA EAYPEDEGTYTFVASNAVGQVSSTANLSLEAPESILH ERIEQEIEMEMKEFSSSFLSAEEEGLHSAELQLSKIN ETLELLSESPVYPTKFDSEKEGTGPIFIKEVSNADIS MGDVATLSVTVIGIPKPKIQWFFNGVLLTPSADYKFV FDGDDHSLIILFTKLEDEGEYTCMASNDYGKTICSAY LKINSKGEGHKDTETESAVAKSLEKLGGPCPPHFLKE LKPIRCAQGLPAIFEYTVVGEPAPTVTWFKENKQLCT SVYYTIIHNPNGSGTFIVNDPQREDSGLYICKAENML GESTCAAELLVLLEDTDMTDTPCKAKSTPEAPEDFPQ TPLKGPAVEALDSEQEIATFVKDTILKAALITEENQQ LSYEHIAKANELSSQLPLGAQELQSILEQDKLTPEST REFLCINGSIHFQPLKEPSPNLQLQIVQSQKTFSKEG ILMPEEPETQAVLSDTEKIFPSAMSIEQINSLTVEPL KTLLAEPEGNYPQSSIEPPMHSYLTSVAEEVLSPKEK TVSDTNREQRVTLQKQEAQSALILSQSLAEGHVESLQ

			SPDVMISQVNYEPLVPSEHSCTEGGKILIESANPLEN AGQDSAVRIEEGKSLRFPLALEEKQVLLKEEHSDNVV MPPDQIIESKREPVAIKKVQEVQGRDLLSKESLLSGI PEEQRLNLKIQICRALQAAVASEQPGLFSEWLRNIEK VEVEAVNITQEPRHIMCMYLVTSAKSVTEEVTIIIED VDPQMANLKMELRDALCAIIYEEIDILTAEGPRIQQG AKTSLQEEMDSFSGSQKVEPITEPEVESKYLISTEEV SYFNVQSRVKYLDATPVTKGVASAVVSDEKQDESLKP SEEKEESSSESGTEEVATVKIQEAEGGLIKEDGPMIH TPLVDTVSEEGDIVHLTTSITNAKEVNWYFENKLVPS DEKFKCLQDQNTYTLVIDKVNTEDHQGEYVCEALNDS GKTATSAKLTVVKRAAPVIKRKIEPLEVALGHLAKFT CEIQSAPNVRFQWFKAGREIYESDKCSIRSSKYISSL EILRTQVVDCGEYTCKASNEYGSVSCTATLTVTEAYP PTFLSRPKSLTTFVGKAAKFICTVTGTPVIETIWQKD GAALSPSPNWRISDAENKHILELSNLTIQDRGVYSCK ASNKFGADICQAELIIIDKPHFIKELEPVQSAINKKV HLECQVDEDRKVTVTWSKDGQKLPPGKDYKICFEDKI ATLEIPLAKLKDSGTYVCTASNEAGSSSCSATVTVRE PPSFVKKVDPSYLMLPGESARLHCKLKGSPVIQVTWF KNNKELSESNTVRMYFVNSEAILDITDVKVEDSGSYS CEAVNDVGSDSCSTEIVIKEPPSFIKTLEPADIVRGT NALLQCEVSGTGPFEISWFKDKKQIRSSKKYRLFSQK SLVCLEIFSFNSADVGEYECVVANEVGKCGCMATHLL KEPPTFVKKVDDLIALGGQTVTLQAAVRGSEPISVTW MKGQEVIREDGKIKMSFSNGVAVLIIPDVQISFGGKY TCLAENEAGSQTSVGELIVKEPAKIIERAELIQVTAG DPATLEYTVAGTPELKPKWYKDGRPLVASKKYRISFK NNVAQLKFYSAELHDSGQYTFEISNEVGSSSCETTFT VLDRDIAPFFTKPLRNVDSVVNGTCRLDCKIAGSLPM RVSWFKDGKEIAASDRYRIAFVEGTASLEIIRVDMND AGNFTCRATNSVGSKDSSGALIVQEPPSFVTKPGSKD VLPGSAVCLKSTFQGSTPLTIRWFKGNKELVSGGSCY ITKEALESSLELYLVKTSDSGTYTCKVSNVAGGVECS ANLFVKEPATFVEKLEPSQLLKKGDATQLACKVTGTP PIKITWFANDREIKESSKHRMSFVESTAVLRLTDVGI EDSGEYMCEAQNEAGSDHCSSIVIVKESPYFTKEFKP IEVLKEYDVMLLAEVAGTPPFEITWFKDNTILRSGRK YKTFIQDHLVSLQILKFVAADAGEYQCRVTNEVGSSI CSARVTLREPPSFIKKIESTSSLRGGTAAFQATLKGS LPITVTWLKDSDEITEDDNIRMTFENNVASLYLSGIE VKHDGKYVCQAKNDAGIQRCSALLSVKEPATITEEAV SIDVTQGDPATLQVKFSGTKEITAKWFKDGQELTLGS KYKISVTDTVSILKIISTEKKDSGEYTFEVQNDVGRS SCKARINVLDLIIPPSFTKKLKKMDSIKGSFIDLECI VAGSHPISIQWFKDDQEISASEKYKFSFHDNTAFLEI SQLEGTDSGTYTCSATNKAGHNQCSGHLTVKEPPYFV EKPQSQDVNPNTRVQLKALVGGTAPMTIKWFKDNKEL HSGAARSVWKDDTSTSLELFAAKATDSGTYICQLSND VGTATSKATLFVKEPPQFIKKPSPVLVLRNGQSTTFE CQITGTPKIRVSWYLDGNEITAIQKHGISFIDGLATF

			QISGARVENSGTYVCEARNDAGTASCSIELKVKEPPT FIRELKPVEVVKYSDVELECEVTGTPPFEVTWLKNNR EIRSSKKYTLTDRVSVFNLHITKCDPSDTGEYQCIVS NEGGSCSCSTRVALKEPPSFIKKIENTTTVLKSSATF QSTVAGSPPISITWLKDDQILDEDDNVYISFVDSVAT LQIRSVDNGHSGRYTCQAKNESGVERCYAFLLVQEPA QIVEKAKSVDVTEKDPMTLECVVAGTPELKVKWLKDG KQIVPSRYFSMSFENNVASFRIQSVMKQDSGQYTFKV ENDFGSSSCDAYLRVLDQNIPPSFTKKLTKMDKVLGS SIHMECKVSGSLPISAQWFKDGKEISTSAKYRLVCHE RSVSLEVNNLELEDTANYTCKVSNVAGDDACSGILTV KEPPSFLVKPGRQQAIPDSTVEFKAILKGTPPFKIKW FKDDVELVSGPKCFIGLEGSTSFLNLYSVDASKTGQY TCHVTNDVGSDSCTTMLLVTEPPKFVKKLEASKIVKA GDSSRLECKIAGSPEIRVVWFRNEHELPASDKYRMTF IDSVAVIQMNNLSTEDSGDFICEAQNPAGSTSCSTKV IVKEPPVFSSFPPIVETLKNAEVSLECELSGTPPFEV VWYKDKRQLRSSKKYKIASKNFHTSIHILNVDTSDIG EYHCKAQNEVGSDTCVCTVKLKEPPRFVSKLNSLTVV AGEPAELQASIEGAQPIFVQWLKEKEEVIRESENIRI TFVENVATLQFAKAEPANAGKYICQIKNDGGMRENMA TLMVLEPAVIVEKAGPMTVTVGETCTLECKVAGTPEL SVEWYKDGKLLTSSQKHKFSFYNKISSLRILSVERQD AGTYTFQVQNNVGKSSCTAVVDVSDRAVPPSFTRRLK NTGGVLGASCILECKVAGSSPISVAWFHEKTKIVSGA KYQTTFSDNVCTLQLNSLDSSDMGNYTCVAANVAGSD ECRAVLTVQEPPSFVKEPEPLEVLPGKNVTFTSVIRG TPPFKVNWFRGARELVKGDRCNIYFEDTVAELELFNI DISQSGEYTCVVSNNAGQASCTTRLFVKEPAAFLKRL SDHSVEPGKSIILESTYTGTLPISVTWKKDGFNITTS EKCNIVTTEKTCILEILNSTKRDAGQYSCEIENEAGR DVCGALVSTLEPPYFVTELEPLEAAVGDSVSLQCQVA GTPEITVSWYKGDTKLRPTPEYRTYFTNNVATLVFNK VNINDSGEYTCKAENSIGTASSKTVFRIQERQLPPSF ARQLKDIEQTVGLPVTLTCRLNGSAPIQVCWYRDGVL LRDDENLQTSFVDNVATLKILQTDLSHSGQYSCSASN PLGTASSSARLTAREPKKSPFFDIKPVSIDVIAGESA DFECHVTGAQPMRITWSKDNKEIRPGGNYTITCVGNT PHLRILKVGKGDSGQYTCQATNDVGKDMCSAQLSVKE PPKFVKKLEASKVAKQGESIQLECKISGSPEIKVSWF RNDSELHESWKYNMSFINSVALLTINEASAEDSGDYI CEAHNGVGDASCSTALTVKAPPVFTQKPSPVGALKGS DVILQCEISGTPPFEVVWVKDRKQVRNSKKFKITSKH FDTSLHILNLEASDVGEYHCKATNEVGSDTCSCSVKF KEPPRFVKKLSDTSTLIGDAVELRAIVEGFQPISVVW LKDRGEVIRESENTRISFIDNIATLQLGSPEASNSGK YICQIKNDAGMRECSAVLTVLEPARIIEKPEPMTVTT GNPFALECVVTGTPELSAKWFKDGRELSADSKHHITF INKVASLKIPCAEMSDKGLYSFEVKNSVGKSNCTVSV HVSDRIVPPSFIRKLKDVNAILGASVVLECRVSGSAP ISVGWFQDGNEIVSGPKCQSSFSENVCTLNLSLLEPS

			DTGIYTCVAANVAGSDECSAVLTVQEPPSFEQTPDSV EVLPGMSLTFTSVIRGTPPFKVKWFKGSRELVPGESC NISLEDFVTELELFEVQPLESGDYSCLVTNDAGSASC TTHLFVKEPATFVKRLADFSVETGSPIVLEATYTGTP PISVSWIKDEYLISQSERCSITMTEKSTILEILESTI EDYAQYSCLIENEAGQDICEALVSVLEPPYFIEPLEH VEAVIGEPATLQCKVDGTPEIRISWYKEHTKLRSAPA YKMQFKNNVASLVINKVDHSDVGEYSCKADNSVGAVA SSAVLVIKARKLPPFFARKLKDVHETLGFPVAFECRI NGSEPLQVSWYKDGVLLKDDANLQTSFVHNVATLQIL QTDQSHIGQYNCSASNPLGTASSSAKLILSEHEVPPF FDLKPVSVDLALGESGTFKCHVTGTAPIKITWAKDNR EIRPGGNYKMTLVENTATLTVLKVGKGDAGQYTCYAS NIAGKDSCSAQLGVQEPPRFIKKLEPSRIVKQDEFTR YECKIGGSPEIKVLWYKDETEIQESSKFRMSFVDSVA VLEMHNLSVEDSGDYTCEAHNAAGSASSSTSLKVKEP PIFRKKPHPIETLKGADVHLECELQGTPPFHVSWYKD KRELRSGKKYKIMSENFLTSIHILNVDAADIGEYQCK ATNDVGSDTCVGSIALKAPPRFVKKLSDISTVVGKEV QLQTTIEGAEPISVVWFKDKGEIVRESDNIWISYSEN IATLQFSRVEPANAGKYTCQIKNDAGMQECFATLSVL EPATIVEKPESIKVTTGDTCTLECTVAGTPELSTKWF KDGKELTSDNKYKISFFNKVSGLKIINVAPSDSGVYS FEVQNPVGKDSCTASLQVSDRTVPPSFTRKLKETNGL SGSSVVMECKVYGSPPISVSWFHEGNEISSGRKYQTT LTDNTCALTVNMLEESDSGDYTCIATNMAGSDECSAP LTVREPPSFVQKPDPMDVLTGTNVTFTSIVKGTPPFS VSWFKGSSELVPGDRCNVSLEDSVAELELFDVDTSQS GEYTCIVSNEAGKASCTTHLYIKAPAKFVKRLNDYSI EKGKPLILEGTFTGTPPISVTWKKNGINVTPSQRCNI TTTEKSAILEIPSSTVEDAGQYNCYIENASGKDSCSA QILILEPPYFVKQLEPVKVSVGDSASLQCQLAGTPEI GVSWYKGDTKLRPTTTYKMHFRNNVATLVFNQVDIND SGEYICKAENSVGEVSASTFLTVQEQKLPPSFSRQLR DVQETVGLPVVFDCAISGSEPISVSWYKDGKPLKDSP NVQTSFLDNTATLNIFKTDRSLAGQYSCTATNPIGSA SSSARLILTEGKNPPFFDIRLAPVDAVVGESADFECH VTGTQPIKVSWAKDSREIRSGGKYQISYLENSAHLTV LKVDKGDSGQYTCYAVNEVGKDSCTAQLNIKERLIPP SFTKRLSETVEETEGNSFKLEGRVAGSQPITVAWYKN NIEIQPTSNCEITFKNNTLVLQVRKAGMNDAGLYTCK VSNDAGSALCTSSIVIKEPKKPPVFDQHLTPVTVSEG EYVQLSCHVQGSEPIRIQWLKAGREIKPSDRCSFSFA SGTAVLELRDVAKADSGDYVCKASNVAGSDTTKSKVT IKDKPAVAPATKKAAVDGRLFFVSEPQSIRVVEKTTA TFIAKVGGDPIPNVKWTKGKWRQLNQGGRVFIHQKGD EAKLEIRDTTKTDSGLYRCVAFNEHGEIESNVNLQVD ERKKQEKIEGDLRAMLKKTPILKKGAGEEEEIDIMEL LKNVDPKEYEKYARMYGITDFRGLLQAFELLKQSQEE ETHRLEIEEIERSERDEKEFEELVSFIQQRLSQTEPV TLIKDIENQTVLKDNDAVFEIDIKINYPEIKLSWYKG

			TEKLEPSDKFEISIDGDRHTLRVKNCQLKDQGNYRLV CGPHIASAKLTVIEPAWERHLQDVTLKEGQTCTMTCQ FSVPNVKSEWFRNGRILKPQGRHKTEVEHKVHKLTIA DVRAEDQGQYTCKYEDLETSAELRIEAEPIQFTKRIQ NIVVSEHQSATFECEVSFDDAIVTWYKGPTELTESQK YNFRNDGRCHYMTIHNVTPDDEGVYSVIARLEPRGEA RSTAELYLTTKEIKLELKPPDIPDSRVPIPTMPIRAV PPEEIPPVVAPPIPLLLPTPEEKKPPPKRIEVTKKAV KKDAKKVVAKPKEMTPREEIVKKPPPPTTLIPAKAPE IIDVSSKAEEVKIMTITRKKEVQKEKEAVYEKKQAVH KEKRVFIESFEEPYDELEVEPYTEPFEQPYYEEPDED YEEIKVEAKKEVHEEWEEDFEEGQEYYEREEGYDEGE EEWEEAYQEREVIQVQKEVYEESHERKVPAKVPEKKA PPPPKVIKKPVIEKIEKTSRRMEEEKVQVTKVPEVSK KIVPQKPSRTPVQEEVIEVKVPAVHTKKMVISEEKMF FASHTEEEVSVTVPEVQKEIVTEEKIHVAISKRVEPP PKVPELPEKPAPEEVAPVPIPKKVEPPAPKVPEVPKK PVPEEKKPVPVPKKEPAAPPKVPEVPKKPVPEEKIPV PVAKKKEAPPAKVPEVQKGVVTEEKITIVTQREESPP PAVPEIPKKKVPEERKPVPRKEEEVPPPPKVPALPKK PVPEEKVAVPVPVAKKAPPPRAEVSKKTVVEEKRFVA EEKLSFAVPQRVEVTRHEVSAEEEWSYSEEEEGVSIS VYREEEREEEEEAEVTEYEVMEEPEEYVVEEKLHIIS KRVEAEPAEVTERQEKKIVLKPKIPAKIEEPPPAKVP EAPKKIVPEKKVPAPVPKKEKVPPPKVPEEPKKPVPE KKVPPKVIKMEEPLPAKVTERHMQITQEEKVLVAVTK KEAPPKARVPEEPKRAVPEEKVLKLKPKREEEPPAKV TEFRKRVVKEEKVSIEAPKREPQPIKEVTIMEEKERA YTLEEEAVSVQREEEYEEYEEYDYKEFEEYEPTEEYD QYEEYEEREYERYEEHEEYITEPEKPIPVKPVPEEPV PTKPKAPPAKVLKKAVPEEKVPVPIPKKLKPPPPKVP EEPKKVFEEKIRISITKREKEQVTEPAAKVPMKPKRV VAEEKVPVPRKEVAPPVRVPEVPKELEPEEVAFEEEV VTHVEEYLVEEEEEYIHEEEEFITEEEVVPVIPVKVP EVPRKPVPEEKKPVPVPKKKEAPPAKVPEVPKKPEEK VPVLIPKKEKPPPAKVPEVPKKPVPEEKVPVPVPKKV EAPPAKVPEVPKKPVPEKKVPVPAPKKVEAPPAKVPE VPKKLIPEEKKPTPVPKKVEAPPPKVPKKREPVPVPV ALPQEEEVLFEEEIVPEEEVLPEEEEVLPEEEEVLPE EEEVLPEEEEIPPEEEEVPPEEEYVPEEEEFVPEEEV LPEVKPKVPVPAPVPEIKKKVTEKKVVIPKKEEAPPA KVPEVPKKVEEKRIILPKEEEVLPVEVTEEPEEEPIS EEEIPEEPPSIEEVEEVAPPRVPEVIKKAVPEAPTPV PKKVEAPPAKVSKKIPEEKVPVPVQKKEAPPAKVPEV PKKVPEKKVLVPKKEAVPPAKGRTVLEEKVSVAFRQE VVVKERLELEVVEAEVEEIPEEEEFHEVEEYFEEGEF HEVEEFIKLEQHRVEEEHRVEKVHRVIEVFEAEEVEV FEKPKAPPKGPEISEKIIPPKKPPTKVVPRKEPPAKV PEVPKKIVVEEKVRVPEEPRVPPTKVPEVLPPKEVVP EKKVPVPPAKKPEAPPPKVPEAPKEVVPEKKVPVPPP KKPEVPPTKVPEVPKAAVPEKKVPEAIPPKPESPPPE

			VPEAPKEVVPEKKVPAAPPKKPEVTPVKVPEAPKEVV PEKKVPVPPPKKPEVPPTKVPEVPKVAVPEKKVPEAI PPKPESPPPEVFEEPEEVALEEPPAEVVEEPEPAAPP QVTVPPKKPVPEKKAPAVVAKKPELPPVKVPEVPKEV VPEKKVPLVVPKKPEAPPAKVPEVPKEVVPEKKVAVP KKPEVPPAKVPEVPKKPVLEEKPAVPVPERAESPPPE VYEEPEEIAPEEEIAPEEEKPVPVAEEEEPEVPPPAV PEEPKKIIPEKKVPVIKKPEAPPPKEPEPEKVIEKPK LKPRPPPPPPAPPKEDVKEKIFQLKAIPKKKVPEKPQ VPEKVELTPLKVPGGEKKVRKLLPERKPEPKEEVVLK SVLRKRPEEEEPKVEPKKLEKVKKPAVPEPPPPKPVE EVEVPTVTKRERKIPEPTKVPEIKPAIPLPAPEPKPK PEAEVKTIKPPPVEPEPTPIAAPVTVPVVGKKAEAKA PKEEAAKPKGPIKGVPKKTPSPIEAERRKLRPGSGGE KPPDEAPFTYQLKAVPLKFVKEIKDIILTESEFVGSS AIFECLVSPSTAITTWMKDGSNIRESPKHRFIADGKD RKLHIIDVQLSDAGEYTCVLRLGNKEKTSTAKLVVEE LPVRFVKTLEEEVTVVKGQPLYLSCELNKERDVVWRK DGKIVVEKPGRIVPGVIGLMRALTINDADDTDAGTYT VTVENANNLECSSCVKVVEVIRDWLVKPIRDQHVKPK GTAIFACDIAKDTPNIKWFKGYDEIPAEPNDKTEILR DGNHLYLKIKNAMPEDIAEYAVEIEGKRYPAKLTLGE REVELLKPIEDVTIYEKESASFDAEISEADIPGQWKL KGELLRPSPTCEIKAEGGKRFLTLHKVKLDQAGEVLY QALNAITTAILTVKEIELDFAVPLKDVTVPERRQARF ECVLTREANVIWSKGPDIIKSSDKFDIIADGKKHILV INDSQFDDEGVYTAEVEGKKTSARLFVTGIRLKFMSP LEDQTVKEGETATFVCELSHEKMHVVWFKNDAKLHTS RTVLISSEGKTHKLEMKEVTLDDISQIKAQVKELSST AQLKVLEADPYFTVKLHDKTAVEKDEITLKCEVSKDV PVKWFKDGEEIVPSPKYSIKADGLRRILKIKKADLKD KGEYVCDCGTDKTKANVTVEARLIKVEKPLYGVEVFV GETAHFEIELSEPDVHGQWKLKGQPLTASPDCEIIED GKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKEL PLIFITPLSDVKVFEKDEAKFECEVSREPKTFRWLKG TQEITGDDRFELIKDGTKHSMVIKSAAFEDEAKYMFE AEDKHTSGKLIIEGIRLKFLTPLKDVTAKEKESAVFT VELSHDNIRVKWFKNDQRLHTTRSVSMQDEGKTHSIT FKDLSIDDTSQIRVEAMGMSSEAKLTVLEGDPYFTGK LQDYTGVEKDEVILQCEISKADAPVKWFKDGKEIKPS KNAVIKADGKKRMLILKKALKSDIGQYTCDCGTDKTS GKLDIEDREIKLVRPLHSVEVMETETARFETEISEDD IHANWKLKGEALLQTPDCEIKEEGKIHSLVLHNCRLD QTGGVDFQAANVKSSAHLRVKPRVIGLLRPLKDVTVT AGETATFDCELSYEDIPVEWYLKGKKLEPSDKVVPRS EGKVHTLTLRDVKLEDAGEVQLTAKDFKTHANLFVKE PPVEFTKPLEDQTVEEGATAVLECEVSRENAKVKWFK NGTEILKSKKYEIVADGRVRKLVIHDCTPEDIKTYTC DAKDFKTSCNLNVVPPHVEFLRPLTDLQVREKEMARF ECELSRENAKVKWFKDGAEIKKGKKYDIISKGAVRIL VINKCLLDDEAEYSCEVRTARTSGMLTVLEEEAVFTK

			NLANIEVSETDTIKLVCEVSKPGAEVIWYKGDEEIIE TGRYEILTEGRKRILVIQNAHLEDAGNYNCRLPSSRT DGKVKVHELAAEFISKPQNLEILEGEKAEFVCSISKE SFPVQWKRDDKTLESGDKYDVIADGKKRVLVVKDATL QDMGTYVVMVGAARAAAHLTVIEKLRIVVPLKDTRVK EQQEVVFNCEVNTEGAKAKWFRNEEAIFDSSKYIILQ KDLVYTLRIRDAHLDDQANYNVSLTNHRGENVKSAAN LIVEEEDLRIVEPLKDIETMEKKSVTFWCKVNRLNVT LKWTKNGEEVPFDNRVSYRVDKYKHMLTIKDCGFPDE GEYIVTAGQDKSVAELLIIEAPTEFVEHLEDQTVTEF DDAVFSCQLSREKANVKWYRNGREIKEGKKYKFEKDG SIHRLIIKDCRLDDECEYACGVEDRKSRARLFVEEIP VEIIRPPQDILEAPGADVVFLAELNKDKVEVQWLRNN MVVVQGDKHQMMSEGKIHRLQICDIKPRDQGEYRFIA KDKEARAKLELAAAPKIKTADQDLVVDVGKPLTMVVP YDAYPKAEAEWFKENEPLSTKTIDTTAEQTSFRILEA KKGDKGRYKIVLQNKHGKAEGFINLKVIDVPGPVRNL EVTETFDGEVSLAWEEPLTDGGSKIIGYVVERRDIKR KTWVLATDRAESCEFTVTGLQKGGVEYLFRVSARNRV GTGEPVETDNPVEARSKYDVPGPPLNVTITDVNRFGV SLTWEPPEYDGGAEITNYVIELRDKTSIRWDTAMTVR AEDLSATVTDVVEGQEYSFRVRAQNRIGVGKPSAATP FVKVADPIERPSPPVNLTSSDQTQSSVQLKWEPPLKD GGSPILGYIIERCEEGKDNWIRCNMKLVPELTYKVTG LEKGNKYLYRVSAENKAGVSDPSEILGPLTADDAFVE PTMDLSAFKDGLEVIVPNPITILVPSTGYPRPTATWC FGDKVLETGDRVKMKTLSAYAELVISPSERSDKGIYT LKLENRVKTISGEIDVNVIARPSAPKELKFGDITKDS VHLTWEPPDDDGGSPLTGYVVEKREVSRKTWTKVMDF VTDLEFTVPDLVQGKEYLFKVCARNKCGPGEPAYVDE PVNMSTPATVPDPPENVKWRDRTANSIFLTWDPPKND GGSRIKGYIVERCPRGSDKWVACGEPVAETKMEVTGL EEGKWYAYRVKALNRQGASKPSRPTEEIQAVDTQEAP EIFLDVKLLAGLTVKAGTKIELPATVTGKPEPKITWT KADMILKQDKRITIENVPKKSTVTIVDSKRSDTGTYI IEAVNVCGRATAVVEVNVLDKPGPPAAFDITDVTNES CLLTWNPPRDDGGSKITNYVVERRATDSEVWHKLSST VKDTNFKATKLIPNKEYIFRVAAENMYGVGEPVQASP ITAKYQFDPPGPPTRLEPSDITKDAVTLTWCEPDDDG GSPITGYWVERLDPDTDKWVRCNKMPVKDTTYRVKGL TNKKKYRFRVLAENLAGPGKPSKSTEPILIKDPIDPP WPPGKPTVKDVGKTSVRLNWTKPEHDGGAKIESYVIE MLKTGTDEWVRVAEGVPTTQHLLPGLMEGQEYSFRVR AVNKAGESEPSEPSDPVLCREKLYPPSPPRWLEVINI TKNTADLKWTVPEKDGGSPITNYIVEKRDVRRKGWQT VDTTVKDTKCTVTPLTEGSLYVFRVAAENAIGQSDYT EIEDSVLAKDTFTTPGPPYALAVVDVTKRHVDLKWEP PKNDGGRPIQRYVIEKKERLGTRWVKAGKTAGPDCNF RVTDVIEGTEVQFQVRAENEAGVGHPSEPTEILSIED PTSPPSPPLDLHVTDAGRKHIAIAWKPPEKNGGSPII GYHVEMCPVGTEKWMRVNSRPIKDLKFKVEEGVVPDK

			EYVLRVRAVNAIGVSEPSEISENVVAKDPDCKPTIDL ETHDIIVIEGEKLSIPVPFRAVPVPTVSWHKDGKEVK ASDRLTMKNDHISAHLEVPKSVRADAGIYTITLENKL GSATASINVKVIGLPGPCKDIKASDITKSSCKLTWEP PEFDGGTPILHYVLERREAGRRTYIPVMSGENKLSWT VKDLIPNGEYFFRVKAVNKVGGGEYIELKNPVIAQDP KQPPDPPVDVEVHNPTAEAMTITWKPPLYDGGSKIMG YIIEKIAKGEERWKRCNEHLVPILTYTAKGLEEGKEY QFRVRAENAAGISEPSRATPPTKAVDPIDAPKVILRT SLEVKRGDEIALDASISGSPYPTITWIKDENVIVPEE IKKRAAPLVRRRKGEVQEEEPFVLPLTQRLSIDNSKK GESQLRVRDSLRPDHGLYMIKVENDHGIAKAPCTVSV LDTPGPPINFVFEDIRKTSVLCKWEPPLDDGGSEIIN YTLEKKDKTKPDSEWIVVTSTLRHCKYSVTKLIEGKE YLFRVRAENRFGPGPPCVSKPLVAKDPFGPPDAPDKP IVEDVTSNSMLVKWNEPKDNGSPILGYWLEKREVNST HWSRVNKSLLNALKANVDGLLEGLTYVFRVCAENAAG PGKFSPPSDPKTAHDPISPPGPPIPRVTDTSSTTIEL EWEPPAFNGGGEIVGYFVDKQLVGTNEWSRCTEKMIK VRQYTVKEIREGADYKLRVSAVNAAGEGPPGETQPVT VAEPQEPPAVELDVSVKGGIQIMAGKTLRIPAVVTGR PVPTKVWTKEEGELDKDRVVIDNVGTKSELIIKDALR KDHGRYVITATNSCGSKFAAARVEVFDVPGPVLDLKP VVTNRKMCLLNWSDPEDDGGSEITGFIIERKDAKMHT WRQPIETERSKCDITGLLEGQEYKFRVIAKNKFGCGP PVEIGPILAVDPLGPPTSPERLTYTERTKSTITLDWK EPRSNGGSPIQGYIIEKRRHDKPDFERVNKRLCPTTS FLVENLDEHQMYEFRVKAVNEIGESEPSLPLNVVIQD DEVPPTIKLRLSVRGDTIKVKAGEPVHIPADVTGLPM PKIEWSKNETVIEKPTDALQITKEEVSRSEAKTELSI PKAVREDKGTYTVTASNRLGSVFRNVHVEVYDRPSPP RNLAVTDIKAESCYLTWDAPLDNGGSEITHYVIDKRD ASRKKAEWEEVTNTAVEKRYGIWKLIPNGQYEFRVRA VNKYGISDECKSDKVVIQDPYRLPGPPGKPKVLARTK GSMLVSWTPPLDNGGSPITGYWLEKREEGSPYWSRVS RAPITKVGLKGVEFNVPRLLEGVKYQFRAMAINAAGI GPPSEPSDPEVAGDPIFPPGPPSCPEVKDKTKSSISL GWKPPAKDGGSPIKGYIVEMQEEGTTDWKRVNEPDKL ITTCECVVPNLKELRKYRFRVKAVNEAGESEPSDTTG EIPATDIQEEPEVFIDIGAQDCLVCKAGSQIRIPAVI KGRPTPKSSWEFDGKAKKAMKDGVHDIPEDAQLETAE NSSVIIIPECKRSHTGKYSITAKNKAGQKTANCRVKV MDVPGPPKDLKVSDITRGSCRLSWKMPDDDGGDRIKG YVIEKRTIDGKAWTKVNPDCGSTTFVVPDLLSEQQYF FRVRAENRFGIGPPVETIQRTTARDPIYPPDPPIKLK IGLITKNTVHLSWKPPKNDGGSPVTHYIVECLAWDPT GTKKEAWRQCNKRDVEELQFTVEDLVEGGEYEFRVKA VNAAGVSKPSATVGPVTVKDQTCPPSIDLKEFMEVEE GTNVNIVAKIKGVPFPTLTWFKAPPKKPDNKEPVLYD THVNKLVVDDTCTLVIPQSRRSDTGLYTITAVNNLGT ASKEMRLNVLGRPGPPVGPIKFESVSADQMTLSWFPP

			KDDGGSKITNYVIEKREANRKTWVHVSSEPKECTYTI PKLLEGHEYVFRIMAQNKYGIGEPLDSEPETARNLFS VPGAPDKPTVSSVTRNSMTVNWEEPEYDGGSPVTGYW LEMKDTTSKRWKRVNRDPIKAMTLGVSYKVTGLIEGS DYQFRVYAINAAGVGPASLPSDPATARDPIAPPGPPF PKVTDWTKSSADLEWSPPLKDGGSKVTGYIVEYKEEG KEEWEKGKDKEVRGTKLVVTGLKEGAFYKFRVRAVNI AGIGEPGEVTDVIEMKDRLVSPDLQLDASVRDRIVVH AGGVIRIIAYVSGKPPPTVTWNMNERTLPQEATIETT AISSSMVIKNCQRSHQGVYSLLAKNEAGERKKTIIVD VLDVPGPVGTPFLAHNLTNESCKLTWFSPEDDGGSPI TNYVIEKRESDRRAWTPVTYTVTRQNATVQGLIQGKA YFFRIAAENSIGMGPFVETSEALVIREPITVPERPED LEVKEVTKNTVTLTWNPPKYDGGSEIINYVLESRLIG TEKFHKVTNDNLLSRKYTVKGLKEGDTYEYRVSAVNI VGQGKPSFCTKPITCKDELAPPTLHLDFRDKLTIRVG EAFALTGRYSGKPKPKVSWFKDEADVLEDDRTHIKTT PATLALEKIKAKRSDSGKYCVVVENSTGSRKGFCQVN VVDRPGPPVGPVSFDEVTKDYMVISWKPPLDDGGSKI TNYIIEKKEVGKDVWMPVTSASAKTTCKVSKLLEGKD YIFRIHAENLYGISDPLVSDSMKAKDRFRVPDAPDQP IVTEVTKDSALVTWNKPHDGGKPITNYILEKRETMSK RWARVTKDPIHPYTKFRVPDLLEGCQYEFRVSAENEI GIGDPSPPSKPVFAKDPIAKPSPPVNPEAIDTTCNSV DLTWQPPRHDGGSKILGYIVEYQKVGDEEWRRANHTP ESCPETKYKVTGLRDGQTYKFRVLAVNAAGESDPAHV PEPVLVKDRLEPPELILDANMAREQHIKVGDTLRLSA IIKGVPFPKVTWKKEDRDAPTKARIDVTPVGSKLEIR NAAHEDGGIYSLTVENPAGSKTVSVKVLVLDKPGPPR DLEVSEIRKDSCYLTWKEPLDDGGSVITNYVVERRDV ASAQWSPLSATSKKKSHFAKHLNEGNQYLFRVAAENQ YGRGPFVETPKPIKALDPLHPPGPPKDLHHVDVDKTE VSLVWNKPDRDGGSPITGYLVEYQEEGTQDWIKFKTV TNLECVVTGLQQGKTYRFRVKAENIVGLGLPDTTIPI ECQEKLVPPSVELDVKLIEGLVVKAGTTVRFPAIIRG VPVPTAKWTTDGSEIKTDEHYTVETDNFSSVLTIKNC LRRDTGEYQITVSNAAGSKTVAVHLTVLDVPGPPTGP INILDVTPEHMTISWQPPKDDGGSPVINYIVEKQDTR KDTWGVVSSGSSKTKLKIPHLQKGCEYVFRVRAENKI GVGPPLDSTPTVAKHKFSPPSPPGKPVVTDITENAAT VSWTLPKSDGGSPITGYYMERREVTGKWVRVNKTPIA DLKFRVTGLYEGNTYEFRVFAENLAGLSKPSPSSD PIKACRPIKPPGPPINPKLKDKSRETADLVWTKPLSD GGSPILGYVVECQKPGTAQWNRINKDELIRQCAFRVP GLIEGNEYRFRIKAANIVGEGEPRELAESVIAKDILH PPEVELDVTCRDVITVRVGQTIRILARVKGRPEPDIT WTKEGKVLVREKRVDLIQDLPRVELQIKEAVRADHGK YIISAKNSSGHAQGSAIVNVLDRPGPCQNLKVTNVTK ENCTISWENPLDNGGSEITNFIVEYRKPNQKGWSIVA SDVTKRLIKANLLANNEYYFRVCAENKVGVGPTIETK TPILAINPIDRPGEPENLHIADKGKTFVYLKWRRPDY

