(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
20 January 2022 (20.01.2022)

WIPO | PCT

(10) International Publication Number
WO 2022/015418 A1

(51) International Patent Classification:
A61P 31/14 (2006.01) *C07K 14/00* (2006.01)

(21) International Application Number:
PCT/US2021/034069

(22) International Filing Date:
25 May 2021 (25.05.2021)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
63/051,474 14 July 2020 (14.07.2020) US
63/067,593 19 August 2020 (19.08.2020) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, IT, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

WO 2022/015418 A1

(54) Title: SARS-COV-2 INHIBITORS

(57) Abstract: Polypeptide inhibitors of SARS-CoV-2 are disclosed comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101, and their use for treating and limiting development of SARS-CoV-2 infection.

[Continued on next page]

Published:

— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
— *with sequence listing part of description (Rule 5.2(a))*

SARS-COV-2 inhibitors

Cross reference

This application claims priority to U.S. Provisional Patent Application Serial Nos. 63/051,474 filed July 14, 2020 and 63/067,593 filed August 19, 2020, each incorporated by reference herein in its entirety.

Federal Funding Statement

This invention was made with government support under Grant No. FA8750-17-C-0219, awarded by the Defense Advanced Research Projects Agency and Grant Nos. HHSN272201700059C and R01 GM120553, awarded by the National Institutes of Health. The government has certain rights in the invention.

Sequence Listing Statement:

A computer readable form of the Sequence Listing is filed with this application by electronic submission and is incorporated into this application by reference in its entirety. The Sequence Listing is contained in the file created on May 25, 2021, having the file name "20-1074-WO_SeqList_ST25" and is 1,112kb in size.

Background

SARS -CoV-2 infection is thought to often start in the nose, with virus replicating there for several before spreading to the broader respiratory system. Delivery of a high concentration of a viral inhibitor into the nose and into the respiratory system generally could therefore potentially provide prophylactic protection, and therapeutic efficacy early in infection, and could be particularly useful for health care workers and others coming into frequent contact with infected individuals.

Summary

In a first aspect the disclosure provides polypeptides comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-17, 19-21, 23-34 and 100-101, wherein the polypeptide

binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD). In one embodiment, amino acid substitutions relative to the reference polypeptide amino acid sequence are selected from the exemplary amino acid substitutions provided in Table 1. In another embodiment, interface residues are identical to those in the reference polypeptide or are conservatively substituted relative to interface residues in the reference polypeptide. In a further embodiment the polypeptides comprise two or more copies of the amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101. In one embodiment, the polypeptide comprises the formula Z1-Z2-Z3, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Z2 comprises an optional amino acid linker; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

wherein Z1 and Z3 may be identical or different.

In another embodiment, the polypeptides comprises the formula B1-B2-Z1-Z2-Z3-B3-B4, wherein:

Z1, Z2, and Z3 are as defined;

B2 and B3 comprise optional amino acid linkers; and

one or both of B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164, wherein one of B1 and B4 may be absent.

In one embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:47-60, 193-355 and 454-588, and a genus selected from those recited in the right hand column of Table 8 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids.

In another embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 356-453 and 595-692, and a genus selected from those recited in the middle column of Table 9 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids.

In a further embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 65-96, wherein in embodiments where a secretion signal is present (MARAWIFFLLCLAGRALA; SEQ ID NO:63) it can be replaced with any other secretion signal.

In other aspects, the disclosure provides nucleic acids encoding the polypeptide of the disclosure, expression vectors comprising the nucleic acids operatively linked to a promoter, host cell comprising a polypeptide, nucleic acid, and/or expression vector of the disclosure, oligomers of the polypeptides of the disclosure, compositions comprising 2, 3, 4, or more copies of the polypeptide any embodiment of the disclosure attached to a support, including but not limited to a polypeptide particle support, and pharmaceutical compositions, comprising a polypeptide, nucleic acid, expression vector, host cell, oligomer, and/or composition of the disclosure, and a pharmaceutically acceptable carrier.

In another aspect, the disclosure provides methods for treating or limiting development of a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of the disclosure, effective to treat or limit development of the infection.

Description of the Figures

Figure 1. Designed Minibinder Proteins For the SARS-CoV-2 Spike Receptor Binding Domain Designs for approach 1, and approach 2, were encoded in long oligonucleotides, and screened for binding to fluorescently tagged RBD on the yeast cell surface. Deep sequencing identified 3 Ace2 helix scaffolded designs (approach 1), and 150 de novo interface designs (approach 2) that were clearly enriched following FACS sorting for RBD binding. Designs were expressed in *E. coli* and purified, and many were found to have

soluble expression, to bind RBD in biolayer interferometry experiments, and could effectively compete with ACE-2 for binding to RBD (example shown in Figure 2). Based on BLI data (e.g. See Figure 2) the RBD binding affinities of minbinders are: LCB1 <1nM, LCB3 <1nM. The affinities of LCB2, LCB4, LCB5, LCB6, LCB7 ,LCB8 range from 1~20nM, with relative strength of different binders being LCB4 > LCB2 > LCB9 = LCB5 > LCB6 > LCB7.

Figure 2. High Affinity Binding of De novo Designed Minibinder to SARS-CoV-2 Spike RBD. Biotinylated Spike RBD protein was loaded to a streptavidin biolayer interferometry (BLI) tip (ForteBio Octet™) and after washing, the tip was dipped into purified Combo 1 anti-RBD minibinder at different concentrations. After loading the tips were placed into buffer alone. (Left and middle) Response curves indicate ~Kd of 300 pM affinity. (Right) If ACE-2 is loaded to RBD tips and then Combo 1 is added, the minibinder rapidly displaces ACE-2 off of the BLI tip.

Figure 3. De novo Designed Minibinder to SARS-CoV-2 Spike RBD is Heat Stable. Purified Combo 1 minibinder was measured for in a circular dichroism spectrometer at 25C, 95C and at 25C after heating to 95C. The CD spectra were all very similar in shape indicating that the protein remains folded in all conditions.

Figure 4. De novo Designed Minibinder to SARS-CoV-2 Spike RBD are Potent in Virus Neutralization Assays. SARS-CoV-2 strain 2019 n-CoV/USA_WA1/2020 was obtained from the Centers for Disease Control and Prevention (gift of Natalie Thornburg). Virus stocks were produced in Vero CCL81 cells (ATCC) and titrated by focus-forming assay on Vero E6 cells. Serial dilutions of mAbs or minibinder were incubated with 102 focus-forming units (FFU) of SARS-CoV-2 for 1 h at 37C. RBD minibinder (or mAb)-virus complexes were added to Vero E6 cell monolayers in 96-well plates and incubated at 37C for 1 h. Subsequently, cells were overlaid with 1% (w/v) methylcellulose in MEM supplemented with 2% FBS. Plates were harvested 30 h later by removing overlays and fixed with 4% PFA in PBS for 20 min at room temperature. Plates were washed and sequentially incubated with 1 μg/mL of CR3022 ([1]) anti-S antibody and HRP-conjugated goat anti-human IgG in PBS supplemented with 0.1% saponin and 0.1% BSA. SARS-CoV-2-infected cell foci were visualized using TrueBlue™ peroxidase substrate (KPL) and quantitated on an ImmunoSpot™ microanalyzer (Cellular Technologies). Data were processed using Prism software (GraphPad Prism™ 8.0).

Figure 5(A-J). LCB1-Fc prophylaxis protects against SARS-CoV-2 infection. (A) Molecular surface representation of three LCB1v1.3 miniproteins bound to individual

protomers of the SARS-CoV-2 spike protein trimer (left: side view; right: top view). (**B**) Binding curves of purified LCB1v1.3 and LCB1-Fc to SARS-CoV-2 RBD as monitored by biolayer interferometry (one experiment performed in technical duplicate). (**C**) Neutralization curves of LCB1v1.3, LCB1-Fc, or control binder against a SARS-CoV-2 WA1/2020 isolate (EC_{50} values: 14.4 pM, 71.8 pM, and >10,000 nM respectively; average of two experiments, each performed in duplicate). (**D-J**) 7 to 8-week-old female and male K18-hACE2 transgenic mice received 250 μg of LCB1-Fc or control binder by i.p. injection one day prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. Tissues were collected at 4 and 7 dpi. (**D**) Weight change following LCB1-Fc administration (mean ± SEM; n = 8, two experiments: two-way ANOVA with Sidak's post-test: *** $P < 0.001$, **** $P < 0.0001$). (**E**) Infectious virus measured by plaque assay at 4 or 7 dpi in the lung (n = 8, two experiments: Mann-Whitney test; *** $P < 0.001$). (**F-J**) Viral RNA levels at 4 or 7 dpi in the lung, heart, spleen, brain, or nasal wash (n = 8, two experiments: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

Figure 6(A-C). LCB1-Fc prophylaxis prevents SARS-CoV-2-mediated lung disease. (**A**) Respiratory mechanics parameters: inspiratory capacity, resistance, elastance tissue damping, quasi-static compliance, and pressure-volume loops measured at 7 dpi (n = 3-6, two experiments: two-way ANOVA with Tukey's post-test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ between indicated groups). (**B**) Hematoxylin and eosin staining of lung sections from mice treated at D-1 and collected at 7 dpi with SARS-CoV-2. Images show low (left) and high (right; boxed region from left) magnification. Scale bars for all images, 100 μm. Representative images from n = 3 mice per group. (**C**) Heat-map of cytokine mRNA levels from lung tissues of SARS-CoV-2 infected mice at 4 dpi. For each cytokine, the fold-change was calculated relative to age-matched naïve control animals after normalization to *Gapdh* and the Log_2(fold change) was plotted (n = 8 mice/group relative to n = 3 naïve controls).