			DGGSPNLSYHVERRLKGSDDWERVHKGSIKETHYMVD RCVENQIYEFRVQTKNEGGESDWVKTEEVVVKEDLQK PVLDLKLSGVLTVKAGDTIRLEAGVRGKPFPEVAWTK DKDATDLTRSPRVKIDTRADSSKFSLTKAKRSDGGKY VVTATNTAGSFVAYATVNVLDKPGPVRNLKIVDVSSD RCTVCWDPPEDDGGCEIQNYILEKCETKRMVWSTYSA TVLTPGTTVTRLIEGNEYIFRVRAENKIGTGPPTESK PVIAKTKYDKPGRPDPPEVTKVSKEEMTVVWNPPEYD GGKSITGYFLEKKEKHSTRWVPVNKSAIPERRMKVQN LLPDHEYQFRVKAENEIGIGEPSLPSRPVVAKDPIEP PGPPTNFRVVDTTKHSITLGWGKPVYDGGAPIIGYVV EMRPKIADASPDEGWKRCNAAAQLVRKEFTVTSLDEN QEYEFRVCAQNQVGIGRPAELKEAIKPKEILEPPEID LDASMRKLVIVRAGCPIRLFAIVRGRPAPKVTWRKVG IDNVVRKGQVDLVDTMAFLVIPNSTRDDSGKYSLTLV NPAGEKAVFVNVRVLDTPGPVSDLKVSDVTKTSCHVS WAPPENDGGSQVTHYIVEKREADRKTWSTVTPEVKKT SFHVTNLVPGNEYYFRVTAVNEYGPGVPTDVPKPVLA SDPLSEPDPPRKLEVTEMTKNSATLAWLPPLRDGGAK IDGYITSYREEEQPADRWTEYSVVKDLSLVVTGLKEG KKYKFRVAARNAVGVSLPREAEGVYEAKEQLLPPKIL MPEQITIKAGKKLRIEAHVYGKPHPTCKWKKGEDEVV TSSHLAVHKADSSSILIIKDVTRKDSGYYSLTAENSS GTDTQKIKVVVMDAPGPPQPPFDISDIDADACSLSWH IPLEDGGSNITNYIVEKCDVSRGDWVTALASVTKTSC RVGKLIPGQEYIFRVRAENRFGISEPLTSPKMVAQFP FGVPSEPKNARVTKVNKDCIFVAWDRPDSDGGSPIIG YLIERKERNSLLWVKANDTLVRSTEYPCAGLVEGLEY SFRIYALNKAGSSPPSKPTEYVTARMPVDPPGKPEVI DVTKSTVSLIWARPKHDGGSKIIGYFVEACKLPGDKW VRCNTAPHQIPQEEYTATGLEEKAQYQFRAIARTAVN ISPPSEPSDPVTILAENVPPRIDLSVAMKSLLTVKAG TNVCLDATVFGKPMPTVSWKKDGTLLKPAEGIKMAMQ RNLCTLELFSVNRKDSGDYTITAENSSGSKSATIKLK VLDKPGPPASVKINKMYSDRAMLSWEPPLEDGGSEIT NYIVDKRETSRPNWAQVSATVPITSCSVEKLIEGHEY QFRICAENKYGVGDPVFTEPAIAKNPYDPPGRCDPPV ISNITKDHMTVSWKPPADDGGSPITGYLLEKRETQAV NWTKVNRKPIIERTLKATGLQEGTEYEFRVTAINKAG PGKPSDASKAAYARDPQYPPGPPAFPKVYDTTRSSVS LSWGKPAYDGGSPIIGYLVEVKRADSDNWVRCNLPQN LQKTRFEVTGLMEDTQYQFRVYAVNKIGYSDPSDVPD KHYPKDILIPPEGELDADLRKTLILRAGVTMRLYVPV KGRPPPKITWSKPNVNLRDRIGLDIKSTDFDTFLRCE NVNKYDAGKYILTLENSCGKKEYTIVVKVLDTPGPPV NVTVKEISKDSAYVTWEPPIIDGGSPIINYVVQKRDA ERKSWSTVTTECSKTSFRVANLEEGKSYFFRVFAENE YGIGDPGETRDAVKASQTPGPVVDLKVRSVSKSSCSI GWKKPHSDGGSRIIGYVVDFLTEENKWQRVMKSLSLQ YSAKDLTEGKEYTFRVSAENENGEGTPSEITVVARDD VVAPDLDLKGLPDLCYLAKENSNFRLKIPIKGKPAPS

			VSWKKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDA GKYTITLKNVAGTKEGTISIKVVGKPGIPTGPIKFDE VTAEAMTLKWAPPKDDGGSEITNYILEKRDSVNNKWV TCASAVQKTTFRVTRLHEGMEYTFRVSAENKYGVGEG LKSEPIVARHPFDVPDAPPPPNIVDVRHDSVSLTWTD PKKTGGSPITGYHLEFKERNSLLWKRANKTPIRMRDF KVTGLTEGLEYEFRVMAINLAGVGKPSLPSEPVVALD PIDPPGKPEVINITRNSVTLIWTEPKYDGGHKLTGYI VEKRDLPSKSWMKANHVNVPECAFTVTDLVEGGKYEF RIRAKNTAGAISAPSESTETIICKDEYEAPTIVLDPT IKDGLTIKAGDTIVLNAISILGKPLPKSSWSKAGKDI RPSDITQITSTPTSSMLTIKYATRKDAGEYTITATNP FGTKVEHVKVTVLDVPGPPGPVEISNVSAEKATLTWT PPLEDGGSPIKSYILEKRETSRLLWTVVSEDIQSCRH VATKLIQGNEYIFRVSAVNHYGKGEPVQSEPVKMVDR FGPPGPPEKPEVSNVTKNTATVSWKRPVDDGGSEITG YHVERREKKSLRWVRAIKTPVSDLRCKVTGLQEGSTY EFRVSAENRAGIGPPSEASDSVLMKDAAYPPGPPSNP HVTDTTKKSASLAWGKPHYDGGLEITGYVVEHQKVGD EAWIKDTTGTALRITQFVVPDLQTKEKYNFRISAIND AGVGEPAVIPDVEIVEREMAPDFELDAELRRTLVVRA GLSIRIFVPIKGRPAPEVTWTKDNINLKNRANIENTE SFTLLIIPECNRYDTGKFVMTIENPAGKKSGFVNVRV LDTPGPVLNLRPTDITKDSVTLHWDLPLIDGGSRITN YIVEKREATRKSYSTATTKCHKCTYKVTGLSEGCEYF FRVMAENEYGIGEPTETTEPVKASEAPSPPDSLNIMD ITKSTVSLAWPKPKHDGGSKITGYVIEAQRKGSDQWT HITTVKGLECVVRNLTEGEEYTFQVMAVNSAGRSAPR ESRPVIVKEQTMLPELDLRGIYQKLVIAKAGDNIKVE IPVLGRPKPTVTWKKGDQILKQTQRVNFETTATSTIL NINECVRSDSGPYPLTARNIVGEVGDVITIQVHDIPG PPTGPIKFDEVSSDFVTFSWDPPENDGGVPISNYVVE MRQTDSTTWVELATTVIRTTYKATRLTTGLEYQFRVK AQNRYGVGPGITSACIVANYPFKVPGPPGTPQVTAVT KDSMTISWHEPLSDGGSPILGYHVERKERNGILWQTV SKALVPGNIFKSSGLTDGIAYEFRVIAENMAGKSKPS KPSEPMLALDPIDPPGKPVPLNITRHTVTLKWAKPEY TGGFKITSYIVEKRDLPNGRWLKANFSNILENEFTVS GLTEDAAYEFRVIAKNAAGAISPPSEPSDAITCRDDV EAPKIKVDVKFKDTVILKAGEAFRLEADVSGRPPPTM EWSKDGKELEGTAKLEIKIADFSTNLVNKDSTRRDSG AYTLTATNPGGFAKHIFNVKVLDRPGPPEGPLAVTEV TSEKCVLSWFPPLDDGGAKIDHYIVQKRETSRLAWTN VASEVQVTKLKVTKLLKGNEYIFRVMAVNKYGVGEPL ESEPVLAVNPYGPPDPPKNPEVTTITKDSMVVCWGHP DSDGGSEIINYIVERRDKAGQRWIKCNKKTLTDLRYK VSGLTEGHEYEFRIMAENAAGISAPSPTSPFYKACDT VFKPGPPGNPRVLDTSRSSISIAWNKPIYDGGSEITG YMVEIALPEEDEWQIVTPPAGLKATSYTITGLTENQE YKIRIYAMNSEGLGEPALVPGTPKAEDRMLPPEIELD ADLRKVVTIRACCTLRLFVPIKGRPAPEVKWARDHGE

			SLDKASIESTSSYTLLIVGNVNRFDSGKYILTVENSS GSKSAFVNVRVLDTPGPPQDLKVKEVTKTSVTLTWDP PLLDGGSKIKNYIVEKRESTRKAYSTVATNCHKTSWK VDQLQEGCSYYFRVLAENEYGIGLPAETAESVKASER PLPPGKITLMDVTRNSVSLSWEKPEHDGGSRILGYIV EMQTKGSDKWATCATVKVTEATITGLIQGEEYSFRVS AQNEKGISDPRQLSVPVIAKDLVIPPAFKLLFNTFTV LAGEDLKVDVPFIGRPTPAVTWHKDNVPLKQTTRVNA ESTENNSLLTIKDACREDVGHYVVKLTNSAGEAIETL NVIVLDKPGPPTGPVKMDEVTADSITLSWGPPKYDGG SSINNYIVEKRDTSTTTWQIVSATVARTTIKACRLKT GCEYQFRIAAENRYGKSTYLNSEPTVAQYPFKVPGPP GTPVVTLSSRDSMEVQWNEPISDGGSRVIGYHLERKE RNSILWVKLNKTPIPQTKFKTTGLEEGVEYEFRVSAE NIVGIGKPSKVSECYVARDPCDPPGRPEAIIVTRNSV TLQWKKPTYDGGSKITGYIVEKKELPEGRWMKASFTN IIDTHFEVTGLVEDHRYEFRVIARNAAGVFSEPSEST GAITARDEVDPPRISMDPKYKDTIVVHAGESFKVDAD IYGKPIPTIQWIKGDQELSNTARLEIKSTDFATSLSV KDAVRVDSGNYILKAKNVAGERSVTVNVKVLDRPGPP EGPVVISGVTAEKCTLAWKPPLQDGGSDIINYIVERR ETSRLVWTVVDANVQTLSCKVTKLLEGNEYTFRIMAV NKYGVGEPLESEPVVAKNPFVVPDAPKAPEVTTVTKD SMIVVWERPASDGGSEILGYVLEKRDKEGIRWTRCHK RLIGELRLRVTGLIENHDYEFRVSAENAAGLSEPSPP SAYQKACDPIYKPGPPNNPKVIDITRSSVFLSWSKPI YDGGCEIQGYIVEKCDVSVGEWTMCTPPTGINKTNIE VEKLLEKHEYNFRICAINKAGVGEHADVPGPIIVEEK LEAPDIDLDLELRKIINIRAGGSLRLFVPIKGRPTPE VKWGKVDGEIRDAAIIDVTSSFTSLVLDNVNRYDSGK YTLTLENSSGTKSAFVTVRVLDTPSPPVNLKVTEITK DSVSITWEPPLLDGGSKIKNYIVEKREATRKSYAAVV TNCHKNSWKIDQLQEGCSYYFRVTAENEYGIGLPAQT ADPIKVAEVPQPPGKITVDDVTRNSVSLSWTKPEHDG GSKIIQYIVEMQAKHSEKWSECARVKSLQAVITNLTQ GEEYLFRVVAVNEKGRSDPRSLAVPIVAKDLVIEPDV KPAFSSYSVQVGQDLKIEVPISGRPKPTITWTKDGLP LKQTTRINVTDSLDLTTLSIKETHKDDGGQYGITVAN VVGQKTASIEIVTLDKPDPPKGPVKFDDVSAESITLS WNPPLYTGGCQITNYIVQKRDTTTTVWDVVSATVART TLKVTKLKTGTEYQFRIFAENRYGQSFALESDPIVAQ YPYKEPGPPGTPFATAISKDSMVIQWHEPVNNGGSPV IGYHLERKERNSILWTKVNKTIIHDTQFKAQNLEEGI EYEFRVYAENIVGVGKASKNSECYVARDPCDPPGTPE PIMVKRNEITLQWTKPVYDGGSMITGYIVEKRDLPDG RWMKASFTNVIETQFTVSGLTEDQRYEFRVIAKNAAG AISKPSDSTGPITAKDEVELPRISMDPKFRDTIVVNA GETFRLEADVHGKPLPTIEWLRGDKEIEESARCEIKN TDFKALLIVKDAIRIDGGQYILRASNVAGSKSFPVNV KVLDRPGPPEGPVQVTGVTSEKCSLTWSPPLQDGGSD ISHYVVEKRETSRLAWTVVASEVVTNSLKVTKLLEGN

			EYVFRIMAVNKYGVGEPLESAPVLMKNPFVLPGPPKS LEVTNIAKDSMTVCWNRPDSDGGSEIIGYIVEKRDRS GIRWIKCNKRRITDLRLRVTGLTEDHEYEFRVSAENA AGVGEPSPATVYYKACDPVFKPGPPTNAHIVDTTKNS ITLAWGKPIYDGGSEILGYVVEICKADEEEWQIVTPQ TGLRVTRFEISKLTEHQEYKIRVCALNKVGLGEATSV PGTVKPEDKLEAPELDLDSELRKGIVVRAGGSARIHI PFKGRPTPEITWSREEGEFTDKVQIEKGVNYTQLSID NCDRNDAGKYILKLENSSGSKSAFVTVKVLDTPGPPQ NLAVKEVRKDSAFLVWEPPIIDGGAKVKNYVIDKRES TRKAYANVSSKCSKTSFKVENLTEGAIYYFRVMAENE FGVGVPVETVDAVKAAEPPSPPGKVTLTDVSQTSASL MWEKPEHDGGSRVLGYVVEMQPKGTEKWSIVAESKVC NAVVTGLSSGQEYQFRVKAYNEKGKSDPRVLGVPVIA KDLTIQPSLKLPFNTYSIQAGEDLKIEIPVIGRPRPN ISWVKDGEPLKQTTRVNVEETATSTVLHIKEGNKDDF GKYTVTATNSAGTATENLSVIVLEKPGPPVGPVRFDE VSADFVVISWEPPAYTGGCQISNYIVEKRDTTTTTWH MVSATVARTTIKITKLKTGTEYQFRIFAENRYGKSAP LDSKAVIVQYPFKEPGPPGTPFVTSISKDQMLVQWHE PVNDGGTKIIGYHLEQKEKNSILWVKLNKTPIQDTKF KTTGLDEGLEYEFKVSAENIVGIGKPSKVSECFVARD PCDPPGRPEAIVITRNNVTLKWKKPAYDGGSKITGYI VEKKDLPDGRWMKASFTNVLETEFTVSGLVEDQRYEF RVIARNAAGNFSEPSDSSGAITARDEIDAPNASLDPK YKDVIVVHAGETFVLEADIRGKPIPDVVWSKDGKELE ETAARMEIKSTIQKTTLVVKDCIRTDGGQYILKLSNV GGTKSIPITVKVLDRPGPPEGPLKVTGVTAEKCYLAW NPPLQDGGANISHYIIEKRETSRLSWTQVSTEVQALN YKVTKLLPGNEYIFRVMAVNKYGIGEPLESGPVTACN PYKPPGPPSTPEVSAITKDSMVVTWARPVDDGGTEIE GYILEKRDKEGVRWTKCNKKTLTDLRLRVTGLTEGHS YEFRVAAENAAGVGEPSEPSVFYRACDALYPPGPPSN PKVTDTSRSSVSLAWSKPIYDGGAPVKGYVVEVKEAA ADEWTTCTPPTGLQGKQFTVTKLKENTEYNFRICAIN SEGVGEPATLPGSVVAQERIEPPEIELDADLRKVVVL RASATLRLFVTIKGRPEPEVKWEKAEGILTDRAQIEV TSSFTMLVIDNVTRFDSGRYNLTLENNSGSKTAFVNV RVLDSPSAPVNLTIREVKKDSVTLSWEPPLIDGGAKI TNYIVEKRETTRKAYATITNNCTKTTFRIENLQEGCS YYFRVLASNEYGIGLPAETTEPVKVSEPPLPPGRVTL VDVTRNTATIKWEKPESDGGSKITGYVVEMQTKGSEK WSTCTQVKTLEATISGLTAGEEYVFRVAAVNEKGRSD PRQLGVPVIARDIEIKPSVELPFHTFNVKAREQLK IDVPFKGRPQATVNWRKDGQTLKETTRVNVSSSKTVT SLSIKEASKEDVGTYELCVSNSAGSITVPITIIVLDR PGPPGPIRIDEVSCDSITISWNPPEYDGGCQISNYIV EKKETTSTTWHIVSQAVARTSIKIVRLTTGSEYQFRV CAENRYGKSSYSESSAVVAEYPFSPPGPPGTPKVVHA TKSTMLVTWQVPVNDGGSRVIGYHLEYKERSSILWSK ANKILIADTQMKVSGLDEGLMYEYRVYAENIAGIGKC

			SKSCEPVPARDPCDPPGQPEVTNITRKSVSLKWSKPH YDGGAKITGYIVERRELPDGRWLKCNYTNIQETYFEV TELTEDQRYEFRVFARNAADSVSEPSESTGPIIVKDD VEPPRVMMDVKFRDVIVVKAGEVLKINADIAGRPLPV ISWAKDGIEIEERARTEIISTDNHTLLTVKDCIRRDT GQYVLTLKNVAGTRSVAVNCKVLDKPGPPAGPLEING LTAEKCSLSWGRPQEDGGADIDYYIVEKRETSHLAWT ICEGELQMTSCKVTKLLKGNEYIFRVTGVNKYGVGEP LESVAIKALDPFTVPSPPTSLEITSVTKESMTLCWSR PESDGGSEISGYIIERREKNSLRWVRVNKKPVYDLRV KSTGLREGCEYEYRVYAENAAGLSLPSETSPLIRAED PVFLPSPPSKPKIVDSGKTTITIAWVKPLFDGGAPIT GYTVEYKKSDDTDWKTSIQSLRGTEYTISGLTTGAEY VFRVKSVNKVGASDPSDSSDPQIAKEREEEPLFDIDS EMRKTLIVKAGASFTMTVPFRGRPVPNVLWSKPDTDL RTRAYVDTTDSRTSLTIENANRNDSGKYTLTIQNVLS AASLTLVVKVLDTPGPPTNITVQDVTKESAVLSWDVP ENDGGAPVKNYHIEKREASKKAWVSVTNNCNRLSYKV TNLQEGAIYYFRVSGENEFGVGIPAETKEGVKITEKP SPPEKLGVTSISKDSVSLTWLKPEHDGGSRIVHYVVE ALEKGQKNWVKCAVAKSTHHVVSGLRENSEYFFRVFA ENQAGLSDPRELLLPVLIKEQLEPPEIDMKNFPSHTV YVRAGSNLKVDIPISGKPLPKVTLSRDGVPLKATMRF NTEITAENLTINLKESVTADAGRYEITAANSSGTTKA FINIVVLDRPGPPTGPVVISDITEESVTLKWEPPKYD GGSQVTNYILLKRETSTAVWTEVSATVARTMMKVMKL TTGEEYQFRIKAENRFGISDHIDSACVTVKLPYTTPG PPSTPWVTNVTRESITVGWHEPVSNGGSAVVGYHLEM KDRNSILWQKANKLVIRTTHFKVTTISAGLIYEFRVY AENAAGVGKPSHPSEPVLAIDACEPPRNVRITDISKN SVSLSWQQPAFDGGSKITGYIVERRDLPDGRWTKASF TNVTETQFIISGLTQNSQYEFRVFARNAVGSISNPSE VVGPITCIDSYGGPVIDLPLEYTEVVKYRAGTSVKLR AGISGKPAPTIEWYKDDKELQTNALVCVENTTDLASI LIKDADRLNSGCYELKLRNAMGSASATIRVQILDKPG PPGGPIEFKTVTAEKITLLWRPPADDGGAKITHYIVE KRETSRVVWSMVSEHLEECIITTTKIIKGNEYIFRVR AVNKYGIGEPLESDSVVAKNAFVTPGPPGIPEVTKIT KNSMTVVWSRPIADGGSDISGYFLEKRDKKSLGWFKV LKETIRDTRQKVTGLTENSDYQYRVCAVNAAGQGPFS EPSEFYKAADPIDPPGPPAKIRIADSTKSSITLGWSK PVYDGGSAVTGYVVEIRQGEEEEWTTVSTKGEVRTTE YVVSNLKPGVNYYFRVSAVNCAGQGEPIEMNEPVQAK DILEAPEIDLDVALRTSVIAKAGEDVQVLIPFKGRPP PTVTWRKDEKNLGSDARYSIENTDSSSLLTIPQVTRN DTGKYILTIENGVGEPKSSTVSVKVLDTPAACQKLQV KHVSRGTVTLLWDPPLIDGGSPIINYVIEKRDATKRT WSVVSHKCSSTSFKLIDLSEKTPFFFRVLAENEIGIG EPCETTEPVKAAEVPAPIRDLSMKDSTKTSVILSWTK PDFDGGSVITEYVVERKGKGEQTWSHAGISKTCEIEV SQLKEQSVLEFRVFAKNEKGLSDPVTIGPITVKELII

			TPEVDLSDIPGAQVTVRIGHNVHLELPYKGKPKPSIS WLKDGLPLKESEFVRFSKTENKITLSIKNAKKEHGGK YTVILDNAVCRIAVPITVITLGPPSKPKGPIRFDEIK ADSVILSWDVPEDNGGGEITCYSIEKRETSQTNWKMV CSSVARTTFKVPNLVKDAEYQFRVRAENRYGVSQPLV SSIIVAKHQFRIPGPPGKPVIYNVTSDGMSLTWDAPV YDGGSEVTGFHVEKKERNSILWQKVNTSPISGREYRA TGLVEGLDYQFRVYAENSAGLSSPSDPSKFTLAVSPV DPPGTPDYIDVTRETITLKWNPPLRDGGSKIVGYSIE KRQGNERWVRCNFTDVSECQYTVTGLSPGDRYEFRII ARNAVGTISPPSQSSGIIMTRDENVPPIVEFGPEYFD GLIIKSGESLRIKALVQGRPVPRVTWFKDGVEIEKRM NMEITDVLGSTSLFVRDATRDHRGVYTVEAKNASGSA KAEIKVKVQDTPGKVVGPIRFTNITGEKMTLWWDAPL NDGCAPITHYIIEKRETSRLAWALIEDKCEAQSYTAI KLINGNEYQFRVSAVNKFGVGRPLDSDPVVAQIQYTV PDAPGIPEPSNITGNSITLTWARPESDGGSEIQQYIL ERREKKSTRWVKVISKRPISETRFKVTGLTEGNEYEF HVMAENAAGVGPASGISRLIKCREPVNPPGPPTVVKV TDTSKTTVSLEWSKPVFDGGMEIIGYIIEMCKADLGD WHKVNAEACVKTRYTVTDLQAGEEYKFRVSAINGAGK GDSCEVTGTIKAVDRLTAPELDIDANFKQTHVVRAGA SIRLFIAYQGRPTPTAVWSKPDSNLSLRADIHTTDSF STLTVENCNRNDAGKYTLTVENNSGSKSITFTVKVLD TPGPPGPITFKDVTRGSATLMWDAPLLDGGARIHHYV VEKREASRRSWQVISEKCTRQIFKVNDLAEGVPYYFR VSAVNEYGVGEPYEMPEPIVATEQPAPPRRLDVVDTS KSSAVLAWLKPDHDGGSRITGYLLEMRQKGSDFWVEA GHTKQLTFTVERLVEKTEYEFRVKAKNDAGYSEPREA FSSVIIKEPQIEPTADLTGITNQLITCKAGSPFTIDV PISGRPAPKVTWKLEEMRLKETDRVSITTTKDRTTLT VKDSMRGDSGRYFLTLENTAGVKTFSVTVVVIGRPGP VTGPIEVSSVSAESCVLSWGEPKDGGGTEITNYIVEK RESGTTAWQLVNSSVKRTQIKVTHLTKYMEYSFRVSS ENRFGVSKPLESAPIIAEHPFVPPSAPTRPEVYHVSA NAMSIRWEEPYHDGGSKIIGYWVEKKERNTILWVKEN KVPCLECNYKVTGLVEGLEYQFRTYALNAAGVSKASE ASRPIMAQNPVDAPGRPEVTDVTRSTVSLIWSAPAYD GGSKVVGYIIERKPVSEVGDGRWLKCNYTIVSDNFFT VTALSEGDTYEFRVLAKNAAGVISKGSESTGPVTCRD EYAPPKAELDARLHGDLVTIRAGSDLVLDAAVGGKPE PKIIWTKGDKELDLCEKVSLQYTGKRATAVIKFCDRS DSGKYTLTVKNASGTKAVSVMVKVLDSPGPCGKLTVS RVTQEKCTLAWSLPQEDGGAEITHYIVERRETSRLNW VIVEGECPTLSYVVTRLIKNNEYIFRVRAVNKYGPGV PVESEPIVARNSFTIPSPPGIPEEVGTGKEHIIIQWT KPESDGGNEISNYLVDKREKKSLRWTRVNKDYVVYDT RLKVTSLMEGCDYQFRVTAVNAAGNSEPSEASNFISC REPSYTPGPPSAPRVVDTTKHSISLAWTKPMYDGGTD IVGYVLEMQEKDTDQWYRVHTNATIRNTEFTVPDLKM GQKYSFRVAAVNVKGMSEYSESIAEIEPVERIEIPDL

			ELADDLKKTVTIRAGASLRLMVSVSGRPPPVITWSKQ GIDLASRAIIDTTESYSLLIVDKVNRYDAGKYTIEAE NQSGKKSATVLVKVYDTPGPCPSVKVKEVSRDSVTIT WEIPTIDGGAPVNNYIVEKREAAMRAFKTVTTKCSKT LYRISGLVEGTMYYFRVLPENIYGIGEPCETSDAVLV SEVPLVPAKLEVVDVTKSTVTLAWEKPLYDGGSRLTG YVLEACKAGTERWMKVVTLKPTVLEHTVTSLNEGEQY LFRIRAQNEKGVSEPRETVTAVTVQDLRVLPTIDLST MPQKTIHVPAGRPVELVIPIAGRPPPAASWFFAGSKL RESERVTVETHTKVAKLTIRETTIRDTGEYTLELKNV TGTTSETIKVIILDKPGPPTGPIKIDEIDATSITISW EPPELDGGAPLSGYVVEQRDAHRPGWLPVSESVTRST FKFTRLTEGNEYVFRVAATNRFGIGSYLQSEVIECRS SIRIPGPPETLQIFDVSRDGMTLTWYPPEDDGGSQVT GYIVERKEVRADRWVRVNKVPVTMTRYRSTGLTEGLE YEHRVTAINARGSGKPSRPSKPIVAMDPIAPPGKPQN PRVTDTTRTSVSLAWSVPEDEGGSKVTGYLIEMQKVD QHEWTKCNTTPTKIREYTLTHLPQGAEYRFRVLACNA GGPGEPAEVPGTVKVTEMLEYPDYELDERYQEGIFVR QGGVIRLTIPIKGKPFPICKWTKEGQDISKRAMIATS ETHTELVIKEADRGDSGTYDLVLENKCGKKAVYIKVR VIGSPNSPEGPLEYDDIQVRSVRVSWRPPADDGGADI LGYILERREVPKAAWYTIDSRVRGTSLVVKGLKENVE YHFRVSAENQFGISKPLKSEEPVTPKTPLNPPEPPSN PPEVLDVTKSSVSLSWSRPKDDGGSRVTGYYIERKET STDKWVRHNKTQITTTMYTVTGLVPDAEYQFRIIAQN DVGLSETSPASEPVVCKDPFDKPSQPGELEILSISKD SVTLQWEKPECDGGKEILGYWVEYRQSGDSAWKKSNK ERIKDKQFTIGGLLEATEYEFRVFAENETGLSRPRRT AMSIKTKLTSGEAPGIRKEMKDVTTKLGEAAQLSCQI VGRPLPDIKWYRFGKELIQSRKYKMSSDGRTHTLTVM TEEQEDEGVYTCIATNEVGEVETSSKLLLQATPQFHP GYPLKEKYYGAVGSTLRLHVMYIGRPVPAMTWFHGQK LLQNSENITIENTEHYTHLVMKNVQRKTHAGKYKVQL SNVFGTVDAILDVEIQDKPDKPTGPIVIEALLKNSAV ISWKPPADDGGSWITNYVVEKCEAKEGAEWQLVSSAI SVTTCRIVNLTENAGYYFRVSAQNTFGISDPLEVSSV VIIKSPFEKPGAPGKPTITAVTKDSCVVAWKPPASDG GAKIRNYYLEKREKKQNKWISVTTEEIRETVFSVKNL IEGLEYEFRVKCENLGGESEWSEISEPITPKSDVPIQ APHFKEELRNLNVRYQSNATLVCKVTGHPKPIVKWYR QGKEIIADGLKYRIQEFKGGYHQLIIASVTDDDATVY QVRATNQGGSVSGTASLEVEVPAKIHLPKTLEGMGAV HALRGEVVSIKIPFSGKPDPVITWQKGQDLIDNNGHY QVIVTRSFTSLVFPNGVERKDAGFYVVCAKNRFGIDQ KTVELDVADVPDPPRGVKVSDVSRDSVNLTWTEPASD GGSKITNYIVEKCATTAERWLRVGQARETRYTVINLF GKTSYQFRVIAENKFGLSKPSEPSEPTITKEDKTRAM NYDEEVDETREVSMTKASHSSTKELYEKYMIAEDLGR GEFGIVHRCVETSSKKTYMAKFVKVKGTDQVLVKKEI SILNIARHRNILHLHESFESMEELVMIFEFISGLDIF

			ERINTSAFELNEREIVSYVHQVCEALQFLHSHNIGHF DIRPENIIYQTRRSSTIKIIEFGQARQLKPGDNFRLL FTAPEYYAPEVHQHDVVSTATDMWSLGTLVYVLLSGI NPFLAETNQQIIENIMNAEYTFDEEAFKEISIEAMDF VDRLLVKERKSRMTASEALQHPWLKQKIERVSTKVIR TLKHRRYYHTLIKKDLNMVVSAARISCGGAIRSQKGV SVAKVKVASIEIGPVSGQIMHAVGEEGGHVKYVCKIE NYDQSTQVTWYFGVRQLENSEKYEITYEDGVAILYVK DITKLDDGTYRCKVVNDYGEDSSYAELFVKGVREVYD YYCRRTMKKIKRRTDTMRLLERPPEFTLPLYNKTAYV GENVRFGVTITVHPEPHVTWYKSGQKIKPGDNDKKYT FESDKGLYQLTINSVTTDDDAEYTVVARNKYGEDSCK AKLTVTLHPPPTDSTLRPMFKRLLANAECQEGQSVCF EIRVSGIPPPTLKWEKDGQPLSLGPNIEIIHEGLDYY ALHIRDTLPEDTGYYRVTATNTAGSTSCQAHLQVERL RYKKQEFKSKEEHERHVQKQIDKTLRMAEILSGTESV PLTQVAKEALREAAVLYKPAVSTKTVKGEFRLEIEEK KEERKLRMPYDVPEPRKYKQTTIEEDQRIKQFVPMSD MKWYKKIRDQYEMPGKLDRVVQKRPKRIRLSRWEQFY VMPLPRITDQYRPKWRIPKLSQDDLEIVRPARRRTPS PDYDFYYRPRRRSLGDISDEELLLPIDDYLAMKRTEE ERLRLEEELELGFSASPPSRSPPHFELSSLRYSSPQA HVKVEETRKDFRYSTYHIPTKAEASTSYAELRERHAQ AAYRQPKQRQRIMAEREDEELLRPVTTTQHLSEYKSE LDFMSKEEKSRKKSRRQREVTEITEIEEEYEISKHAQ RESSSSASRLLRRRRSLSPTYIELMRPVSELIRSRPQ PAEEYEDDTERRSPTPERTRPRSPSPVSSERSLSRFE RSARFDIFSRYESMKAALKTQKTSERKYEVLSQQPFT LDHAPRITLRMRSHRVPCGQNTRFILNVQSKPTAEVK WYHNGVELQESSKIHYTNTSGVLTLEILDCHTDDSGT YRAVCTNYKGEASDYATLDVTGGDYTTYASQRRDEEV PRSVFPELTRTEAYAVSSFKKTSEMEASSSVREVKSQ MTETRESLSSYEHSASAEMKSAALEEKSLEEKSTTRK IKTTLAARILTKPRSMTVYEGESARFSCDTDGEPVPT VTWLRKGQVLSTSARHQVTTTKYKSTFEISSVQASDE GNYSVVVENSEGKQEAEFTLTIQKARVTEKAVTSPPR VKSPEPRVKSPEAVKSPKRVKSPEPSHPKAVSPTETK PTPTEKVQHLPVSAPPKITQFLKAEASKEIAKLTCVV ESSVLRAKEVTWYKDGKKLKENGHFQFHYSADGTYEL KINNLTESDQGEYVCEISGEGGTSKTNLQFMGQAFKS IHEKVSKISETKKSDQKTTESTVTRKTEPKAPEPISS KPVIVTGLQDTTVSSDSVAKFAVKATGEPRPTAIWTK DGKAITQGGKYKLSEDKGGFFLEIHKTDTSDSGLYTC TVKNSAGSVSSSCKLTIKAIKDTEAQKVSTQKTSEIT PQKKAVVQEEISQKALRSEEIKMSEAKSQEKLALKEE ASKVLISEEVKKSAATSLEKSIVHEEITKTSQASEEV RTHAEIKAFSTQMSINEGQRLVLKANIAGATDVKWVL NGVELTNSEEYRYGVSGSDQTLTIKQASHRDEGILTC ISKTKEGIVKCQYDLTLSKELSDAPAFISQPRSQNIN EGQNVLFTCEISGEPSPEIEWFKNNLPISISSNVSIS RSRNVYSLEIRNASVSDSGKYTIKAKNFRGQCSATAS

			LMVLPLVEEPSREVVLRTSGDTSLQGSFSSQSVQMSA SKQEASFSSFSSSSASSMTEMKFASMSAQSMSSMQES FVEMSSSSFMGISNMTQLESSTSKMLKAGIRGIPPKI EALPSDISIDEGKVLTVACAFTGEPTPEVTWSCGGRK IHSQEQGRFHIENTDDLTTLIIMDVQKQDGGLYTLSL GNEFGSDSATVNIHIRSI
Cytoplasmic dynein 1 heavy chain 1 (DYNC1H1)	DYNC1H1 Syndrome	236	MSEPGGGGGEDGSAGLEVSAVQNVADVSVLQKHLRKL VPLLLEDGGEAPAALEAALEEKSALEQMRKFLSDPQV HTVLVERSTLKEDVGDEGEEEKEFISYNINIDIHYGV KSNSLAFIKRTPVIDADKPVSSQLRVLTLSEDSPYET LHSFISNAVAPFFKSYIRESGKADRDGDKMAPSVEKK IAELEMGLLHLQQNIEIPEISLPIHPMITNVAKQCYE RGEKPKVTDFGDKVEDPTFLNQLQSGVNRWIREIQKV TKLDRDPASGTALQEISFWLNLERALYRIQEKRESPE VLLTLDILKHGKRFHATVSFDTDTGLKQALETVNDYN PLMKDFPLNDLLSATELDKIRQALVAIFTHLRKIRNT KYPIQRALRLVEAISRDLSSQLLKVLGTRKLMHVAYE EFEKVMVACFEVFQTWDDEYEKLQVLLRDIVKRKREE NLKMVWRINPAHRKLQARLDQMRKFRRQHEQLRAVIV RVLRPQVTAVAQQNQGEVPEPQDMKVAEVLFDAADAN AIEEVNLAYENVKEVDGLDVSKEGTEAWEAAMKRYDE RIDRVETRITARLRDQLGTAKNANEMFRIFSRFNALF VRPHIRGAIREYQTQLIQRVKDDIESLHDKFKVQYPQ SQACKMSHVRDLPPVSGSIIWAKQIDRQLTAYMKRVE DVLGKGWENHVEGQKLKQDGDSFRMKLNTQEIFDDWA RKVQQRNLGVSGRIFTIESTRVRGRTGNVLKLKVNFL PEIITLSKEVRNLKWLGFRVPLAIVNKAHQANQLYPF AISLIESVRTYERTCEKVEERNTISLLVAGLKKEVQA LIAEGIALVWESYKLDPYVQRLAETVFNFQEKVDDLL IIEEKIDLEVRSLETCMYDHKTFSEILNRVQKAVDDL NLHSYSNLPIWVNKLDMEIERILGVRLQAGLRAWTQV LLGQAEDKAEVDMDTDAPQVSHKPGGEPKIKNVVHEL RITNQVIYLNPPIEECRYKLYQEMFAWKMVVLSLPRI QSQRYQVGVHYELTEEEKFYRNALTRMPDGPVALEES YSAVMGIVSEVEQYVKVWLQYQCLWDMQAENIYNRLG EDLNKWQALLVQIRKARGTFDNAETKKEFGPVVIDYG KVQSKVNLKYDSWHKEVLSKFGQMLGSNMTEFHSQIS KSRQELEQHSVDTASTSDAVTFITYVQSLKRKIKQFE KQVELYRNGQRLLEKQRFQFPPSWLYIDNIEGEWGAF NDIMRRKDSAIQQQVANLQMKIVQEDRAVESRTTDLL TDWEKTKPVTGNLRPEEALQALTIYEGKFGRLKDDRE KCAKAKEALELTDTGLLSGSEERVQVALEELQDLKGV WSELSKVWEQIDQMKEQPWVSVQPRKLRQNLDALLNQ LKSFPARLRQYASYEFVQRLLKGYMKINMLVIELKSE ALKDRHWKQLMKRLHVNWVVSELTLGQIWDVDLQKNE AIVKDVLLVAQGEMALEEFLKQIREVWNTYELDLVNY QNKCRLIRGWDDLFNKVKEHINSVSAMKLSPYYKVFE EDALSWEDKLNRIMALFDVWIDVQRRWVYLEGIFTGS ADIKHLLPVETQRFQSISTEFLALMKKVSKSPLVMDV LNIQGVQRSLERLADLLGKIQKALGEYLERERSSFPR FYFVGDEDLLEIIGNSKNVAKLQKHFKKMFAGVSSII

			LNEDNSVVLGISSREGEEVMFKTPVSITEHPKINEWL TLVEKEMRVTLAKLLAESVTEVEIFGKATSIDPNTYI TWIDKYQAQLVVLSAQIAWSENVETALSSMGGGGDAA PLHSVLSNVEVTLNVLADSVLMEQPPLRRRKLEHLIT ELVHQRDVTRSLIKSKIDNAKSFEWLSQMRFYFDPKQ TDVLQQLSIQMANAKFNYGFEYLGVQDKLVQTPLTDR CYLTMTQALEARLGGSPFGPAGTGKTESVKALGHQLG RFVLVFNCDETFDFQAMGRIFVGLCQVGAWGCFDEFN RLEERMLSAVSQQVQCIQEALREHSNPNYDKTSAPIT CELLNKQVKVSPDMAIFITMNPGYAGRSNLPDNLKKL FRSLAMTKPDRQLIAQVMLYSQGFRTAEVLANKIVPF FKLCDEQLSSQSHYDFGLRALKSVLVSAGNVKRERIQ KIKREKEERGEAVDEGEIAENLPEQEILIQSVCETMV PKLVAEDIPLLFSLLSDVFPGVQYHRGEMTALREELK KVCQEMYLTYGDGEEVGGMWVEKVLQLYQITQINHGL MMVGPSGSGKSMAWRVLLKALERLEGVEGVAHIIDPK AISKDHLYGTLDPNTREWTDGLFTHVLRKIIDSVRGE LQKRQWIVFDGDVDPEWVENLNSVLDDNKLLTLPNGE RLSLPPNVRIMFEVQDLKYATLATVSRCGMVWFSEDV LSTDMIFNNFLARLRSIPLDEGEDEAQRRRKGKEDEG EEAASPMLQIQRDAATIMQPYFTSNGLVTKALEHAFQ LEHIMDLTRLRCLGSLFSMLHQACRNVAQYNANHPDF PMQIEQLERYIQRYLVYAILWSLSGDSRLKMRAELGE YIRRITTVPLPTAPNIPIIDYEVSISGEWSPWQAKVP QIEVETHKVAAPDVVVPTLDTVRHEALLYTWLAEHKP LVLCGPPGSGKTMTLFSALRALPDMEVVGLNFSSATT PELLLKTFDHYCEYRRTPNGVVLAPVQLGKWLVLFCD EINLPDMDKYGTQRVISFIRQMVEHGGFYRTSDQTW VKLERIQFVGACNPPTDPGRKPLSHRFLRHVPVVYVD YPGPASLTQIYGTFNRAMLRLIPSLRTYAEPLTAAMV EFYTMSQERFTQDTQPHYIYSPREMTRWVRGIFEALR PLETLPVEGLIRIWAHEALRLFQDRLVEDEERRWTDE NIDTVALKHFPNIDREKAMSRPILYSNWLSKDYIPVD QEELRDYVKARLKVFYEEELDVPLVLFNEVLDHVLRI DRIFRQPQGHLLLIGVSGAGKTTLSRFVAWMNGLSVY QIKVHRKYTGEDFDEDLRTVLRRSGCKNEKIAFIMDE SNVLDSGFLERMNTLLANGEVPGLFEGDEYATLMTQC KEGAQKEGLMLDSHEELYKWFTSQVIRNLHVVFTMNP SSEGLKDRAATSPALFNRCVLNWFGDWSTEALYQVGK EFTSKMDLEKPNYIVPDYMPVVYDKLPQPPSHREAIV NSCVFVHQTLHQANARLAKRGGRTMAITPRHYLDFIN HYANLFHEKRSELEEQQMHLNVGLRKIKETVDQVEEL RRDLRIKSQELEVKNAAANDKLKKMVKDQQEAEKKKV MSQEIQEQLHKQQEVIADKQMSVKEDLDKVEPAVIEA QNAVKSIKKQHLVEVRSMANPPAAVKLALESICLLLG ESTTDWKQIRSIIMRENFIPTIVNFSAEEISDAIREK MKKNYMSNPSYNYEIVNRASLACGPMVKWAIAQLNYA DMLKRVEPLRNELQKLEDDAKDNQQKANEVEQMIRDL EASIARYKEEYAVLISEAQAIKADLAAVEAKVNRSTA LLKSLSAERERWEKTSETFKNQMSTIAGDCLLSAAFI AYAGYFDQQMRQNLFTTWSHHLQQANIQFRTDIARTE

			YLSNADERLRWQASSLPADDLCTENAIMLKRFNRYPL IIDPSGQATEFIMNEYKDRKITRTSFLDDAFRKNLES ALRFGNPLLVQDVESYDPVLNPVLNREVRRTGGRVLI TLGDQDIDLSPSFVIFLSTRDPTVEFPPDLCSRVTFV NFTVTRSSLQSQCLNEVLKAERPDVDEKRSDLLKLQG EFQLRLRQLEKSLLQALNEVKGRILDDDTIITTLENL KREAAEVTRKVEETDIVMQEVETVSQQYLPLSTACSS IYFTMESLKQIHFLYQYSLQFFLDIYHNVLYENPNLK GVTDHTQRLSIITKDLFQVAFNRVARGMLHQDHITFA MLLARIKLKGTVGEPTYDAEFQHFLRGNEIVLSAGST PRIQGLTVEQAEAVVRLSCLPAFKDLIAKVQADEQFG IWLDSSSPEQTVPYLWSEETPATPIGQAIHRLLLIQA FRPDRLLAMAHMFVSTNLGESFMSIMEQPLDLTHIVG TEVKPNTPVLMCSVPGYDASGHVEDLAAEQNTQITSI AIGSAEGFNQADKAINTAVKSGRWVMLKNVHLAPGWL MQLEKKLHSLQPHACFRLFLTMEINPKVPVNLLRAGR IFVFEPPPGVKANMLRTFSSIPVSRICKSPNERARLY FLLAWFHAIIQERLRYAPLGWSKKYEFGESDLRSACD TVDTWLDDTAKGRQNISPDKIPWSALKTLMAQSIYGG RVDNEFDQRLLNTFLERLFTTRSFDSEFKLACKVDGH KDIQMPDGIRREEFVQWVELLPDTQTPSWLGLPNNAE RVLLTTQGVDMISKMLKMQMLEDEDDLAYAETEKKTR TDSTSDGRPAWMRTLHTTASNWLHLIPQTLSHLKRTV ENIKDPLFRFFEREVKMGAKLLQDVRQDLADVVQVCE GKKKQTNYLRTLINELVKGILPRSWSHYTVPAGMTVI QWVSDFSERIKQLQNISLAAASGGAKELKNIHVCLGG LFVPEAYITATRQYVAQANSWSLEELCLEVNVTTSQG ATLDACSFGVTGLKLQGATCNNNKLSLSNAISTALPL TQLRWVKQTNTEKKASVVTLPVYLNFTRADLIFTVDF EIATKEDPRSFYERGVAVLCTE
TRIO and F-actin-binding protein (TRIO)	TRIO-Related ID	237	MEEVPGDALCEHFEANILTQNRCQNCFHPEEAHGARY QELRSPSGAEVPYCDLPRCPPAPEDPLSASTSGCQSV VDPGLRPGPKRGPSPSAGLPEEGPTAAPRSRSRELEA VPYLEGLTTSLCGSCNEDPGSDPTSSPDSATPDDTSN SSSVDWDTVERQEEEAPSWDELAVMIPRRPREGPRAD SSQRAPSLLTRSPVGGDAAGQKKEDTGGGGRSAGQHW ARLRGESGLSLERHRSTLTQASSMTPHSGPRSTTSQA SPAQRDTAQAASTREIPRASSPHRITQRDTSRASSTQ QEISRASSTQQETSRASSTQEDTPRASSTQEDTPRAS STQWNTPRASSPSRSTQLDNPRTSSTQQDNPQTSFPT CTPQRENPRTPCVQQDDPRASSPNRTTQRENSRTSCA QRDNPKASRTSSPNRATRDNPRTSCAQRDNPRASSPS RATRDNPTTSCAQRDNPRASRTSSPNRATRDNPRTSC AQRDNPRASSPSRATRDNPTTSCAQRDNPRASRTSSP NRATRDNPRTSCAQRDNPRASSPNRAARDNPTTSCAQ RDNPRASRTSSPNRATRDNPRTSCAQRDNPRASSPNR ATRDNPTTSCAQRDNPRASRTSSPNRATRDNPRTSCA QRDNPRASSPNRTTQQDSPRTSCARRDDPRASSPNRT IQQENPRTSCALRDNPRASSPSRTIQQENPRTSCAQR DDPRASSPNRTTQQENPRTSCARRDNPRASSRNRTIQ RDNPRTSCAQRDNPRASSPNRTIQQENLRTSCTRQDN

			PRTSSPNRATRDNPRTSCAQRDNLRASSPIRATQQDN PRTCIQQNIPRSSSTQQDNPKTSCTKRDNLRPTCTQR DRTQSFSFQRDNPGTSSSQCCTQKENLRPSSPHRSTQ WNNPRNSSPHRTNKDIPWASFPLRPTQSDGPRTSSPS RSKQSEVPWASIALRPTQGDRPQTSSPSRPAQHDP PQSSFGPTQYNLPSRATSSSHNPGHQSTSRTSSPVYP AAYGAPLTSPEPSQPPCAVCIGHRDAPRASSPPRYLQ HDPFPFFPEPRAPESEPPHHEPPYIPPAVCIGHRDAP RASSPPRHTQFDPFPFLPDTSDAEHQCQSPQHEPLQL PAPVCIGYRDAPRASSPPRQAPEPSLLFQDLPRASTE SLVPSMDSLHECPHIPTPVCIGHRDAPSFSSPPRQAP EPSLFFQDPPGTSMESLAPSTDSLHGSPVLIPQVCIG HRDAPRASSPPRHPPSDLAFLAPSPSPGSSGGSRGSA PPGETRHNLEREEYTVLADLPPPRRLAQRQPGPQAQC SSGGRTHSPGRAEVERLFGQERRKSEAAGAFQAQDEG RSQQPSQGQSQLLRRQSSPAPSRQVTMLPAKQAELTR RSQAEPPHPWSPEKRPEGDRQLQGSPLPPRTSARTPE RELRTQRPLESGQAGPRQPLGVWQSQEEPPGSQGPH RHLERSWSSQEGGLGPGGWWGCGEPSLGAAKAPEGAW GGTSREYKESWGQPEAWEEKPTHELPRELGKRSPLTS PPENWGGPAESSQSWHSGTPTAVGWGAEGACPYPRGS ERRPELDWRDLLGLLRAPGEGVWARVPSLDWEGLLEL LQARLPRKDPAGHRDDLARALGPELGPPGTNDVPEQE SHSQPEGWAEATPVNGHSPALQSQSPVQLPSACTSTQ WPKIKVTRGPATATLAGLEQTGPLGSRSTAKGPSLPE LQFQPEEPEESEPSRGDPLTDQKQADSADKRPAEGKA GSPLKGRLVTSWRMPGDRPTLFNPFLLSLGVLRWRRP DLLNFKKGWMSILDEPGEPPSPSLTTTSTSQWKKHWF VLTDSSLKYYRDSTAEEADELDGEIDLRSCTDVTEYA VQRNYGFQIHTKDAVYTLSAMTSGIRRNWIEALRKTV RPTSAPDVTKLSDSNKENALHSYSTQKGPLKAGEQRA GSEVISRGGPRKADGQRQALDYVELSPLTQASPQRAR TPARTPDRLAKQEELERDLAQRSEERRKWFEATDSRT PEVPAGEGPRRGLGAPLTEDQQNRLSEEIEKKWQELE KLPLRENKRVPLTALLNQSRGERRGPPSDGHEALEKE VQALRAQLEAWRLQGEAPQSALRSQEDGHIPPGYISQ EACERSLAEMESSHQQVMEELQRHHERELQRLQQEKE WLLAEETAATASAIEAMKKAYQEELSRELSKTRSLQQ GPDGLRKQHQSDVEALKRELQVLSEQYSQKCLEIGAL MRQAEEREHTLRRCQQEGQELLRHNQELHGRLSEEID QLRGFIASQGMGNGCGRSNERSSCELEVLLRVKENEL QYLKKEVQCLRDELQMMQKDKRFTSGKYQDVYVELSH IKTRSEREIEQLKEHLRLAMAALQEKESMRNSLAE
Probable ubiquitin carboxyl-terminal hydrolase FAF-X (USP9X)	USP9X Development Disorder	238	MTATTRGSPVGGNDNQGQAPDGQSQPPLQQNQTSSPD SSNENSPATPPDEQGQGDAPPQLEDEEPAFPHTDLAK LDDMINRPRWVVPVLPKGELEVLLEAAIDLSKKGLDV KSEACQRFFRDGLTISFTKILTDEAVSGWKFEIHRCI INNTHRLVELCVAKLSQDWFPLLELLAMALNPHCKFH IYNGTRPCESVSSSVQLPEDELFARSPDPRSPKGWLV DLLNKFGTLNGFQILHDRFINGSALNVQIIAALIKPF GQCYEFLTLHTVKKYFLPIIEMVPQFLENLTDEELKK

			EAKNEAKNDALSMIIKSLKNLASRVPGQEETVKNLEI FRLKMILRLLQISSFNGKMNALNEVNKVISSVSYYTH RHGNPEEEEWLTAERMAEWIQQNNILSIVLRDSLHQP QYVEKLEKILRFVIKEKALTLQDLDNIWAAQAGKHEA IVKNVHDLLAKLAWDFSPEQLDHLFDCFKASWTNAS KKQREKLLELIRRLAEDDKDGVMAHKVLNLLWNLAHS DDVPVDIMDLALSAHIKILDYSCSQDRDTQKIQWIDR FIEELRTNDKWVIPALKQIREICSLFGEAPQNLSQTQ RSPHVFYRHDLINQLQHNHALVTLVAENLATYMESMR LYARDHEDYDPQTVRLGSRYSHVQEVQERLNFLRFLL KDGQLWLCAPQAKQIWKCLAENAVYLCDREACFKWYS KLMGDEPDLDPDINKDFFESNVLQLDPSLLTENGMKC FERFFKAVNCREGKLVAKRRAYMMDDLELIGLDYLWR VVIQSNDDIASRAIDLLKEIYTNLGPRLQVNQVVIHE DFIQSCFDRLKASYDTLCVLDGDKDSVNCARQEAVRM VRVLTVLREYINECDSDYHEERTILPMSRAFRGKHLS FVVRFPNQGRQVDDLEVWSHTNDTIGSVRRCILNRIK ANVAHTKIELFVGGELIDPADDRKLIGQLNLKDKSLI TAKLTQISSNMPSSPDSSSDSSTGSPGNHGNHYSDGP NPEVESCLPGVIMSLHPRYISFLWQVADLGSSLNMPP LRDGARVLMKLMPPDSTTIEKLRAICLDHAKLGESSL SPSLDSLFFGPSASQVLYLTEVVYALLMPAGAPLADD SSDFQFHFLKSGGLPLVLSMLTRNNFLPNADMETRRG AYLNALKIAKLLLTAIGYGHVRAVAEACQPGVEGVNP MTQINQVTHDQAVVLQSALQSIPNPSSECMLRNVSVR LAQQISDEASRYMPDICVIRAIQKIIWASGCGSLQLV FSPNEEITKIYEKTNAGNEPDLEDEQVCCEALEVMTL CFALIPTALDALSKEKAWQTFIIDLLLHCHSKTVRQV AQEQFFLMCTRCCMGHRPLLFFITLLFTVLGSTARER AKHSGDYFTLLRHLLNYAYNSNINVPNAEVLLNNEID WLKRIRDDVKRTGETGIEETILEGHLGVTKELLAFQT SEKKFHIGCEKGGANLIKELIDDFIFPASNVYLQYMR NGELPAEQAIPVCGSPPTINAGFELLVALAVGCVRNL KQIVDSLTEMYYIGTAITTCEALTEWEYLPPVGPRPP KGFVGLKNAGATCYMNSVIQQLYMIPSIRNGILAIEG TGSDVDDDMSGDEKQDNESNVDPRDDVFGYPQQFEDK PALSKTEDRKEYNIGVLRHLQVIFGHLAASRLQYYVP RGFWKQFRLWGEPVNLREQHDALEFFNSLVDSLDEAL KALGHPAMLSKVLGGSFADQKICQGCPHRYECEESFT TLNVDIRNHQNLLDSLEQYVKGDLLEGANAYHCEKCN KKVDTVKRLLIKKLPPVLAIQLKRFDYDWERECAIKF NDYFEFPRELDMEPYTVAGVAKLEGDNVNPESQLIQQ SEQSESETAGSTKYRLVGVLVHSGQASGGHYYSYIIQ RNGGDGERNRWYKFDDGDVTECKMDDDEEMKNQCFGG EYMGEVFDHMMKRMSYRRQKRWWNAYILFYERMDTID QDDELIRYISELAITTRPHQIIMPSAIERSVRKQNVQ FMHNRMQYSMEYFQFMKKLLTCNGVYLNPPPGQDHLL PEAEEITMISIQLAARFLFTTGFHTKKVVRGSASDWY DALCILLRHSKNVRFWFAHNVLFNVSNRFSEYLLECP SAEVRGAFAKLIVFIAHFSLQDGPCPSPFASPGPSSQ AYDNLSLSDHLLRAVLNLLRREVSEHGRHLQQYFNLF

			VMYANLGVAEKTQLLKLSVPATFMLVSLDEGPGPPIK YQYAELGKLYSVVSQLIRCCNVSSRMQSSINGNPPLP NPFGDPNLSQPIMPIQQNVADILFVRTSYVKKIIEDC SNSEETVKLLRFCCWENPQFSSTVLSELLWQVAYSYT YELRPYLDLLLQILLIEDSWQTHRIHNALKGIPDDRD GLFDTIQRSKNHYQKRAYQCIKCMVALFSNCPVAYQI LQGNGDLKRKWTWAVEWLGDELERRPYTGNPQYTYNN WSPPVQSNETSNGYFLERSHSARMTLAKACELCPEEE PDDQDAPDEHESPPPEDAPLYPHSPGSQYQQNNHVHG QPYTGPAAHHMNNPQRTGQRAQENYEGSEEVSPPQTK DQ
Pyrin domain-containing protein 2 (PYDC2)	-	287	MASSAELDFNLQALLEQLSQDELSKFKSLIRTISLGK ELQTVPQTEVDKANGKQLVEIFTSHSCSYWAGMAAIQ VFEKMNQTHLSGRADEHCVMPPP
Cystatin-B (CSTB)	Epilepsy, progressive myoclonic 1 (EPM1)	288	MMCGAPSATQPATAETQHIADQVRSQLEEKENKKFPV FKAVSFKSQVVAGTNYFIKVHVGDEDFVHLRVFQSLP HENKPLTLSNYQTNKAKHDELTYF
Pterin-4-alpha-carbinolamine dehydratase (PCBD1)	Hyperphenylalaninemia, BH4-deficient, D (HPABH4D)	289	MAGKAHRLSAEERDQLLPNLRAVGWNELEGRDAIFKQ FHFKDFNRAFGFMTRVALQAEKLDHHPEWFNVYNKVH ITLSTHECAGLSERDINLASFIEQVAVSMT

5.3.2.2 Anti-SYNGAP1 Single Domain Antibodies

[00191] In one aspect, provided herein is a single domain antibody (e.g., a VHH) that specifically binds SYNGAP1 (e.g., human SYNGAP1). In some embodiments, the single domain antibody is a VHH (i.e. a nanobody). In some embodiments, the VHH comprises three complementarity determining regions: VH CDR1, VH CDR2, and VH CDR3. The CDRs below are defined according to Kabat.

[00192] In some embodiments, the VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and/or a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00193] In some embodiments, the VHH comprises a CDR1 that comprises the amino acid

sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00194] In some embodiments, the VHH comprises a CDR1 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 290; a CDR2 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% to the amino acid sequence of SEQ ID NO: 291; and a CDR3 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 292.

[00195] In some embodiments, the VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00196] In some embodiments, the VHH comprises a CDR1 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 294; a CDR2 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% to the amino acid sequence of SEQ ID NO: 295; and a CDR3 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 296.

[00197] In some embodiments, the VHH comprises a VH CDR1 that comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID

NO: 300 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00198] In some embodiments, the VHH comprises a CDR1 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 298; a CDR2 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% to the amino acid sequence of SEQ ID NO: 299; and a CDR3 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 300.

[00199] In some embodiments, the VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00200] In some embodiments, the VHH comprises a CDR1 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 302; a CDR2 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% to the amino acid sequence of SEQ ID NO: 303; and a CDR3 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 304.

[00201] In some embodiments, the VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00202] In some embodiments, the VHH comprises a CDR1 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 306; a CDR2 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% to the amino acid sequence of SEQ ID NO: 307; and a CDR3 that comprises an

amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 308.

[00203] In some embodiments, the VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00204] In some embodiments, the VHH comprises a CDR1 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 310; a CDR2 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% to the amino acid sequence of SEQ ID NO: 311; and a CDR3 that comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 312.

[00205] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293, 297, 301, 305, 309, or 312.

[00206] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293.

[00207] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 297.

[00208] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 301.

[00209] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 305.

[00210] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 309.

[00211] In some embodiments, the VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 313.

[00212] Also provided herein are $(VHH)_2$ antibodies that specifically bind SYNGAP1. The first VHH and the second VHH of a $(VHH)_2$ may be directly connected or indirectly connected via an amino acid linker. Exemplary amino acid linkers include the amino acid sequence of any one of SEQ ID NOS: 375-384. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 375-384. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 375. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 376. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 377. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 378. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 379. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 380. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 381. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 382. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 383. In some embodiments, the amino acid sequence of the linker is at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 384.

[00213] In some embodiments, the $(VHH)_2$ comprises a first VHH comprising a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 with 1, 2, or 3 amino acid

modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and/or a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a second VHH comprising a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and/or a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00214] In some embodiments, the $(VHH)_2$ comprises a first VHH comprising a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition), operably connected (optionally via an amino acid linker) to a second VHH, wherein the second VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00215] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises a CDR1 that

comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition), operably connected (optionally via an amino acid linker) to a second VHH, wherein the second VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00216] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition), operably connected (optionally via an amino acid linker) to a second VHH, wherein the second VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00217] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID

NO: 302 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition), operably connected (optionally via an amino acid linker) to a second VHH, wherein the second VHH comprises a comprising a VH CDR1 that comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00218] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition), operably connected (optionally via an amino acid linker) to a second VHH, wherein the second VHH comprises a comprising a CDR1 that comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00219] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a

CDR2 that comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition), operably connected (optionally via an amino acid linker) to a second VHH, wherein the second VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and a CDR3 that comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00220] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293, 297, 301, 305, 309, or 313; and a second VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293, 297, 301, 305, 309, or 313.

[00221] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293; and a second VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293.

[00222] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 297; and a second VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 297.

[00223] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 301; and a second VHH that comprises an amino acid

sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 301.

[00224] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 305; and a second VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 305.

[00225] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 309; and a second VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 309.

[00226] In some embodiments, the $(VHH)_2$ comprises a first VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 313; and a second VHH that comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 313.

[00227] In some embodiments, the $(VHH)_2$ comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 314. In some embodiments, the $(VHH)_2$ comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 315. In some embodiments, the $(VHH)_2$ comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 316. In some embodiments, the $(VHH)_2$ comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 317. In some embodiments, the $(VHH)_2$ comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 318. In some embodiments, the $(VHH)_2$ comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 319.

[00228] In some embodiments, the anti-SYNGAP1 VHH is one described in Table 3.

[00229] The amino acid sequence of anti-SYNGAP1 VHHs is provided in Table 3 below.

Table 3. Amino Acid Sequence of Anti- SynGAP1 VHHs. The CDRs are defined according to Kabat.

Description		SEQ ID NO	Amino Acid Sequence
FLX00152	CDR1	290	GFSFSNFP
	CDR2	291	INQDGRNT
	CDR3	292	QAIRTTTHFDS
	VHH	293	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSS
FLX00153	CDR1	294	GFTFSNYR
	CDR2	295	IDRSGTYT
	CDR3	296	AADRRLIVDLTPEVYDH
	VHH	297	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSS
FLX00154	CDR1	298	GFIFSSYQ
	CDR2	299	INTGGWNT
	CDR3	300	AADRWMVAKIVGGDLDFDS
	VHH	301	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSS
FLX00155	CDR1	302	GFAFGSYD
	CDR2	303	ITPGGGGT
	CDR3	304	YYCAKNFYGNGG
	VHH	305	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSS
FLX00156	CDR1	306	GFTFGTHA
	CDR2	307	ISSGGGGT
	CDR3	308	NSPSNIANDN
	VHH	309	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSS
FLX00157	CDR1	310	ERTFGHYA
	CDR2	311	ISWKGGTT
	CDR3	312	AARNTMSGSMSSSAYPY
	VHH	313	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSS

[00230] The amino acid sequence of anti-SYNGAP1 VHH_2's is provided in Table 4 below.

Table 4. Amino Acid Sequence of Anti- SynGAP1 VHH_2s

Description	SEQ ID NO:	Amino Acid Sequence
FLX00152	314	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVRQAPGKGRE WVADINQDGRNTYYADSVKGRFTISRDNAKTTVYLQMNNLNPEDTA VYYCQAIRTTTHFDSWGQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS* QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVRQAPGKGRE WVADINQDGRNTYYADSVKGRFTISRDNAKTTVYLQMNNLNPEDTA VYYCQAIRTTTHFDSWGQGTQVTVSS
FLX00153	315	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVRMAPGKGLE WVSDIDRSGTYTYYADSVKGRFAISRDNAKNTVYLQMNSLKPEDTA VYYCAADRRLIVDLTPEVYDHWGQGTQVTVSS*GGGGSGGGGSGGGG SGGGGS*QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVRMA PGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAKNTVYLQMNSL KPEDTAVYYCAADRRLIVDLTPEVYDHWGQGTQVTVSS
FLX00154	316	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVRQAPGKGLE WVADINTGGWNTYYADSVKGRFTISRDNAKNTLYLEMNSLKPEDTA VYYCAADRWMVAKIVGGDLDFDSWGQGTQVTVSS*GGGGSGGGGSGG GGSGGGGS*QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAKNTLYLEMN SLKPEDTAVYYCAADRWMVAKIVGGDLDFDSWGQGTQVTVSS
FLX00155	317	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVRQAPGQGPE WVSAITPGGGGTFYAYYSDSVKGRFAISRDNAKNTLTLQMNSLKPD DTAMYYCAKNFYGNGGRGHGTQVTVSS*GGGGSGGGGSGGGGSGGGG S*QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVRQAPGQGP EWVSAITPGGGGTFYAYYSDSVKGRFAISRDNAKNTLTLQMNSLKP DDTAMYYCAKNFYGNGGRGHGTQVTVSS
FLX00156	318	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVRWAPGKGFE WVSTISSGGGGTRYADSVKGRFTISRDNAKNTVYLQMDNLKPEDTA VYYCNSPSNIANDNWGQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*Q VQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVRWAPGKGFEW VSTISSGGGGTRYADSVKGRFTISRDNAKNTVYLQMDNLKPEDTAV YYCNSPSNIANDNWGQGTQVTVSS
FLX00157	319	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFRQAPGKERE FVATISWKGGTTGYAHSVKGRFTISRDSAKNMVYLQMNSLKPEDTA VYYCAARNTMSGSMSSSAYPYWGQGTQVTVSS*GGGGSGGGGSGGGG SGGGGS*QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFRQA PGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAKNMVYLQMNSL KPEDTAVYYCAARNTMSGSMSSSAYPYWGQGTQVTVSS

5.3.3 Orientation and Linkers

[00231] In some embodiments, the effector domain is N-terminal of the targeting domain in the fusion protein. In some embodiments, the targeting domain is N-terminal of the effector domain in the fusion protein. In some embodiments, the effector domain is operably connected (directly

or indirectly) to the C terminus of the targeting domain. In some embodiments, the effector domain is operably connected (directly or indirectly) to the N terminus of the targeting domain. In some embodiments, the effector domain is directly operably connected to the C terminus of the targeting domain. In some embodiments, the effector domain is directly operably connected to the N terminus of the targeting domain.

[00232] In some embodiments, the effector domain is indirectly operably connected to the C terminus of the targeting domain. In some embodiments, the effector domain is indirectly operably connected to the N terminus of the targeting domain. One or more amino acid sequences comprising e.g., a linker, or encoding one or more polypeptides may be positioned between the effector moiety and the targeting moiety. In some embodiments, the effector domain is indirectly operably connected to the C terminus of the targeting domain through a peptide linker. In some embodiments, the effector domain is indirectly operably connected to the N terminus of the targeting domain through a peptide linker.

[00233] Each component of the fusion protein described herein can be directly linked to the other to indirectly linked to the other via a peptide linker. In some embodiments, the linker is one or any combination of a cleavable linker, a non-cleavable linker, a peptide linker, a flexible linker, a rigid linker, a helical linker, or a non-helical linker. In some embodiments, the linker is a peptide linker. In some embodiments, the linker is a peptide linker that comprises glycine or serine, or both glycine and serine amino acid residues. In some embodiments, the peptide linker comprises from or from about 2-25, 5-25, 10-25, 15-25, 20-25, 2-20, 5-20, 10-20, 15-20, 2-15, 5-15, 10-15, 2-10, or 5-10 amino acids. In some embodiments, the linker is a peptide linker that consists of glycine or serine, or both glycine and serine amino acid residues. In some embodiments, the peptide linker consists of from or from about 2-25, 5-25, 10-25, 15-25, 20-25, 2-20, 5-20, 10-20, 15-20, 2-15, 5-15, 10-15, 2-10, or 5-10 amino acids. In some embodiments, the peptide linker comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acid residues. In some embodiments, the linker is at least 11 amino acids in length. In some embodiments, the linker is at least 15 amino acids in length. In some embodiments, the linker is 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acid residues in length.

[00234] In some embodiments, the linker is a glycine/serine linker, e.g., a peptide linker substantially consisting of the amino acids glycine and serine. In some embodiments, the linker is

a glycine/serine/proline linker, e.g., a peptide linker substantially consisting of the amino acids glycine, serine, and proline.

[00235] In some embodiments, the amino acid sequence of the linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition). In some embodiments, the amino acid sequence of the linker consists of the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00236] In some embodiments, the amino acid sequence of the linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition). In some embodiments, the amino acid sequence of the linker consists of the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00237] The amino acid sequence of exemplary linkers for use in any one or more of the fusion proteins described herein is provided in Table 5 below.

Table 5. Amino Acid Sequence of Exemplary Linkers

Amino Acid Sequence	SEQ ID NO
GGGGSGGGGSGGGGSGGGGSGGGGS	375
GGGGSGGGGSGGGGSGGGGS	376
GGGGSGGGGSGGGGS	377
GGGGSGGGGS	378
GGGGS	379
SGGGGSGGGGSGGGGS	380
SGGGGSGGGGSGGGG	381
SGGGGSGGGG	382
SGGGG	383
GGSGG	384
AHFKISGEKRPSTDPGKKAKNPKKKKKKDP	402
AHRAKKMSKTHA	403
ASPEYVNLPINGNG	404
CTKRPRW	405
DKAKRVSRNKSEKKRR	406
EELRLKEELLKGIYA	407
EEQLRRRKNSRLNNTG	408
EVLKVIRTGKRKKKAWKRMVTKVC	409

HHHHHHHHHHHHQPH	410
HKKKHPDASVNFSEFSK	411
HKRTKKNLS	412
IINGRKLKLKKSRRRSSQTSNNSFTSRRS	413
KAEQERRK	414
KEKRKRREELFIEQKKRK	415
KKGKDEWFSRGKKP	416
KKGPSVQKRKKTNLS	417
KKKTVINDLLHYKKEK	418
KKNGGKGKNKPSAKIKK	419
KKPKWDDFKKKKK	420
KKRKKDNLS	421
KKRRKRRRK	422
KKRRRRARK	423
KKSKRGR	424
KKSRKRGS	425
KKSTALSRELGKIMRRR	426
KKSYQDPEIIAHSRPRK	427
KKTGKNRKLKSKRVKTR	428
KKVSIAGQSGKLWRWKR	429
KKYENVVIKRSPRKRGRPRK	430
KNKKRK	431
KPKKKR	432
KRAMKDDSHGNSTSPKRRK	433
KRANSNLVAAYEKAKKK	434
KRASEDTTSGSPPKKSSAGPKR	435
KRFKRRWMVRKMKTKK	436
KRGLNSSFETSPKKVK	437
KRGNSSIGPNDLSKRKQRKK	438
KRIHSVSLSQSQIDPSKKVKRAK	439
KRKGKLKNKGSKRKK	440
KRRRRRRREKRKR	441
KRSNDRTYSPEEEKQRRA	442
KRTVATNGDASGAHRAKKMSK	443
KRVYNKGEDEQEHLPKGKKR	444
KSGKAPRRRAVSMDNSNK	445
KVNFLDMSLDDIIIYKELE	446
KVQHRIAKKTTRRRR	447
LSPSLSPL	448
MDSLLMNRRKFLYQFKNVRWAKGRRETYLC	449
MPQNEYIELHRKRYGYRLDYHEKKRKKESREAHERSKKAKKMIGLKAKLYHK	450
MVQLRPRASR	451
NNKLLAKRRKGGASPKDDPMDDIK	452
NYKRPMDGTYGPPAKRHEGE	453
PDTKRAKLDSSETTMVKKK	454
PEKRTKI	455
PGGRGKKK	456
PGKMDKGEHRQERRDRPY	457
PKKGDKYDKTD	458

PKKKSRK	459
PKKNKPE	460
PKKRAKV	461
PKPKKLKVE	462
PKRGRGR	463
PKRRLVDDA	464
PKRRRTY	465
PLFKRR	466
PLRKAKR	467
PPAKRKCIF	468
PPARRRRL	469
PPKKKRKV	470
PPNKRMKVKH	471
PPRIYPQLPSAPT	472
PQRSPFPKSSVKR	473
PRPRKVPR	474
PRRRVQRKR	475
PRRVRLK	476
PSRKRPR	477
PSSKKRKV	478
PTKKRVK	479
QRPGPYDRP	480
RGKGGKGLGKGGAKRHRK	481
RKAGKGGGGHKTTKKRSAKDEKVP	482
RKIKLKRAK	483
RKIKRKRAK	484
RKKEAPGPREELRSRGR	485
RKKRKGK	486
RKKRRQRRR	487
RKKSIPLSIKNLKRKHKRKKNKITR	488
RKLVKPKNTKMKTKLRTNPY	489
RKRLILSDKGQLDWKK	490
RKRLKSK	491
RKRRVRDNM	492
RKRSPKDKKEKDLDGAGKRRKT	493
RKRTPRVDGQTGENDMNKRRRK	494
RLPVRRRRRR	495
RLRFRKPKSK	496
RQQRKR	497
RRDLNSSFETSPKKVK	498
RRDRAKLR	499
RRGDGRRR	500
RRGRKRKAEKQ	501
RRKKRR	502
RRKRSKSEDMDSVESKRRR	503
RRKRSR	504
RRPKGKTLQKRKPK	505
RRRGFERFGPDNMGRKRK	506
RRRGKNKVAAQNCRK	507

RRRKRRNLS	508
RRRQKQKGGASRRR	509
RRRREGPRARRRR	510
RRTIRLKLVYDKCDRSCKIQKKNRNKCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKL KAE	511
RRVPQRKEVSRCRKCRK	512
RVGGRRQAVECIEDLLNEPGQPLDLSCKRPRP	513
RVVKLRIAP	514
RVVRRR	515
SKRKTKISRKTR	516
SYVKTVPNRTRTYIKL	517
TGKNEAKKRKIA	518
TLSPASSPSSVSCPVIPASTDESPGSALNI	519

5.3.3.1 Conditional Constructs

[00238] Also described herein are constructs that comprise a targeting domain (e.g., a VHH, $(VHH)_2$) bound to an effector domain (e.g., an effector domain that comprises a catalytic domain of an deubiquitinase, or an effector domain that comprises a deubiquitinase). In some embodiments, the association of the targeting domain and the effector domain is mediated by binding of a first agent (e.g., a small molecule, protein, or peptide) attached to the targeting domain and a second agent (e.g., a small, molecule, protein, or peptide) attached to the effector domain. For example, in one embodiment, the targeting domain may be attached to a first agent that specifically binds to a second agent that is attached to the effector domain. In some embodiments, specific binding of the first agent to the second agent is mediated by addition of a third agent (e.g., a small molecule).