Figure 7(A-J). Post-exposure delivery of anti-RBD binders reduces SARS-CoV-2 burden. (**A-G**) 7 to 8-week-old female and male K18-hACE2 transgenic mice received 250 μg of LCB1-Fc or control binder by i.p. injection one day after i.n. inoculation with 10^3 PFU of SARS-CoV-2. Tissues were collected at 4 or 7 dpi. (**A**) Weight change following LCB1-Fc administration (mean ± SEM; n = 6, two experiments: two-way ANOVA with Sidak's post-test: ** $P < 0.01$, **** $P < 0.0001$). (**B**) Infectious virus in the lung measured by plaque assay at 4 or 7 dpi in the lung (n = 6, two experiments: ** $P < 0.01$). (**C-G**) Viral RNA levels

at 4 or 7 dpi in the lung, heart, spleen, brain, or nasal wash (n = 6, two experiments: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$). (**H**) Hematoxylin and eosin staining of lung sections from mice treated at D+1 and collected at 7 dpi with SARS-CoV-2. Images show low (left) and high (right; boxed region from left) magnification. Scale bars for all images, 100 μm. Representative images from n = 3 mice per group. (**I-J**) 7 to 8-week-old male K18-hACE2 transgenic mice received a single 50 μg i.n. dose of LCB1v1.3 or control binder at one- or two-days post-inoculation with 10^3 PFU of SARS-CoV-2. Viral RNA levels at 7 dpi in the lung (**I**) or nasal wash (**J**) (n = 6, two experiments: one-way ANOVA: ns, not significant, * $P < 0.05$, **** $P < 0.0001$).

Figure 8(A-K). Intranasal administration of LCB1v1.3 reduces viral infection even when given 5 days prior to SARS-CoV-2 exposure. (**A-D**) 7 to 8-week-old female K18-hACE2 transgenic mice received a single i.n. 50 μg dose of LCB1v1.3 or control binder at the indicated time prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. Tissues were collected at 4 or 7 dpi and viral RNA levels were determined (n = 5-6 animals per group, two-experiments: two-way ANOVA with Sidak's post-test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$). (**E-J**) 7 to 8-week-old female K18-hACE2 transgenic mice received the indicated i.n. dose of LCB1v1.3 or control binder at one day prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. (**E**) Weight change following LCB1v1.3 or control binder administration (mean ± SEM; n = 6, two experiments: two-way ANOVA with Sidak's post-test compared to the control binder treated group: ** $P < 0.01$, **** $P < 0.0001$). (**F-J**) Viral RNA levels at 7 dpi in the lung, heart, spleen, brain, or nasal wash (n = 6, two experiments: Kruskal-Wallis ANOVA with Dunn's post-test: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). (**K**) Hematoxylin and eosin staining of lung sections from mice treated with a single i.n. 50 μg dose of LCB1v1.3 or control binder at D-1 and collected at 7 dpi with SARS-CoV-2. Images show low (left) and high (right; boxed region from left) magnification. Scale bars for all images, 100 μm. Representative images from n = 3 mice per group.

Figure 9(A-H). Immunogenicity of LCB1v1.3 and protection from challenge. (**A**) Scheme of experimental details. K18-hACE2 transgenic mice (n = 10 to 12 per group) were treated every 3 days with 50 μg of LCB1v1.3 or control binder by i.n. administration. On day 18 post-treatment, animals were bled and anti-LCB1v1.3 antibodies were measured. The following day, animals were challenged with 10^3 PFU of SARS-CoV-2, and tissues were collected at 7 dpi. (**B**) Binding of serum antibodies to LCB1v1.3 as measured by ELISA

(three experiments). Dashed line indicated limit of detection of the assay. (**C**) Weight change following LCB1v1.3 or control binder administration (mean ± SEM; two experiments: two-way ANOVA with Sidak's post-test: **** $P < 0.0001$). (**D-H**) Viral RNA levels at 7 dpi in the lung, heart, spleen, brain, or nasal wash (two experiments: Mann-Whitney test: * $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$).

Figure 10(A-M). LCB1v1.3 protects mice against B.1.1.7 variant and WA1/2020 E484K/N501Y/D614G strains. (**A**) Neutralization of LCB1v1.3 against B.1.1.7 or WA1/2020 E484K/N501Y/D614G SARS-CoV-2 (EC_{50} values: 802 pM and 667 pM, respectively; mean of two experiments, each performed in duplicate). (**B-G**) 7 to 8-week-old female K18-hACE2 transgenic mice were treated with a single 50 μg i.n. dose of LCB1v1.3 or control binder at 1 day prior to i.n. inoculation with 10^3 PFU of B.1.1.7. (**B**) Weight change following LCB1v1.3 or control binder administration (mean ± SEM; n = 6, two experiments: two-way ANOVA with Sidak's post-test: *** $P < 0.001$, **** $P < 0.0001$). (**C-G**) Viral RNA levels at 6 dpi in the lung, heart, spleen, nasal wash, or brain (n = 6, two experiments: Mann-Whitney test: * $P < 0.05$, ** $P < 0.01$). (**H-M**) 8-week-old male K18-hACE2 transgenic mice were treated with a single 50 μg i.n. dose of LCB1v1.3 or control binder at 1 day prior to i.n. inoculation with 10^3 PFU of WA1/2020 E484K/N501Y/D614G. (**H**) Weight change following LCB1v1.3 or control binder administration (mean ± SEM; n = 6, two experiments: two-way ANOVA with Sidak's post-test: * $P < 0.05$, **** $P < 0.0001$). (**I-M**) Viral RNA levels at 6 dpi in the lung, heart, spleen, nasal wash, or brain (n = 6, two experiments: Mann-Whitney test: * $P < 0.05$, ** $P < 0.01$).

Figure 11. Cytokine and chemokine induction following SARS-CoV-2 infection. Individual plots for cytokine and chemokine RNA levels in the lungs of SARS-CoV-2 infected mice at 4 dpi following treatment with control or LCB1-Fc binders (n = 8 per group, two experiments: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). Data were used to generate the heat-map in **Figure 6C**.

Figure 12(A-C). Intranasal delivery of LCB1v1.3 at 1 or 2 days post-SARS-CoV-2 infection reduces viral burden, Related to Fig 7. (**A-C**) 7 to 8-week-old male K18-hACE2 transgenic mice received a single 50 μg i.n. dose of LCB1v1.3 or control binder at one- or two-days post-inoculation with 10^3 PFU of SARS-CoV-2. Viral RNA levels at 7 dpi in the heart (**A**), spleen (**B**), or brain (**C**) (n = 6, two experiments: one-way ANOVA: * $P < 0.05$, ** $P < 0.01$).

Figure 13. Intranasal prophylaxis of LCB1v1.3 reduces weight loss, Related to Fig 8. 7 to 8-week-old female K18-hACE2 transgenic mice received a single 50 μg i.n. dose of LCB1v1.3 or control binder at the indicated time prior to i.n. inoculation with 10^3 PFU of SARS-CoV-2. Weight change was recorded daily (mean ± SEM; n = 6, two experiments: two-way ANOVA with Sidak's post-test: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

Figure 14(A-B). Multivalent minibinders simultaneously engage multiple epitopes on the pre-fusion SARS-CoV-2 spike protein resulting in extremely slow dissociation rates. (**A,B**) Dissociation of the minibinder construct and the receptor binding domain (RBD) (**A**) or the hexapro spike protein (S6P) (**B**) complex was monitored via competition with 100-fold molar excess of untagged M1 using AlphaLISA™ (Mean ± SEM, n=3).

Figure 15(A-F). Cryo-EM structures of multivalent minibinders in complex with the SARS-CoV-2 S glycoprotein. (**A**) Ribbon diagram representations of all three minibinders bound to the RBD. (**B**) Cryo-EM map of F31-G10 in complex with two RBDs. (**C**) Cryo-EM map of F231-P24 in complex with three RBDs. (**D**) Design model of H2-1 bound to the S glycoprotein. (**E**) Cryo-EM map of H2-1 in complex with the S glycoprotein in two orthogonal orientations. (**F**) Cryo-EM map showing the interacting residues of the H2-1 and S glycoprotein interface.

Figure 16(A-F). Multivalency enhances both the breadth and potency of neutralization against SARS-CoV-2 variants by minibinders. (**A**) Dissociation of minibinder constructs from S6P variants after 24 hours was measured via competition with untagged H2-0 using AlphaLISA (mean, n=3). Cells containing an X indicate insufficient signal in the no competitor condition to quantify the fraction of protein bound. (**B**) Competition of minibinder constructs with ACE2 for S6P was measured via ELISA (mean, n=2). (**C**) Neutralization curves of minibinder constructs against SARS-CoV-2 pseudovirus variants (mean, n=2) (**D**) Table summarizing neutralization potencies of multivalent minibinder constructs against SARS-CoV-2 pseudovirus variants. N/A indicates an IC_{50} value above the tested concentration range and an IC_{50} greater than 50,000 pM. (**E**) Neutralization curves of minibinder constructs against authentic SARS-CoV-2 isolates (mean, n=2). (**F**) Table summarizing neutralization potencies of multivalent minibinder constructs against authentic SARS-CoV-2 isolates.

Figure 17(A-C). Top multivalent minibinder candidates are escape resistant and protect mice from SARS-CoV-2 infection via pre-exposure intranasal administration. (**A**)

Plaque assays were performed to isolate VSV-SARS-CoV-2 chimera virus escape mutants against a control neutralizing antibody (2B04) and the F231-P12 and H2-1 multivalent minibinders. Images are representative of 35 replicate wells per multivalent minibinder. Large plaques, highlighted by black arrows, are indicative of escape. (**B**, **C**) K18-hACE2-transgenic mice (n=6/timepoint) were dosed with 50ug H2-0 by intranasal administration (i.n., 2 x 25 µl doses per nostril, 100 µl total) 24h prior (T-24h) to infection with 10^3 plaque forming units of SARS-CoV-2 Variants B.1.1.7, B1.351, B.1.1.24 intranasally at Day 0. (**B**) Daily weight change following infection (mean ± SEM; n = 6, two-way ANOVA with Sidak's post-test: * $P < 0.05$, *** $P < 0.001$, **** $P < 0.0001$). (**C**) After days post infection (6dpi) animals (n=6/timepoint) were sacrificed and analyzed for the presence of SARS-CoV-2 viral RNA by quantitative real time RT-PCR in the lung, heart, spleen, brain, or nasal wash (n = 6: Mann-Whitney test: ns, not significant, * $P < 0.05$, ** $P < 0.01$).

Detailed Description

All references cited are herein incorporated by reference in their entirety. Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: Molecular Cloning: A Laboratory Manual (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), Gene Expression Technology (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in Methods in Enzymology (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); PCR Protocols: A Guide to Methods and Applications (Innis, et al. 1990. Academic Press, San Diego, CA), Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed. (R.I. Freshney. 1987. Liss, Inc. New York, NY), Gene Transfer and Expression Protocols, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

As used herein, the singular forms "a", "an" and "the" include plural referents unless the context clearly dictates otherwise.

As used herein, the amino acid residues are abbreviated as follows: alanine (Ala; A), asparagine (Asn; N), aspartic acid (Asp; D), arginine (Arg; R), cysteine (Cys; C), glutamic acid (Glu; E), glutamine (Gln; Q), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

In all embodiments of polypeptides disclosed herein, an N-terminal methionine residue is optional (i.e.: may be present or absent).

All embodiments of any aspect of the disclosure can be used in combination, unless the context clearly dictates otherwise.

Unless the context clearly requires otherwise, throughout the description and the claims, the words 'comprise', 'comprising', and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of "including, but not limited to". Words using the singular or plural number also include the plural and singular number, respectively. Additionally, the words "herein," "above," and "below" and words of similar import, when used in this application, shall refer to this application as a whole and not to any particular portions of the application.

In a first aspect, the disclosure provides polypeptides comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101, wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

>LCB1-1
DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:1)

>LCB1-2
DKEEILNKIYEIMRLLDELGNAEASMRVSDLILEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:2)

>LCB1-3
DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:3)

>LCB1-4
DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:4)

>LCB1-5
DKENILQKIYEIMKTLDQLGHAEASMNVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:5)

LCB1_v1.1_Cys
DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERC(SEQ ID NO:6)

>LCB1_v1.2
DKENILQKIYEIMKTLDQLGHAEASMYVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:7)

>LCB1_v1.3
DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:8)

>LCB1_v1.4

DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDENLLEEAEQLLQEVER (SEQ ID NO:9)

>LCB1_v1.5 (LCB1_v1.3 with N-link Glycosylation)

DKENILQKIYEIMKTLEQLGHAEASMNVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:10)

>LCB2-1

SDDEDSVRYLLYMAELRYEQGNPEKAKKILEMAEFIAKRNNNEELERLVREVKKRL (SEQ ID NO:11)

>LCB2-2

SDDEDAVRYLLYMAELLYKQGNPEEAKKLLELAEFIAKRNNNEELERLVREVKKRL (SEQ ID NO:12)

>LCB3-1

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13)

>LCB3-2

NDDELLMLVTDLVAEALLFAKDEEIKKRVFTLFELADKAYKNNDRDTLSKVVSELKELLERLQ (SEQ ID NO:14)

> LCB3_v1.2

NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)

>LCB3-4

NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFENATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:16)

>LCB3_v1.1

NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNNDRQKLEKVVEELKELLERLLS (SEQ ID NO:17)

>LCB3_v1.3

NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:19)

>LCB3_v1.4

NDDELHMQMTDLVYEALHKAKDEEFQKHVFQLFEKATKARKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:20)

>LCB3_v1.5

NDDELHMQMTDLVYEALHKAKDEEMQKRVFQLFEQADKAYKTKDRQKLEKVVEELKELLERLLS (SEQ ID NO:21)

>LCB4-1

QREKRLKQLEMLLEYAIERNDPYLMFDVAVEMLRLAEENNDERIIERAKRILEEYE (SEQ ID NO:23)

>LCB4-2

DREERLKYLEMLLELAVERNDPYLIFDVAIELLRLAEENNDERIYERAKRILEEVE (SEQ ID NO:24)

>LCB5-1

SLEELKEQVKELKKELSPEMRRLIEEALRFLEEGNPAMAMMVLSDLVYQLGDPRVIDLYMLVTKT (SEQ ID NO:25)

>LCB5-2

SLEEVKEILKELKKELSPEDRRLIEEALRLLEEGNPAMASMVLSDLVFLLGDPRVIELLMLVTKT (SEQ ID NO:26)

>LCB6-1

DREQRLVRFLVRLASKFNLSPEQILQLFEVLEELLERGVSEEEIRKQLEEVAKELG (SEQ ID NO:27)

>LCB6-2

DREQRLVRFLVRLASKFNLSMEQILILFDVLEELLERGVSEEEIRKILEEVAKEL (SEQ ID NO:28)

>LCB7-1

DDDIRYLIYMAKLRLEQGNPEEAEKVLEMARFLAERLGMEELLKEVRELLRKIEELR (SEQ ID NO:29)

>LCB7-2

DDDVRYLIYMAKLLLEQGNPEEAEKVLESARFAAELLGNEELLKEVRELLRKIEELR (SEQ ID NO:30)

>LCB8-1

PIIELLREAKEKNDEFAISDALYLVNELLQRTGDPRLEEVLYLIWRALKEKDPRLLDRAIELFER (SEQ ID NO:31)

>LCB8-2

PVTELLREAKEKNDPMAISDALFLVFELAQRTGDPRLEEVLFLIWRALKEKDPRLLDRAIELFER (SEQ ID NO:32)

>AHB1-1

DEDLEELERLYRKAEEVAKEAKDASRRGDDERAKEQMERAMRLFDQVFELAQELQEKQTDGNRQKATHLDKAVKE AADELYQRVR(SEQ ID NO:33)

>AHB1-2

DEDLEELERLYRKAEEVAKEAEEASRRGDKERAKELLERALHLFDQVFELAQELQEKLTDEKRQKATHLDKAVHE AADELYQRVR (SEQ ID NO:34)

>AHB2-1

ELEERVMHLLDQVSELAHELLHKLTGEELQRATHFDKWANEAILELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO:100)

>AHB2-2_

ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO:101)

As detailed in the examples that follows, the polypeptides bind with high affinity to the SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

In all of embodiments herein, the percent identity requirement does not include any additional functional domain that may be incorporated in the polypeptide. In one embodiment, 1, 2, or 3 amino acids may be deleted from the N and/or C terminus.

The polypeptides have been subjected to extensive mutational analysis as described in the examples that follow, permitting determination of allowable substitutions at each residue within the polypeptide. Exemplary substitutions are as shown in **Table 1** (The number denotes the residue number, and the letters denote the single letter amino acids that can be present at that residue). Thus, in one embodiment, amino acid substitutions relative to the reference polypeptide amino acid sequence (i.e.: one of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101) are selected from the exemplary amino acid substitutions provided in Table 1.

Table 1: Exemplary substitutions:

LCB1 (SEQ ID NOS:1-10 and 102-136)

1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
3 -- A,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
6 -- A,C,I,L,M,Q,T,V
7 -- A,C,D,E,F,G,H,M,N,P,Q,R,S,V,W,Y
8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
9 -- C,I,L,M,N,Q,T,V
10 -- C,F,V,W,Y
11 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
12 -- A,C,D,H,I,L,M,N,S,T,V,Y
13 -- C,I,M,Q
14 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
15 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
16 -- C,F,I,L,M,T,V
17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,K,L,M,N,Q,R,S,T,W

21 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
22 -- A,C,D,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y
23 -- C,E,M,N,P,Q,S,T,V
24 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
25 -- A,C,G,M,N,Q,S,T,V
26 -- M,N,V
27 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
28 -- A,C,G,I,L,S,T,V
29 -- A,C,S,V,W
30 -- D
31 -- A,C,D,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
32 -- C,F,H,I,L,M,N,P,T,V
33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
35 -- A,C,D,F,H,M,Q,V,W,Y
36 -- A,C,D,E,G,H,I,L,M,N,Q,R,S,T,V,W,Y
37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
39 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
40 -- D,E,G,H,N,P,Q
41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
44 -- A,C,D,E,F,G,H,I,K,L,M,Q,R,S,V,W,Y
45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
47 -- A,C,G,P,S,T,V
48 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
50 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
51 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB2 (SEQ ID NOS:11-12)
1 -- A,C,D,E,G,N,P,S,T
2 -- D,M,P,Q,Y
3 -- A,D,E,N,Q

4 -- C,D,E,V
5 -- D
6 -- A,C,D,E,G,N,Q,S,T,V
7 -- A,C,G,I,L,M,P,S,T,V
8 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
9 -- D,N,Y
10 -- I,L,T
11 -- C,E,G,I,L,M,W
12 -- F,H,Y
13 -- E,M,Q,R,V
14 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
15 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V
16 -- C,H,L,T
17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y
21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
22 -- A,C,D,E,G,I,K,L,N,P,Q,R,S,T,V
23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
25 -- A,C,E,G,H,I,K,N,P,Q,R,S,T,Y
26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
28 -- H,K,R,T,Y
29 -- C,D,E,H,I,K,L,M,N,P,Q,R,S,T,V,Y
30 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,S,T,V,W,Y
31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y
32 -- F,H,I,K,L,M,P,Q,R,Y
33 -- A,C,G,P,S,T
34 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
35 -- F,H,Y
36 -- A,C,E,H,I,L,M,S,V
37 -- A,C,E,G,H,L,M,Q,R,S,T,V,W
38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
39 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V
40 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

45 -- A,C,E,F,I,L,M,P,S,T,V,W,Y
46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
48 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
49 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB3 (SEQ ID NOS:13-17, 19-21 and 137-163)
1 -- C,E,F,I,M,N,T,W
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
3 -- D,G,L,M,N,S,Y
4 -- A,C,E,F,H,K,Q,T
5 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
7 -- A,C,D,F,I,L,M,P,R,S,V,W
8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
9 -- A,C,E,F,G,H,I,L,M,N,Q,R,S,T,V,Y
10 -- A,C,F,G,H,K,M,N,Q,R,S,T,Y
11 -- D,F,H,L,M,N,Q
12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
13 -- A,F,I,L,M,N,Q,S,T,V
14 -- A,C,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
16 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y
17 -- A,C,D,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W
18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