[00239] For example, a conditional construct includes an KBP/FRB-based dimerization switch, e.g., as described in US20170081411 (the entire contents of which are incorporated by reference herein), can be utilized herein. FKBP12 (FKBP or FK506 binding protein) is an abundant cytoplasmic protein that serves as the initial intracellular target for the natural product immunosuppressive drug, rapamycin. Rapamycin binds to FKBP and to the large PI3K homolog FRAP (RAFT, mTOR), thereby acting to dimerize these molecules. In some embodiments, an FKBP/FRAP based switch, also referred to herein as an FKBP/FRB based switch, can utilize a heterodimerization molecule, e.g., rapamycin or a rapamycin analog. FRB is a 93 amino acid portion of FRAP, that is sufficient for binding the FKBP-rapamycin complex (Chen, J., Zheng, X. F., Brown, E. J. & Schreiber, S. L. (1995) Identification of an 11-kDa FKBP12-rapamycin-binding domain within the 289-kDa FKBP12-rapamycin-associated protein and characterization of a

critical serine residue. Proc Natl Acad Sci USA 92: 4947-51), the entire contents of which is incorporated by reference herein. For example, the targeting domain can be attached to FKBP and the effector domain attached to FRB. Thereby, the association of the targeting domain and the effector domain is mediated by rapamycin and only takes place in the presence of rapamycin.

[00240] Exemplary conditional activation systems that can be used here include, but are not limited to those described in US20170081411; Lajoie MJ, et al. Designed protein logic to target cells with precise combinations of surface antigens. Science. 2020 Sep 25;369(6511):1637-1643. doi: 10.1126/science.aba6527. Epub 2020 Aug 20. PMID: 32820060; Farrants H, et al. Chemogenetic Control of Nanobodies. Nat Methods. 2020 Mar;17(3):279-282. doi: 10.1038/s41592-020-0746-7. Epub 2020 Feb 17. PMID: 32066961; and US20170081411, the entire contents of each of which is incorporated by reference herein for all purposes.

5.3.4 Exemplary Fusion Proteins

[00241] Exemplary fusion proteins are described below. Exemplary fusion proteins of the present disclosure include, but are not limited to, those described below. In some embodiments, the fusion protein comprises an effector domain comprising a catalytic domain of a cysteine protease deubiquitinase, or a functional fragment or functional variant thereof; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00242] In some embodiments, the fusion protein comprises an effector domain comprising a catalytic domain of a metalloprotease deubiquitinase, or a functional fragment or functional variant thereof; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, or USP9X, PYDC2, CSTB, or PCBD1.

[00243] In some embodiments, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the deubiquitinase is a ubiquitin-specific protease (USP), a ubiquitin C-terminal hydrolase (UCH), a Machado-Josephin domain protease (MJD), an ovarian tumour protease (OTU), a

MINDY protease, or a ZUFSP protease; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00244] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the deubiquitinase is USP1, USP2, USP3, USP4, USP5, USP6, USP7, USP8, USP9X, USP9Y, USP10, USP11, USP12, USP13, USP14, USP15, USP16, USP17, USP17L2, USP17L3, USP17L4, USP17L5, USP17L7, USP17L8, USP18, USP19, USP20, USP21, USP22, USP23, USP24, USP25, USP26, USP27X, USP28, USP29, USP30, USP31, USP32, USP33, USP34, USP35, USP36, USP37, USP38, USP39, USP40, USP41, USP42, USP43, USP44, USP45, USP46, BAP1, UCHL1, UCHL3, UCHL5, ATXN3 ATXN3L, OTUB1, OTUB2 MINDY1, MINDY2, MINDY3, MINDY4, or ZUP1; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00245] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the deubiquitinase is described in Table 1; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00246] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the catalytic domain is described in Table 1; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00247] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%,

85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00248] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein is CDKL5, ATP7B, STXBP1, SYNGAP1, GRN, JAG1, DEPDC5, TSC2, TSC1, KIF1A, DNM1, SHANK3, DMD, RP1, TTN, DYNC1H1, TRIO, USP9X, PYDC2, CSTB, or PCBD1.

[00249] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 221-238 or 287-289.

[00250] In one embodiment, the fusion protein comprises an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof, wherein the catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286; and a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein, wherein the cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS:

221-238 or 287-289.

[00251] The amino acid sequence of exemplary SYNGAP1 targeting fusion proteins are provided in Table 6 below.

Table 6. Amino acid sequence of exemplary SYNGAP1 targeting enDub fusion proteins

Description	SEQ ID NO:	Amino Acid Sequence
FLX00152 – Cezanne	320	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQ DDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSN EHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLV ALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAAS LGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQ TQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTN GANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVA DTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVL AYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLH FAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSY MNVKWIPLSSDAQAPLAQ
FLX00153 – Cezanne	321	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSSPPSFSEGSGGSRTPEKGFSDREPTRPPR PILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNG GGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLI EQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNC LLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKR RWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPR MHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRR PIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCH RSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEY KLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKL HLLHSYMNVKWIPLSSDAQAPLAQ
FLX00154 – Cezanne	322	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSSPPSFSEGSGGSRTPEKGFSDREPTRP PRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSS NGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERD LIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDG NCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEAL KRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSE PRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVL RRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQ CHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDS EYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEV KLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00155 – Cezanne	323	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD

		NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQR QDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGS NEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSML VALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAA SLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQ QTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGT NGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVV ADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLV LAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPL HFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHS YMNVKWIPLSSDAQAPLAQ
FLX00156 – Cezanne	324	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQD DIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNE HPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVA LEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASL GMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQT QQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNG ANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVAD TMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLA YDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHF AVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYM NVKWIPLSSDAQAPLAQ
FLX00157 – Cezanne	325	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSSPPSFSEGSGGSRTPEKGFSDREPTRPPR PILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNG GGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLI EQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNC LLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKR RWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPR MHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRR PIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCH RSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEY KLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKL HLLHSYMNVKWIPLSSDAQAPLAQ
FLX00152 – GSSSS linker – Cezanne	326	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPRP ILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGG GGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIE QSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCL LHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRR WRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRM HLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRP IVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHR

		SPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYK LLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLH LLHSYMNVKWIPLSSDAQAPLAQ
FLX00153 – GSSSS linker – Cezanne	327	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSSGSSSSPPSFSEGSGGSRTPEKGFSDREP TRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSH VSSNGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFI ERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATT GDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEK EALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLA SSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLA HVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVP ASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPL TDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILS LEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00154 – GSSSS linker – Cezanne	328	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSSGSSSSPPSFSEGSGGSRTPEKGFSDR EPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLAR SHVSSNGGGGSNEHPLEMPICAFQLPDLTVYNEDFRS FIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLA TTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGV EKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIK LASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFV LAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLE VPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVI PLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVI LSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00155 – GSSSS linker – Cezanne	329	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPR PILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNG GGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLI EQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNC LLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKR RWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPR MHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRR PIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCH RSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEY KLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKL HLLHSYMNVKWIPLSSDAQAPLAQ
FLX00156 – GSSSS linker – Cezanne	330	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPI LQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGG GGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQ

		SMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLL HAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRW RWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMH LGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPI VVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRS PLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKL LPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHL LHSYMNVKWIPLSSDAQAPLAQ
FLX00157 – GSSSS linker – Cezanne	331	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSSGSSSSPPSFSEGSGGSRTPEKGFSDREP TRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSH VSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFI ERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATT GDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEK EALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLA SSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLA HVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVP ASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPL TDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILS LEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00152 – (GSSSS)2 linker – Cezanne	332	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDREPT RPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHV SSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIE RDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTG DGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKE ALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLAS SEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAH VLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPA SQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLT DSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSL EVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00153 – (GSSSS)2 linker – Cezanne	333	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSSGSSSSGSSSSPPSFSEGSGGSRTPEKGF SDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVS LARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNED FRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLL PLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALME KGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNE LIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFH VFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYL PLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQ AVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLA SVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00154 – (GSSSS)2	334	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR

linker – Cezanne		QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSSGSSSSGSSSSPPSFSEGSGGSRTPEK GFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSI VSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYN EDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQR LLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYAL MEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEW NELIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEE FHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGI YLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTK EQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVR LASVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00155 – (GSSSS)2 linker – Cezanne	335	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDREP TRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSH VSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFI ERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATT GDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEK EALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLA SSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLA HVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVP ASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPL TDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILS LEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00156 – (GSSSS)2 linker – Cezanne	336	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTR PPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHVS SNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIER DLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGD GNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEA LKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASS EPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHV LRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPAS QCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTD SEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLE VKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00157 – (GSSSS)2 linker – Cezanne	337	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSSGSSSSGSSSSPPSFSEGSGGSRTPEKGF SDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVS LARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNED FRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLL PLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALME KGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNE LIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFH

		VFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYL PLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQ AVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLA SVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00152 – (GSSSS)3 linker – Cezanne	338	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSSGSSSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFS DREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSL ARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDF RSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLP LATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEK GVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNEL IKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHV FVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLP LEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQA VIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLAS VILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00153 – (GSSSS)3 linker – Cezanne	339	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSSGSSSSGSSSSGSSSSPPSFSEGSGGSRT PEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHAS SSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLT VYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPT SQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKAL YALMEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQ KEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYES LEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPF GGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKE NTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSD NVRLASVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLA Q
FLX00154 – (GSSSS)3 linker – Cezanne	340	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSSGSSSSGSSSSGSSSSPPSFSEGSGGS RTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISH ASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPD LTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSVD PTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRK ALYALMEKGVEKEALKRRWRWQQTQQNKESGLVYTEDE WQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVY ESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPI PFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQ KENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDD SDNVRLASVILSLEVKLHLLHSYMNVKWIPLSSDAQAP LAQ
FLX00155 – (GSSSS)3 linker – Cezanne	341	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ

		VTVSSGSSSSGSSSSGSSSSPPSFSEGSGGSRTPEKGF SDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVS LARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNED FRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLL PLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALME KGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNE LIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFH VFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYL PLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQ AVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLA SVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00156 – (GSSSS)3 linker – Cezanne	342	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSSGSSSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSD REPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLA RSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFR SFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPL ATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKG VEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELI KLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVF VLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPL EVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAV IPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASV ILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00157 – (GSSSS)3 linker – Cezanne	343	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSSGSSSSGSSSSGSSSSPPSFSEGSGGSRT PEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHAS SSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLT VYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPT SQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKAL YALMEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQ KEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYES LEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPF GGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKE NTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSD NVRLASVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLA Q
FLX00152 VHH_2 – Cezanne	344	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQP GGSLRLSCAASGFSFSNFPMMWVRQAPGKGREWVADIN QDGRNTYYADSVKGRFTISRDNAKTTVYLQMNNLNPED TAVYYCQAIRTTTHFDSWGQGTQVTVSSPPSFSEGSGG SRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGIS HASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLP DLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSV DPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLR

		KALYALMEKGVEKEALKRRWRWQQTQQNKESGLVYTED EWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPV YESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAP IPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSME QKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKD DSDNVRLASVILSLEVKLHLLHSYMNVKWIPLSSDAQA PLAQ
FLX00153 VHH_2 – Cezanne	345	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QLQLVESG GGLVQPGESLRLSCAASGFTFSNYRMYWVRMAPGKGLE WVSDIDRSGTYTYYADSVKGRFAISRDNAKNTVYLQMN SLKPEDTAVYYCAADRRLIVDLTPEVYDHWGQGTQVTV SSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDD IVQEKRLSRGISHASSSIVSLARSHVSSNGGGGSNEH PLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVAL EQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLG MWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQ QNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGA NCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVADT MLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAY DQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFA VDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMN VKWIPLSSDAQAPLAQ
FLX00154 VHH_2 – Cezanne	346	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVE SGGGLVQPGGSLRLSCAASGFIFSSYQMAWVRQAPGKG LEWVADINTGGWNTYYADSVKGRFTISRDNAKNTLYLE MNSLKPEDTAVYYCAADRWMVAKIVGGDLDFDSWGQGT QVTVSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQ RQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGG SNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSM LVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHA ASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRW QQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLG TNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVV VADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPL VLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLP LHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLH SYMNVKWIPLSSDAQAPLAQ
FLX00155 VHH_2 – Cezanne	347	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQ PGGSLRLSCAASGFAFGSYDMSWVRQAPGQGPEWVSAI TPGGGGTFYAYYSDSVKGRFAISRDNAKNTLTLQMNSL KPDDTAMYYCAKNFYGNGGRGHGTQVTVSSPPSFSEGS GGSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRG

		ISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQ LPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWV SVDPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLM LRKALYALMEKGVEKEALKRRWRWQQTQQNKESGLVYT EDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEE PVYESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAF APIPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVS MEQKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWG KDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPLSSDA QAPLAQ
FLX00156 VHH_2 – Cezanne	348	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQPG GSLRLACAASGFTFGTHAMHWVRWAPGKGFEWVSTISS GGGGTRYADSVKGRFTISRDNAKNTVYLQMDNLKPEDT AVYYCNSPSNIANDNWGQGTQVTVSSPPSFSEGSGGSR TPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHA SSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDL TVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDP TSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKA LYALMEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEW QKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYE SLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIP FGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQK ENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDS DNVRLASVILSLEVKLHLLHSYMNVKWIPLSSDAQAPL AQ
FLX00157 VHH_2 – Cezanne	349	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESG GGLVQAGASLRLSCAASERTFGHYAMGWFRQAPGKERE FVATISWKGGTTGYAHSVKGRFTISRDSAKNMVYLQMN SLKPEDTAVYYCAARNTMSGSMSSSAYPYWGQGTQVTV SSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDD IVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEH PLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVAL EQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLG MWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQ QNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGA NCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVADT MLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAY DQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFA VDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMN VKWIPLSSDAQAPLAQ
FLX00152 VHH_2 – GSSSS linker – Cezanne	350	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQP GGSLRLSCAASGFSFSNFPMMWVRQAPGKGREWVADIN

		QDGRNTYYADSVKGRFTISRDNAKTTVYLQMNNLNPED TAVYYCQAIRTTTHFDSWGQGTQVTVSSGSSSSPPSFS EGSGGSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRL SRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPIC AFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLN WWVSVDPTSQRLLPLATTGDGNCLLHAASLGMWGFHDR DLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKESGL VYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGGVES SEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRDSGG EAFAPIPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSA LVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGW EWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPLS SDAQAPLAQ
FLX00153 VHH_2 – GSSSS linker – Cezanne	351	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QLQLVESG GGLVQPGESLRLSCAASGFTFSNYRMYWVRMAPGKGLE WVSDIDRSGTYTYYADSVKGRFAISRDNAKNTVYLQMN SLKPEDTAVYYCAADRRLIVDLTPEVYDHWGQGTQVTV SSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPIL QRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGG GSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQS MLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLH AASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWR WQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHL GTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIV VVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSP LVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLL PLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLL HSYMNVKWIPLSSDAQAPLAQ
FLX00154 VHH_2 – GSSSS linker – Cezanne	352	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVE SGGGLVQPGGSLRLSCAASGFIFSSYQMAWVRQAPGKG LEWVADINTGGWNTYYADSVKGRFTISRDNAKNTLYLE MNSLKPEDTAVYYCAADRWMVAKIVGGDLDFDSWGQGT QVTVSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPP RPILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSN GGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDL IEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGN CLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALK RRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEP RMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLR RPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQC HRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSE YKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVK LHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00155 VHH_2 – GSSSS linker – Cezanne	353	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD

		NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQ PGGSLRLSCAASGFAFGSYDMSWVRQAPGQGPEWVSAI TPGGGGTFYAYYSDSVKGRFAISRDNAKNTLTLQMNSL KPDDTAMYYCAKNFYGNGGRGHGTQVTVSSGSSSSPPS FSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIVQEK RLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEMP ICAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQAGR LNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMWGFH DRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKES GLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGGV ESSEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRDS GGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAYDQAHF SALVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVDPGK GWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIP LSSDAQAPLAQ
FLX00156 VHH_2 – GSSSS linker – Cezanne	354	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQPG GSLRLACAASGFTFGTHAMHWVRWAPGKGFEWVSTISS GGGGTRYADSVKGRFTISRDNAKNTVYLQMDNLKPEDT AVYYCNSPSNIANDNWGQGTQVTVSSGSSSSPPSFSEG SGGSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSR GISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAF QLPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWW VSVDPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDL MLRKALYALMEKGVEKEALKRRWRWQQTQQNKESGLVY TEDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSE EPVYESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEA FAPIPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALV SMEQKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEW GKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPLSSD AQAPLAQ
FLX00157 VHH_2 – GSSSS linker – Cezanne	355	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESG GGLVQAGASLRLSCAASERTFGHYAMGWFRQAPGKERE FVATISWKGGTTGYAHSVKGRFTISRDSAKNMVYLQMN SLKPEDTAVYYCAARNTMSGSMSSSAYPYWGQGTQVTV SSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPIL QRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGG GSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQS MLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLH AASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWR WQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHL GTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIV VVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSP LVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLL PLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLL

		HSYMNVKWIPLSSDAQAPLAQ
FLX00152 VHH_2 – (GSSSS)2 linker – Cezanne	356	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQP GGSLRLSCAASGFSFSNFPMMWVRQAPGKGREWVADIN QDGRNTYYADSVKGRFTISRDNAKTTVYLQMNNLNPED TAVYYCQAIRTTTHFDSWGQGTQVTVSSGSSSSGSSSS PPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIV QEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPL EMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQ AGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMW GFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQN KESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANC GGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVADTML RDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAYDQ AHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVD PGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVK WIPLSSDAQAPLAQ
FLX00153 VHH_2 – (GSSSS)2 linker – Cezanne	357	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QLQLVESG GGLVQPGESLRLSCAASGFTFSNYRMYWVRMAPGKGLE WVSDIDRSGTYTYYADSVKGRFAISRDNAKNTVYLQMN SLKPEDTAVYYCAADRRLIVDLTPEVYDHWGQGTQVTV SSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRP PRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSS NGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERD LIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDG NCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEAL KRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSE PRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVL RRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQ CHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDS EYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEV KLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00154 VHH_2 – (GSSSS)2 linker – Cezanne	358	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVE SGGGLVQPGGSLRLSCAASGFIFSSYQMAWVRQAPGKG LEWVADINTGGWNTYYADSVKGRFTISRDNAKNTLYLE MNSLKPEDTAVYYCAADRWMVAKIVGGDLDFDSWGQGT QVTVSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDRE PTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARS HVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSF IERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLAT TGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVE KEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKL ASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVL

		AHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEV PASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIP LTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVIL SLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00155 VHH_2 – (GSSSS)2 linker – Cezanne	359	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQ PGGSLRLSCAASGFAFGSYDMSWVRQAPGQGPEWVSAI TPGGGGTFYAYYSDSVKGRFAISRDNAKNTLTLQMNSL KPDDTAMYYCAKNFYGNGGRGHGTQVTVSSGSSSSGSS SSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDD IVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEH PLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVAL EQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLG MWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQ QNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGA NCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVADT MLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAY DQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFA VDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMN VKWIPLSSDAQAPLAQ
FLX00156 VHH_2 – (GSSSS)2 linker – Cezanne	360	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQPG GSLRLACAASGFTFGTHAMHWVRWAPGKGFEWVSTISS GGGGTRYADSVKGRFTISRDNAKNTVYLQMDNLKPEDT AVYYCNSPSNIANDNWGQGTQVTVSSGSSSSGSSSSPP SFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIVQE KRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEM PICAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQAG RLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMWGF HDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKE SGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGG VESSEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRD SGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAYDQAH FSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVDPG KGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWI PLSSDAQAPLAQ
FLX00157 VHH_2 – (GSSSS)2 linker – Cezanne	361	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESG GGLVQAGASLRLSCAASERTFGHYAMGWFRQAPGKERE FVATISWKGGTTGYAHSVKGRFTISRDSAKNMVYLQMN SLKPEDTAVYYCAARNTMSGSMSSSAYPYWGQGTQVTV SSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRP PRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSS NGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERD LIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDG

		NCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEAL KRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSE PRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVL RRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQ CHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDS EYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEV KLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00152 VHH_2 – (GSSSS)3 linker – Cezanne	362	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQP GGSLRLSCAASGFSFSNFPMMWVRQAPGKGREWVADIN QDGRNTYYADSVKGRFTISRDNAKTTVYLQMNNLNPED TAVYYCQAIRTTTHFDSWGQGTQVTVSSGSSSSGSSSS GSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQR QDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGS NEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSML VALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAA SLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQ QTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGT NGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVV ADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLV LAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPL HFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHS YMNVKWIPLSSDAQAPLAQ
FLX00153 VHH_2 – (GSSSS)3linker – Cezanne	363	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QLQLVESG GGLVQPGESLRLSCAASGFTFSNYRMYWVRMAPGKGLE WVSDIDRSGTYTYYADSVKGRFAISRDNAKNTVYLQMN SLKPEDTAVYYCAADRRLIVDLTPEVYDHWGQGTQVTV SSGSSSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDR EPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLAR SHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRS FIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLA TTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGV EKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIK LASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFV LAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLE VPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVI PLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVI LSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00154 VHH_2 – (GSSSS)3linker – Cezanne	364	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVE SGGGLVQPGGSLRLSCAASGFIFSSYQMAWVRQAPGKG LEWVADINTGGWNTYYADSVKGRFTISRDNAKNTLYLE MNSLKPEDTAVYYCAADRWMVAKIVGGDLDFDSWGQGT QVTVSSGSSSSGSSSSGSSSSPPSFSEGSGGSRTPEKG

		FSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIV SLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNE DFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRL LPLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALM EKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWN ELIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEF HVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIY LPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKE QAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRL ASVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FLX00155 VHH_2 – (GSSSS)3 linker – Cezanne	365	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQ PGGSLRLSCAASGFAFGSYDMSWVRQAPGQGPEWVSAI TPGGGGTFYAYYSDSVKGRFAISRDNAKNTLTLQMNSL KPDDTAMYYCAKNFYGNGGRGHGTQVTVSSGSSSSGSS SSGSSSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPIL QRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGG GSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQS MLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLH AASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWR WQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHL GTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIV VVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSP LVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLL PLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLL HSYMNVKWIPLSSDAQAPLAQ
FLX00156 VHH_2 – (GSSSS)3 linker – Cezanne	366	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESGGGLVQPG GSLRLACAASGFTFGTHAMHWVRWAPGKGFEWVSTISS GGGGTRYADSVKGRFTISRDNAKNTVYLQMDNLKPEDT AVYYCNSPSNIANDNWGQGTQVTVSSGSSSSGSSSSGS SSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQD DIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGSNE HPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVA LEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASL GMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQT QQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNG ANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVAD TMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLA YDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHF AVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYM NVKWIPLSSDAQAPLAQ
FLX00157 VHH_2 – (GSSSS)3 linker – Cezanne	367	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSS*GGGGSGGGGSGGGGSGGGGS*QVQLVESG GGLVQAGASLRLSCAASERTFGHYAMGWFRQAPGKERE

		FVATISWKGGTTGYAHSVKGRFTISRDSAKNMVYLQMN SLKPEDTAVYYCAARNTMSGSMSSSAYPYWGQGTQVTV SSGSSSSGSSSSGSSSSPPSFSEGSGGSRTPEKGFSDR EPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLAR SHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRS FIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLA TTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGV EKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIK LASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFV LAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLE VPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVI PLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVI LSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ

[00252] In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 320-367. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 320. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 321. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 322. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 323. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 324. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 325. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the

amino acid sequence of SEQ ID NO: 326. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 327. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 328. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 329. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 330. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 331. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 332. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 333. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 334. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 335. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 336. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 337. In some embodiments, the fusion

protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 338. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 339. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 340. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 341. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 342. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 343. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 344. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 345. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 346. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 347. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 348. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 349. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 350. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 351. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 352. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 353. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 354. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 355. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 356. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 357. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 358. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 359. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 360. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 361. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 362. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 363. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 364. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 365. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 366. In some embodiments, the fusion protein comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 367.

[00253] In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 320-367. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 320. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 321. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,

88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 322. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 323. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 324. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 325. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 326. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 327. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 328. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 329. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 330. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 331. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 332. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or

100% identical to the amino acid sequence of SEQ ID NO: 333. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 334. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 335. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 336. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 337. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 338. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 339. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 340. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 341. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 342. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 343. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 344. In some

embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 345. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 346. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 347. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 348. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 349. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 350. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 351. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 352. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 353. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 354. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 355. In some embodiments, the fusion protein consists of an amino acid sequence at

least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 356. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 357. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 358. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 359. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 360. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 361. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 362. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 363. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 364. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 365. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 366. In some embodiments, the fusion protein consists of an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 367.

5.3.4.1 Additional Exemplary Embodiments

[00254] Additional exemplary embodiments of fusion proteins described herein are provided below, which should not be construed as limiting.

[00255] Embodiment 1. A fusion protein comprising: (a) an effector moiety comprising a functional fragment of a human deubiquitinase that is capable of mediating deubiquitination, wherein the human deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112, and a targeting moiety comprising a VHH, $(VHH)_2$. or scFv that specifically binds to a cytosolic protein.

[00256] Embodiment 2. A fusion protein comprising an effector moiety comprising a functional fragment of a human deubiquitinase that is capable of mediating deubiquitination that comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286, and a targeting moiety comprising a VHH, $(VHH)_2$, or scFv that specifically binds to a cytosolic protein.

[00257] Embodiment 3. A fusion protein comprising an effector moiety comprising a functional fragment of a human deubiquitinase that is capable of mediating deubiquitination that comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286, and a targeting moiety comprising a VHH, $(VHH)_2$, or scFv that specifically binds to a cytosolic protein.

[00258] Embodiment 4. The fusion protein of any one of Embodiments 1-3, wherein the cytosolic protein is cyclin-dependent kinase-like 5 (CDKL5), copper-transporting ATPase 2 (ATP7B), syntaxin-binding protein 1 (STXBP1), Ras/Rap GTPase-activating protein (SYNGAP1), progranulin (GRN), protein jagged-1 (JAG1), GATOR complex protein DEPDC5 (DEPDC5), tuberin (TSC2), hamartin (TSC1), kinesin-like protein KIF1A (KIF1A), dynamin-1 (DNM1), SH3 and multiple ankyrin repeat domains protein 3 (SHANK3), dystrophin (DMD), oxygen-regulated protein 1 (RP1), titin (TTN), cytoplasmic dynein 1 heavy chain 1 (DYNC1H1), TRIO and F-actin-binding protein (TRIO), probable ubiquitin carboxyl-terminal hydrolase FAF-

X (USP9X), Pyrin domain-containing protein 2 (PYDC2), cystatin-B (CSTB), or pterin-4-alpha-carbinolamine dehydratase (PCBD1).

[00259] Embodiment 5. The fusion protein of any one of Embodiments 1-4, wherein said cytosolic protein is SHANK3, SYNGAP1, PYCD2, CSTB, or PCBD1.

[00260] Embodiment 6. The fusion protein of any one of Embodiments 1-5, wherein said cytosolic protein is SHANK3, SYNGAP1, CSTB, or PCBD1.

[00261] Embodiment 7. The fusion protein of any one of Embodiments 1-6, wherein said cytosolic protein is SYNGAP1.

[00262] Embodiment 8. The fusion protein of any one of Embodiments 1-7, wherein said targeting moiety is a VHH or $(VHH)_2$.

[00263] Embodiment 9. The fusion protein of any one of Embodiments 1-8, wherein said targeting moiety comprises a VHH described in Table 3.

[00264] Embodiment 10. The fusion protein of any one of Embodiments 1-9, wherein said targeting moiety comprises a VHH that comprises a CDR1, CDR2, and CDR3 of a VHH that is described in Table 3.

[00265] Embodiment 11. The fusion protein of any one of Embodiments 1-10, wherein said VHH comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and/or a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00266] Embodiment 12. The fusion protein of any one of Embodiments 1-11, wherein said targeting moiety comprises a VHH that comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a VHH that is described in Table 3.

[00267] Embodiment 13. The fusion protein of any one of Embodiments 1-12, wherein said targeting moiety comprises a VHH that comprises an amino acid sequence at least 80%, 81%,

82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313.

[00268] Embodiment 14. The fusion protein of any one of Embodiments 1-13, wherein said targeting moiety comprises a $(VHH)_2$ comprising a first VHH described in Table 3 and a second VHH described in Table 3.

[00269] Embodiment 15. The fusion protein of Embodiment 14, wherein the amino acid sequence of said first VHH is 100% identical to the amino acid sequence of said second VHH.

[00270] Embodiment 16. The fusion protein of any one of Embodiments 14-15, wherein said first $(VHH)_2$ comprises a CDR1, CDR2, and CDR3 of a VHH that is described in Table 3; and said second $(VHH)_2$ comprises a CDR1, CDR2, and CDR3 of a VHH that is described in Table 3.

[00271] Embodiment 17. The fusion protein of any one of Embodiments 14-16, wherein said first $(VHH)_2$ comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and/or a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and said first $(VHH)_2$ comprises a CDR1 that comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); a CDR2 that comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition); and/or a CDR3 that comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 with 1, 2, or 3 amino acid modifications (e.g., a substitution, deletion, or addition).

[00272] Embodiment 18. The fusion protein of any one of Embodiments 14-17, wherein said first $(VHH)_2$ comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence

of a VHH that is described in Table 3; and said second $(VHH)_2$ comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a VHH that is described in Table 3.

[00273] Embodiment 19. The fusion protein of any one of Embodiments 14-18, wherein said first $(VHH)_2$ comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313; and said second $(VHH)_2$ comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313.

[00274] Embodiment 21.The fusion protein of any one of Embodiments 1-19, wherein said effector moiety comprising a functional fragment of a human deubiquitinase that is capable of mediating deubiquitination that comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286, and a targeting moiety; and said targeting moiety comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, 313, or 314-319.

[00275] Embodiment 20. The fusion protein of any one of Embodiments 1-19, comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 320-367.

5.3.5 Methods of Making Fusion Proteins

[00276] Fusion proteins described herein can be made by any conventional technique known in the art, for example, recombinant techniques or chemical synthesis (*e.g.*, solid phase peptide synthesis). In some embodiments, the fusion protein is made through recombinant expression in a cell (e.g., a eukaryotic cell, e.g., a mammalian cell). Briefly, the fusion protein can be made by synthesizing the DNA encoding the fusion protein and cloning the DNA into any suitable expression vector. Numerous cloning vectors are known to those of skill in the art, and the selection of an appropriate cloning vector is a matter of choice. The gene can be placed under the control of

a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator and/or one or more enhancer elements, so that the DNA sequence encoding the fusion protein is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. Heterologous leader sequences can be added to the coding sequence that causes the secretion of the expressed polypeptide from the host organism. Other regulatory sequences may also be desirable which allow for regulation of expression of the protein sequences relative to the growth of the host cell. Such regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

[00277] The expression vector may then be used to transform an appropriate host cell. A number of mammalian cell lines are known in the art and include immortalized cell lines available from the American Type Culture Collection (ATCC), such as, but not limited to, Chinese hamster ovary (CHO) cells, CHO-suspension cells (CHO-S), HeLa cells, HEK293, baby hamster kidney (BHK) cells, monkey kidney cells (COS), VERO, HepG2, MadinDarby bovine kidney (MDBK) cells, NOS, U2OS, A549, HT1080, CAD, P19, NIH3T3, L929, N2a, MCF-7, Y79, SO-Rb50, DUKX-X11, and J558L.

[00278] Depending on the expression system and host selected, the fusion protein is produced by growing host cells transformed by an expression vector described above under conditions whereby the fusion protein is expressed. The fusion protein is then isolated from the host cells and purified. If the expression system secretes the fusion protein into growth media, the fusion protein can be purified directly from the media. If the fusion protein is not secreted, it is isolated from cell lysates. The selection of the appropriate growth conditions and recovery methods are within the skill of the art. Once purified, the amino acid sequences of the fusion proteins can be determined, i.e., by repetitive cycles of Edman degradation, followed by amino acid analysis by HPLC. Other methods of amino acid sequencing are also known in the art. Once purified, the functionality of

the fusion protein can be assessed, *e.g.*, as described herein, *e.g.*, utilizing a bifunctional ELISA.

[00279] As described above, functionality of the fusion protein can be tested by any method known in the art. Each functionality can be measured in a separate assay. For example, binding of the targeting domain to the target protein can be measure using an enzyme linked immunosorbent assay (ELISA). Catalytic activity of the effector domain can be measured using any standard deubiquitinase activity assay known in the art. For example, BioVision Deubiquitinase Activity Assay Kit (Fluorometric) Catalog # K485-100 according to the manufacturer's instructions. The deubiquitinase activity of a fusion protein described herein can be measured for example by using a fluorescent deubiquitinase substrate to detect deubiquitinase activity upon cleavage of the fluorescent substrate. The deubiquitinase activity can also be measured according to the materials and methods set forth in the Examples provided herein.

5.4 Nucleic Acids, Host Cells, Vectors, and Viral Particles

[00280] In one aspect, provided herein are nucleic acid molecules encoding a fusion protein described herein. In some embodiments, the nucleic acid molecule is a DNA molecule. In some embodiments, the nucleic acid molecule is an RNA molecule. In some embodiments, the nucleic acid molecule contains at least one modified nucleic acid (e.g., that increases stability of the nucleic acid molecule), e.g., phosphorothioate, N6-methyladenosine (m6A), N6,2′-O-dimethyladenosine (m6Am), 8-oxo-7,8-dihydroguanosine (8-oxoG), pseudouridine (Ψ), 5-methylcytidine (m5C), and N4-acetylcytidine (ac4C).

[00281] In one aspect, provided herein is a host cell (or population of host cells) comprising a nucleic acid encoding a fusion protein described herein. In some embodiments, the nucleic acid is incorporated into the genome of the host cell. In some embodiments, the nucleic acid is not incorporated into the genome of the host cell. In some embodiments, the nucleic acid is present in the cell episomally. In some embodiments, the host cell is a human cell. In some embodiments, the host cell is a mammalian cell. In some embodiments, the host cell is a mouse, rat, hamster, guinea pig, cat, dog, or human cell. In some embodiments, the host cell is modified in vitro, ex vivo, or in vivo.

[00282] The nucleic acid can be introduced into the host cell by any suitable method known in the art (e.g., as described herein). For example, a viral delivery system (e.g., a retrovirus, an adenovirus, an adeno associated virus, a herpes virus, a lentivirus, a pox virus, a vaccinia virus, a

vesicular stomatitis virus, a polio virus, a Newcastle's Disease virus, an Epstein-Barr virus, an influenza virus, a reoviruses, a myxoma virus, a maraba virus, a rhabdovirus, or a coxsackie virus delivery system) can be utilized to deliver a nucleic acid (e.g., DNA or RNA molecule) encoding the fusion protein for expression with the host cell. In some embodiments, the nucleic acid encoding the fusion protein is present episomally within the host cell. In some embodiments, the nucleic acid encoding the fusion protein is incorporated into the genome of the host cell. In some embodiments, the virus replication competent. In some embodiments, the virus is replication deficient.

[00283] In some embodiments, a nucleic acid (DNA or RNA) is delivered to the host cell using a non-viral vector (e.g., a plasmid) encoding the fusion protein. In some embodiments, the nucleic acid encoding the fusion protein is present episomally within the host cell. In some embodiments, the nucleic acid encoding the fusion protein is incorporated into the genome of the host cell. Exemplary non-viral transfection methods known in the art include, but are not limited to, direct delivery of DNA such as by ex vivo transfection, by injection (e.g., microinjection), electroporation, liposome mediated transfection, receptor-mediated transfection, microprojectile bombardment, by agitation with silicon carbide fibers Through the application of techniques such as these cells may be stably or transiently transfected with a nucleic acid encoding a fusion protein described herein to express the encoded fusion protein.