28 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
29 -- A,C,D,E,F,G,I,L,M,N,P,S,T,V,W,Y
30 -- C,E,F,H,L,N,S,W,Y
31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
33 -- A,C,E,F,I,K,P,Q,S,V,W,Y
34 -- A,D,E,F,G,H,M,N,P,Q,R,S,V,W,Y
35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
36 -- A,C,E,G,H,I,M,N,Q,S,T,V
37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
40 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
48 -- A,C,E,F,G,I,K,L,M,N,P,Q,S,T,V,W
49 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,E,F,G,H,I,K,L,M,N,Q,S,T,V,W,Y
56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
57 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
59 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
60 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
61 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
62 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
63 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
64 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB4 (SEQ ID NO:23-24)
1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 -- C,D,H,K,N,Q,R,Y
6 -- A,C,F,G,I,K,L,M,P,Q,R,S,T,V,Y
7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
8 -- A,C,H,I,M,N,Q,R,S,T,V,Y
9 -- A,C,D,G,H,I,K,L,M,N,Q,R,S,T,V,Y
10 -- A,C,D,E,M,N,P,Q,S,T,V
11 -- C,D,G,H,I,K,L,M,N,P,R,S,T,V
12 -- F,G,I,L
13 -- F,I,L,M,S,V,Y
14 -- A,C,D,E,G,L,M,N,Q,R,S,T,V
15 -- C,E,F,G,H,I,L,M,S,V,W,Y
16 -- A,G,T,Y
17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
18 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- C,D,Q,Y
22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
23 -- E,F,H,Y
24 -- A,F,G,I,L,M,W
25 -- A,C,E,G,H,I,K,L,M,N,Q,R,S,T,V,Y
26 -- C,F,H,I,L,N,S,T,V,W
27 -- D,Q,W,Y
28 -- A,C,D,I,L,V,Y
29 -- A,C,E,G,K,L,N,Q,R,S,T
30 -- C,I,L,M,P,T,V
31 -- C,D,E
32 -- A,C,E,I,L,M,Q,S,T,V,Y
33 -- A,C,E,F,G,H,I,K,L,M,Q,R,S,T,V,Y
34 -- C,D,F,G,H,L,M,N,P,R,S,T,W,Y
35 -- A,C,E,F,G,H,I,K,L,N,P,R,T,V,W
36 -- A,C,G,S,T,V
37 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y
38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
40 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y
41 -- A,C,D,E,G,H,K,N,Q,S,W
42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

44 -- A,E,F,G,H,I,K,L,M,N,Q,R,S,T,V
45 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
46 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
47 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
48 -- A,C,M,S,T,V
49 -- A,H,I,K,L,M,N,Q,R,S,T,V,W,Y
50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
51 -- A,F,I,K,L,M,R,T,V,W,Y
52 -- F,I,K,L,M,V
53 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB5 (SEQ ID NO:25-26)
1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
9 -- A,C,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y
10 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
11 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
12 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y
13 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
14 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
23 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,W,Y
24 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y
25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

27 -- A,C,G,H,I,S,T,V
28 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
30 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
31 -- A,C,E,F,H,I,K,L,M,N,Q,S,T,V,W,Y
32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
35 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
37 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,D,E,G,I,L,M,N,P,Q,S,T,V,W
39 -- A,C,F,G,L,M,N,S,T,V,W
40 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y
41 -- C,H,I,L,M,P,R
42 -- A,C,E,G,H,I,L,M,P,T,V,Y
43 -- C,I,L,M,Q,T,V
44 -- A,C,D,F,G,H,I,M,S,T
45 -- D,Y
46 -- A,C,D,F,I,L,R,V
47 -- C,E,G,I,V
48 -- F,I,V,W,Y
49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
50 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
52 -- C,D,E,H,I,K,N,P,Q,R,S,T,Y
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
56 -- F,I,L,M,T,V,W
57 -- A,C,D,E,F,G,H,N,P,Q,R,S,T,W,Y
58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
59 -- A,C,F,I,L,M,T,V,Y
60 -- C,F,M,N,V,Y
61 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
62 -- A,C,F,G,I,L,M,S,T,V,W
63 -- A,C,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
64 -- A,C,E,F,G,H,K,L,N,P,R,S,T,W,Y
65 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB6 (SEQ ID NO:27-28)

1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
3 -- E,W
4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
6 -- F,L,M,R,S
7 -- H,T,V
8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
9 -- F,M
10 -- A,K,L,W
11 -- D,E,G,V,Y
12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
13 -- E,L
14 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
17 -- F,N,P,S
18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
19 -- L,N,Q,V
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
23 -- C,D,P,Q,R,W
24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
27 -- D,H,L,S,W
28 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
30 -- L,Q,V,W
31 -- I,K,L,S
32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
33 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
34 -- A,F,L,T,V
35 -- C,D,G,H,K,L,N,T
36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
40 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
44 -- F,I
45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
48 -- L,Q,R,T
49 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
51 -- C,V,Y
52 -- A,E,H,K
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- C,F,H,L,P,W,Y
56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB7 (SEQ ID NO:29-30)
1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- I,T,V
5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
7 -- L,P,Y
8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
9 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
10 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
11 -- A
12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
13 -- A,L,P
14 -- H,L,R,T,Y
15 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
17 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
18 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
23 -- A,S
24 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

25 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
26 -- C,G,S,V,Y
27 -- K,L,M,W
28 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
29 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
30 -- A,Y
31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
33 -- A,C,F,I,K,L,V,W
34 -- A,H,L
35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
36 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
39 -- A,C,K,L,M,N
40 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
41 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
42 -- A,C,D,L,V
43 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
44 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
45 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
46 -- Q,S,V
47 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
48 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
49 -- E,L
50 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
52 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
53 -- I
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
56 -- L,M,N,R
57 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

LCB8 (SEQ ID NO:31-32)
1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- C,F,I,L,M,S,V,W,Y
3 -- A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
5 -- A,C,F,G,I,K,L,M,Q,S,T,V,W,Y
6 -- H,I,K,L,M

7 -- A,H,I,K,L,M,N,P,Q,R,W,Y

8 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

9 -- A,C,F,G,I,L,M,S,Y

10 -- A,F,H,K,L,M,Q,R,S

11 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

12 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y

13 -- A,C,D,E,F,G,H,M,N,Q,S,W,Y

14 -- C,D,E,H,N,Q,S

15 -- A,D,E,F,H,I,L,M,N,P,Q,S,T,V,W,Y

16 -- C,F,M,N,R,Y

17 -- A,C,I,L,M,Q,R,V

18 -- A,C,F,H,I,L,M,T,V,Y

19 -- I,Q,S

20 -- D,N

21 -- A,C,G,S,V

22 -- A,C,I,L,M,V

23 -- C,F,R,T,W,Y

24 -- A,C,D,E,F,G,H,I,L,M,N,Q,R,S,T,V,W,Y

25 -- C,E,S,T,V,Y

26 -- A,C,D,E,F,G,H,N,Q,S,T

27 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V

28 -- C,E,F,G,H,I,K,L,M,Q,R,W,Y

29 -- A,C,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y

30 -- A,C,E,G,H,K,M,N,P,Q,R,T

31 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,Y

32 -- A,C,D,E,G,H,I,K,N,Q,R,S,T,W

33 -- A,C,E,G,H,K,M,N,P,Q,R,S,W,Y

34 -- C,D,E,F,H,M,N,W,Y

35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,Y

36 -- A,C,D,E,F,G,H,K,L,M,N,Q,R,S,T,V,W,Y

37 -- F,G,H,I,L,M,S,T,Y

38 -- D,E,H,Q,W,Y

39 -- C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y

40 -- A,C,E,G,H,I,K,M,P,V,Y

41 -- C,F,H,I,K,L,M,R,S,T,V

42 -- E,F,I,T,W,Y

43 -- A,C,D,E,F,H,I,L,M,N,Q,R,S,T,V,W,Y

44 -- C,G,I,K,L,M,T,V,Y

45 -- G,S,W,Y

46 -- C,I,K,L,M,N,Q,R,S,T

47 -- A,C,E,N,Q,S,T,V

48 -- C,D,E,F,H,I,L,M,W
49 -- C,D,F,H,K,L,M,N,Q,R,T
50 -- A,C,D,E,N,Y
51 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
52 -- A,C,D,E,G,H,K,L,M,N,Q,R,S,T
53 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y
54 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
55 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,S,T,V,W,Y
56 -- C,I,L,M
57 -- A,C,D,E,G,I,N,Q,S,T
58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
59 -- A,C,G,P,S
60 -- A,C,E,F,G,I,L,M,N,Q,S,T,V
61 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
62 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
63 -- A,C,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y
64 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,S,T,V
65 -- A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,W,Y

AHB1 (SEQ ID NOS:33-34)
1 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
2 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
3 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
4 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
5 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
6 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
7 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
8 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
9 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
10 -- A,C,F,H,I,K,L,M,N,Q,R,S,T,V,W,Y
11 -- F,N,Y
12 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
13 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
14 -- A,D,G
15 -- A,C,D,E,G,H,I,K,L,M,N,Q,R,S,T,V
16 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
17 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
18 -- A,C,D,E,F,G,H,I,L,M,N,Q,S,T,V,W,Y
19 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
20 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
21 -- A,C,E,G,S,V

22 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
23 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
24 -- A,C,D,E,F,H,K,L,M,N,Q,R,S,T,V,Y
25 -- A,C,D,F,G,H,L,M,N,Q,R,S,T,V,W,Y
26 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
27 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
28 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,Y
29 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
30 -- A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
31 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
32 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
33 -- A,G,S
34 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
35 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
36 -- A,C,D,E,F,G,H,K,L,M,N,P,Q,R,S,T,V,W,Y
37 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
38 -- A,C,E,G,H,M,P,Q
39 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
40 -- A,C,D,E,G,K,N,Q,R,S,T
41 -- A,C,D,E,F,G,H,I,L,M,N,P,Q,S,T,V,W,Y
42 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
43 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,S,T,V,W,Y
44 -- E,F,H,Q,S,W,Y
45 -- D,N
46 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
47 -- C,T,V
48 -- F,S,W,Y
49 -- A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y
50 -- A,C,F,H,I,K,L,M,N,Q,R,S,T,V,W,Y
51 -- A,D,G,H,N,S
52 -- H,K,Q,R
53 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
54 -- A,C,H,I,K,L,M,N,P,Q,R,S,T,V
55 -- A,C,E,G,H,K,N,Q,R,S,T
56 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
57 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
58 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
59 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
60 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
61 -- A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
62 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

63 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
64 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
65 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
66 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
67 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
68 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
69 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
70 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
71 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
72 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
73 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
74 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
75 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
76 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
77 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
78 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
79 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
80 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
81 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
82 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
83 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
84 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y
85 -- A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y

AHB2 (SEQ ID NO:101-102 and 164)

1 -- C,G,A,V,F,Y,W,S,Q,D,E,R,K
2 -- C,P,G,V,I,M,L,F,Y,W,S,N,Q,D,E,R,H
3 -- C,G,A,V,I,F,S,T,D,E,K
4 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
5 -- C,P,G,A,V,M,L,Y,W,S,N,Q,D,E,R,K,H
6 -- G,A,V,I,F,S,T,D,H
7 -- C,P,G,V,I,M,L,F,W,S,T,N,Q,E,R,K,H
8 -- C,P,G,A,V,M,L,Y,W,S,T,N,Q,D,E,R,K,H
9 -- C,P,G,A,V,I,M,L,F,W,S,T,N,Q,D,E,R,K,H
10 -- C,P,G,A,V,I,L,Y,W,S,T,N,E,R,K
11 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,H
12 -- C,P,G,A,V,I,L,F,Y,W,S,T,N,Q,D,E,R,K,H
13 -- C,G,A,V,M,L,F,W,S,T,N,E,H
14 -- C,P,G,A,V,I,Y,S,T,N,D,E,R,H
15 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K
16 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

17 -- C,P,G,A,V,L,Y,W,S,T,Q,D,E,R
18 -- C,P,A,V,I,M,F,Y,N,Q,R,K,H
19 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
20 -- C,P,G,A,V,M,L,Y,W,N,Q,E,R,K,H
21 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,E,R,K,H
22 -- C,P,G,A,V,M,L,F,Y,S,T,N,Q,D,E,R,K,H
23 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,E,R,K
24 -- C,P,G,A,V,I,M,L,F,Y,W,S,Q,E,R,H
25 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,R,H
26 -- C,G,A,V,L,Y,S,N,D,R,K,H
27 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
28 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
29 -- C,P,G,V,I,M,L,F,Y,W,S,T,N,Q,D,R,K,H
30 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
31 -- C,G,A,V,I,M,L,F,Y,W,S,T,Q,D,E,R,K,H
32 -- P,G,A,V,I,L,W,S,T,D,R,H
33 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,E,R,K,H
34 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
35 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
36 -- C,P,G,A,V,I,L,F,Y,S,T,N,Q,D,E,R,H
37 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
38 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,Q,E,R,K
39 -- C,P,G,A,V,I,W,S,Q,E,R,H
40 -- C,P,G,A,V,I,L,Y,W,S,T,N,D,E,R,K,H
41 -- C,P,G,A,V,I,M,L,Y,W,S,T,N,Q,D,E,R,K,H
42 -- C,P,G,A,V,M,L,Y,W,S,T,N,Q,D,E,R,K,H
43 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
44 -- C,P,G,A,V,I,M,L,F,W,S,T,Q,D,E,R,H
45 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
46 -- C,P,G,A,V,I,M,L,F,S,T,Q,E,R,K
47 -- C,G,A,V,I,M,L,F,W,S,T,N,Q,D,E,R,H
48 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,E,R,K
49 -- C,P,G,A,V,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
50 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
51 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
52 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
53 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,D,E,R,K,H
54 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
55 -- C,P,G,A,V,I,M,L,F,Y,S,T,N,Q,D,E,R,K,H
56 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
57 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H

58 -- C,G,A,V,I,M,L,F,Y,W,S,T,N,E,R,K,H
59 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
60 -- C,G,A,V,I,M,L,F,Y,W,S,T,Q,D,E,R,K
61 -- C,P,G,A,V,I,M,L,F,Y,W,S,N,Q,D,E,R,K,H
62 -- C,G,A,V,L,S,T,N,D,E,K,H
63 -- C,P,G,A,V,I,L,F,Y,W,S,T,N,Q,D,E,R,K,H
64 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,H
65 -- C,G,A,V,I,M,L,F,Y,S,T,N,R,K,H
66 -- C,P,G,A,V,I,M,L,W,T,Q,E,R
67 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
68 -- C,P,G,A,V,I,L,F,Y,W,S,T,N,Q,D,E,R,H
69 -- P,G,V,I,M,L,Y,W,S,T,Q,R,K
70 -- C,P,G,A,V,I,M,L,F,Y,W,S,T,N,Q,D,E,R,K,H
71 -- C,G,A,V,L,F,W,S,Q,D,E,R,K
72 -- C,V,I,L,S
73 -- P,G,A,V,S,T,E
74 -- C,A,L,F,Y,S,T,R,H
75 -- C,P,G,V,I,L,F,W,S,N,D,E,R,K

The residue numbers of the interface residues which are within 8A to the RBD target are listed in **Table 2** for the various design types. In another embodiment, amino acid residues at the interface residues listed in Table 2 are either identical at that residue to the reference sequence, or may be substituted by a conservative amino acid substitution. Such conservative amino acid substitutions involve replacing a residue by a residue having similar physiochemical characteristics, e.g., substituting one aliphatic residue for another (such as Ile, Val, Leu, or Ala for one another), or substitution of one polar residue for another (such as between Lys and Arg; Glu and Asp; or Gln and Asn). Other such conservative substitutions, e.g., substitutions of entire regions having similar hydrophobicity characteristics, are known. Amino acids can be grouped according to similarities in the properties of their side chains (in A. L. Lehninger, in Biochemistry, second ed., pp. 73-75, Worth Publishers, New York (1975)): (1) non-polar: Ala (A), Val (V), Leu (L), Ile (I), Pro (P), Phe (F), Trp (W), Met (M); (2) uncharged polar: Gly (G), Ser (S), Thr (T), Cys (C), Tyr (Y), Asn (N), Gln (Q); (3) acidic: Asp (D), Glu (E); (4) basic: Lys (K), Arg (R), His (H). Alternatively, naturally occurring residues can be divided into groups based on common side-chain properties: (1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile; (2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln; (3) acidic: Asp, Glu; (4) basic: His, Lys, Arg; (5) residues that influence chain orientation: Gly, Pro; (6) aromatic: Trp, Tyr, Phe. Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Particular conservative substitutions

include, for example; Ala into Gly or into Ser; Arg into Lys; Asn into Gln or into H is; Asp into Glu; Cys into Ser; Gln into Asn; Glu into Asp; Gly into Ala or into Pro; His into Asn or into Gln; Ile into Leu or into Val; Leu into Ile or into Val; Lys into Arg, into Gln or into Glu; Met into Leu, into Tyr or into Ile; Phe into Met, into Leu or into Tyr; Ser into Thr; Thr into Ser; Trp into Tyr; Tyr into Trp; and/or Phe into Val, into Ile or into Leu.

Table 2: Interface residues

'LCB1': [3, 6, 7, 10, 13, 17, 20, 22, 23, 25, 26, 29, 32, 33, 36],
'LCB2': [1, 2, 5, 6, 9, 12, 13, 16, 20, 32, 35, 39],
'LCB3': [1, 3, 4, 6, 7, 10, 11, 13, 14, 15, 18, 27, 30, 33, 34, 37],
'LCB4': [8, 11, 12, 15, 23, 24, 26, 27, 28, 30, 31, 34, 56],
'LCB5': [35, 37, 38, 40, 41, 44, 47, 48, 53, 56, 60, 63],
'LCB6': [3, 4, 7, 8, 11, 12, 14, 15, 21, 24, 25, 28, 31, 32, 35],
'LCB7': [2, 3, 6, 7, 9, 10, 13, 17, 29, 32, 33, 36],
'LCB8': [14, 15, 16, 19, 22, 23, 26, 29, 30, 38, 41, 42, 45],
'AHB1', [34, 38, 41, 45, 48, 49, 52, 63, 64, 67, 68, 70, 71, 74, 78, 81, 82, 85],
'AHB2', [4, 7, 11, 14, 15, 18, 21, 26, 29, 30, 33, 34, 36, 37, 40, 43, 44, 47, 48].

In one embodiment, amino acid residues at the interface residues listed in Table 2 are identical at that residue to the reference sequence.

In another embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10, 13-17, 19-21, 33-34, and 100-101.

In one embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10 and 102-136 (see Table 3).

Table 3: LCB1 exemplary variants

Name	Binder Protein
LCB1_4N	DKENILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 102)
LCB1_4K	DKEKILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 103)
LCB1_14K	DKEWILQKIYEIMKLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ

	ID NO: 104)
LCB1_15T	DKEWILQKIYEIMRTLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 105)
LCB1_18Q	DKEWILQKIYEIMRLLDQLGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 106)
LCB1_18K	DKEWILQKIYEIMRLLDKLGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 107)
LCB1_27Q	DKEWILQKIYEIMRLLDELGHAEASMQVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 108)
LCB1_27Y	DKEWILQKIYEIMRLLDELGHAEASMYVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 109)
LCB1_17E	DKEWILQKIYEIMRLLEELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 110)
LCB1_17R	DKEWILQKIYEIMRLLRELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 111)
LCB1_42N	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDENLLEEAERLLEEVER(SEQ ID NO: 112)
LCB1_49Q	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAEQLLEEVER(SEQ ID NO: 113)
LCB1_52Q	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLQEVER(SEQ ID NO: 114)
LCB1_32L	DKEWILQKIYEIMRLLDELGHAEASMRVSDLLYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 115)
LCB1_28A	DKEWILQKIYEIMRLLDELGHAEASMRASDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 116)
LCB1_v1.3_ACH1	DKENILQKIYEIMKTLEQLGHAEASMYVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 117)
LCB1_v1.3_ACH2	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDENLLEEAERLLEEVER(SEQ ID NO: 118)
LCB1_v1.3_ACH3	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAEQLLEEVER(SEQ ID NO: 119)
LCB1_v1.3_ACH4	DKENILQKIYEIMKTLEQLGHAEASMYVSDLIYEFMKQGDENLLEEAEQLLEEVER(SEQ ID NO: 120)
LCB1_v1.3_ACH5	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDENLLEEAEQLLEEVER(SEQ ID NO: 121)
LCB1_v1.3_1	DRENILQKIYEIMKELEKLGHAEASMQVSDLIYEFMQDKDERLLEEAERLLEEVKR(SEQ ID NO: 122)
LCB1_v1.3_2	DRENILQKIYEIMKELRQLGHAEASMQVSDLIYEFMKTKDKRLLEEAERLLEEVKR(SEQ ID NO: 123)
LCB1_v1.3_3	DRENILQKIYEIMKTLRRLGHAEASMQVSDLIYEFMQDKDKRLLEEAERLLEEVQR(SEQ ID NO: 124)
LCB1_v1.3_4	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 125)
LCB1_v1.3_5	DRENILQKIYEIMKTLEKLGHAEASMQASDLIYEFMKTKDERLLEEAERLLEEVQR(SEQ ID NO: 126)
LCB1_v1.3_6	DKENILQKIYEIMKTLRALGHAEASMQVSDLIYEFMQTKDERLLEEAERLLEEVKR(SEQ ID NO: 127)
LCB1_v1.3_7	DKENVLQKIYEIMKTLEKLGHAEASMQVSDLIYEFMQTKDKRLLEEAERLLEEVQR(SEQ ID NO: 128)
LCB1_v1.3_15	DRENILQKIYEIMKELEKLGHAEASMQVSDLIYEFMQDKDENLLEEAERLLEEVKR(SEQ ID NO: 129)
LCB1_v1.3_16	DRENILQKIYEIMKELRQLGHAEASMQVSDLIYEFMKTKDKNLLEEAERLLEEVKR(SEQ ID NO: 130)
LCB1_v1.3_17	DRENILQKIYEIMKTLRRLGHAEASMQVSDLIYEFMQDKDKNLLEEAERLLEEVQR(SEQ ID NO: 131)
LCB1_v1.3_19	DRENILQKIYEIMKTLEKLGHAEASMQASDLIYEFMKTKDENLLEEAERLLEEVQR(SEQ ID NO: 132)
LCB1_v1.3_20	DKENILQKIYEIMKTLRALGHAEASMQVSDLIYEFMQTKDENLLEEAERLLEEVKR(SEQ ID NO: 133)
LCB1_v1.3_21	DKENVLQKIYEIMKTLEKLGHAEASMQVSDLIYEFMQTKDKNLLEEAERLLEEVQR(SEQ ID NO: 134)