[00284] In one aspect, provided herein are vectors comprising a nucleic acid encoding a fusion protein described herein (e.g., a nucleic acid described herein). In some embodiments, the vector is a viral vector. Exemplary viral vectors include, but are not limited to, retroviral vectors, adenoviral vectors, adeno associated viral vectors, herpes viral vectors, lentiviral vectors, pox viral vectors, vaccinia viral vectors, vesicular stomatitis viral vectors, polio viral vectors, Newcastle's Disease viral vectors, Epstein-Barr viral vectors, influenza viral vectors, reovirus vectors, myxoma viral vectors, maraba viral vectors, rhabdoviral vectors, and coxsackie viral vectors. In some embodiments, the vector is a non-viral vector. In some embodiments, the non-viral vector is a plasmid.

[00285] In one aspect, provided herein is a viral particle (or population of viral particles) that comprise a nucleic acid encoding a fusion protein described herein (e.g., a nucleic acid described herein). In some embodiments, the viral particle is an RNA virus. In some embodiments, the viral particle is a DNA virus. In some embodiments, the viral particle comprises a double stranded

genome. In some embodiments, the viral particle comprises a single stranded genome. Exemplary viral particles include, but are not limited to, a retrovirus, an adenovirus, an adeno associated virus, a herpes virus, a lentivirus, a pox virus, a vaccinia virus, a vesicular stomatitis virus, a polio virus, a Newcastle's Disease virus, an Epstein-Barr virus, an influenza virus, a reoviruses, a myxoma virus, a maraba virus, a rhabdovirus, or a coxsackie.

5.5 Pharmaceutical Compositions

[00286] In one aspect, provided herein are pharmaceutical compositions comprising 1) a fusion protein described herein, a nucleic acid encoding a fusion protein described herein, a vector comprising a nucleic acid encoding a fusion protein described herein, or a viral particle comprising a nucleic acid encoding a fusion protein described herein; and 2) at least one pharmaceutically acceptable carrier, excipient, stabilizer buffer, diluent, surfactant, preservative and/or adjuvant, etc (see, e.g., Remington's Pharmaceutical Sciences (1990) Mack Publishing Co., Easton, PA). A person of ordinary skill in the art can select suitable excipient for inclusion in the pharmaceutical composition. For example, the formulation of the pharmaceutical composition may differ based on the route of administration (e.g., intravenous, subcutaneous, etc.), and/or the active molecule contained within the pharmaceutical composition (e.g., a viral particle, a non-viral vector, a nucleic acid not contained within a vector).

[00287] Acceptable carriers, excipients, or stabilizers are preferably nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, or other organic acids; antioxidants including ascorbic acid or methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol;or m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, or other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[00288] In one embodiment, the present disclosure provides a pharmaceutical composition comprising a fusion protein described herein for use as a medicament. In another embodiment, the disclosure provides a pharmaceutical composition for use in a method for the treatment of cancer. In some embodiments, pharmaceutical compositions comprise a fusion protein disclosed herein, and optionally one or more additional prophylactic or therapeutic agents, in a pharmaceutically acceptable carrier.

[00289] A pharmaceutical composition may be formulated for any route of administration to a subject. Specific examples of routes of administration include parenteral administration (*e.g.*, intravenous, subcutaneous, intramuscular). In some embodiments, the pharmaceutical composition is formulated for intravenous administration. In some embodiments, the pharmaceutical composition is formulated for subcutaneous administration. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions. The injectables can contain one or more excipients. Exemplary excipients include, for example, water, saline, dextrose, glycerol or ethanol. In addition, if desired, the pharmaceutical compositions to be administered can also contain minor amounts of non-toxic auxiliary substances such as wetting or emulsifying agents, pH buffering agents, stabilizers, solubility enhancers, or other such agents, such as for example, sodium acetate, sorbitan monolaurate, triethanolamine oleate or cyclodextrins.

[00290] In some embodiments, the pharmaceutical composition is formulated for intravenous administration. Suitable carriers for intravenous administration include physiological saline or phosphate buffered saline (PBS), or solutions containing thickening or solubilizing agents, such as glucose, polyethylene glycol, or polypropylene glycol or mixtures thereof.

[00291] The compositions to be used for *in vivo* administration can be sterile. This is readily accomplished by filtration through, *e.g.,* sterile filtration membranes.

[00292] Pharmaceutically acceptable carriers used in the parenteral preparations described herein include for example, aqueous vehicles, nonaqueous vehicles, antimicrobial agents, isotonic agents, buffers, antioxidants, local anesthetics, suspending and dispersing agents, emulsifying agents, sequestering or chelating agents or other pharmaceutically acceptable substances. Examples of aqueous vehicles, which can be incorporated in one or more of the formulations described herein, include sodium chloride injection, Ringer's injection, isotonic dextrose injection, sterile water injection, dextrose or lactated Ringer's injection. Nonaqueous parenteral vehicles,

which can be incorporated in one or more of the formulations described herein, include fixed oils of vegetable origin, cottonseed oil, corn oil, sesame oil or peanut oil. Antimicrobial agents in bacteriostatic or fungistatic concentrations can be added to the parenteral preparations described herein and packaged in multiple-dose containers, which include phenols or cresols, mercurials, benzyl alcohol, chlorobutanol, methyl and propyl p-hydroxybenzoic acid esters, thimerosal, benzalkonium chloride or benzethonium chloride. Isotonic agents, which can be incorporated in one or more of the formulations described herein, include sodium chloride or dextrose. Buffers, which can be incorporated in one or more of the formulations described herein, include phosphate or citrate. Antioxidants, which can be incorporated in one or more of the formulations described herein, include sodium bisulfate. Local anesthetics, which can be incorporated in one or more of the formulations described herein, include procaine hydrochloride. Suspending and dispersing agents, which can be incorporated in one or more of the formulations described herein, include sodium carboxymethylcelluose, hydroxypropyl methylcellulose or polyvinylpyrrolidone. Emulsifying agents, which can be incorporated in one or more of the formulations described herein, include Polysorbate 80 (TWEEN® 80). A sequestering or chelating agent of metal ions, which can be incorporated in one or more of the formulations described herein, is EDTA. Pharmaceutical carriers, which can be incorporated in one or more of the formulations described herein, also include ethyl alcohol, polyethylene glycol or propylene glycol for water miscible vehicles; orsodium hydroxide, hydrochloric acid, citric acid or lactic acid for pH adjustment.

[00293] The precise dose to be employed in a pharmaceutical composition will also depend on the route of administration, and the seriousness of the condition caused by it, and should be decided according to the judgment of the practitioner and each subject's circumstances. For example, effective doses may also vary depending upon means of administration, target site, physiological state of the subject (including age, body weight, and health), other medications administered, or whether therapy is prophylactic or therapeutic. Therapeutic dosages are preferably titrated to optimize safety and efficacy.

5.6 Methods of Therapeutic Use

[00294] In one aspect, provided herein are methods of treating a disease in a subject by administering to the subject having the disease a fusion protein described herein, a nucleic acid encoding a fusion protein described herein, a vector comprising a nucleic acid encoding a fusion

protein described herein, or a viral particle comprising a nucleic acid encoding a fusion protein described herein.

[00295] The fusion protein can be delivered to host cells via any method known in the art. For example, a viral delivery system (e.g., a retrovirus, an adenovirus, an adeno associated virus, a herpes virus, a lentivirus, a pox virus, a vaccinia virus, a vesicular stomatitis virus, a polio virus, a Newcastle's Disease virus, an Epstein-Barr virus, an influenza virus, a reoviruses, a myxoma virus, a maraba virus, a rhabdovirus, an enadenotucirev or a coxsackie) can be utilized to deliver a nucleic acid (e.g., DNA or RNA molecule) encoding the fusion protein for expression within a population of cells of a subject. In some embodiments, the nucleic acid encoding the fusion protein is present episomally within the population of cells of the subject. In some embodiments, the nucleic acid encoding the fusion protein is incorporated into the genome of the population of cells of the subject. In some embodiments, the virus is replication competent. In some embodiments, the virus is replication deficient.

[00296] In some embodiments, the fusion protein is administered to the subject. In some embodiments, a nucleic acid (DNA or RNA) is administered to the subject. In some embodiments, the nucleic acid (DNA or RNA) is complexed within a carrier (e.g., a nanoparticle, a liposome, a microsphere). In some embodiments, a nucleic acid (DNA or RNA) within a non-viral vector (e.g., a plasmid) encoding the fusion protein is administered to the subject.

5.6.1 Administration

[00297] The fusion protein can be delivered to host cells via any method known in the art. For example, a viral delivery system (e.g., a retrovirus, an adenovirus, an adeno associated virus, a herpes virus, a lentivirus, a pox virus, a vaccinia virus, a vesicular stomatitis virus, a polio virus, a Newcastle's Disease virus, an Epstein-Barr virus, an influenza virus, a reoviruses, a myxoma virus, a maraba virus, a rhabdovirus, an enadenotucirev or a coxsackie) can be utilized to deliver a nucleic acid (e.g., DNA or RNA molecule) encoding the fusion protein for expression within a population of cells of a subject. In some embodiments, the nucleic acid encoding the fusion protein is present episomally within the population of cells of the subject. In some embodiments, the nucleic acid encoding the fusion protein is incorporated into the genome of the population of cells of the subject. In some embodiments, the virus is replication competent. In some embodiments, the virus is replication deficient.

[00298] In some embodiments, the fusion protein is administered to the subject. In some embodiments, a nucleic acid (DNA or RNA) is administered to the subject. In some embodiments, the nucleic acid (DNA or RNA) is complexed within a carrier (e.g., a nanoparticle, a liposome, a microsphere). In some embodiments, a nucleic acid (DNA or RNA) within a non-viral vector (e.g., a plasmid) encoding the fusion protein is administered to the subject.

[00299] In some embodiment, the fusion protein is administered parenterally. In some embodiments, the fusion protein is administered via intravenous, intramuscular, intraarterial, intrathecal, intralymphatic, intralesional, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural or intrasternal injection or infusion. In some embodiments, the fusion protein is intravenously administered. In some embodiments, the fusion protein is subcutaneously administered. In some embodiments, the fusion protein is administered via a non-parenteral route, or orally. Other non-parenteral routes include a topical, epidermal or mucosal route of administration, for example, intranasally, vaginally, rectally, sublingually or topically. Administering can also be performed, for example, once, a plurality of times, and/or over one or more extended periods.

[00300] In some embodiments, the methods disclosed herein are used in place of standard of care therapies. In certain embodiments, a standard of care therapy is used in combination with any method disclosed herein. In some embodiments, the methods disclosed herein are used after standard of care therapy has failed. In some embodiments, the fusion protein is co-administered, administered prior to, or administered after, an additional therapeutic agent. In some embodiments, the disease is a genetic disease.

5.6.2 Exemplary Genetic Diseases

[00301] In some embodiments, the disease is associated with decreased expression of a functional target cytosolic protein. In some embodiments, the disease is associated with decreased stability of a functional target cytosolic protein. In some embodiments, the disease is associated with increased ubiquitination of a target cytosolic protein. In some embodiments, the disease is associated with increased ubiquitination and degradation of a target cytosolic protein. In some embodiments, the disease is a haploinsufficiency disease.

[00302] In some embodiments, the disease is a genetic disease. In some embodiments, the

genetic disease is associated with decreased expression of a functional target cytosolic protein. In some embodiments, the genetic disease is associated with decreased stability of a functional target cytosolic protein. In some embodiments, the genetic disease is associated with increased ubiquitination of a target cytosolic protein. In some embodiments, the genetic disease is associated with increased ubiquitination and degradation of a target cytosolic protein. In some embodiments, the genetic disease is a haploinsufficiency disease.

[00303] In some embodiments, the disease is an epileptic encephalopathy. In some embodiments, the epileptic encephalopathy is an early infantile epileptic encephalopathy. In some embodiments, the early infantile epileptic encephalopathy is early infantile epileptic encephalopathy type 4, or early infantile epileptic encephalopathy type 4.

[00304] In some embodiments, the disease is SYNGAP1 encephalopathy, CDKL5 deficiency disorder, STXBP1 encephalopathy early, early infantile epileptic encephalopathy type 2, Wilson disease, early infantile epileptic encephalopathy type 4, Mental retardation, autosomal dominant 5, aphasia, primary progressive & FTD (frontotemporal degeneration), alagille syndrome 1, Epilepsy, familial focal, with variable foci 1, Tuberous sclerosis-2, Tuberous sclerosis-1, KIF1A-associated neurological disorder, encephalopathy, Phelan-McDermid syndrome, Becker Muscular Dystrophy, RP1, retinitis pigmentosa 1, dilated cardiomyopathy 1G, DYNC1H1 Syndrome, TRIO-Related intellectual disability (ID), or USP9X development disorder.

[00305] In some embodiments, the target cytosolic protein is SYNGAP1, and the disease is SYNGAP1 encephalopathy. In some embodiments, the target cytosolic protein is SYNGAP1, and the disease is Mental retardation, autosomal dominant 5. In some embodiments, the target cytosolic protein is CDKL5, and the disease is CDKL5 deficiency disorder. In some embodiments, the target cytosolic protein is CDKL5, and the disease is an early infantile epileptic encephalopathy. In some embodiments, the target cytosolic protein is CDKL5, and the disease is early infantile epileptic encephalopathy type 2. In some embodiments, the target cytosolic protein is ATP7B, and the disease is Wilson disease. In some embodiments, the target cytosolic protein is STXBP1, and the disease is STXBP1 encephalopathy. In some embodiments, the target cytosolic protein is STXBP1, and the disease is an early infantile epileptic encephalopathy. In some embodiments, the target cytosolic protein is STXBP1, and the disease is early infantile epileptic encephalopathy type 4. In some embodiments, the target cytosolic protein is GRN, and the disease is aphasia, primary progressive & FTD (frontotemporal degeneration). In some embodiments, the target cytosolic

protein is JAG1, and the disease is alagille syndrome 1. In some embodiments, the target cytosolic protein is DEPDC5, and the disease is epilepsy (e.g., familial focal, with variable foci 1). In some embodiments, the target cytosolic protein is TSC2, and the disease is tuberous sclerosis. In some embodiments, the target cytosolic protein is TSC2, and the disease is tuberous sclerosis type 2. In some embodiments, the target cytosolic protein is TSC2, and the disease is tuberous sclerosis type 1. In some embodiments, the target cytosolic protein is TSC1, and the disease is tuberous sclerosis. In some embodiments, the target cytosolic protein is TSC1, and the disease is tuberous sclerosis type 1. In some embodiments, the target cytosolic protein is TSC1, and the disease is tuberous sclerosis type 2. In some embodiments, the target cytosolic protein is KIF1A, and the disease is KIF1A-associated neurological disorder. In some embodiments, the target cytosolic protein is DNM1, and the disease is a DNM1 encephalopathy. In some embodiments, the target cytosolic protein is DNM1, and the disease is encephalopathy. In some embodiments, the target cytosolic protein is SHANK3, and the disease is Phelan-McDermid syndrome. In some embodiments, the target cytosolic protein is DMD, and the disease is Becker Muscular Dystrophy. In some embodiments, the target cytosolic protein is RP1, and the disease is retinitis pigmentosa 1. In some embodiments, the target cytosolic protein is TTN, and the disease is dilated cardiomyopathy 1G. In some embodiments, the target cytosolic protein is DYNC1H1, and the disease is DYNC1H1 Syndrome. In some embodiments, the target cytosolic protein is TRIO, and the disease is TRIO-Related intellectual disability (ID). In some embodiments, the target cytosolic protein is USP9X, and the disease is USP9X development disorder. In some embodiments, the target cytosolic protein is CSTB, and the disease is epilepsy, progressive myoclonic 1 (EPM1). In some embodiments, the target cytosolic protein is PCBD1, and the disease is hyperphenylalaninemia, BH4-deficient, D (HPABH4D).

5.7 Kits

[00306] In one aspect, provided herein are kits comprising a fusion protein described herein, a nucleic acid encoding a fusion protein described herein, a vector comprising a nucleic acid encoding a fusion protein described herein, or a viral particle comprising a nucleic acid encoding a fusion protein described herein, for therapeutic uses. Kits typically include a label indicating the intended use of the contents of the kit and instructions for use. The term label includes any writing, or recorded material supplied on or with the kit, or which otherwise accompanies the kit.

Accordingly, this disclosure provides a kit for treating a subject afflicted with a disease (*e.g.*, a genetic disease), the kit comprising: (a) a dosage of a fusion protein, a nucleic acid encoding a fusion protein described herein, a vector comprising a nucleic acid encoding a fusion protein described herein, or a viral particle comprising a nucleic acid encoding a fusion described herein; and (b) instructions for using the fusion protein in any of the therapy methods disclosed herein.

6. EXAMPLES

[00307] The present invention is further illustrated by the following examples which should not be construed as further limiting.

6.1 Example 1. Generation of Targeted Engineered Deubiquitinases

[00308] This example provides general experimental methods of using fluorescent tagged target proteins together with fluorophore tagged engineered deubiquitinases (enDUBs) to demonstrate up-regulation of expression in the context of an enDUB. For illustrative purposes the constructs disclosed below will be synthesized in a suitable vector for mammalian expression. Generally, the target protein will be expressed with a C-terminal YFP followed by a P2A cleavage signal and an mCherry protein as a second reporter (Target protein – YFP – P2A – mCherry). This construct will be co-transfected in the presence of a trifunctional fusion protein comprising of a CFP protein followed by a P2A signal and a nanobody specifically binding to YPF followed by the engineered DUB (CFP – P2A - Anti-YFPnanobody – enDUB). In applications for drug treatment the targeting nanobodies (or other specific binders) will be directed to the wild type (or disease-causing mutant) protein in the cell to be upregulated while the enDUB is fused to a binding protein directed to the target protein. Target protein binding moieties could be any antibody or antibody fragments, nanobodies, or any other non-antibody scaffold such as fibronectins, anticalins, ankyrin repeats or natural binding proteins interacting specifically with the target protein to be upregulated. The amino acid sequence of the components of the test fusion proteins is provided in Table 7 below.

Table 7. Amino Acid Sequence of Components of test fusion proteins

Description	SEQ ID NO	Amino Acid Sequence
Target Proteins		
LCK kinase	239	MGCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRD PLVTYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILE QSGEWWKAQSLTTGQEGFIPFNFVAKANSLEPEPWFFKNLSRKDAE

		RQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIR NLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQ KPWWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLK QGSMSPDAFLAEANLMKQLQHQRLVRLYAVVTQEPIYIITEYMENG SLVDFLKTPSGIKLTINKLLDMAAQIAEGMAFIEERNYIHRDLRAA NILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEAINY GTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMV RPDNCPEELYQLMRLCWKERPEDRPTFDYLRSVLEDFFTATEGQYQ PQP
YES1 kinase	240	MGCIKSKENKSPAIKYRPENTPEPVSTSVSHYGAEPTTVSPCPSSS AKGTAVNFSSLSMTPFGGSSGVTPFGGASSSFSVVPSSYPAGLTGG VTIFVALYDYEARTTEDLSFKKGERFQIINNTEGDWWEARSIATGK NGYIPSNYVAPADSIQAEEWYFGKMGRKDAERLLLNPGNQRGIFLV RESETTKGAYSLSIRDWDEIRGDNVKHYKIRKLDNGGYYITTRAQF DTLQKLVKHYTEHADGLCHKLTTVCPTVKPQTQGLAKDAWEIPRES LRLEVKLGQGCFGEVWMGTWNGTTKVAIKTLKPGTMMPEAFLQEAQ IMKKLRHDKLVPLYAVVSEEPIYIVTEFMSKGSLLDFLKEGDGKYL KLPQLVDMAAQIADGMAYIERMNYIHRDLRAANILVGENLVCKIAD FGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGI LQTELVTKGRVPYPGMVNREVLEQVERGYRMPCPQGCPESLHELMN LCWKKDPDERPTFEYIQSFLEDYFTATEPQYQPGENL
Aurora kinase A	241	MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQR VLCPSNSSQRVPLQAQKLVSSHKPVQNQKQKQLQATSVPHPVSRPL NNTQKSKQPLPSAPENNPEEELASKQKNEESKKRQWALEDFEIGRP LGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRREVEI QSHLRHPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDE QRTATYITELANALSYCHSKRVIHRDIKPENLLLGSAGELKIADFG WSVHAPSSRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEF LVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRLLKHNP SQRPMLREVLEHPWITANSSKPSNCQNKESASKQS
Fluorescent Proteins		
YFP	242	VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKF ICTTGKLPVPWPTLVTTFGYGLQCFARYPDHMKQHDFFKSAMPEGY VQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILG HKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQ NTPIGDGPVLLPDNHYLSYQSALSKDPNEKRDHMVLLEFVTAAGIT LGMDELYK
mCherry	243	MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGT QTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSF PEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDG PVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKT TYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGG MDELYK
CFP	244	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYK

A2 Peptides		
P2A	245	GSGATNFSLLKQAGDVEENPGP
T2A	246	GSGEGRGSLLTCGDVEENPGP
E2A	247	GSGQCTNYALLKLAGDVESNPGP
Target Binders		
YFP targeting nanobody	248	QVQLVESGGALVQPGGSLRLSCAASGFPVNRYSMRWYRQAPGKERE WVAGMSSAGDRSSYEDSVKGRFTISRDDARNTVYLQMNSLKPEDTA VYYCNVNVGFEYWGQGTQVTVSS
LCK binder (monobody)	249	GSVSSVPTKLEVVAATPTSLLISWDAPAVTVDFYHITYGETGGNSP VQEFTVPGSKSTATISGLKPGVDYTITVYAYVSYPEYYFPSPISIN YRT
YES1 Kinase binder (monobody)	250	GSVSSVPTKLEVVAATPTSLLISWDAPAVTVDYYFITYGETGGNSP VQEFTVPGSKSTATISGLKPGVDYTITVYAWYYYDDEYYMNESSPI SINYRT
Aurora kinase A binder (monobody)	251	GSVSSVPTKLEVVAATPTSLLISWDAPAVTVVHYVITYGETGGNSP VQEFTVPGSKSTATISGLKPGVDYTITVYAIDFYWGSYSPISINYR T
EnDUBS		
Cezanne	252	PPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRG ISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYN EDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTG DGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRW QQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGG VESSEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAP IPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQ AVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEV KLHLLHSYMNVKWIPLSSDAQAPLAQ
OTUD1	253	DEKLALYLAEVEKQDKYLRQRNKYRFHIIPDGNCLYRAVSKTVYGD QSLHRELREQTVHYIADHLDHFSPLIEGDVGEFIIAAAQDGAWAGY PELLAMGQMLNVNIHLTTGGRLESPTVSTMIHYLGPEDSLRPSIWL SWLSNGHYDAVFDHSYPNPEYDNWCKQTQVQRKRDEELAKSMAISL SKMYIEQNACS
TRABID	254	LEVDFKKLKQIKNRMKKTDWLFLNACVGVVEGDLAAIEAYKSSGGD IARQLTADEVRLLNRPSAFDVGYTLVHLAIRFQRQDMLAILLTEVS QQAAKCIPAMVCPELTEQIRREIAASLHQRKGDFACYFLTDLVTFT LPADIEDLPPTVQEKLFDEVLDRDVQKELEEESPIINWSLELATRL DSRLYALWNRTAGDCLLDSVLQATWGIYDKDSVLRKALHDSLHDCS HWFYTRWKDWESWYSQSFGLHFSLREEQWQEDWAFILSLASQPGAS LEQTHIFVLAHILRRPIIVYGVKYYKSFRGETLGYTRFQGVYLPLL WEQSFCWKSPIALGYTRGHFSALVAMENDGYGNRGAGANLNTDDDV TITFLPLVDSERKLLHVHFLSAQELGNEEQQEKLLREWLDCCVTEG GVLVAMQKSSRRRNHPLVTQMVEKWLDRYRQIRPCTSLS
USP21	255	SDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRDFCL RRDFRQEVPGGGRAQELTEAFADVIGALWHPDSCEAVNPTRFRAVF QKYVPSFSGYSQQDAQEFLKLLMERLHLEINRRGRRAPPILANGPV

		PSPPRRGGALLEEPELSDDDRANLMWKRYLEREDSKIVDLFVGQLK SCLKCQACGYRSTTFEVFCDLSLPIPKKGFAGGKVSLRDCFNLFTK EEELESENAPVCDRCRQKTRSTKKLTVQRFPRILVLHLNRFSASRG SIKKSSVGVDFPLQRLSLGDFASDKAGSPVYQLYALCNHSGSVHYG HYTALCRCQTGWHVYNDSRVSPVSENQVASSEGYVLFYQLMQEPPR CL
OTUD4	256	ATPMDAYLRKLGLYRKLVAKDGSCLFRAVAEQVLHSQSRHVEVRMA CIHYLRENREKFEAFIEGSFEEYLKRLENPQEWVGQVEISALSLMY RKDFIIYREPNVSPSQVTENNFPEKVLLCFSNGNHYDIVYPIKYKE SSAMCQSLLYELLYEKVFKTDVSKIVMELDTLEVADE
Human USP3 (full length) nuclear located	257	MECPHLSSSVCIAPDSAKFPNGSPSSWCCSVCRSNKSPWVCLTCSS VHCGRYVNGHAKKHYEDAQVPLTNHKKSEKQDKVQHTVCMDCSSYS TYCYRCDDFVVNDTKLGLVQKVREHLQNLENSAFTADRHKKRKLLE NSTLNSKLLKVNGSTTAICATGLRNLGNTCFMNAILQSLSNIEQFC CYFKELPAVELRNGKTAGRRTYHTRSQGDNNVSLVEEFRKTLCALW QGSQTAFSPESLFYVVWKIMPNFRGYQQQDAHEFMRYLLDHLHLEL QGGFNGVSRSAILQENSTLSASNKCCINGASTVVTAIFGGILQNEV NCLICGTESRKFDPFLDLSLDIPSQFRSKRSKNQENGPVCSLRDCL RSFTDLEELDETELYMCHKCKKKQKSTKKFWIQKLPKVLCLHLKRF HWTAYLRNKVDTYVEFPLRGLDMKCYLLEPENSGPESCLYDLAAVV VHHGSGVGSGHYTAYATHEGRWFHFNDSTVTLTDEETVVKAKAYIL FYVEHQAKAGSDKL

[00309] The amino acid sequence of the test fusion proteins is provided in Table 8 below.

Table 8. Amino acid sequence of exemplary test fusion proteins

Description	SEQ ID NO	Amino Acid Sequence
LCK Kinase Target – YFP-P2A – mCherrry	258	MGCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRD PLVTYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILE QSGEWWKAQSLTTGQEGFIPFNFVAKANSLEPEPWFFKNLSRKDAE RQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIR NLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPQ KPWWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLK QGSMSPDAFLAEANLMKQLQHQRLVRLYAVVTQEPIYIITEYMENG SLVDFLKTPSGIKLTINKLLDMAAQIAEGMAFIEERNYIHRDLRAA NILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEAINY GTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMV RPDNCPEELYQLMRLCWKERPEDRPTFDYLRSVLEDFFTATEGQYQ PQPVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT LKFICTTGKLPVPWPTLVTTFGYGLQCFARYPDHMKQHDFFKSAMP EGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGN ILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADH YQQNTPIGDGPVLLPDNHYLSYQSALSKDPNEKRDHMVLLEFVTAA GITLGMDELYKGSGATNFSLLKQAGDVEENPGPMVSKGEEDNMAII KEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPL PFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFE DGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEAS SERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

YES1 Kinase Target – YFP-P2A – mCherrry	259	MGCIKSKENKSPAIKYRPENTPEPVSTSVSHYGAEPTTVSPCPSSS AKGTAVNFSSLSMTPFGGSSGVTPFGGASSSFSVVPSSYPAGLTGG VTIFVALYDYEARTTEDLSFKKGERFQIINNTEGDWWEARSIATGK NGYIPSNYVAPADSIQAEEWYFGKMGRKDAERLLLNPGNQRGIFLV RESETTKGAYSLSIRDWDEIRGDNVKHYKIRKLDNGGYYITTRAQF DTLQKLVKHYTEHADGLCHKLTTVCPTVKPQTQGLAKDAWEIPRES LRLEVKLGQGCFGEVWMGTWNGTTKVAIKTLKPGTMMPEAFLQEAQ IMKKLRHDKLVPLYAVVSEEPIYIVTEFMSKGSLLDFLKEGDGKYL KLPQLVDMAAQIADGMAYIERMNYIHRDLRAANILVGENLVCKIAD FGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGI LQTELVTKGRVPYPGMVNREVLEQVERGYRMPCPQGCPESLHELMN LCWKKDPDERPTFEYIQSFLEDYFTATEPQYQPGENLVSKGEELFT GVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPV PWPTLVTTFGYGLQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFK DDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNS HNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPV LLPDNHYLSYQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKG SGATNFSLLKQAGDVEENPGPMVSKGEEDNMAIIKEFMRFKVHMEG SVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFM YGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSS LQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALK GEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSH NEDYTIVEQYERAEGRHSTGGMDELYK
Aurora Kinase A Target – YFP-P2A – mCherrry	260	MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQR VLCPSNSSQRVPLQAQKLVSSHKPVQNQKQKQLQATSVPHPVSRPL NNTQKSKQPLPSAPENNPEEELASKQKNEESKKRQWALEDFEIGRP LGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRREVEI QSHLRHPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDE QRTATYITELANALSYCHSKRVIHRDIKPENLLLGSAGELKIADFG WSVHAPSSRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEF LVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRLLKHNP SQRPMLREVLEHPWITANSSKPSNCQNKESASKQSVSKGEELFTGV VPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPW PTLVTTFGYGLQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDD GNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHN VYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL PDNHYLSYQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKGSG ATNFSLLKQAGDVEENPGPMVSKGEEDNMAIIKEFMRFKVHMEGSV NGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYG SKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQ DGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGE IKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNE DYTIVEQYERAEGRHSTGGMDELYK
CFP- P2A-Cezanne enDUB	261	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPPPSFSEGSGGSRTPE KGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSH VSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQS

		MLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMWG FHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKESGLVYTE DEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEF HVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPAS QCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPL HFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIP LSSDAQAPLAQ
CFP- P2A-OTUD1 enDUB	262	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPDEKLALYLAEVEKQD KYLRQRNKYRFHIIPDGNCLYRAVSKTVYGDQSLHRELREQTVHYI ADHLDHFSPLIEGDVGEFIIAAAQDGAWAGYPELLAMGQMLNVNIH LTTGGRLESPTVSTMIHYLGPEDSLRPSIWLSWLSNGHYDAVFDHS YPNPEYDNWCKQTQVQRKRDEELAKSMAISLSKMYIEQNACS
CFP- P2A-TRABID enDUB	263	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPLEVDFKKLKQIKNRM KKTDWLFLNACVGVVEGDLAAIEAYKSSGGDIARQLTADEVRLLNR PSAFDVGYTLVHLAIRFQRQDMLAILLTEVSQQAAKCIPAMVCPEL TEQIRREIAASLHQRKGDFACYFLTDLVTFTLPADIEDLPPTVQEK LFDEVLDRDVQKELEEESPIINWSLELATRLDSRLYALWNRTAGDC LLDSVLQATWGIYDKDSVLRKALHDSLHDCSHWFYTRWKDWESWYS QSFGLHFSLREEQWQEDWAFILSLASQPGASLEQTHIFVLAHILRR PIIVYGVKYYKSFRGETLGYTRFQGVYLPLLWEQSFCWKSPIALGY TRGHFSALVAMENDGYGNRGAGANLNTDDDVTITFLPLVDSERKLL HVHFLSAQELGNEEQQEKLLREWLDCCVTEGGVLVAMQKSSRRRNH PLVTQMVEKWLDRYRQIRPCTSLS
CFP- P2A-USP21 enDUB	264	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPSDDKMAHHTLLLGSG HVGLRNLGNTCFLNAVLQCLSSTRPLRDFCLRRDFRQEVPGGGRAQ ELTEAFADVIGALWHPDSCEAVNPTRFRAVFQKYVPSFSGYSQQDA QEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGALLEEPE LSDDDRANLMWKRYLEREDSKIVDLFVGQLKSCLKCQACGYRSTTF EVFCDLSLPIPKKGFAGGKVSLRDCFNLFTKEEELESENAPVCDRC RQKTRSTKKLTVQRFPRILVLHLNRFSASRGSIKKSSVGVDFPLQR LSLGDFASDKAGSPVYQLYALCNHSGSVHYGHYTALCRCQTGWHVY NDSRVSPVSENQVASSEGYVLFYQLMQEPPRCL
CFP- P2A-OTUD4 enDUB	265	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ

		QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPATPMDAYLRKLGLYR KLVAKDGSCLFRAVAEQVLHSQSRHVEVRMACIHYLRENREKFEAF IEGSFEEYLKRLENPQEWVGQVEISALSLMYRKDFIIYREPNVSPS QVTENNFPEKVLLCFSNGNHYDIVYPIKYKESSAMCQSLLYELLYE KVFKTDVSKIVMELDTLEVADE
CFP-P2A-a-YFPnanobody-Cezanne enDUB	266	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPQVQLVESGGALVQPG GSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYE DSVKGRFTISRDDARNTVYLQMNSLKPEDTAVYYCNVNVGFEYWGQ GTQVTVSSPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIV QEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQ LPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQR LLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKE ALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLG TNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRD SGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSME QKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLA SVILSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
CFP-P2A-a-YFPnanobody-OTUD1 enDUB	267	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPQVQLVESGGALVQPG GSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYE DSVKGRFTISRDDARNTVYLQMNSLKPEDTAVYYCNVNVGFEYWGQ GTQVTVSSDEKLALYLAEVEKQDKYLRQRNKYRFHIIPDGNCLYRA VSKTVYGDQSLHRELREQTVHYIADHLDHFSPLIEGDVGEFIIAAA QDGAWAGYPELLAMGQMLNVNIHLTTGGRLESPTVSTMIHYLGPED SLRPSIWLSWLSNGHYDAVFDHSYPNPEYDNWCKQTQVQRKRDEEL AKSMAISLSKMYIEQNACS
CFP-P2A-a-YFPnanobody-TRABID enDUB	268	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPQVQLVESGGALVQPG GSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYE DSVKGRFTISRDDARNTVYLQMNSLKPEDTAVYYCNVNVGFEYWGQ GTQVTVSSLEVDFKKLKQIKNRMKKTDWLFLNACVGVVEGDLAAIE AYKSSGGDIARQLTADEVRLLNRPSAFDVGYTLVHLAIRFQRQDML AILLTEVSQQAAKCIPAMVCPELTEQIRREIAASLHQRKGDFACYF LTDLVTFTLPADIEDLPPTVQEKLFDEVLDRDVQKELEEESPIINW SLELATRLDSRLYALWNRTAGDCLLDSVLQATWGIYDKDSVLRKAL HDSLHDCSHWFYTRWKDWESWYSQSFGLHFSLREEQWQEDWAFILS LASQPGASLEQTHIFVLAHILRRPIIVYGVKYYKSFRGETLGYTRF