LCB1_v2.2	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
LCB1_v2.2_ompT	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTR(SEQ ID NO: 136)

The polypeptides may contain a substantial number of mutations while retaining binding activity, as detailed in the examples that follow. In one embodiment, the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:1 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or all 18 residues selected from the group consisting of 2, 4, 5, 14, 15, 17, 18, 27, 28, 32, 37, 38, 39, 41, 42, 49, 52, and 55. In another embodiment, the substitutions are selected from the substitutions listed in Table 4, either individually (i.e.: any single mutation listed in the Table) or in combinations in a given row.

Table 4: Exemplary LCB1 substitutions

Name	Parent	Mutations from WT									
LCB1_1	LCB1	W4N	R14K	L15T	E18Q	R27Q	K38Q				
LCB1_2	LCB1	W4N	R14K	L15T	E18Q	R27Y	K38Q				
LCB1_3	LCB1	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q			
LCB1_4	LCB1	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R42N	R49Q	E52Q
LCB1_4N	LCB1	W4N									
LCB1_4K	LCB1	W4K									
LCB1_14K	LCB1	R14K									
LCB1_15T	LCB1	L15T									
LCB1_18Q	LCB1	E18Q									
LCB1_18K	LCB1	E18K									
LCB1_27Q	LCB1	R27Q									
LCB1_27Y	LCB1	R27Y									
LCB1_38Q	LCB1	K38Q									
LCB1_17E	LCB1	D17E									
LCB1_17R	LCB1	D17R									
LCB1_42N	LCB1	R42N									
LCB1_49Q	LCB1	R49Q									
LCB1_52Q	LCB1	E52Q									
LCB1_32L	LCB1	I32L									
LCB1_28A	LCB1	V28A									
LCB1_v1.3	LCB1	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q			
LCB1_v1.3_ACH1	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Y	K38Q			
LCB1_v1.3_ACH2	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R42N		
LCB1_v1.3_ACH3	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R49Q		
LCB1_v1.3_ACH4	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Y	K38Q	R42N	R49Q	
LCB1_v1.3_ACH5	LCB1_v1.3	W4N	R14K	L15T	D17E	E18Q	R27Q	K38Q	R42N	R49Q	
LCB1_v1.3_1	LCB1_v1.3 E55K	K2R	W4N	R14K	L15E	D17E	E18K	R27Q	K37Q	K38D	G39K

LCB1_v1.3_2	LCB1_v1.3 E55K	K2R	W4N	R14K	L15E	D17R	E18Q	R27Q	K38T	G39K	E41K
LCB1_v1.3_3	LCB1_v1.3 E41K	K2R E55Q	W4N	R14K	L15T	D17R	E18R	R27Q	K37Q	K38D	G39K
LCB1_v1.3_4	LCB1_v1.3	W4N	I5V	R14K	L15E	D17E	E18R	R27Q	K38T	G39K	E55K
LCB1_v1.3_5	LCB1_v1.3 E55Q	K2R	W4N	R14K	L15T	D17E	E18K	R27Q	V28A	K38T	G39K
LCB1_v1.3_6	LCB1_v1.3	W4N	R14K	L15T	D17R	E18A	R27Q	K37Q	K38T	G39K	E55K
LCB1_v1.3_7	LCB1_v1.3 E41K	W4N E55Q	I5V	R14K	L15T	D17E	E18K	R27Q	K37Q	K38T	G39K
LCB1_v1.3_15	LCB1_v1.3 R42N	K2R E55K	W4N	R14K	L15E	D17E	E18K	R27Q	K37Q	K38D	G39K
LCB1_v1.3_16	LCB1_v1.3 R42N	K2R E55K	W4N	R14K	L15E	D17R	E18Q	R27Q	K38T	G39K	E41K
LCB1_v1.3_17	LCB1_v1.3 E41K	K2R R42N	W4N E55Q	R14K	L15T	D17R	E18R	R27Q	K37Q	K38D	G39K
LCB1_v1.3_19	LCB1_v1.3 R42N	K2R E55Q	W4N	R14K	L15T	D17E	E18K	R27Q	V28A	K38T	G39K
LCB1_v1.3_20	LCB1_v1.3 E55K	W4N	R14K	L15T	D17R	E18A	R27Q	K37Q	K38T	G39K	R42N
LCB1_v1.3_21	LCB1_v1.3 E41K	W4N R42N	I5V E55Q	R14K	L15T	D17E	E18K	R27Q	K37Q	K38T	G39K
LCB1_v2.2	LCB1_v1.3 E55K	W4N	I5V	R14K	L15E	D17E	E18R	R27Q	K38T	G39K	R42N
LCB1_v2.2_ompT	LCB1_v1.3 E55T	W4N	I5V	R14K	L15E	D17E	E18R	R27Q	K38T	G39K	R42N

In another embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163 (see Table 5).

Table 5: LCB3 exemplary variants

Name	**Binder Protein**
LCB3_8Q	NDDELHMQMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 137)
LCB3_8T	NDDELHMTMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 138)
LCB3_19K	NDDELHMLMTDLVYEALHKAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 139)
LCB3_19I	NDDELHMLMTDLVYEALHIAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 140)
LCB3_25F	NDDELHMLMTDLVYEALHFAKDEEFKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 141)
LCB3_25M	NDDELHMLMTDLVYEALHFAKDEEMKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 142)
LCB3_26Q	NDDELHMLMTDLVYEALHFAKDEEIQKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 143)
LCB3_28H	NDDELHMLMTDLVYEALHFAKDEEIKKHVFQLFELADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 144)
LCB3_35K	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEKADKAYKNNDRQKLEKVVEELKELLE RLLS(SEQ ID NO: 145)
LCB3_37T	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELATKAYKNNDRQKLEKVVEELKELLE

RLLS(SEQ ID NO: 146)

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKARKNNDRQKLEKVVEELKELLE

LCB3_40R RLLS(SEQ ID NO: 147)

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNKDRQKLEKVVEELKELLE

LCB3_43K RLLS(SEQ ID NO: 148)

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFGLADKAYKNNDRQKLEKVVEELKELLE

LCB3_34G RLLS(SEQ ID NO: 149)

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFYLADKAYKNNDRQKLEKVVEELKELLE

LCB3_34Y RLLS(SEQ ID NO: 150)

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFTLADKAYKNNDRQKLEKVVEELKELLE

LCB3_34T RLLS(SEQ ID NO: 151)

NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLKKVVEELKELLE

LCB3_49K RLLS(SEQ ID NO: 152)

LCB3_v1.2_AC NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFGKATKAYKNKDRQKLEKVVEELKELLE

H1 RLLS(SEQ ID NO: 153)

LCB3_v1.2_AC NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFYKATKAYKNKDRQKLEKVVEELKELLE

H2 RLLS(SEQ ID NO: 154)

NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE

LCB3_v2.2 RLLS(SEQ ID NO: 155)

NDDELHMQMTDLVYEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_2 RLLS(SEQ ID NO: 156)

NDDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKARKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_3 RLLS(SEQ ID NO: 157)

NDDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKARKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_4 RLLS(SEQ ID NO: 158)

NDDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_5 RLLS(SEQ ID NO: 159)

NEDELHMQMTDLVWEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_6 RLLS(SEQ ID NO: 160)

NDDELHMQMTDLVWEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_7 RLLS(SEQ ID NO: 161)

NLDELHMQMTDLVYEALHFAKTEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLE

LCB3_v1.3_15 RLLS(SEQ ID NO: 162)

NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLE

LCB3_v2.3 RILS(SEQ ID NO: 163)

The polypeptides may contain a substantial number of mutations while retaining binding activity, as detailed in the examples that follow. In one embodiment, the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:13 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or all 20 residues selected from the group consisting 2, 6, 8, 9, 13, 14, 19, 22, 25, 26, 28, 29, 34, 35, 37, 40, 43, 45, 49, and 62. In another embodiment, the substitutions are selected from the substitutions listed in Table 6, either individually or in combinations in a given row.