		QGVYLPLLWEQSFCWKSPIALGYTRGHFSALVAMENDGYGNRGAGA NLNTDDDVTITFLPLVDSERKLLHVHFLSAQELGNEEQQEKLLREW LDCCVTEGGVLVAMQKSSRRRNHPLVTQMVEKWLDRYRQIRPCTSL
CFP-P2A-a-YFPnanobody-USP21 enDUB	269	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPQVQLVESGGALVQPG GSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYE DSVKGRFTISRDDARNTVYLQMNSLKPEDTAVYYCNVNVGFEYWGQ GTQVTVSSSDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSST RPLRDFCLRRDFRQEVPGGGRAQELTEAFADVIGALWHPDSCEAVN PTRFRAVFQKYVPSFSGYSQQDAQEFLKLLMERLHLEINRRGRRAP PILANGPVPSPPRRGGALLEEPELSDDDRANLMWKRYLEREDSKIV DLFVGQLKSCLKCQACGYRSTTFEVFCDLSLPIPKKGFAGGKVSLR DCFNLFTKEEELESENAPVCDRCRQKTRSTKKLTVQRFPRILVLHL NRFSASRGSIKKSSVGVDFPLQRLSLGDFASDKAGSPVYQLYALCN HSGSVHYGHYTALCRCQTGWHVYNDSRVSPVSENQVASSEGYVLFY QLMQEPPRCL
CFP-P2A-a-YFPnanobody-OTUD4 enDUB	270	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPQVQLVESGGALVQPG GSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYE DSVKGRFTISRDDARNTVYLQMNSLKPEDTAVYYCNVNVGFEYWGQ GTQVTVSSATPMDAYLRKLGLYRKLVAKDGSCLFRAVAEQVLHSQS RHVEVRMACIHYLRENREKFEAFIEGSFEEYLKRLENPQEWVGQVE ISALSLMYRKDFIIYREPNVSPSQVTENNFPEKVLLCFSNGNHYDI VYPIKYKESSAMCQSLLYELLYEKVFKTDVSKIVMELDTLEVADE
CFP-P2A -anti-LCK Kinase targeting binder-Cezanne enDUB	271	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVLYYLITYGETGDHWSGHQAFEVPGSKSTAT ISGLKPGVDYTITVYAHAESYGESYSPISINYRTPPSFSEGSGGSR TPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLA RSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLI EQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLG MWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKESGLV YTEDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYESL EEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEV PASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKL LPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVK WIPLSSDAQAPLAQ
CFP-P2A -anti-LCK Kinase	272	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG

targeting binder-OTUD1 enDUB		YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVLYYLITYGETGDHWSGHQAFEVPGSKSTAT ISGLKPGVDYTITVYAHAESYGESYSPISINYRTDEKLALYLAEVE KQDKYLRQRNKYRFHIIPDGNCLYRAVSKTVYGDQSLHRELREQTV HYIADHLDHFSPLIEGDVGEFIIAAAQDGAWAGYPELLAMGQMLNV NIHLTTGGRLESPTVSTMIHYLGPEDSLRPSIWLSWLSNGHYDAVF DHSYPNPEYDNWCKQTQVQRKRDEELAKSMAISLSKMYIEQNACS
CFP-P2A -anti-LCK Kinase targeting binder-TRABID enDUB	273	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVLYYLITYGETGDHWSGHQAFEVPGSKSTAT ISGLKPGVDYTITVYAHAESYGESYSPISINYRTLEVDFKKLKQIK NRMKKTDWLFLNACVGVVEGDLAAIEAYKSSGGDIARQLTADEVRL LNRPSAFDVGYTLVHLAIRFQRQDMLAILLTEVSQQAAKCIPAMVC PELTEQIRREIAASLHQRKGDFACYFLTDLVTFTLPADIEDLPPTV QEKLFDEVLDRDVQKELEEESPIINWSLELATRLDSRLYALWNRTA GDCLLDSVLQATWGIYDKDSVLRKALHDSLHDCSHWFYTRWKDWES WYSQSFGLHFSLREEQWQEDWAFILSLASQPGASLEQTHIFVLAHI LRRPIIVYGVKYYKSFRGETLGYTRFQGVYLPLLWEQSFCWKSPIA LGYTRGHFSALVAMENDGYGNRGAGANLNTDDDVTITFLPLVDSER KLLHVHFLSAQELGNEEQQEKLLREWLDCCVTEGGVLVAMQKSSRR RNHPLVTQMVEKWLDRYRQIRPCTSLS
CFP-P2A -anti-LCK Kinase targeting binder-USP21 enDUB	274	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNF GSVSSVPTKLEVVAATPTSLLISWDAPAVTVLYYLITYGETGDHWS GHQAFEVPGSKSTATISGLKPGVDYTITVYAHAESYGESYSPISIN YRTSDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRD FCLRRDFRQEVPGGGRAQELTEAFADVIGALWHPDSCEAVNPTRFR AVFQKYVPSFSGYSQQDAQEFLKLLMERLHLEINRRGRRAPPILAN GPVPSPPRRGGALLEEPELSDDDRANLMWKRYLEREDSKIVDLFVG QLKSCLKCQACGYRSTTFEVFCDLSLPIPKKGFAGGKVSLRDCFNL FTKEEELESENAPVCDRCRQKTRSTKKLTVQRFPRILVLHLNRFSA SRGSIKKSSVGVDFPLQRLSLGDFASDKAGSPVYQLYALCNHSGSV HYGHYTALCRCQTGWHVYNDSRVSPVSENQVASSEGYVLFYQLMQE PPRCL
CFP-P2A -anti-LCK Kinase targeting binder-OTUD4 enDUB	275	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA

		TPTSLLISWDAPAVTVLYYLITYGETGDHWSGHQAFEVPGSKSTAT ISGLKPGVDYTITVYAHAESYGESYSPISINYRTATPMDAYLRKLG LYRKLVAKDGSCLFRAVAEQVLHSQSRHVEVRMACIHYLRENREKF EAFIEGSFEEYLKRLENPQEWVGQVEISALSLMYRKDFIIYREPNV SPSQVTENNFPEKVLLCFSNGNHYDIVYPIKYKESSAMCQSLLYEL LYEKVFKTDVSKIVMELDTLEVADE
CFP-P2A -anti-YES1 Kinase targeting binder-Cezanne enDUB	276	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVDYYFITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAWYYYDDEYYMNESSPISINYRTPPSFSEGSG GSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIV SLARSHVSSNGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIER DLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAA SLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKES GLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVY ESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLP LEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSE YKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYM NVKWIPLSSDAQAPLAQ
CFP-P2A -anti-YES1 Kinase targeting binder-OTUD1 enDUB	277	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVDYYFITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAWYYYDDEYYMNESSPISINYRTDEKLALYLA EVEKQDKYLRQRNKYRFHIIPDGNCLYRAVSKTVYGDQSLHRELRE QTVHYIADHLDHFSPLIEGDVGEFIIAAAQDGAWAGYPELLAMGQM LNVNIHLTTGGRLESPTVSTMIHYLGPEDSLRPSIWLSWLSNGHYD AVFDHSYPNPEYDNWCKQTQVQRKRDEELAKSMAISLSKMYIEQNA CS
CFP-P2A -anti-YES1 Kinase targeting binder-TRABID enDUB	278	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVDYYFITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAWYYYDDEYYMNESSPISINYRTLEVDFKKLK QIKNRMKKTDWLFLNACVGVVEGDLAAIEAYKSSGGDIARQLTADE VRLLNRPSAFDVGYTLVHLAIRFQRQDMLAILLTEVSQQAAKCIPA MVCPELTEQIRREIAASLHQRKGDFACYFLTDLVTFTLPADIEDLP PTVQEKLFDEVLDRDVQKELEEESPIINWSLELATRLDSRLYALWN RTAGDCLLDSVLQATWGIYDKDSVLRKALHDSLHDCSHWFYTRWKD WESWYSQSFGLHFSLREEQWQEDWAFILSLASQPGASLEQTHIFVL AHILRRPIIVYGVKYYKSFRGETLGYTRFQGVYLPLLWEQSFCWKS

		PIALGYTRGHFSALVAMENDGYGNRGAGANLNTDDDVTITFLPLVD SERKLLHVHFLSAQELGNEEQQEKLLREWLDCCVTEGGVLVAMQKS SRRRNHPLVTQMVEKWLDRYRQIRPCTSLS
CFP-P2A -anti-YES1 Kinase targeting binder-USP21 enDUB	279	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVDYYFITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAWYYYDDEYYMNESSPISINYRTSDDKMAHHT LLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRDFCLRRDFRQEVP GGGRAQELTEAFADVIGALWHPDSCEAVNPTRFRAVFQKYVPSFSG YSQQDAQEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGA LLEEPELSDDDRANLMWKRYLEREDSKIVDLFVGQLKSCLKCQACG YRSTTFEVFCDLSLPIPKKGFAGGKVSLRDCFNLFTKEEELESENA PVCDRCRQKTRSTKKLTVQRFPRILVLHLNRFSASRGSIKKSSVGV DFPLQRLSLGDFASDKAGSPVYQLYALCNHSGSVHYGHYTALCRCQ TGWHVYNDSRVSPVSENQVASSEGYVLFYQLMQEPPRCL
CFP-P2A -anti-YES1 Kinase targeting binder-OTUD4 enDUB	280	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVDYYFITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAWYYYDDEYYMNESSPISINYRTATPMDAYLR KLGLYRKLVAKDGSCLFRAVAEQVLHSQSRHVEVRMACIHYLRENR EKFEAFIEGSFEEYLKRLENPQEWVGQVEISALSLMYRKDFIIYRE PNVSPSQVTENNFPEKVLLCFSNGNHYDIVYPIKYKESSAMCQSLL YELLYEKVFKTDVSKIVMELDTLEVADE
CFP-P2A -anti-Aroura Kinase A targeting binder- Cezanne enDUB	281	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVVHYVITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAIDFYWGSYSPISINYRTPPSFSEGSGGSRTP EKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARS HVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQ SMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMW GFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKESGLVYT EDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEE FHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPA SQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLP LHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWI PLSSDAQAPLAQ
CFP-P2A -anti-Aroura Kinase A targeting	282	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL

binder- OTUD1 enDUB		GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVVHYVITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAIDFYWGSYSPISINYRTDEKLALYLAEVEKQ DKYLRQRNKYRFHIIPDGNCLYRAVSKTVYGDQSLHRELREQTVHY IADHLDHFSPLIEGDVGEFIIAAAQDGAWAGYPELLAMGQMLNVNI HLTTGGRLESPTVSTMIHYLGPEDSLRPSIWLSWLSNGHYDAVFDH SYPNPEYDNWCKQTQVQRKRDEELAKSMAISLSKMYIEQNACS
CFP-P2A -anti-Aroura Kinase A targeting binder- TRABID enDUB	283	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVVHYVITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAIDFYWGSYSPISINYRTLEVDFKKLKQIKNR MKKTDWLFLNACVGVVEGDLAAIEAYKSSGGDIARQLTADEVRLLN RPSAFDVGYTLVHLAIRFQRQDMLAILLTEVSQQAAKCIPAMVCPE LTEQIRREIAASLHQRKGDFACYFLTDLVTFTLPADIEDLPPTVQE KLFDEVLDRDVQKELEESPIINWSLELATRLDSRLYALWNRTAGD CLLDSVLQATWGIYDKDSVLRKALHDSLHDCSHWFYTRWKDWESWY SQSFGLHFSLREEQWQEDWAFILSLASQPGASLEQTHIFVLAHILR RPIIVYGVKYYKSFRGETLGYTRFQGVYLPLLWEQSFCWKSPIALG YTRGHFSALVAMENDGYGNRGAGANLNTDDDVTITFLPLVDSERKL LHVHFLSAQELGNEEQQEKLLREWLDCCVTEGGVLVAMQKSSRRRN HPLVTQMVEKWLDRYRQIRPCTSLS
CFP-P2A -anti-Aroura Kinase A targeting binder- USP21 enDUB	284	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVVHYVITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAIDFYWGSYSPISINYRTSDDKMAHHTLLLGS GHVGLRNLGNTCFLNAVLQCLSSTRPLRDFCLRRDFRQEVPGGGRA QELTEAFADVIGALWHPDSCEAVNPTRFRAVFQKYVPSFSGYSQQD AQEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGALLEEP ELSDDDRANLMWKRYLEREDSKIVDLFVGQLKSCLKCQACGYRSTT FEVFCDLSLPIPKKGFAGGKVSLRDCFNLFTKEEELESENAPVCDR CRQKTRSTKKLTVQRFPRILVLHLNRFSASRGSIKKSSVGVDFPLQ RLSLGDFASDKAGSPVYQLYALCNHSGSVHYGHYTALCRCQTGWHV YNDSRVSPVSENQVASSEGYVLFYQLMQEPPRCL
CFP-P2A -anti-Aroura Kinase A targeting binder- OTUD4 enDUB	285	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLK FICTTGKLPVPWPTLVTTLTWGVQCFSRYPDHMKQHDFFKSAMPEG YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNIL GHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQ QNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGI TLGMDELYKGSGATNFSLLKQAGDVEENPGPGSVSSVPTKLEVVAA TPTSLLISWDAPAVTVVHYVITYGETGGNSPVQEFTVPGSKSTATI SGLKPGVDYTITVYAIDFYWGSYSPISINYRTATPMDAYLRKLGLY

		RKLVAKDGSCLFRAVAEQVLHSQSRHVEVRMACIHYLRENREKFEA FIEGSFEEYLKRLENPQEWVGQVEISALSLMYRKDFIIYREPNVSP SQVTENNFPEKVLLCFSNGNHYDIVYPIKYKESSAMCQSLLYELLY EKVFKTDVSKIVMELDTLEVADE

6.2 Example 2. Testing of Targeted Engineered Deubiquitinases

[00310] To demonstrate upregulation of a target protein in the context of a specific targeting enDUB the following experiments will be performed.

Schematic constructs used:

- Control experiment using non-targeting enDUB fusion
  - Target – YFP- P2A – mCherrry
  - CFP- P2A- enDUB (nontargeting control enDUB)
- Test constructs for up-regulation:
  - Target- YFP-P2A-mCherry
  - CFP-P2A-a-YFPnanobody-enDUB
- Or specific targeting enDUB fusion composed of
  - CFP-P2A -anti-targeting binder-enDUB

[00311] Co-transfection of both plasmids carrying the YFP tagged target protein together with the enDUB fused to a target binding protein into HEK cells will be performed. A control construct carrying the enDUB in the absence of the targeting binder will also be co-transfected together with the labeled target protein. After 24-48 hours the transfected cells will be analyzed by FACS or upregulation over the control. The mCherry signal on the target protein will be used to normalize for transfection efficiency while the CFP signal will be used to normalize for the transfection efficiency of the enDUB constructs. The YFP fused to the target protein is the read-out for target gene expression and will be plotted vs the signal in the control transfection. Relative increase in the YFP fluorescence over control will demonstrate upregulation in the presence of the enDUB.

6.3 Example 3. Screening Assay for Testing Fusion Proteins

[00312] The following example describes an assay to analyze the ability of a targeted engineered deubiquitinase (enDub) (e.g., an enDub described herein) to increase expression of a target protein. Generally, the assay involves tagging the target protein with a fluorescent tag (e.g., NanoLuciferase (NLuc)) and an alfa-tag (α-Tag); and tagging a fusion protein of the enDub and

an anti-alfa Tag nanobody with a different fluorescent tag (e.g., Firefly Luciferase (FLuc)) through a cleavable linker. The use of two different fluorescent tags enables normalization of the signal to compensate for variation in transfection/expression, as the second fluorescent tag is rapidly cleaved from the enDub-anti-alfa tag fusion protein inside the cell through cleavage of the cleavable linker. FIG. 2 provides a general schematic of the cellular aspects of the assay. The protocol, including materials and methods is described below.

[00313] CHO-K1 cells were digested with 0.25% (w/v) Trypsin-EDTA, at 37°C, for 5min. Complete medium was added for the CHO-K1 cell cultures to stop the digestion. The CHO-K1 cells were centrifuges at 800 rpm for 5 minutes. After centrifugation, the supernatant was discarded and the CHO-K1 cells were resuspend in 2 mL culture medium and counted. 10^6 CHO-K1 cells were electroporated under 440V with 0.5ug of a plasmid encoding the target protein tagged with NLuc and alfa-tag, and 1ug of a plasmid encoding a) enDub-anti-alfa tag nanobody-FLuc fusion protein (experimental), b) the enDub (control), or the anti-alfa tag nanobody (control). 5E+4 cells/well were placed in in 24 well plates and cultured for 24h, at 37°C, 5% CO_2. The cells were digested with 0.25% (w/v) Trypsin-EDTA, at 37°C for 5min. Complete medium was added to the culture to stop the digestion and the cells were counted for use in NanoGlo® Dual Luciferase® Assay (Promega), which enables detection of FLuc and NLuc® in a single sample. The NanoGlo® Dual Luciferase® Assay was carried out according to manufacturer's instructions (Promega, Nano-Glo® Dual-Luciferase® Reporter Assay Technical Manual #TM426). Briefly, 1E+4 cells/well were placed in 96 well black plates and cultured for 24h, at 37°C, 5% CO_2. The plates were removed from the incubator and allowed to equilibrate to room temperature. The samples were modified as needed to have a starting volume of 80µl per well. All sample wells were injected with 80µl of ONE-Glo™ EX Reagent and incubated for 3 minutes. The firefly luminescence was read in all sample wells using a 1-second integration time. All sample wells were injected with 80µl of NanoDLR™ Stop & Glo® Reagent; and incubated for 5 minutes. The NanoLuc® luminescence of all sample wells was read using a 1-second integration time. The dispensing lines were cleaned according to manufacturer's instructions (Nano-Glo® Dual-Luciferase® Reporter Assay Technical Manual #TM426.) and the data analyzed.

[00314] The amino acid sequence of the components of the fusion proteins used in the assay are detailed in Table 9 below.

Table 9. Amino acid sequence of components of test fusion proteins

Description		SEQ ID NO	Amino Acid Sequence
Fluorescent Protein	NanoLuc	385	VFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQ NLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGL SGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLV IDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTL WNGNKIIDERLINPDGSLLFRVTINGVTGWRLC ERILA
	Firefly Luciferase	386	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRY ALVPGTIAFTDAHIEVDITYAEYFEMSVRLAEA MKRYGLNTNHRIVVCSENSLQFFMPVLGALFIG VAVAPANDIYNERELLNSMGISQPTVVFVSKKG LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMY TFVTSHLPPGFNEYDFVPESFDRDKTIALIMNS SGSTGLPKGVALPHRTACVRFSHARDPIFGNQI IPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAK STLIDKYDLSNLHEIASGGAPLSKEVGEAVAKR FHLPGIRQGYGLTETTSAILITPEGDDKPGAVG KVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDED EHFFIVDRLKSLIKYKGYQVAPAELESILLQHP NIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTE KEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLK
Alfa Tag		387	PSRLEEELRRRLTEP
P2A		388	GSGATNFSLLKQAGDVEENPGP
Cezanne (Exemplary Catalytic Domain)		389	PPSFSEGSGGSRTPEKGFSDREPTRPPRPILQR QDDIVQEKRLSRGISHASSSIVSLARSHVSSNG GGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFI ERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLL PLATTGDGNCLLHAASLGMWGFHDRDLMLRKAL YALMEKGVEKEALKRRWRWQQTQQNKESGLVYT EDEWQKEWNELIKLASSEPRMHLGTNGANCGGV ESSEEPVYESLEEFHVFVLAHVLRRPIVVVADT MLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSP LVLAYDQAHFSALVSMEQKENTKEQAVIPLTDS EYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVI LSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ

[00315] The amino acid sequence of exemplary target fusion proteins comprising a target protein, NLuc, and the alfa tag are detailed in Table 10 below.

Table 10. Amino Acid Sequence of exemplary Target Protein – NLuc – Alfa Tag Fusion Proteins

Test Protein	SEQ ID NO	Amino Acid Sequence
Shank3-nanoluc-alfa-tag-fusion	390	MDGPGASAVVVRVGIPDLQQTKCLRLDPAAPVWAAKQRVLCALNH SLQDALNYGLFQPPSRGRAGKFLDEERLLQEYPPNLDTPLPYLEF RYKRRVYAQNLIDDKQFAKLHTKANLKKFMDYVQLHSTDKVARLL DKGLDPNFHDPDSGECPLSLAAQLDNATDLLKVLKNGGAHLDFRT RDGLTAVHCATRQRNAAALTTLLDLGASPDYKDSRGLTPLYHSAL

		GGGDALCCELLLHDHAQLGITDENGWQEIHQACRFGHVQHLEHLL FYGADMGAQNASGNTALHICALYNQESCARVLLFRGANRDVRNYN SQTAFQVAIIAGNFELAEVIKTHKDSDVVPFRETPSYAKRRRLAG PSGLASPRPLQRSASDINLKGEAQPAASPGPSLRSLPHQLLLQRL QEEKDRDRDADQESNISGPLAGRAGQSKISPSGPGGPGPAPGPGP APPAPPAPPPRGPKRKLYSAVPGRKFIAVKAHSPQGEGEIPLHRG EAVKVLSIGEGGFWEGTVKGRTGWFPADCVEEVQMRQHDTRPETR EDRTKRLFRHYTVGSYDSLTSHSDYVIDDKVAVLQKRDHEGFGFV LRGAKAETPIEEFTPTPAFPALQYLESVDVEGVAWRAGLRTGDFL IEVNGVNVVKVGHKQVVALIRQGGNRLVMKVVSVTRKPEEDGARR RAPPPPKRAPSTTLTLRSKSMTAELEELASIRRRKGEKLDEMLAA AAEPTLRPDIADADSRAATVKQRPTSRRITPAEISSLFERQGLPG PEKLPGSLRKGIPRTKSVGEDEKLASLLEGRFPRSTSMQDPVREG RGIPPPPQTAPPPPPAPYYFDSGPPPAFSPPPPPGRAYDTVRSSF KPGLEARLGAGAAGLYEPGAALGPLPYPERQKRARSMIILQDSAP ESGDAPRPPPAATPPERPKRRPRPPGPDSPYANLGAFSASLFAPS KPQRRKSPLVKQLQVEDAQERAALAVGSPGPGGGSFAREPSPTHR GPRPGGLDYGAGDGPGLAFGGPGPAKDRRLEERRRSTVFLSVGAI EGSAPGADLPSLQPSRSIDERLLGTGPTAGRDLLLPSPVSALKPL VSGPSLGPSGSTFIHPLTGKPLDPSSPLALALAARERALASQAPS RSPTPVHSPDADRPGPLFVDVQARDPERGSLASPAFSPRSPAWIP VPARREAEKVPREERKSPEDKKSMILSVLDTSLQRPAGLIVVHAT SNGQEPSRLGGAEEERPGTPELAPAPMQSAAVAEPLPSPRAQPPG GTPADAGPGQGSSEEEPELVFAVNLPPAQLSSSDEETREELARIG LVPPPEEFANGVLLATPLAGPGPSPTTVPSPASGKPSSEPPPAPE SAADSGVEEADTRSSSDPHLETTSTISTVSSMSTLSSESGELTDT HTSFADGHTFLLEKPPVPPKPKLKSPLGKGPVTFRDPLLKQSSDS ELMAQQHHAASAGLASAAGPARPRYLFQRRSKLWGDPVESRGLPG PEDDKPTVISELSSRLQQLNKDTRSLGEEPVGGLGSLLDPAKKSP IAAARLFSSLGELSSISAQRSPGGPGGGASYSVRPSGRYPVARRA PSPVKPASLERVEGLGAGAGGAGRPFGLTPPTILKSSSLSIPHEP KEVRFVVRSVSARSRSPSPSPLPSPASGPGPGAPGPRRPFQQKPL QLWSKFDVGDWLESIHLGEHRDRFEDHEIEGAHLPALTKDDFVEL GVTRVGHRMNIERALRQLDGSKVPVFTLEDFVGDWRQTAGYNLDQ VLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGL SGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYF GRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTI NGVTGWRLCERILAGGGGSPSRLEEELRRRLTEP
CDKL5-nanoluc-alfa-tag-fusion	391	MKIPNIGNVMNKFEILGVVGEGAYGVVLKCRHKETHEIVAIKKFK DSEENEEVKETTLRELKMLRTLKQENIVELKEAFRRRGKLYLVFE YVEKNMLELLEEMPNGVPPEKVKSYIYQLIKAIHWCHKNDIVHRD IKPENLLISHNDVLKLCDFGFARNLSEGNNANYTEYVATRWYRSP ELLLGAPYGKSVDMWSVGCILGELSDGQPLFPGESEIDQLFTIQK VLGPLPSEQMKLFYSNPRFHGLRFPAVNHPQSLERRYLGILNSVL LDLMKNLLKLDPADRYLTEQCLNHPTFQTQRLLDRSPSRSAKRKP YHVESSTLSNRNQAGKSTALQSHHRSNSKDIQNLSVGLPRADEGL PANESFLNGNLAGASLSPLHTKTYQASSQPGSTSKDLTNNNIPHL LSPKEAKSKTEFDFNIDPKPSEGPGTKYLKSNSRSQQNRHSFMES SQSKAGTLQPNEKQSRHSYIDTIPQSSRSPSYRTKAKSHGALSDS KSVSNLSEARAQIAEPSTSRYFPSSCLDLNSPTSPTPTRHSDTRT LLSPSGRNNRNEGTLDSRRTTTRHSKTMEELKLPEHMDSSHSHSL

		SAPHESFSYGLGYTSPFSSQQRPHRHSMYVTRDKVRAKGLDGSLS IGQGMAARANSLQLLSPQPGEQLPPEMTVARSSVKETSREGTSSF HTRQKSEGGVYHDPHSDDGTAPKENRHLYNDPVPRRVGSFYRVPS PRPDNSFHENNVSTRVSSLPSESSSGTNHSKRQPAFDPWKSPENI SHSEQLKEKEKQGFFRSMKKKKKKSQTVPNSDSPDLLTLQKSIHS ASTPSSRPKEWRPEKISDLQTQSQPLKSLRKLLHLSSASNHPASS DPRFQPLTAQQTKNSFSEIRIHPLSQASGGSSNIRQEPAPKGRPA LQLPGQMDPGWHVSSVTRSATEGPSYSEQLGAKSGPNGHPYNRTN RSRMPNLNDLKETALKVPVFTLEDFVGDWRQTAGYNLDQVLEQGG VSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMG QIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEG IAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGW RLCERILAGGGGSPSRLEEELRRRLTEP
STXBP1-nanoluc-alfa-tag-fusion	392	MAPIGLKAVVGEKIMHDVIKKVKKKGEWKVLVVDQLSMRMLSSCC KMTDIMTEGITIVEDINKRREPLPSLEAVYLITPSEKSVHSLISD FKDPPTAKYRAAHVFFTDSCPDALFNELVKSRAAKVIKTLTEINI AFLPYESQVYSLDSADSFQSFYSPHKAQMKNPILERLAEQIATLC ATLKEYPAVRYRGEYKDNALLAQLIQDKLDAYKADDPTMGEGPDK ARSQLLILDRGFDPSSPVLHELTFQAMSYDLLPIENDVYKYETSG IGEARVKEVLLDEDDDLWIALRHKHIAEVSQEVTRSLKDFSSSKR MNTGEKTTMRDLSQMLKKMPQYQKELSKYSTHLHLAEDCMKHYQG TVDKLCRVEQDLAMGTDAEGEKIKDPMRAIVPILLDANVSTYDKI RIILLYIFLKNGITEENLNKLIQHAQIPPEDSEIITNMAHLGVPI VTDSTLRRRSKPERKERISEQTYQLSRWTPIIKDIMEDTIEDKLD TKHYPYISTRSSASFSTTAVSARYGHWHKNKAPGEYRSGPRLIIF ILGGVSLNEMRCAYEVTQANGKWEVLIGSTHILTPQKLLDTLKKL NKTDEEISSKVPVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQ NLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIF KVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDG KKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERI LAGGGGSPSRLEEELRRRLTEP
DNM1-nanoluc-alfa-tag-fusion	393	MGNRGMEDLIPLVNRLQDAFSAIGQNADLDLPQIAVVGGQSAGKS SVLENFVGRDFLPRGSGIVTRRPLVLQLVNATTEYAEFLHCKGKK FTDFEEVRLEIEAETDRVTGTNKGISPVPINLRVYSPHVLNLTLV DLPGMTKVPVGDQPPDIEFQIRDMLMQFVTKENCLILAVSPANSD LANSDALKVAKEVDPQGQRTIGVITKLDLMDEGTDARDVLENKLL PLRRGYIGVVNRSQKDIDGKKDITAALAAERKFFLSHPSYRHLAD RMGTPYLQKVLNQQLTNHIRDTLPGLRNKLQSQLLSIEKEVEEYK NFRPDDPARKTKALLQMVQQFAVDFEKRIEGSGDQIDTYELSGGA RINRIFHERFPFELVKMEFDEKELRREISYAIKNIHGIRTGLFTP DMAFETIVKKQVKKIREPCLKCVDMVISELISTVRQCTKKLQQYP RLREEMERIVTTHIREREGRTKEQVMLLIDIELAYMNTNHEDFIG FANAQQRSNQMNKKKTSGNQDEILVIRKGWLTINNIGIMKGGSKE YWFVLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGFMSSKHI FALFNTEQRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV GDKEKASETEENGSDSFMHSMDPQLERQVETIRNLVDSYMAIVNK TVRDLMPKTIMHLMINNTKEFIFSELLANLYSCGDQNTLMEESAE QAQRRDEMLRMYHALKEALSIIGDINTTTVSTPMPPPVDDSWLQV QSVPAGRRSPTSSPTPQRRAPAVPPARPGSRGPAPGPPPAGSALG GAPPVPSRPGASPDPFGPPPQVPSRPNRAPPGVPSRSGQASPSRP ESPRPPFDLKVPVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQ

		NLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIF KVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDG KKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERI LAGGGGSPSRLEEELRRRLTEP
KIF1A-nanoluc-alfa-tag-fusion	394	MAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKE TPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEMLQHAFEGYN VCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDLFSRINDTTN DNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVREHPLLGPYVED LSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIF TQKRHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGAN INKSLTTLGKVISALAEMDSGPNKNKKKKTDFIPYRDSVLTWLL RENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIRCNAVI NEDPNNKLIRELKDEVTRLRDLLYAQGLGDITDMTNALVGMSPSS SLSALSSRAASVSSLHERILFAPGSEEAIERLKETEKIIAELNET WEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPHLV NLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEH CVFRSDSRGGSEAVVTLEPCEGADTYVNGKKVTEPSILRSGNRII MGKSHVFRFNHPEQARQERERTPCAETPAEPVDWAFAQRELLEKQ GIDMKQEMEQRLQELEDQYRREREEATYLLEQQRLDYESKLEALQ KQMDSRYYPEVNEEEEEPEDEVQWTERECELALWAFRKWKWYQFT SLRDLLWGNAIFLKEANAISVELKKKVQFQFVLLTDTLYSPLPPD LLPPEAAKDRETRPFPRTIVAVEVQDQKNGATHYWTLEKLRQRLD LMREMYDRAAEVPSSVIEDCDNVVTGGDPFYDRFPWFRLVGRAFV YLSNLLYPVPLVHRVAIVSEKGEVKGFLRVAVQAISADEEAPDYG SGVRQSGTAKISFDDQHFEKFQSESCPVVGMSRSGTSQEELRIVE GQGQGADVGPSADEVNNNTCSAVPPEGLLLDSSEKAALDGPLDAA LDHLRLGNTFTFRVTVLQASSISAEYADIFCQFNFIHRHDEAFST EPLKNTGRGPPLGFYHVQNIAVEVTKSFIEYIKSQPIVFEVFGHY QQHPFPPLCKDVLSPLRPSRRHFPRVMPLSKPVPATKLSTLTRPC PGPCHCKYDLLVYFEICELEANGDYIPAVVDHRGGMPCMGTFLLH QGIQRRITVTLLHETGSHIRWKEVRELVVGRIRNTPETDESLIDP NILSLNILSSGYIHPAQDDRTFYQFEAAWDSSMHNSLLLNRVTPY REKIYMTLSAYIEMENCTQPAVVTKDFCMVFYSRDAKLPASRSIR NLFGSGSLRASESNRVTGVYELSLCHVADAGSPGMQRRRRRVLDT SVAYVRGEENLAGWRPRSDSLILDHQWELEKLSLLQEVEKTRHYL LLREKLETAQRPVPEALSPAFSEDSESHGSSSASSPLSAEGRPSP LEAPNERQRELAVKCLRLLTHTFNREYTHSHVCVSASESKLSEMS VTLLRDPSMSPLGVATLTPSSTCPSLVEGRYGATDLRTPQPCSRP ASPEPELLPEADSKKLPSPARATETDKEPQRLLVPDIQEIRVSPI VSKKGYLHFLEPHTSGWARRFVVVRRPYAYMYNSDKDTVERFVLN LATAQVEYSEDQQAMLKTPNTFAVCTEHRGILLQAASDKDMHDWL YAFNPLLAGTIRSKLSRRRSAQMRVKVPVFTLEDFVGDWRQTAGY NLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIP YEGLSGDQMGQIEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNM IDYFGRPYEGIAVFDGKKITVTGTLWNGNKIIDERLINPDGSLLF RVTINGVTGWRLCERILAGGGGSPSRLEEELRRRLTEP
SYNGAP1 - nanoluc-alfa-tag-fusion	395	MSRSRASIHRGSIPAMSYAPFRDVRGPSMHRTQYVHSPYDRPGWN PRFCIISGNQLLMLDEDEIHPLLIRDRRSESSRNKLLRRTVSVPV EGRPHGEHEYHLGRSRRKSVPGGKQYSMEGAPAAPFRPSQGFLSR RLKSSIKRTKSQPKLDRTSSFRQILPRFRSADHDRARLMQSFKES

		HSHESLLSPSSAAEALELNLDEDSIIKPVHSSILGQEFCFEVTTS SGTKCFACRSAAERDKWIENLQRAVKPNKDNSRRVDNVLKLWIIE ARELPPKKRYYCELCLDDMLYARTTSKPRSASGDTVFWGEHFEFN NLPAVRALRLHLYRDSDKKRKKDKAGYVGLVTVPVATLAGRHFTE QWYPVTLPTGSGGSGGMGSGGGGGSGGGSGGKGKGGCPAVRLKAR YQTMSILPMELYKEFAEYVTNHYRMLCAVLEPALNVKGKEEVASA LVHILQSTGKAKDFLSDMAMSEVDRFMEREHLIFRENTLATKAIE EYMRLIGQKYLKDAIGEFIRALYESEENCEVDPIKCTASSLAEHQ ANLRMCCELALCKVVNSHCVFPRELKEVFASWRLRCAERGREDIA DRLISASLFLRFLCPAIMSPSLFGLMQEYPDEQTSRTLTLIAKVI QNLANFSKFTSKEDFLGFMNEFLELEWGSMQQFLYEISNLDTLTN SSSFEGYIDLGRELSTLHALLWEVLPQLSKEALLKLGPLPRLLND ISTALRNPNIQRQPSRQSERPRPQPVVLRGPSAEMQGYMMRDLNS SIDLQSFMARGLNSSMDMARLPSPTKEKPPPPPPGGGKDLFYVSR PPLARSSPAYCTSSSDITEPEQKMLSVNKSVSMLDLQGDGPGGRL NSSSVSNLAAVGDLLHSSQASLTAALGLRPAPAGRLSQGSGSSIT AAGMRLSQMGVTTDGVPAQQLRIPLSFQNPLFHMAADGPGPPGGH GGGGGHGPPSSHHHHHHHHHRGGEPPGDTFAPFHGYSKSEDLSS GVPKPPAASILHSHSYSDEFGPSGTDFTRRQLSLQDNLQHMLSPP QITIGPQRPAPSGPGGGSGGGSGGGGGGQPPPLQRGKSQQLTVSA AQKPRPSSGNLLQSPEPSYGPARPRQQSLSKEGSIGGSGGSGGGG GGGLKPSITKQHSQTPSTLNPTMPASERTVAWVSNMPHLSADIES AHIEREEYKLKEYSKSMDESRLDRVKEYEEEIHSLKERLHMSNRK LEEYERRLLSQEEQTSKILMQYQARLEQSEKRLRQQQAEKDSQIK SIIGRLMLVEEELRRDHPAMAEPLPEPKKRLLDAQERQLPPLGPT NPRVTLAPPWNGLAPPAPPPPPRLQITENGEFRNTADHKVPVFTL EDFVGDWRQTAGYNLDQVLEQGGVSSLFQNLGVSVTPIQRIVLSG ENGLKIDIHVIIPYEGLSGDQMGQIEKIFKVVYPVDDHHFKVILH YGTLVIDGVTPNMIDYFGRPYEGIAVFDGKKITVTGTLWNGNKII DERLINPDGSLLFRVTINGVTGWRLCERILAGGGGSPSRLEEELR RRLTEP
PYDC2-nanoluc-alfa-tag-fusion	396	MASSAELDFNLQALLEQLSQDELSKFKSLIRTISLGKELQTVPQT EVDKANGKQLVEIFTSHSCSYWAGMAAIQVFEKMNQTHLSGRADE HCVMPPPKVPVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQNL GVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFKV VYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGKK ITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERILA GGGGSPSRLEEELRRRLTEP
CSTB-nanoluc-alfa-tag-fusion	397	MMCGAPSATQPATAETQHIADQVRSQLEEKENKKFPVFKAVSFKS QVVAGTNYFIKVHVGDEDFVHLRVFQSLPHENKPLTLSNYQTNKA KHDELTYFKVPVFTLEDFVGDWRQTAGYNLDQVLEQGGVSSLFQN LGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQIEKIFK VVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGIAVFDGK KITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWRLCERIL AGGGGSPSRLEEELRRRLTEP
PCBD1-nanoluc-alfa-tag-fusion	398	MAGKAHRLSAEERDQLLPNLRAVGWNELEGRDAIFKQFHFKDFNR AFGFMTRVALQAEKLDHHPEWFNVYNKVHITLSTHECAGLSERDI NLASFIEQVAVSMTKVPVFTLEDFVGDWRQTAGYNLDQVLEQGGV SSLFQNLGVSVTPIQRIVLSGENGLKIDIHVIIPYEGLSGDQMGQ IEKIFKVVYPVDDHHFKVILHYGTLVIDGVTPNMIDYFGRPYEGI

		AVFDGKKITVTGTLWNGNKIIDERLINPDGSLLFRVTINGVTGWR LCERILAGGGGSPSRLEEELRRRLTEP

[00316] The amino acid sequence of exemplary fusion proteins comprising a control or a targeted engineered deubiquitinase are detailed in Table 11 below.

Table 11. Amino Acid Sequence of exemplary enDub Control and Screening Fusion Proteins

Description	SEQ ID NO	Amino Acid Sequence
FireflyLuciferase-P2A-nano (Control)	399	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDA HIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQFFM PVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKGLQK ILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYD FVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDP IFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEE ELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASG GAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPG AVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNP EATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVA PAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTE KEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILI KAKKGGKIAVTRLKGSGATNFSLLKQAGDVEENPGPRSGTGSSGE VQLQESGGGLVQPGGSLRLSCTASGVTISALNAMAMGWYRQAPGE RRVMVAAVSERGNAMYRESVQGRFTVTRDFTNKMVSLQMDNLKPE DTAVYYCHVLEDRVDSFHDYWGQGTQVTVSS
FireflyLuciferase-P2A-Cezanne (Control)	400	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDA HIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQFFM PVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKGLQK ILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYD FVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDP IFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEE ELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASG GAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPG AVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNP EATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVA PAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTE KEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILI KAKKGGKIAVTRLKGSGATNFSLLKQAGDVEENPGPRSGTGSPPS FSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGIS HASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNE DFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTG DGNCLLHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWR WQQTQQNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANC GGVESSEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEA FAPIPFGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKEN TKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVI LSLEVKLHLLHSYMNVKWIPLSSDAQAPLAQ
FireflyLuciferase-P2A-a_alfatag_nano-Cezanne	401	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDA HIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQFFM PVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKGLQK

		ILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYD FVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDP IFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEE ELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASG GAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPG AVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNP EATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVA PAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTE KEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILI KAKKGGKIAVTRLKGSGATNFSLLKQAGDVEENPGPRSGTGSSGE VQLQESGGGLVQPGGSLRLSCTASGVTISALNAMAMGWYRQAPGE RRVMVAAVSERGNAMYRESVQGRFTVTRDFTNKMVSLQMDNLKPE DTAVYYCHVLEDRVDSFHDYWGQGTQVTVSSGAPGSGPPSFSEGS GGSRTPEKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSS IVSLARSHVSSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSF IERDLIEQSMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCL LHAASLGMWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQ QNKESGLVYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGGVES SEEPVYESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIP FGGIYLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQA VIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEV KLHLLHSYMNVKWIPLSSDAQAPLAQ

[00317] The assay was conducted with utilizing the tagged proteins and targeted enDubs described above in Tables 7 and 8. The results of the SHANK3 targeting are shown in FIG. 3, showing a 2.4-fold increase in SHANK3 protein expression relative to the control. The results from the SYNGAP1 targeting are shown in **FIG. 4**, showing a 3.1-fold increase in SYNGAP1 protein expression relative to the control. The results of the PYDC2 targeting are shown in **FIG. 5**, showing a 2.64-fold increase in PYDC2 protein expression. The results of the CSTB targeting are shown in **FIG. 6**, showing a 1.61-fold increase in CSTB protein expression. The results of the PCBD1 targeting are shown in **FIG. 7**, showing a 1.13-fold increase in PCBD1 protein expression. The control used for the PYDC2, CSTB, and PCBD1 experiments is the engineered deubiquitinase without the nanobody targeting the alfa-tag. Normalization of transduction efficiency was performed using the firefly luciferase signal as the reference and the ratio between NLuc signal divided by firefly luciferase signal plotted on the y axes.

6.4 Example 4. Generation of Anti-SYNGAP-1 VHH

[00318] Anti-SYNGAP-1 VHHs (i.e. nanobodies) were generated according to the materials and methods below.

6.4.1 Antigen Expression

[00319] cDNA of His-SynGAP-EC[1186-1277] (Uniprot #Q96PV0) with 6His tag at 5'/N-terminal was chemically synthesized with codon optimization for bacterial systems, then sub-cloned in an expression vector. Full protein sequence is as follows: MGSHHHHHHSGKSMDESRLDRVKEYEEEIHSLKERLHMSNRKLEEYERRLLSQEEQTSKILMQY QARLEQSEKRLRQQQAEKDSQIKSIIGRLMLVEEELRRDHPAMAEPLPEPKKRLLDAQERQLPP LGPT (SEQ ID NO: 368). His-SynGAP-EC[1186-1277] was expressed in E. coli, then purified by affinity against 6His-tag using Nickel resin. Purification test results of His-SynGAP-EC [1186-1277] in E. coli are shown in FIG. 8. 4.08MG of His-SynGAP-EC [1186-1277] was produced with a molecular weight of 15.75kDA and a pI of 7.38.

6.4.2 Phage Display

[00320] A series of camelid VHHs were screened for binding to the His-SynGAP-EC[1186-1277] produced above. Briefly, a tube was coated with His-SynGAP-EC[1186-1277], washed, blocked, washed, incubated with a phase library expressing camelid VHHs, washed, and the phages expressing camelid VHH binders that bound to His-SynGAP-EC[1186-1277] were eluted from the tube with glycine-HCL. The concentration of the eluted phages was determined. First, the eluted phages were added to *E. Coli* TG1. TG1 was poured onto a plate and cultured upside down. The PFU was calculated based on the number of plaques (i.e. dead TG1) on the plate. The eluted phages were added to TG1 followed infection by helper phage and cultured. Phages were precipitated with PEG/NaCl and subsequently resuspended. The phages were screened using a polyclonal ELISA and a monoclonal ELISA. Briefly, the polyclonal ELISA was carried out utilizing a plate coated with His-SynGAP-EC[1186-1277] (4μg/mL) or control buffer. The coated plate was washed, blocked, washed, and incubated with the amplified eluted phages. Subsequently the plate was washed and incubated with anti-phage-HRP antibody, washed, and incubated with TMB followed by HCL. The result readings were taken at 450nm. The monoclonal phase ELISA was carried out according to the following. Single TG1 clones randomly selected from plates (described above) were cultured with helper phage. A total of 192 clones from round 3 +96 clones from round 4+ 96 clones from round 5 were selected. The clones were centrifuged and the supernatant (i.e. the phages) were collected. A plate was coated with His-SynGAP-EC[1186-1277] (4 μg/ml) or control buffer. The plate was washed, blocked, washed, incubated with the selected

phages, washed, incubated with anti-phage-HRP antibody, washed, and incubated with TMB followed by HCL. The results were read of 450nm.

[00321] Six anti-His-SynGAP-EC[1186-1277] VHHs were identified and sequenced from the above. The amino acid sequence of the six anti-His-SynGAP-EC[1186-1277] VHHs is disclosed in Table 12 below.

Table 12. Amino Acid Sequence of Anti- SynGAP VHHs

Description		SEQ ID NO	Amino Acid Sequence
FLX00152	CDR1	290	GFSFSNFP
	CDR2	291	INQDGRNT
	CDR3	292	QAIRTTTHFDS
	VH	293	QVQLVESGGGLVQPGGSLRLSCAASGFSFSNFPMMWVR QAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQV TVSS
FLX00153	CDR1	294	GFTFSNYR
	CDR2	295	IDRSGTYT
	CDR3	296	AADRRLIVDLTPEVYDH
	VH	297	QLQLVESGGGLVQPGESLRLSCAASGFTFSNYRMYWVR MAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHW GQGTQVTVSS
FLX00154	CDR1	298	GFIFSSYQ
	CDR2	299	INTGGWNT
	CDR3	300	AADRWMVAKIVGGDLDFDS
	VH	301	QVQLVESGGGLVQPGGSLRLSCAASGFIFSSYQMAWVR QAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFD SWGQGTQVTVSS
FLX00155	CDR1	302	GFAFGSYD
	CDR2	303	ITPGGGGT
	CDR3	304	YYCAKNFYGNGG
	VH	305	QVQLVESGGGLVQPGGSLRLSCAASGFAFGSYDMSWVR QAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQ VTVSS
FLX00156	CDR1	306	GFTFGTHA
	CDR2	307	ISSGGGGT
	CDR3	308	NSPSNIANDN
	VH	309	QVQLVESGGGLVQPGGSLRLACAASGFTFGTHAMHWVR WAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVT VSS
FLX00157	CDR1	310	ERTFGHYA
	CDR2	311	ISWKGGTT
	CDR3	312	AARNTMSGSMSSSAYPY

	VH	313	QVQLVESGGGLVQAGASLRLSCAASERTFGHYAMGWFR QAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYW GQGTQVTVSS

6.5 Example 5. Deubiquitinase Activity of Anti-SYNGAP1 targeted enDubs

[00322] EnDubs targeting SYNGAP1 were constructed using the anti-SYNGAP1 nanobodies described in above in Example 4. The experimental fusion proteins contained from N to C terminus: FireflyLuciferase-P2A-anti-syngap1 nanobody-Cezanne catalytic domain. The amino acid sequence of each of the experimental anti-SYNGAP1 enDubs is provided below in Table 13.

[00323] Table 13 provides the amino acid sequence of exemplary anti-SYNGAP1 enDubs.

Table 13. Amino Acid Sequence of Anti-SYNGAP1 enDubs

Description	SEQ ID NO	Amino Acid Sequence
FireflyLuciferase-P2A-anti-syngap1_FLX00157-Cezanne	369	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTD AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQF FMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKG LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGF NEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFS HARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILIT PEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKS LIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAV VVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLKGSGATNFSLLKQAGDVEE NPGPRSGTGSSGQVQLVESGGGLVQAGASLRLSCAASERTFGHY AMGWFRQAPGKEREFVATISWKGGTTGYAHSVKGRFTISRDSAK NMVYLQMNSLKPEDTAVYYCAARNTMSGSMSSSAYPYWGQGTQV TVSSGGGGSGGGGSGGGGSGGGGSQVQLVESGGGLVQAGASLRL SCAASERTFGHYAMGWFRQAPGKEREFVATISWKGGTTGYAHSV KGRFTISRDSAKNMVYLQMNSLKPEDTAVYYCAARNTMSGSMSS SAYPYWGQGTQVTVSSGAPGSGPPSFSEGSGGSRTPEKGFSDRE PTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHVSSNG GGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLV ALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMWGF HDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKESGLVYT EDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPVYESL EEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPL EVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDS EYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLH SYMNVKWIPLSSDAQAPLAQ
FireflyLuciferase-P2A-anti-syngap1_FLX0015	370	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTD AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQF FMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKG

6-Cezanne		LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGF NEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFS HARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILIT PEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKS LIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAV VVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLKGSGATNFSLLKQAGDVEE NPGPRSGTGSSGQVQLVESGGGLVQPGGSLRLACAASGFTFGTH AMHWVRWAPGKGFEWVSTISSGGGGTRYADSVKGRFTISRDNAK NTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVTVSSGGG GSGGGGSGGGGSGGGGSQVQLVESGGGLVQPGGSLRLACAASGF TFGTHAMHWVRWAPGKGFEWVSTISSGGGGTRYADSVKGRFTIS RDNAKNTVYLQMDNLKPEDTAVYYCNSPSNIANDNWGQGTQVTV SSGAPGSGPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDD IVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPI CAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSV DPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYAL MEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKL ASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRR PIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVL AYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVDPG KGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPLSSDA QAPLAQ
FireflyLuciferase-P2A-anti-syngap1_FLX00155-Cezanne	371	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTD AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQF FMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKG LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGF NEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFS HARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILIT PEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKS LIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAV VVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLKGSGATNFSLLKQAGDVEE NPGPRSGTGSSGQVQLVESGGGLVQPGGSLRLSCAASGFAFGSY DMSWVRQAPGQGPEWVSAITPGGGGTFYAYYSDSVKGRFAISRD NAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGTQVTVSSG GGGSGGGGSGGGGSGGGGSQVQLVESGGGLVQPGGSLRLSCAAS GFAFGSYDMSWVRQAPGQGPEWVSAITPGGGGTFYAYYSDSVKG RFAISRDNAKNTLTLQMNSLKPDDTAMYYCAKNFYGNGGRGHGT QVTVSSGAPGSGPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQ RQDDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPL EMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNW WVSVDPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKA LYALMEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNE LIKLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAH

		VLRRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRS PLVLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFA VDPGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPL SSDAQAPLAQ
FireflyLuciferase-P2A-anti-syngap1_FLX00154-Cezanne	372	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTD AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQF FMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKG LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGF NEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFS HARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILIT PEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKS LIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAV VVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLKGSGATNFSLLKQAGDVEE NPGPRSGTGSSGQVQLVESGGGLVQPGGSLRLSCAASGFIFSSY QMAWVRQAPGKGLEWVADINTGGWNTYYADSVKGRFTISRDNAK NTLYLEMNSLKPEDTAVYYCAADRWMVAKIVGGDLDFDSWGQGT QVTVSSGGGGSGGGGSGGGGSGGGGSQVQLVESGGGLVQPGGSL RLSCAASGFIFSSYQMAWVRQAPGKGLEWVADINTGGWNTYYAD SVKGRFTISRDNAKNTLYLEMNSLKPEDTAVYYCAADRWMVAKI VGGDLDFDSWGQGTQVTVSSGAPGSGPPSFSEGSGGSRTPEKGF SDREPTRPPRPILQRQDDIVQEKRLSRGISHASSSIVSLARSHV SSNGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQ SMLVALEQAGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLG MWGFHDRDLMLRKALYALMEKGVEKEALKRRWRWQQTQQNKESG LVYTEDEWQKEWNELIKLASSEPRMHLGTNGANCGGVESSEEPV YESLEEFHVFVLAHVLRRPIVVVADTMLRDSGGEAFAPIPFGGI YLPLEVPASQCHRSPLVLAYDQAHFSALVSMEQKENTKEQAVIP LTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVILSLEVKL HLLHSYMNVKWIPLSSDAQAPLAQ
FireflyLuciferase-P2A-anti-syngap1_FLX00153-Cezanne	373	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTD AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQF FMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKG LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGF NEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFS HARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILIT PEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKS LIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAV VVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLKGSGATNFSLLKQAGDVEE NPGPRSGTGSSGQLQLVESGGGLVQPGESLRLSCAASGFTFSNY RMYWVRMAPGKGLEWVSDIDRSGTYTYYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCAADRRLIVDLTPEVYDHWGQGTQV TVSSGAPGSGPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQ DDIVQEKRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEM

		PICAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWV SVDPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKALY ALMEKGVEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELI KLASSEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVL RRPIVVVADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPL VLAYDQAHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVD PGKGWEWGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPLSS DAQAPLAQ
FireflyLuciferase-P2A-anti-syngap1_FLX00152-Cezanne	374	MEDAKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTD AHIEVDITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQF FMPVLGALFIGVAVAPANDIYNERELLNSMGISQPTVVFVSKKG LQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGF NEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFS HARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILIT PEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPM IMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKS LIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAV VVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTG KLDARKIREILIKAKKGGKIAVTRLKGSGATNFSLLKQAGDVEE NPGPRSGTGSSGQVQLVESGGGLVQPGGSLRLSCAASGFSFSNF PMMWVRQAPGKGREWVADINQDGRNTYYADSVKGRFTISRDNAK TTVYLQMNNLNPEDTAVYYCQAIRTTTHFDSWGQGTQVTVSSGA PGSGPPSFSEGSGGSRTPEKGFSDREPTRPPRPILQRQDDIVQE KRLSRGISHASSSIVSLARSHVSSNGGGGGSNEHPLEMPICAFQ LPDLTVYNEDFRSFIERDLIEQSMLVALEQAGRLNWWVSVDPTS QRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKALYALMEKG VEKEALKRRWRWQQTQQNKESGLVYTEDEWQKEWNELIKLASSE PRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRRPIVV VADTMLRDSGGEAFAPIPFGGIYLPLEVPASQCHRSPLVLAYDQ AHFSALVSMEQKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWE WGKDDSDNVRLASVILSLEVKLHLLHSYMNVKWIPLSSDAQAPL AQ

[00324] Each of the constructs in Table 13 was tested as described in Example 3. As shown in **FIG. 9**, each of the SYNGAP1 targeted nanobodies showed an increase in SYNGAP1 expression of at least 2-fold over the control.

* * *

[00325] The invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[00326] All references (e.g., publications or patents or patent applications) cited herein are

incorporated herein by reference in their entireties and for all purposes to the same extent as if each individual reference (e.g., publication or patent or patent application) was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

Other embodiments are within the following claims.

CLAIMS

What is claimed is:

1. A fusion protein comprising:
    a. an effector domain comprising a catalytic domain of a deubiquitinase, or a functional fragment or functional variant thereof; and
    b. a targeting domain comprising a targeting moiety that specifically binds a cytosolic protein.

2. The fusion protein of claim 1, wherein said deubiquitinase is a cysteine protease or a metalloprotease.

3. The fusion protein of claim 2, wherein said deubiquitinase is a cysteine protease.

4. The fusion protein of claim 3, wherein said cysteine protease is a ubiquitin-specific protease (USP), a ubiquitin C-terminal hydrolase (UCH), a Machado-Josephin domain protease (MJD), an ovarian tumour protease (OTU), a MINDY protease, or a ZUFSP protease.

5. The fusion protein of claim 4, wherein said cysteine protease is a USP.

6. The fusion protein of claim 5, wherein said USP is USP1, USP2, USP3, USP4, USP5, USP6, USP7, USP8, USP9X, USP9Y, USP10, USP11, USP12, USP13, USP14, USP15, USP16, USP17, USP17L2, USP17L3, USP17L4, USP17L5, USP17L7, USP17L8, USP18, USP19, USP20, USP21, USP22, USP23, USP24, USP25, USP26, USP27X, USP28, USP29, USP30, USP31, USP32, USP33, USP34, USP35, USP36, USP37, USP38, USP39, USP40, USP41, USP42, USP43, USP44, USP45, or USP46.

7. The fusion protein of claim 4, wherein said cysteine protease is a UCH.

8. The fusion protein of claim 7, wherein said UCH is BAP1, UCHL1, UCHL3, or UCHL5.

9. The fusion protein of claim 4, wherein said cysteine protease is a MJD.

10. The fusion protein of claim 9, wherein said MJD is ATXN3 or ATXN3L.

11. The fusion protein of claim 4, wherein said cysteine protease is an OTU.

12. The fusion protein of claim 11, wherein said OTU is OTUB1 or OTUB2.

13. The fusion protein of claim 4, wherein said cysteine protease is a MINDY.

14. The fusion protein of claim 13, wherein said MINDY MINDY1, MINDY2, MINDY3, or MINDY4.

15. The fusion protein of claim 4, wherein said cysteine protease is a ZUFSP.

16. The fusion protein of claim 15, wherein said ZUFSP is ZUP1.

17. The fusion protein of claim 2, wherein said deubiquitinase is a metalloprotease.

18. The fusion protein of claim 17, wherein said metalloprotease is a Jab1/Mov34/Mpr1 Pad1 N-terminal+ (MPN+) (JAMM) domain protease.

19. The fusion protein of any one of the preceding claims, wherein said deubiquitinase comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112.

20. The fusion protein of any one of the preceding claims, wherein said catalytic domain comprises a catalytic domain derived from a deubiquitinase comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 1-112.

21. The fusion protein of any one of the preceding claims, wherein said catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286.

22. The fusion protein of any one of the preceding claims, wherein said catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286.

23. The fusion protein of any one of the preceding claim, wherein said catalytic domain comprises an amino acid sequence that is a functional fragment of the amino acid sequence of any one of SEQ ID NOS: 1-112.

24. The fusion protein of any one of the preceding claim, wherein said catalytic domain comprises an amino acid sequence that is a functional fragment of the amino acid sequence of any one of SEQ ID NOS: 113-220 or 286.

25. The fusion protein of any one of the preceding claims, wherein said moiety that specifically binds a cytosolic protein comprises an antibody, or functional fragment or functional variant thereof.

26. The fusion protein of claim 25, wherein said antibody, or functional fragment or functional variant thereof, comprises a full-length antibody, a single chain variable fragment (scFv), a scFv2, a scFv-Fc, a Fab, a Fab', a F(ab')2, a F(v), a VHH, or a $(VHH)_2$.

27. The fusion protein of claim 26, wherein said antibody, or functional fragment or functional variant thereof, comprises a VHH or a $(VHH)_2$.

28. The fusion protein of any one of the preceding claims, wherein said cytosolic protein is cyclin-dependent kinase-like 5 (CDKL5), copper-transporting ATPase 2 (ATP7B), syntaxin-binding protein 1 (STXBP1), Ras/Rap GTPase-activating protein (SYNGAP1), progranulin (GRN), protein jagged-1 (JAG1), GATOR complex protein DEPDC5 (DEPDC5), tuberin (TSC2), hamartin (TSC1), kinesin-like protein KIF1A (KIF1A), dynamin-1 (DNM1), SH3 and multiple ankyrin repeat domains protein 3 (SHANK3), dystrophin (DMD), oxygen-regulated protein 1 (RP1), titin (TTN), cytoplasmic dynein 1 heavy chain 1 (DYNC1H1), TRIO and F-actin-binding protein (TRIO), probable ubiquitin carboxyl-terminal hydrolase FAF-X (USP9X), cystatin-B (CSTB), or pterin-4-alpha-carbinolamine dehydratase (PCBD1).

29. The fusion protein of any one of the preceding claims, wherein said cytosolic protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 221-328 or 287-289.

30. The fusion protein of any one of the preceding claims, wherein said effector domain is directly operably connected to said targeting domain.

31. The fusion protein of any one of claims 1-29, wherein said effector domain is indirectly operably connected to said targeting domain.

32. The fusion protein of claim 31, wherein said effector domain is indirectly operably connected to said targeting domain via a peptide linker.

33. The fusion protein of claim 32, wherein said effector domain is indirectly fused to said targeting domain via a peptide linker of sufficient length such that said effector domain and said targeting domain can simultaneous bind the respective target proteins.

34. The fusion protein of claim 32 or 33, wherein said peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications.

35. The fusion protein of claim 34, wherein said peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications.

36. The fusion protein of any one of the preceding claims, wherein said effector domain is operably connected either directly or indirectly to the C terminus of said targeting domain.

37. The fusion protein of any one of claims 1-35, wherein said effector moiety is operably connected either directly or indirectly to the N terminus of said targeting domain.

38. A nucleic acid molecule encoding the fusion protein of any one of claims 1-37.

39. The nucleic acid molecule of claim 38, wherein said nucleic acid molecule is a DNA molecule.

40. The nucleic acid molecule of claim 38, wherein said nucleic acid molecule is an RNA molecule.

41. A vector comprising the nucleic acid molecule of any one of claims 38-40.

42. The vector of claim 41, wherein said vector is a plasmid or a viral vector.

43. A viral particle comprising the nucleic acid molecule of any one of claims 38-40.

44. An in vitro cell or population of cells comprising the fusion protein of any one of claims 1-37, the nucleic acid molecule of any one of claims 38-40, or the vector of any one of claims 41-42.

45. A pharmaceutical composition comprising the fusion protein of any one of claims 1-37, the nucleic acid molecule of any one of claims 38-40, the vector of any one of claims 41-42, or the viral particle of claim 43, and an excipient.

46. A method of making the fusion protein of any one of claims 1-37, comprising

a. introducing into an in vitro cell or population of cells the nucleic acid molecule of any one of claims 38-40, the vector of any one of claims 41-42, the viral particle of claim 43;

b. culturing the cell or population of cells in a culture medium under conditions suitable for expression of the fusion protein,

c. isolating the fusion protein from the culture medium, and

d. optionally purifying the fusion protein.

47. A method of treating or preventing a disease in a subject comprising administering the fusion protein of any one of claims 1-37, the nucleic acid molecule of any one of claims 38-40,

the vector of any one of claims 41-42, the viral particle of claim 43, or the pharmaceutical composition of claim 45, to a subject in need thereof.

48. The method of claim 47, wherein the subject is human.

49. The method of claim 47 or 48, wherein said disease is associated with decreased expression of a functional version of the cytosolic protein relative to a non-diseased control.

50. The method of any one of claims 47-49, wherein the disease is associated with decreased stability of a functional version of the cytosolic protein relative to a non-diseased control.

51. The method of any one of claims 47-50, wherein said disease is associated with increased ubiquitination of the cytosolic protein relative to a non-diseased control.

52. The method of any one of claims 47-51, wherein said disease is associated with increased ubiquitination and degradation of the cytosolic protein relative to a non-diseased control.

53. The method of any one of claims 47-52, wherein said disease is a genetic disease.

54. The method of any one of claims 47-53, wherein said disease is SYNGAP1 encephalopathy, CDKL5 deficiency disorder, STXBP1 encephalopathy, early infantile epileptic encephalopathy type 2, Wilson disease, early infantile epileptic encephalopathy type 4, mental retardation autosomal dominant 5, aphasia, alagille syndrome 1, epilepsy, tuberous sclerosis-2, tuberous sclerosis-1, KIF1A-associated neurological disorder, encephalopathy, Phelan-McDermid syndrome, Becker Muscular Dystrophy, RP1, retinitis pigmentosa 1, dilated cardiomyopathy 1G, DYNC1H1 Syndrome, TRIO-Related intellectual disability (ID), USP9X Development Disorder, epilepsy, progressive myoclonic 1 (EPM1), or hyperphenylalaninemia BH4-deficient D (HPABH4D).

55. The method of any one of claims 47-54, wherein

a. said target cytosolic protein is SYNGAP1, and said disease is SYNGAP1 encephalopathy;

b. said target cytosolic protein is SYNGAP1, and said disease is Mental retardation autosomal dominant 5.

c. said target cytosolic protein is CDKL5, and said disease is CDKL5 deficiency disorder;

d. said target cytosolic protein is CDKL5, and said disease is an early infantile epileptic encephalopathy

e. said target cytosolic protein is CDKL5, and said disease is early infantile epileptic encephalopathy type 2;
f. said target cytosolic protein is ATP7B, and said disease is Wilson disease;
g. said target cytosolic protein is STXBP1, and said disease is STXBP1 encephalopathy;
h. said target cytosolic protein is STXBP1, and said disease is an early infantile epileptic encephalopathy;
i. said target cytosolic protein is STXBP1, and said disease is early infantile epileptic encephalopathy type 4;
j. said target cytosolic protein is GRN, and said disease is aphasia primary progressive & FTD (frontotemporal degeneration);
k. said target cytosolic protein is JAG1, and said disease is alagille syndrome 1;
l. said target cytosolic protein is DEPDC5, and said disease is epilepsy (e.g., familial focal, with variable foci 1);
m. said target cytosolic protein is TSC2, and said disease is tuberous sclerosis;
n. said target cytosolic protein is TSC2, and said disease is tuberous sclerosis type 2;
o. said target cytosolic protein is TSC2, and said disease is tuberous sclerosis type 1;
p. said target cytosolic protein is TSC1, and said disease is tuberous sclerosis;
q. said target cytosolic protein is TSC1, and said disease is tuberous sclerosis type 1;
r. said target cytosolic protein is TSC1, and said disease is tuberous sclerosis type 2;
s. said target cytosolic protein is KIF1A, and said disease is KIF1A-associated neurological disorder;
t. said target cytosolic protein is DNM1, and said disease is a DNM1 encephalopathy;
u. said target cytosolic protein is DNM1, and said disease is encephalopathy;
v. said target cytosolic protein is SHANK3, and said disease is Phelan-McDermid syndrome;
w. said target cytosolic protein is DMD, and said disease is Becker Muscular Dystrophy;
x. said target cytosolic protein is RP1, and said disease is retinitis pigmentosa 1;

y. said target cytosolic protein is TTN, and said disease is dilated cardiomyopathy 1G;

z. said target cytosolic protein is DYNC1H1, and said disease is DYNC1H1 Syndrome;

aa. said target cytosolic protein is TRIO, and said disease is TRIO-Related intellectual disability (ID);

bb. said target cytosolic protein is USP9X, and said disease is USP9X development disorder;

cc. said target cytosolic protein is CSTB, and the disease is epilepsy, progressive myoclonic 1 (EPM1); or

dd. the target cytosolic protein is PCBD1, and the disease is hyperphenylalaninemia, BH4-deficient, D (HPABH4D).

56. The method of any one of claims 47-55, wherein said disease is a haploinsufficiency disease.

57. The method of any one of claims 47-56, wherein said fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered at a therapeutically effective dose.

58. The method of any one of claims 47-57, wherein said fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered systematically or locally.

59. The method of any one of claims 47-58, wherein said fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered intravenously, subcutaneously, or intramuscularly.

60. The fusion protein of any one of claims 1-37, the polynucleotide of claim 38, the DNA of claim 39, the RNA of claim 40, the vector of any one of claims 41-42, the viral particle of claim 43, or the pharmaceutical composition of claim 45 for use as a medicament.

61. The fusion protein of any one of claims 1-37, the polynucleotide of claim 38, the DNA of claim 39, the RNA of claim 40, the vector of any one of claims 41-42, the viral particle of claim 43, or the pharmaceutical composition of claim 45 for use in treating or inhibiting a genetic disorder.

62. A single variable domain antibody (VHH) that specifically binds SYNGAP1 comprising three complementarity determining regions: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312, or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 comprising 1, 2, or 3 amino acid modifications.

63. The VHH of claim 62, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 comprising 1, 2, or 3 amino acid modifications.

64. The VHH of claim 62, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 comprising 1, 2, or 3 amino acid modifications.

65. The VHH of claim 62, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 comprising 1, 2, or 3 amino acid modifications.

66. The VHH of claim 62, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 comprising 1, 2, or 3 amino acid modifications.

67. The VHH of claim 62, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 comprising 1, 2, or 3 amino acid modifications.

68. The VHH of claim 62, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 comprising 1, 2, or 3 amino acid modifications.

69. The VHH of any one of claims 62-68, wherein said VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313.

70. A $(VHH)_2$ comprising a first VHH that specifically binds SYNGAP1 comprising three complementarity determining regions: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312, or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 comprising 1, 2, or 3 amino acid modifications; and

a second VHH that specifically binds SYNGAP1 comprising three complementarity determining regions: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310, or the amino acid sequence of SEQ ID NO: 290, 294, 298, 302, 306, or 310 comprising 1, 2, or 3 amino acid modifications;

e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311, or the amino acid sequence of SEQ ID NO: 291, 295, 299, 303, 307, or 311 comprising 1, 2, or 3 amino acid modifications; and/or

f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312, or the amino acid sequence of SEQ ID NO: 292, 296, 300, 304, 308, or 312 comprising 1, 2, or 3 amino acid modifications;

wherein the first VHH and the second VHH are directly or indirectly operably connected.

71. The $(VHH)_2$ of claim 70, wherein the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 comprising 1, 2, or 3 amino acid modifications; and

the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 290, or the amino acid sequence of SEQ ID NO: 290 comprising 1, 2, or 3 amino acid modifications;

e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 291, or the amino acid sequence of SEQ ID NO: 291 comprising 1, 2, or 3 amino acid modifications; and/or

f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 292, or the amino acid sequence of SEQ ID NO: 292 comprising 1, 2, or 3 amino acid modifications.

72. The $(VHH)_2$ of claim 70, wherein the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 comprising 1, 2, or 3 amino acid modifications; and

the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 294, or the amino acid sequence of SEQ ID NO: 294 comprising 1, 2, or 3 amino acid modifications;

e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 295, or the amino acid sequence of SEQ ID NO: 295 comprising 1, 2, or 3 amino acid modifications; and/or

f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 296, or the amino acid sequence of SEQ ID NO: 296 comprising 1, 2, or 3 amino acid modifications.

73. The $(VHH)_2$ of claim 70, wherein the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 comprising 1, 2, or 3 amino acid modifications; and

the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 298, or the amino acid sequence of SEQ ID NO: 298 comprising 1, 2, or 3 amino acid modifications;

e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 299, or the amino acid sequence of SEQ ID NO: 299 comprising 1, 2, or 3 amino acid modifications; and/or

f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 300, or the amino acid sequence of SEQ ID NO: 300 comprising 1, 2, or 3 amino acid modifications.

74. The $(VHH)_2$ of claim 70, wherein the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 comprising 1, 2, or 3 amino acid modifications; and

the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 302, or the amino acid sequence of SEQ ID NO: 302 comprising 1, 2, or 3 amino acid modifications;

e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 303, or the amino acid sequence of SEQ ID NO: 303 comprising 1, 2, or 3 amino acid modifications; and/or

f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 304, or the amino acid sequence of SEQ ID NO: 304 comprising 1, 2, or 3 amino acid modifications.

75. The $(VHH)_2$ of claim 70, wherein the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 comprising 1, 2, or 3 amino acid modifications; and/or

c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 comprising 1, 2, or 3 amino acid modifications; and

the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 306, or the amino acid sequence of SEQ ID NO: 306 comprising 1, 2, or 3 amino acid modifications;

e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 307, or the amino acid sequence of SEQ ID NO: 307 comprising 1, 2, or 3 amino acid modifications; and/or

f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 308, or the amino acid sequence of SEQ ID NO: 308 comprising 1, 2, or 3 amino acid modifications.

76. The $(VHH)_2$ of claim 70, wherein the first VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

a. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 comprising 1, 2, or 3 amino acid modifications;

b. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 comprising 1, 2, or 3 amino acid modifications; and/or
c. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 comprising 1, 2, or 3 amino acid modifications; and

the second VHH comprises three CDRs: CDR1, CDR2, and CDR3, wherein

d. the amino acid sequence of CDR1 comprises the amino acid sequence of SEQ ID NO: 310, or the amino acid sequence of SEQ ID NO: 310 comprising 1, 2, or 3 amino acid modifications;
e. the amino acid sequence of CDR2 comprises the amino acid sequence of SEQ ID NO: 311, or the amino acid sequence of SEQ ID NO: 311 comprising 1, 2, or 3 amino acid modifications; and/or
f. the amino acid sequence of CDR3 comprises the amino acid sequence of SEQ ID NO: 312, or the amino acid sequence of SEQ ID NO: 312 comprising 1, 2, or 3 amino acid modifications.

77. The $(VHH)_2$ of any one of claims 70, wherein said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313; and said second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 293, 297, 301, 305, 309, or 313.

78. The $(VHH)_2$ of any one of claims 70, wherein

a. said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293; and said second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 293;
b. said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 297; and said second VHH comprises an amino acid sequence at

least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 297;

c. said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 301; and said second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 301;

d. said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 305; and said second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 305;

e. said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 309; and said second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 309; or

f. said first VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 313; and said second VHH comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 313.

79. The $(VHH)_2$ of any one of claims 62-78, wherein said first VHH is operably connected to said second VHH via a peptide linker.

80. The $(VHH)_2$ of claim 62-78, wherein said peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications.

81. The $(VHH)_2$ of claim 80, wherein said peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications.

82. The $(VHH)_2$ of any one of claims 70-81, wherein said $(VHH)_2$ comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 314-319.

83. A nucleic acid molecule encoding the VHH of any one of claims 62-69 or the $(VHH)_2$ of any one of claims 70-82.

84. The nucleic acid molecule of claim 83, wherein said nucleic acid molecule is a DNA molecule.

85. The nucleic acid molecule of claim 83, wherein said nucleic acid molecule is an RNA molecule.

86. A vector comprising the nucleic acid molecule of any one of claims 83-85.

87. The vector of claim 86, wherein said vector is a plasmid or a viral vector.

88. A viral particle comprising the nucleic acid molecule of any one of claims 83-85

89. An in vitro cell or population of cells comprising the VHH of any one of claims 62-69 or the $(VHH)_2$ of any one of claims 70-82, the nucleic acid molecule of any one of claims 83-85, or the vector of any one of claims 86-87.

90. A pharmaceutical composition comprising the VHH of any one of claims 62-69 or the $(VHH)_2$ of any one of claims 70-82, the nucleic acid molecule of any one of claims 83-85, the vector of any one of claims 86-87, or the viral particle of claim 88, and an excipient.

91. A method of making the VHH of any one of claims 62-69 or the $(VHH)_2$ of any one of claims 70-82, comprising

a. introducing into an in vitro cell or population of cells the nucleic acid molecule of any one of claims 83-85, the vector of any one of claims 86-87, the viral particle of claim 88;
b. culturing the cell or population of cells in a culture medium under conditions suitable for expression of the fusion protein,
c. isolating the fusion protein from the culture medium, and
d. optionally purifying the fusion protein.

92. The fusion protein of any one of claims 1-37, wherein said targeting domain comprises a VHH of any one of claims 62-69, or a $(VHH)_2$ of any one of claims 70-82.

93. The fusion protein of claim 92, wherein said catalytic domain comprises an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 286.

94. The fusion protein of any one of claims 92-93, wherein said effector domain is indirectly fused to said targeting domain via a peptide linker of sufficient length such that said effector domain and said targeting domain can simultaneous bind the respective target proteins.

95. The fusion protein of claim 94, wherein said peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519, or the amino acid sequence of any one of SEQ ID NOS: 375-384 or 402-519 comprising 1, 2, or 3 amino acid modifications.

96. The fusion protein of claim 95, wherein said peptide linker comprises the amino acid sequence of any one of SEQ ID NOS: 375-384, or the amino acid sequence of any one of SEQ ID NOS: 375-384 comprising 1, 2, or 3 amino acid modifications.

97. The fusion protein of any one of claims 92-96, wherein said effector domain is operably connected either directly or indirectly to the C terminus of said targeting domain.

98. The fusion protein of any one of claims 92-97, wherein said effector moiety is operably connected either directly or indirectly to the N terminus of said targeting domain.

99. The fusion protein of any one of claims 9-98, wherein said fusion protein comprises an amino acid sequence at least at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOS: 320-367.

100. A nucleic acid molecule encoding the fusion protein of any one of claims 92-99.

101. The nucleic acid molecule of claim 100, wherein said nucleic acid molecule is a DNA molecule.

102. The nucleic acid molecule of claim 100, wherein said nucleic acid molecule is an RNA molecule.

103. A vector comprising the nucleic acid molecule of any one of claims 99-102.

104. The vector of claim 103, wherein said vector is a plasmid or a viral vector.

105. A viral particle comprising the nucleic acid molecule of any one of claims 99-102.

106. An in vitro cell or population of cells comprising the fusion protein of any one of claims 92-99, the nucleic acid molecule of any one of claims 100-102, or the vector of any one of claims 103-104.

107. A pharmaceutical composition comprising the fusion protein of any one of claims 92-99, the nucleic acid molecule of any one of claims 100-102, the vector of any one of claims 103-104, or the viral particle of claim 105, and an excipient.

108. A method of making the fusion protein of any one of claims 92-99, comprising

a. introducing into an in vitro cell or population of cells the nucleic acid molecule of any one of claims 100-102, the vector of any one of claims 103-104, the viral particle of claim 105;
b. culturing the cell or population of cells in a culture medium under conditions suitable for expression of the fusion protein,
c. isolating the fusion protein from the culture medium, and
d. optionally purifying the fusion protein.

109. A method of treating or preventing a disease in a subject comprising administering the fusion protein of any one of claims 92-99, the nucleic acid molecule of any one of claims 100-102, the vector of any one of claims 103-104, the viral particle of claim 105, or the pharmaceutical composition of claim 107, to a subject in need thereof.

110. The method of claim 109, wherein the subject is human.

111. The method of any one of claims 109-110, wherein said disease is SYNGAP1 encephalopathy.

112. The method of any one of claims 108-110, wherein said fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered at a therapeutically effective dose.

113. The method of any one of claims 109-112, wherein said fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered systematically or locally.

114. The method of any one of claims 109-113, wherein said fusion protein, nucleic acid molecule, vector, viral particle, or pharmaceutical composition is administered intravenously, subcutaneously, or intramuscularly.

115. The fusion protein of any one of claims 92-99, the polynucleotide of claim 100, the DNA of claim 101, the RNA of claim 102, the vector of any one of claims 103-104, the viral particle of claim 105, or the pharmaceutical composition of claim 107 for use as a medicament.

116. The fusion protein of any one of claims 92-99, the polynucleotide of claim 100, the DNA of claim 101, the RNA of claim 102, the vector of any one of claims 103-104, the viral particle of claim 105, or the pharmaceutical composition of claim 107 for use in treating or inhibiting a genetic disorder.

FIG. 1A

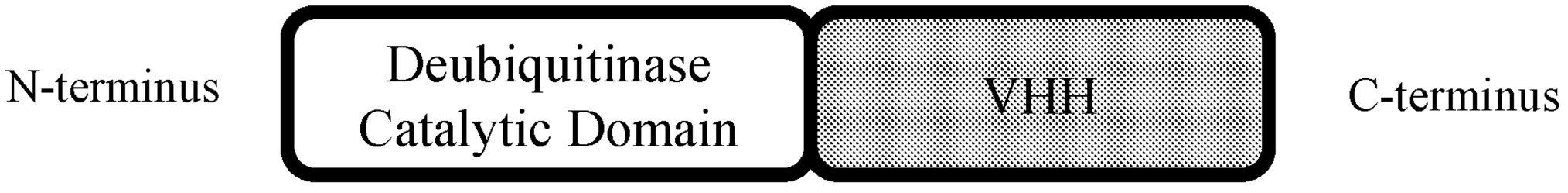

FIG. 1B

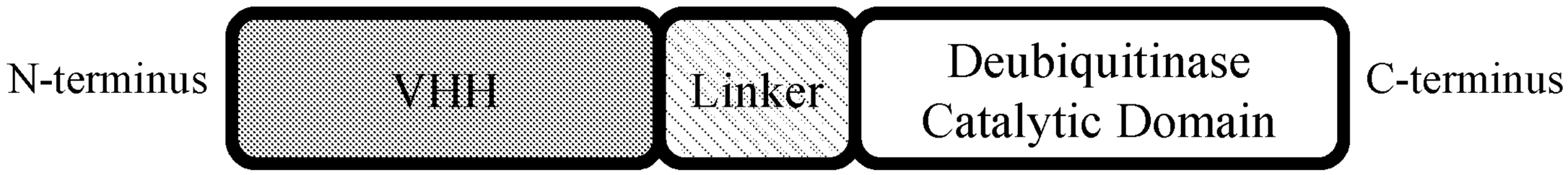

FIG. 1C

FIG. 1D

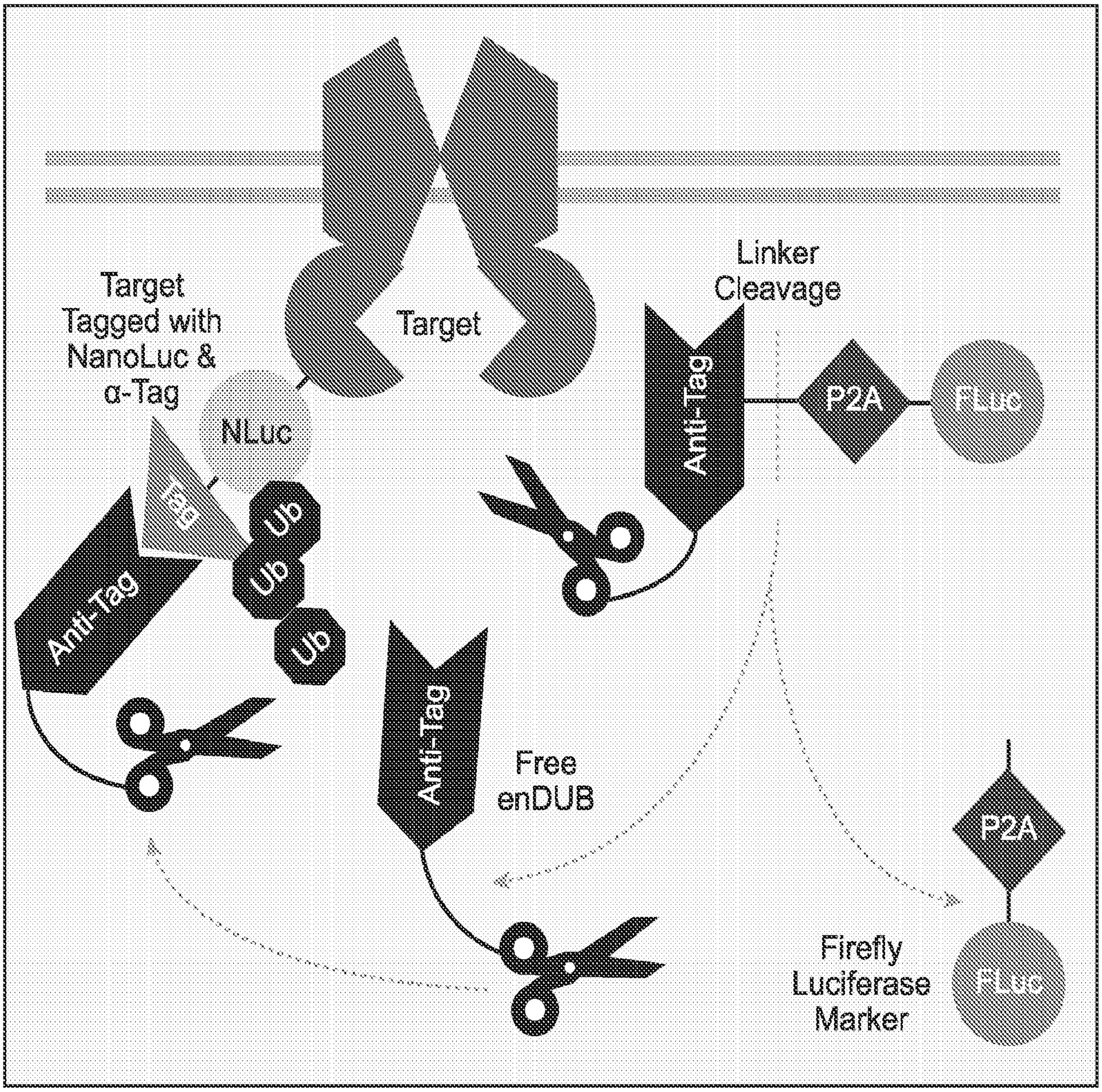
Target
Tagged with
NanoLuc &
α-Tag
NLuc
Target
Linker
Cleavage
Anti-Tag
P2A
FLuc
Ub
Ub
Ub
Anti-Tag
Anti-Tag
Free
enDUB
P2A
Firefly
Luciferase
Marker
FLuc

FIG. 2

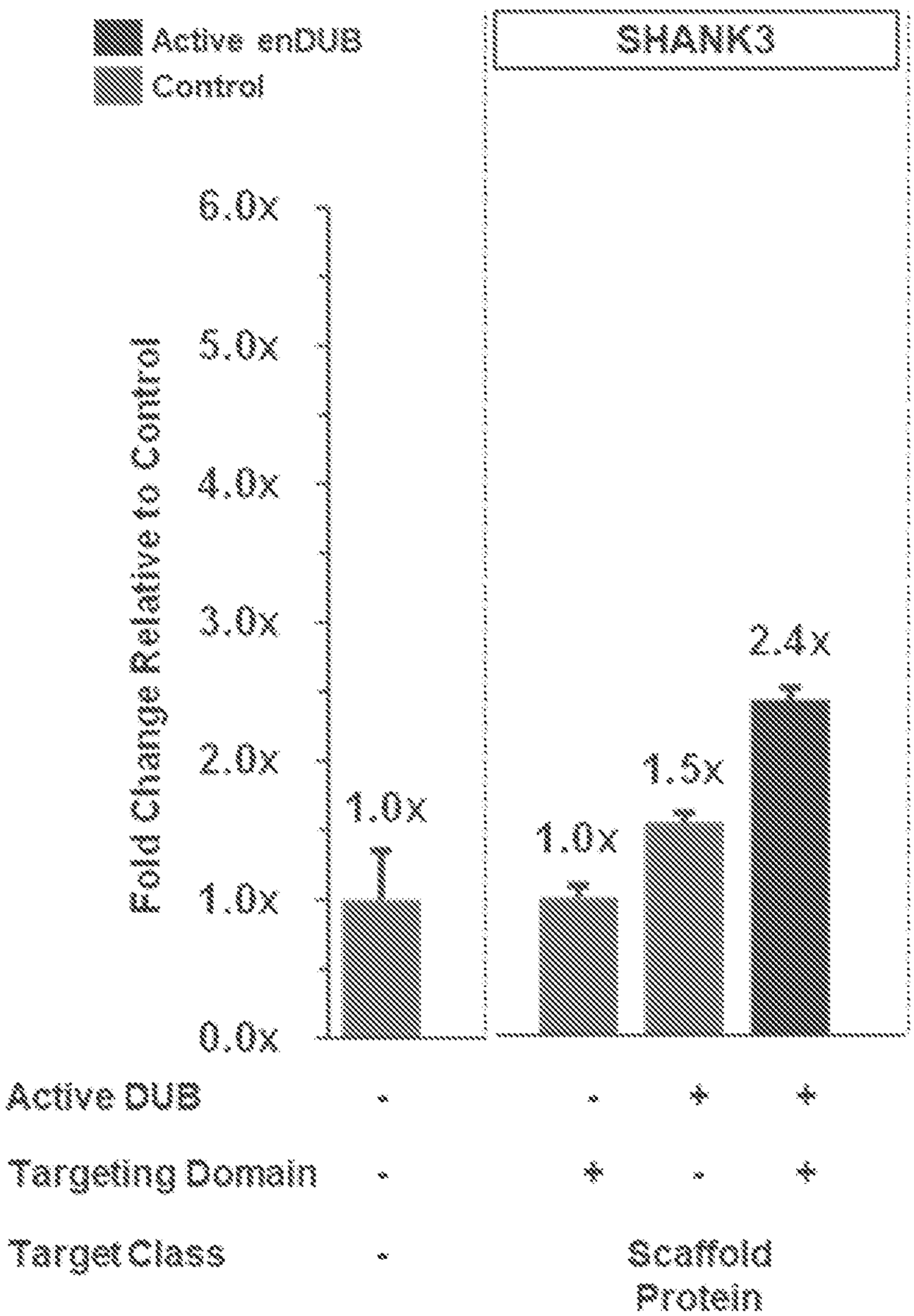
Active enDUB
Control
SHANK3
Fold Change Relative to Control
0.0x
1.0x
2.0x
3.0x
4.0x
5.0x
6.0x
1.0x
1.0x
1.5x
2.4x
Active DUB
Targeting Domain
Target Class
Scaffold Protein

FIG. 3

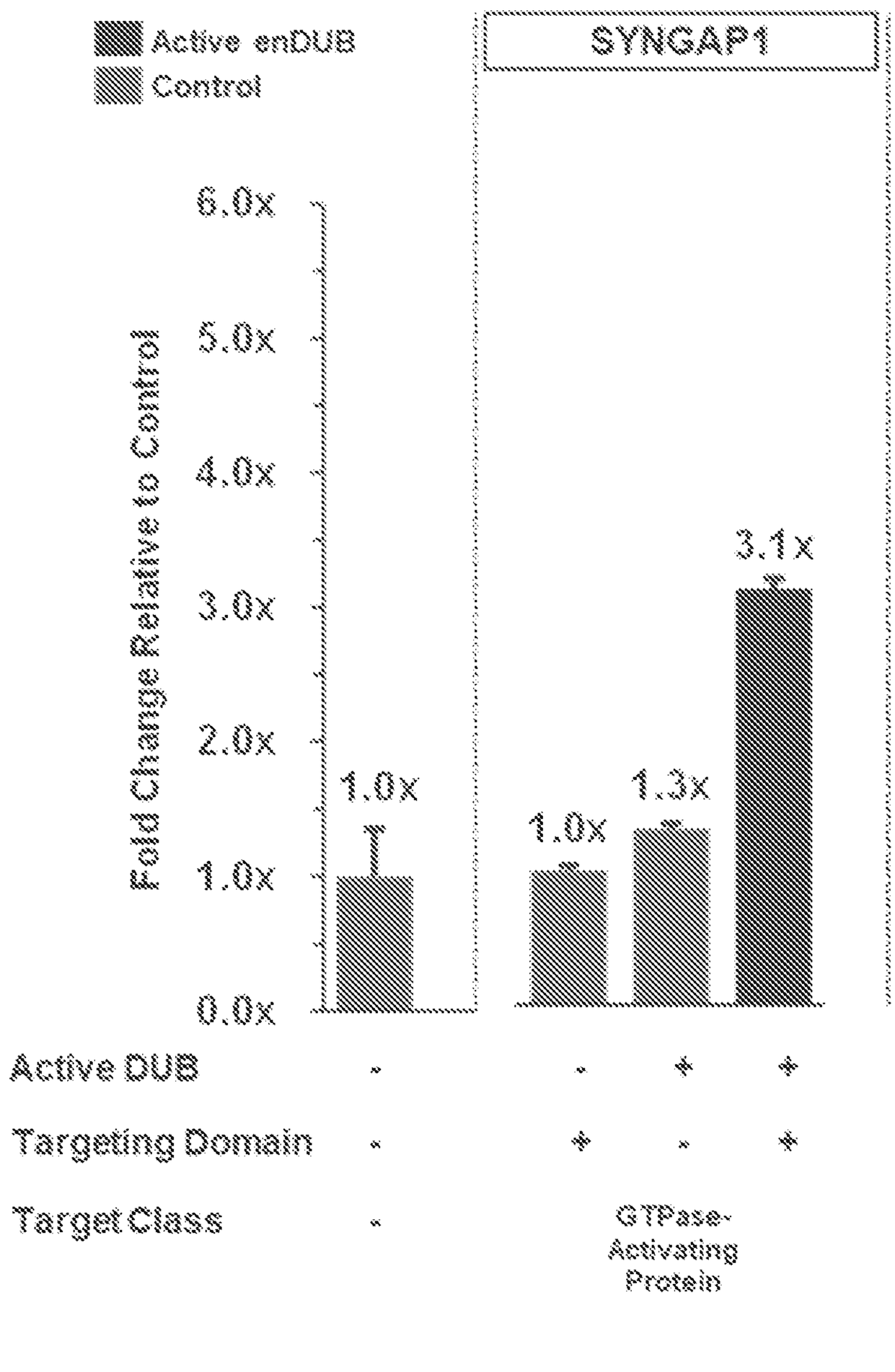
Active enDUB
Control
SYNGAP1
Fold Change Relative to Control
6.0x
5.0x
4.0x
3.0x
2.0x
1.0x
0.0x
1.0x
1.0x
1.3x
3.1x
Active DUB
Targeting Domain
Target Class
GTPase-Activating Protein

FIG. 4

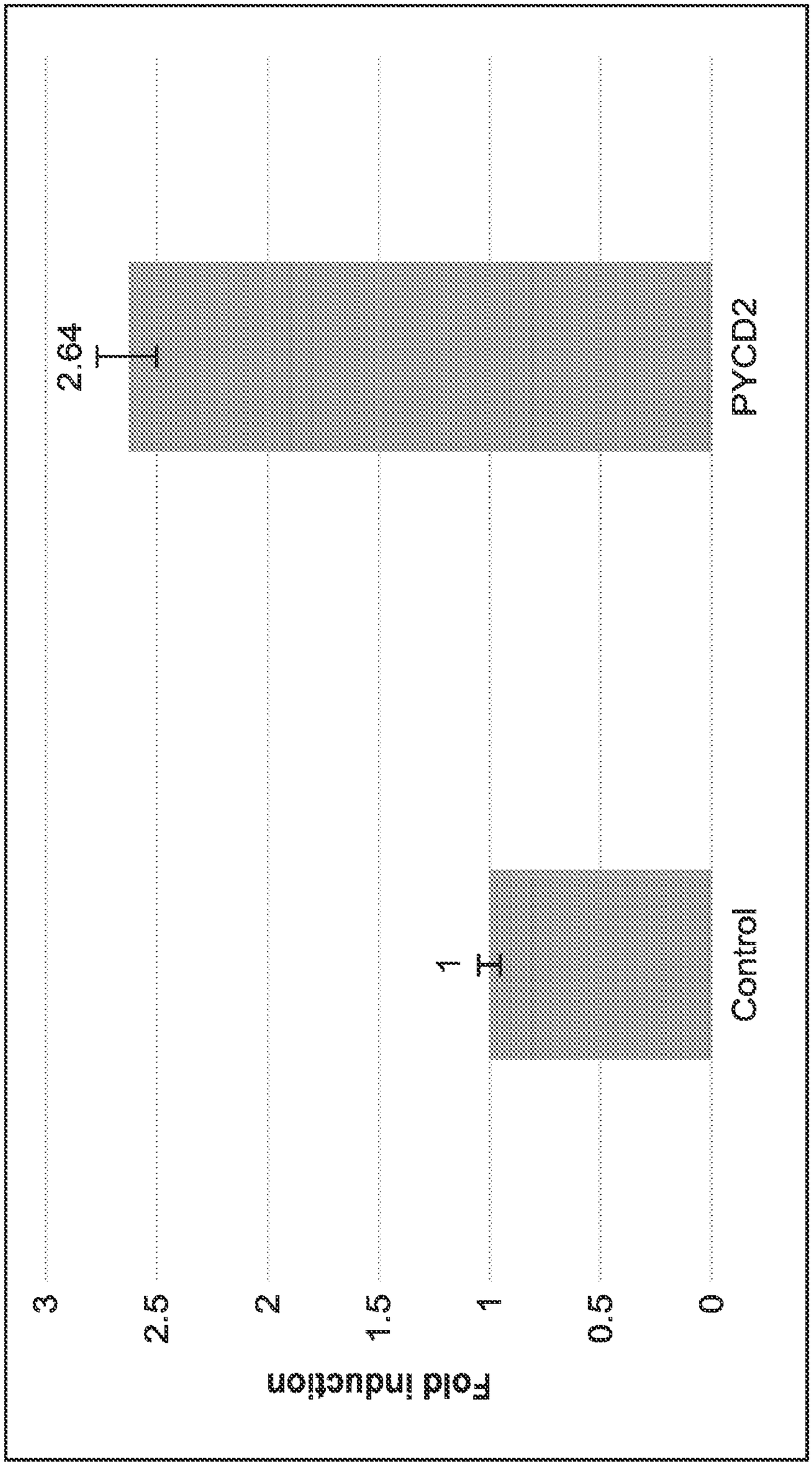

FIG. 5

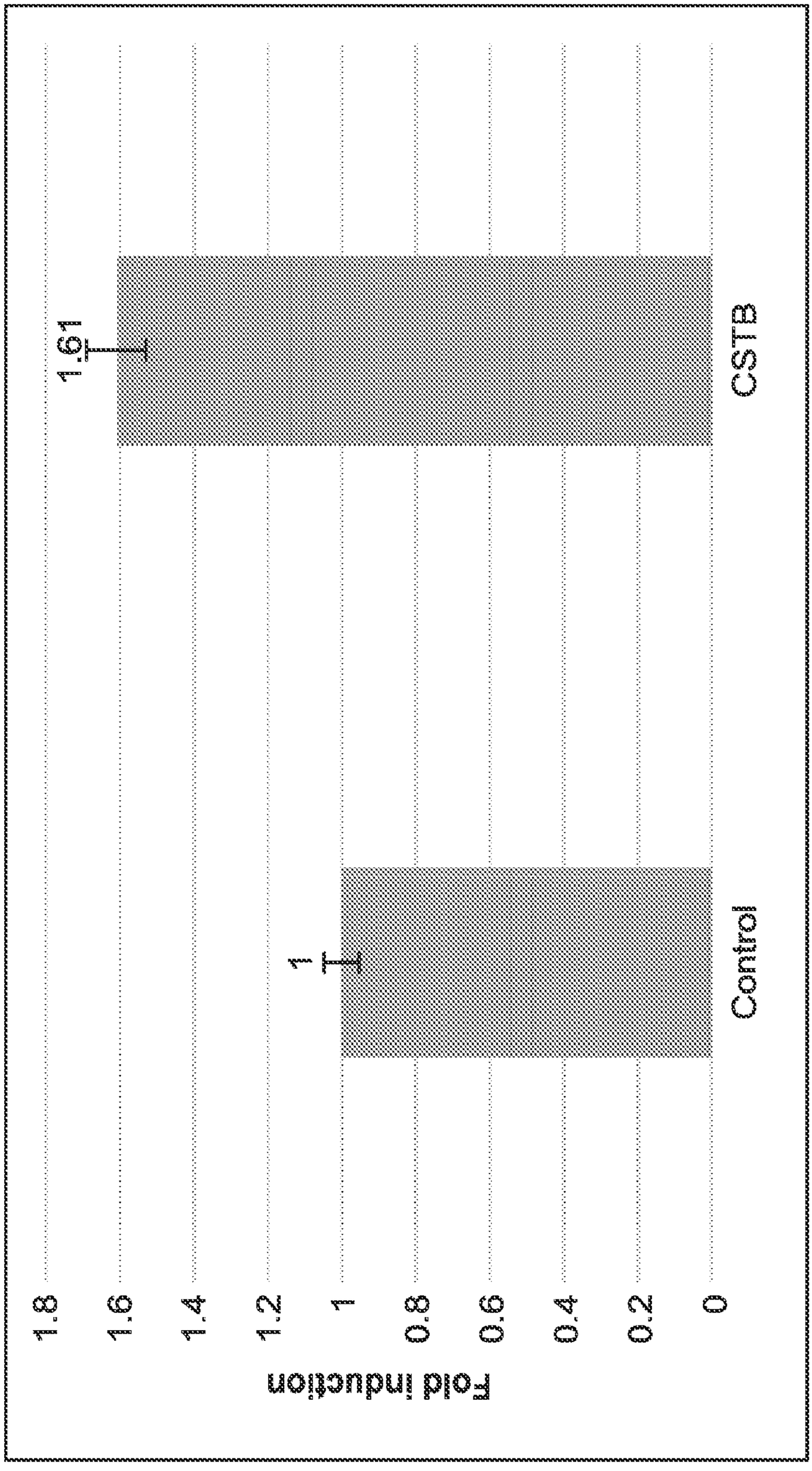

FIG. 6

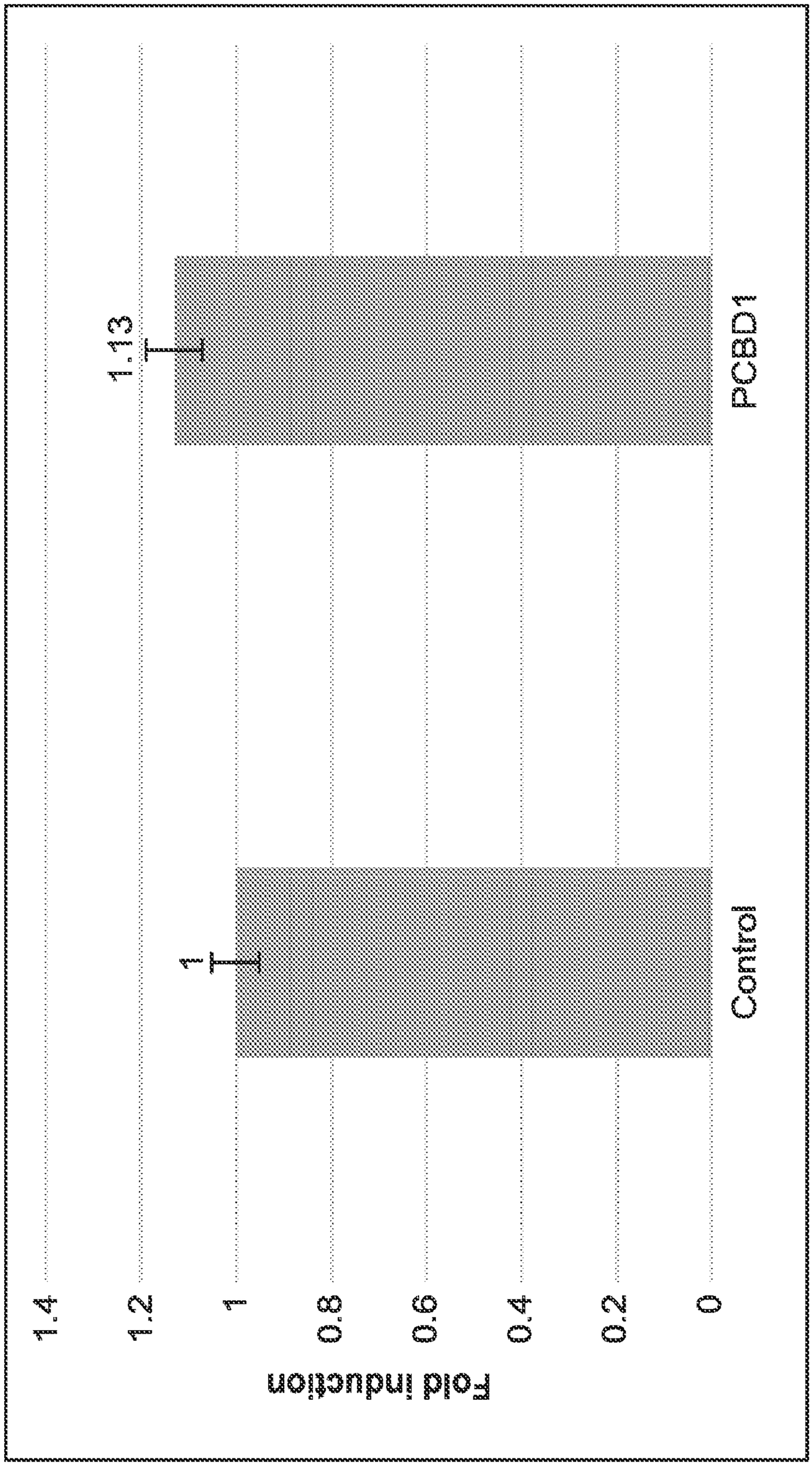

FIG. 7

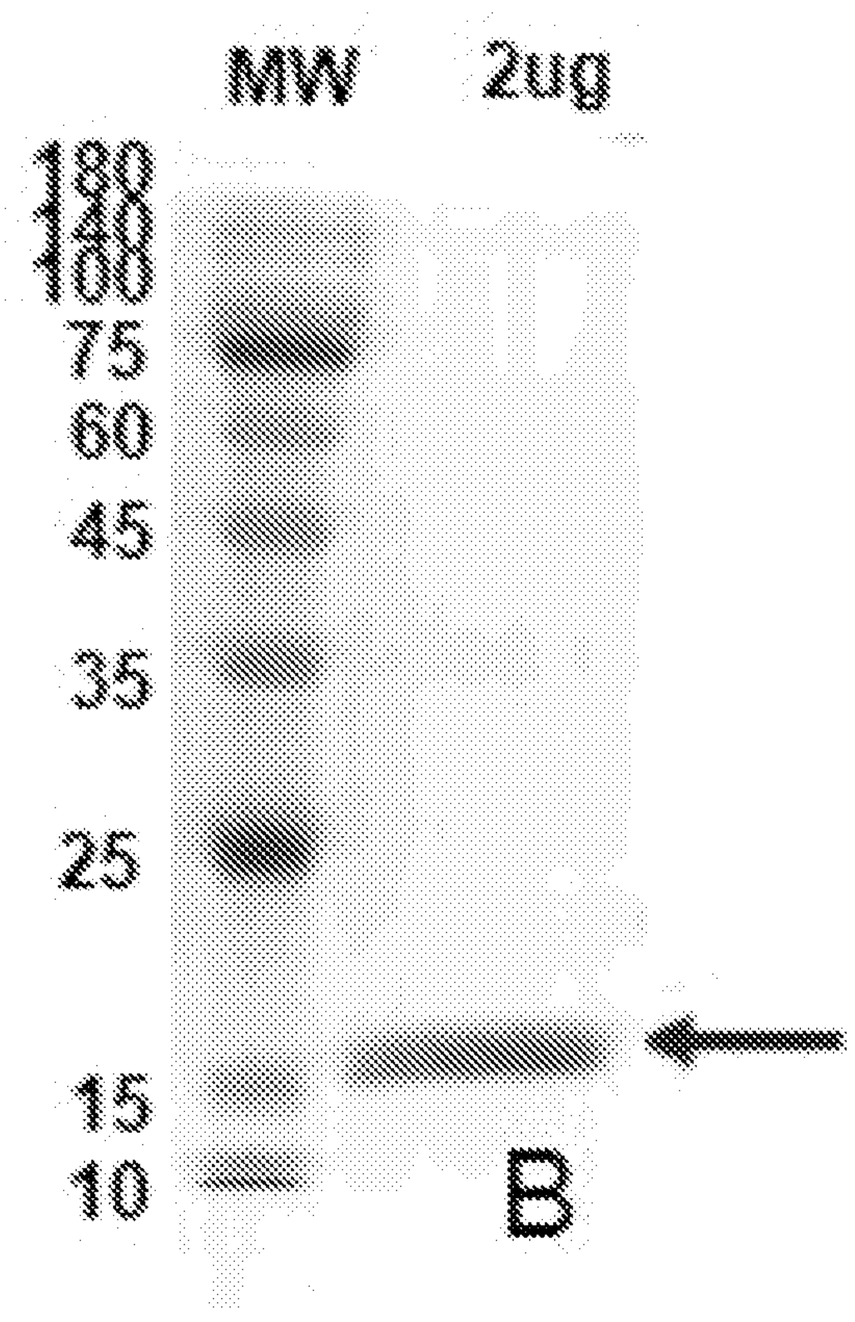

FIG. 8

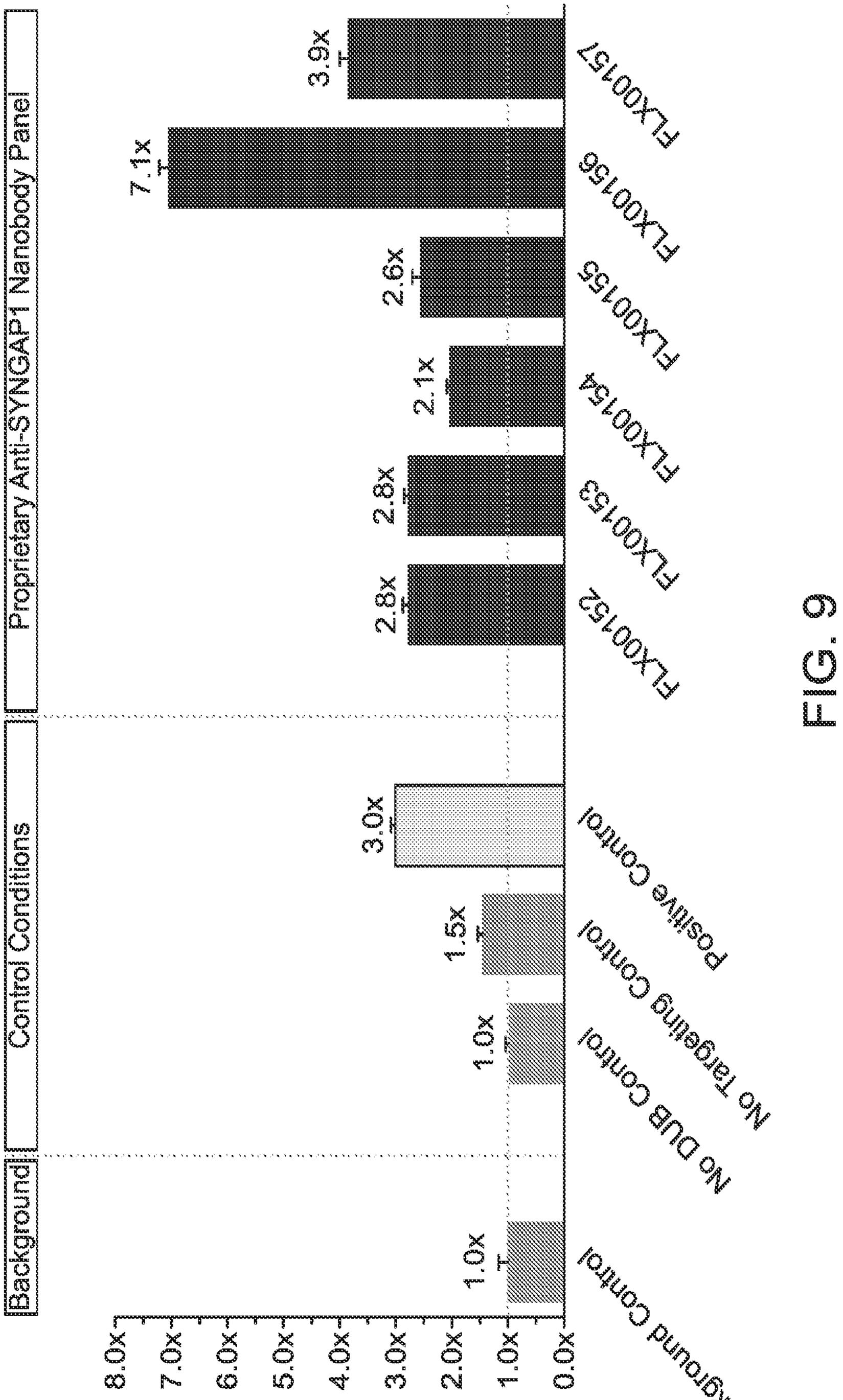
Proprietary Anti-SYNGAP1 Nanobody Panel
Control Conditions
Background
3.9x
7.1x
2.6x
2.1x
2.8x
2.8x
2.8x
3.0x
1.5x
1.0x
1.0x
FLX00157
FLX00156
FLX00155
FLX00154
FLX00153
FLX00152
Positive Control
No targeting Control
No DUB Control
Background Control
8.0x
7.0x
6.0x
5.0x
4.0x
3.0x
2.0x
1.0x
0.0x
Fold change Relative to Control

FIG. 6