Table 6: Exemplary LCB3 substitutions

Name	Parent	Mutations from WT						
LCB3_1	LCB3	L8Q	I25F	K26Q	R28H	L35K	D37T	
LCB3_2	LCB3	L8Q	K26Q	R28H	L35K	D37T	N43K	
LCB3_3	LCB3	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K

LCB3_4	LCB3	L8Q	F19K	I25F	K26Q	R28H	L35K	D37T	Y40R, N43K
LCB3_8Q	LCB3	L8Q							
LCB3_8T	LCB3	L8T							
LCB3_19K	LCB3	F19K							
LCB3_19I	LCB3	F19I							
LCB3_25F	LCB3	I25F							
LCB3_25M	LCB3	I25M							
LCB3_26Q	LCB3	K26Q							
LCB3_28H	LCB3	R28H							
LCB3_35K	LCB3	L35K							
LCB3_37T	LCB3	D37T							
LCB3_40R	LCB3	Y40R							
LCB3_43K	LCB3	N43K							
LCB3_34G	LCB3	E34G							
LCB3_34Y	LCB3	E34Y							
LCB3_34T	LCB3	E34T							
LCB3_49K	LCB3	E49K							
LCB3_v1.2	LCB3	L8Q	K26Q	R28H	L35K	D37T	N43K		
LCB3_v1.2_ACH1	LCB3_v1.2	L8Q	K26Q	R28H	E34G	L35K	D37T	N43K	
LCB3_v1.2_ACH2	LCB3_v1.2	L8Q	K26Q	R28H	E34Y	L35K	D37T	N43K	
LCB3_v2.2	LCB3_v1.3	D2L	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_2	LCB3_v1.3	L8Q	D22T	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_3	LCB3_v1.3	L8Q	I25F	K26Q	R28H	L35K	D37R	N43K	
LCB3_v1.3_4	LCB3_v1.3	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37R	N43K
LCB3_v1.3_5	LCB3_v1.3	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37T	N43K
LCB3_v1.3_6	LCB3_v1.3	D2E	L8Q	Y14W	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v1.3_7	LCB3_v1.3	L8Q	Y14W	D22T	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v1.3	LCB3_v1.2	L8Q	I25F	K26Q	R28H	L35K	D37T	N43K	
LCB3_v1.3_15	LCB3_v1.3	D2L	L8Q	D22T	I25F	K26Q	R28H	L35K	D37T, N43K
LCB3_v2.3	LCB1_v2.1	D2I	H6L	L8Q	M9V	V13I	I25F	K26Q	R28H, V29A, L35K, D37T, N43K, R45K, L62I

In a further embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:33-34 and 100-101 and 164 (see Table 7).

Table 7: AHB2 exemplary variant

AHB2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEH
v2	LEELART (SEQ ID NO: 164)

In one embodiment, the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:101 at or both residues selected from the group consisting 63 and 75. In a further embodiment, the substitutions comprise R63A and/or K75T.

In all embodiments disclosed herein, the polypeptides may comprise one or more additional functional groups or residues as deemed appropriate for an intended use. In one embodiment, the polypeptides may further comprise one or more added cysteine residues at the N-terminus and/or C-terminus. In another embodiment, the polypeptides may further comprise an N-linked glycosylation site (i.e.: NX(S/T), where X is any amino acid).

In another embodiment, the polypeptides may comprise two or more (i.e.: 2, 3, 4, 5, or more) copies of the amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101. In this embodiment, 2 or more of the binders are linked. In one embodiment, the two or more copies of the polypeptide are all identical; in another embodiment, the two or more copies of the polypeptide are not all identical. In any of these embodiments, the two or more copies of the polypeptide may be separated by amino acid linker sequences, though such linkers are not required. The amino acid linkers may be of any length and amino acid composition as suitable for an intended purpose. In one embodiment, the amino acid linkers are independently between 2-100 or 3-100 amino acids in length.

In another embodiment, the amino acid linker sequences comprise Gly-Ser rich (at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% Gly-Ser residues) amino acid linkers. In a further embodiment, the Gly-Ser rich linkers comprise an amino acid sequence selected from the group consisting of GG and SEQ ID NOs:35-46 and 165-171

GSGS (SEQ ID NO:35)

GGSGGS (SEQ ID NO:36)

SGGSGGSGGSG (SEQ ID NO:37)

GGSGGSGSGGSG (SEQ ID NO:38)

GGSGSSGGSGSGSG (SEQ ID NO:39)

GGSGSGGSGSGSGGS (SEQ ID NO:40)

SGGSGSGSGGSGSGS (SEQ ID NO:41)

GGGSGGGSSGGSGGSSGGGSGGGS (SEQ ID NO:42)

GGGSGGGGSGGGGSGGGGSGGGGSGGGGSG (SEQ ID NO:43)

GGGSGGGSGGSGGSGGGSGGGSGSGGSGGGGSGGGS (SEQ ID NO:44)

GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO:45)

SGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO:46)

GGSGGGGSGGGGSGGGGSGG (SEQ ID NO: 165)

GGSGGGGSGGGGSGG(SEQ ID NO: 166)

GGSGGGGSGG(SEQ ID NO: 167)

GGGGSGGGG(SEQ ID NO: 168)

GGGSGGG(SEQ ID NO: 169)

GGSGG(SEQ ID NO: 170)

GGSGSSG(SEQ ID NO: 171)

In another embodiment, the amino acid linker sequences may comprise Pro-rich (at least 15%, 20%, 25%, or greater Pro residues) amino acid linkers. Non-limiting and exemplary embodiments may comprise an amino acid sequence selected from the group consisting of SEQ ID NOs:97-98 and 172-176.

AGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASG(SEQ ID NO:97)

GSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSAS(SEQ ID NO:98)

GGASPAAPAPASPAAPAPSAPAGG (SEQ ID NO: 172)

GGASPAAPAPASPAGG(SEQ ID NO: 173)

GGASPAAPAPGG(SEQ ID NO: 174)

GGASPAAPAGG(SEQ ID NO: 175)

GGSSGPSTPPTPSPSTPPTPSPSPGGSSG(SEQ ID NO: 176)

In further non-limiting embodiments, the amino acid linkers may comprise the amino acid sequence selected from the group consisting of SEQ ID NOS: 99 and 177-178.

GGSSAGSPTSTGTSSATPSGSGTGG(SEQ ID NO: 177)

GGSSGEAAAKEAAAKEAAAKGSSGG(SEQ ID NO: 178)

GGSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGGSSG(SEQ ID NO: 99)

In one embodiment, the polypeptide comprises the formula Z1-Z2-Z3, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Z2 comprises an optional amino acid linker; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

wherein Z1 and Z3 may be identical or different. In one embodiment, Z1 and Z3 are identical; in another embodiment Z1 and Z3 are different. In embodiments where Z1 and Z3 differ, each may be a variant of a given starting monomer (ex: Z1 comprises the amino acid sequence of SEQ ID NO:1 (LCB1), and Z3 comprises the amino acid sequence of SEQ ID NO: 102-136. Any such combination of the monomers disclosed herein may be used. It will further be understood that the polypeptides may comprise 2, 3, 4, 5, or more monomers of any embodiment disclosed herein. In embodiments where there are 3 or more monomers, all 3 monomers may be identical; 2 monomers may be identical and one may differ, or all 3 monomers may be different.

In one embodiment employing LCB1 and variants thereof, Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

In another embodiment employing LCB3 and variants thereof,

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

In another embodiment employing AHB and variants thereof,

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

In one embodiment, one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

In another embodiment, one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

In a further embodiment, one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting SEQ ID NOS: 13-17, 19-21 and 137-163; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

In another embodiment of any of the other embodiments disclosed herein, the polypeptide comprises at least 3 monomers (i.e.: 3, 4, 5, or more). In one such embodiment, the polypeptide comprises the formula B1-B2-Z1-Z2-Z3-B3-B4, wherein:

Z1, Z2, and Z3 are as defined above;

B2 and B3 comprise optional amino acid linkers; and

one or both of B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164, wherein one of B1 and B4 may be absent. In one embodiment, one of B1 and B4 is absent. In another embodiment, both B1 and B4 are present. In one embodiment, B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164. In this embodiment, B1 and B4 may be identical or may be different. In one embodiment, B1 when present and B4 when present, are identical to one or both of Z1 and Z3. In another embodiment, B1 when present and B4 when present, are not identical to either of Z1 and Z3.

In one embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10, 13-17, 19-21, 33-34, 100-101, and 102-164.

In another embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

In a further embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

In a still further embodiment, B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

In various embodiments when both B1 and B4 are present,

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least

50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163;

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164, or
- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

In various non-limiting embodiments, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:47-60, 193-355, and 454-588 and a genus selected from those recited in the right hand column of Table 8 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids. In all embodiments, any N-terminal methionine residues may be present or absent in the polypeptide. In one embodiment, any N-terminal methionine residues are absent in the polypeptide.

>LCB1-6GS-LCB1
DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:47)

>LCB1-12GS-LCB1
DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGGSGSGGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:48)

>LCB1-24GS-LCB1

DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGSGGGSSGGSGGSSGGGSGGGSDKE
WILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:49)

>LCB1-36GS-LCB1
DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGSGGGSGGSGGSGGGSGGGSGSGGS
GGGGSGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:50)

>LCB1_v1.1-GSLCB1_v1.1(1GS1)
DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSGGGGSGG
GGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEF
MKQGDERLLEEAERLLEEVER (SEQ ID NO:51)

>LCB1_v1.1-PRO-LCB1_v1.1(1PRO1)
DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPP
TPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEF
MKQGDERLLEEAERLLEEVER (SEQ ID NO:52)

>LCB3_v1.2-GS3-LCB3_v1.2(3GS3)
NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQK
HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:53)

>LCB3_v1.2-PRO-LCB3_v1.2(3PRO3)
NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPP
TPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQK
HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:54)

>LCB1_v1.1-GS-LCB3_v1.2(1GS3)
DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSGGGGSGG
GGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK
ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:55)

>LCB3_v1.2-GS-LCB1_v1.1(3GS1)
NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQ
VSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:56)

>LCB3_v1.2-10GS-LCB1_v1.1(LCB3-GS10-LCB1)
NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGSGDKENILQKI
YEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:57)

>LCB1_v1.1-PRO-LCB3_v1.2(1PRO3)
DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGSGGSPVPSTPPTPSPSTPP
TPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEK
ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:58)

>LCB3_v1.2-PRO-LCB1_v1.1(3PRO1)
NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPP
TPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQ
VSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:59)

>36175(5_LCB1_linker14)
DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSSGGSGSGSGDKEWILQKIYEIM
RLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSSGGSGSGSGDKEWILQKIYEIMRLLDELGHAEASM
RVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSSGGSGSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKG

DERLLEEAERLLEEVERGGSGSSGGSGSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:60)

Table 8. Daisy Chain Designs

Name	Protein	Annotated: X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids
1GS1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO: 193)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:4)
1PRO1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 194)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)
3GS3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 195)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:15)
3PRO3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 196)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO:15)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO:15)
1GS3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSNDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 197)	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO:15)
3GS1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 198)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO:15)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)
1PRO3	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID	X1-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)-X2-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ

	NO: 199)	ID NO:15)
3PRO1	MEKKIGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGGGGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 200)	X1-NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO:15)-X2-DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO:4)
CSL-LCB1-GS15-LCB1	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 201)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)
CSL-LCB3-GS15-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO: 202)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS (SEQ ID NO:13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)
CSL-LCB1-GS20-LCB1	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGGGSGGGGSGGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 203)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)
CSL-LCB3-GS20-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO: 204)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X2-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)
CSL-LCB1-GS20-LCB1-GS20-LCB1	MEKKISAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSGSGSSGSGSSGSGSSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSSGGSSSGGSSSGGSSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 205)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X3-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)
CSL-LCB3-GS20-LCB3-GS20-LCB3	MEKKISAWSHPQFEKGGSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO: 206)	X1-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X2-DDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X3-NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)
CSL-LCB1-XTENx2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSTSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 207)	X1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X2-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)
CSL-LCB1-XTENx	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGSPAGS	x1-DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)

3	PTSTGTSGSGDKEWILQKIYEIMRLLDELGHAEASM RVSDLIYEFMKKGDERLLEEAERLLEEVERGSAGGS PAGSPTSTGTSGSGDKEWILQKIYEIMRLLDELGHA EASMRVSDLIYEFMKKGDERLLEEAERLLEEVER(S EQ ID NO: 208)	-X2- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1) -X3- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)
CSL-LCB3-XTENx2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGS AGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALH FAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEE LKELLERLLS(SEQ ID NO: 209)	X1- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13) -X2- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)
CSL-LCB3-XTENx3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGS AGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALH FAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEE LKELLERLLSGSAGGSPAGSPTSTGTSGSGNDDELH MLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKN NDRQKLEKVVEELKELLERLLS(SEQ ID NO: 210)	X1- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13) -X2- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13) -X3- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)
C-LCB1-GS20-LCB1-GS20-LCB1-LS	MEKKISSGDKEWILQKIYEIMRLLDELGHAEASMRV SDLIYEFMKKGDERLLEEAERLLEEVERGSSGSGSS GSGSSGSGSSGSDKEWILQKIYEIMRLLDELGHAEA SMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSSS GGSSSGGSSSGGSSSGDKEWILQKIYEIMRLLDELG HAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER GGSGSSGSAWSHPQFEK(SEQ ID NO: 211)	X1- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1) -X2- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1) -X3- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1) -X4
C-LCB3-GS20-LCB3-GS20-LCB3-LS	MEKKISSGNDDELHMLMTDLVYEALHFAKDEEIKKR VFQLFELADKAYKNNDRQKLEKVVEELKELLERLLS GSSGSGSSGSGSSGSGSSGSNDDELHMLMTDLVYEA LHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVV EELKELLERLLSGSSSGGSSSGGSSSGGSSSGNDDE LHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAY KNNDRQKLEKVVEELKELLERLLSGGSGSSGSAWSH PQFEK(SEQ ID NO: 212)	X1- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X2- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X3- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X4
CSL-LCB1-XTEN25x3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKEWILQKIYEIMRLLDELGHAEASMRVSD LIYEFMKKGDERLLEEAERLLEEVERGGSSAGSPTS TGTSSATPSGSGTGGDKEWILQKIYEIMRLLDELGH AEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG GSSAGSPTSTGTSSATPSGSGTGGDKEWILQKIYEI MRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAE RLLEEVER(SEQ ID NO: 213)	X1- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X2- DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)-X3 DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEF MKKGDERLLEEAERLLEEVER(SEQ ID NO: 1)
CSL-LCB3-XTEN25x3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNDDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGG SSAGSPTSTGTSSATPSGSGTGGNDDELHMLMTDLV YEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLE KVVEELKELLERLLSGGSSAGSPTSTGTSSATPSGS GTGGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQL FELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO: 214)	X1NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLF ELADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X2- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)-X3- NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS(SEQ ID NO:13)
LCB1_v1.3_	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGGGSSG	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER (SEQ ID

GS_2X	GGSSGGGSSGGGSSGDKENILQKIYEIMKTLEQLGH AEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 215)	NO:8)-X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ XTEN_ 2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTS TGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGH AEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 216)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ EAAAK _2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAK EAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGH AEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 217)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ Pro_2 X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPP TPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLE QLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEE VER(SEQ ID NO: 218)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ Ub_2X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVK TLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQR LIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGG SSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVER(SEQ ID NO: 219)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ XTEN_ 3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSAGSPTS TGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGH AEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEI MKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAE RLLEEVER(SEQ ID NO: 220)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X3- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ EAAAK _3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGEAAAK EAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGH AEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEI MKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAE RLLEEVER(SEQ ID NO: 221)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X3- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ Pro_3 X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPP TPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLE QLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEE VERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKEN ILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGD ERLLEEAERLLEEVER(SEQ ID NO: 222)	X1- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X3- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
LCB1_ v1.3_ Ub_3X	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVK TLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQR LIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGG SSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLT	X1DKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVER(SEQ ID NO:8)-X2- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)- X3- DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEF

	GKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIF AGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGGSSG DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFM KQGDERLLEEAERLLEEVER(SEQ ID NO: 223)	MKQGDERLLEEAERLLEEVER(SEQ ID NO:8)
1GS1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSG GGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 224)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
1Pro1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPP TPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELE RLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEE VKR(SEQ ID NO: 225)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3GS3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLV YEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLS(SEQ ID NO: 226)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
3Pro3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQM TDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDR QKLEKVVEELKELLERLLS(SEQ ID NO: 227)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
1GS1_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGG GSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHA EASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGG SGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 228)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
1Pro1_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPT PSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELER LGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEV KRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQ FEK(SEQ ID NO: 229)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
3GS3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGS SGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGGSGSSGSAWSHPQFEKGGGSG GGSGGSAWSHPQFEK(SEQ ID NO: 230)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
3Pro3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGS SGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMT DLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQ KLEKVVEELKELLERLLSGGSGSSGSAWSHPQFEKG GGSGGGSGGSAWSHPQFEK(SEQ ID NO: 231)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
1GS1GS1_NT	MEKKISAWSHPQFEKGGSGSSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERL LEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENV	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO:

S	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE NLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGG GSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLI YEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 232)	135)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
1Pro1 Pro1_ NTS	MEKKISAWSHPQFEKGGSGSSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERL LEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGD KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTP PTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEA SMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 233)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3GS3G S3_NT S	MEKKISAWSHPQFEKGGSGSSGNLDELHMQMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGG SSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSG GGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLS(SEQ ID NO: 234)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
3Pro3 Pro3_ NTS	MEKKISAWSHPQFEKGGSGSSGNLDELHMQMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSP SPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSG GSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQ MTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKD RQKLEKVVEELKELLERLLS(SEQ ID NO: 235)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
1GS1G S1_CT S	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGG GSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHA EASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGG SSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER LLEEVKRGGSGSSGSAWSHPQFEK(SEQ ID NO: 236)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
1Pro1 Pro1_ CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPT PSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELER LGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEV KRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENV LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE NLLEEAERLLEEVKRGGSGSSGSAWSHPQFEK(SEQ ID NO: 237)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
3GS3G S3_CT S	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGS SGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-

	VVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGGG SSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGS SGSAWSHPQFEK(SEQ ID NO: 238)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X4
3Pro3_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGS SGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMT DLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQ KLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPP TPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLER LLSGGSGSSGSAWSHPQFEK(SEQ ID NO: 239)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X4
1GS3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSG GGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLS(SEQ ID NO: 240)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
1Pro3_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPP TPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEAL HFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVE ELKELLERLLS(SEQ ID NO: 241)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)X-2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
3GS1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER LLEEVKR(SEQ ID NO: 242)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3Pro1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG SSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLE EAERLLEEVKR(SEQ ID NO: 243)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
1GS3_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGG GSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKEL LERLLSGGSGSSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK(SEQ ID NO: 244)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
1Pro3_CTS	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPT PSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALH FAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEE LKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGGSG GSAWSHPQFEK(SEQ ID NO: 245)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
3GS1_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGS SGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERL	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-

	LEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 246)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
3Pro1_CTS	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 247)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
3-GS10-1-L_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 248)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3-GS10-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 249)	X1-}NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3-GS15-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 250)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3-GS20-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 251)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
1-GS10-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 252)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
1-GS15-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 253)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
1-GS20-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 254)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-1_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGDKENVLQKIYEIMKELE	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO:101)-X2-

	RLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEE VKR(SEQ ID NO: 255)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
2-1_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAE RLLEEVKR(SEQ ID NO: 256)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO:101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
2-1_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGGGSSGDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERL LEEAERLLEEVKR(SEQ ID NO: 257)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK (SEQ ID NO:101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
2-2-1_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEARRILEHLEELARKGGSSGGGSS GGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 258)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3
2-2-1_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEARRILEHLEELARKGGSSGGGSS GGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 259)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3
2-2-1_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVM HVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEARRILEHLEELARKGGSS GGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLG HAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO: 260)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3
2-2-2_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVM HVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 261)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)
2-2-2_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 262)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)
2-2-2_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVM HVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEARRILEHLEELARK(SEQ	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE

	ID NO: 263)	ELARK(SEQ ID NO:101)
2-2-2_GS10	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 264)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
2-2-2_GS15	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 265)	X1ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
2-2-2_GS20	MSKIKSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 266)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
AHB2-AHB2_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 267)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
LCB3-LCB1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 268)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
AHB2-LCB1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 269)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO:101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
AHB2_3x_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 270)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
3-2-1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF	X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ

	QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVS ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEARRILEHLEELARKGGASPAAPAPA SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SE Q ID NO: 271)	ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3
2-3-1_PAS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLD ELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKA YKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPA SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SE Q ID NO: 272)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
1-1-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAP ASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHA EASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGG ASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERL LEEVKR(SEQ ID NO: 273)	X1- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-2-2_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWA TEMMLELIKSDDEREIREIEEEARRILEHLEELARK GGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQ VSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 274)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)
3-3-3_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGG ASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVY EALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLSGGASPAAPAPASPAAPAPSAPA GGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFE KATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 275)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
2-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGASPAAPAPASPAAPAPSAPAGGELE EQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWA TEMMLELIKSDDEREIREIEEEARRILEHLEELARK GGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE RLLEEVKR(SEQ ID NO: 276)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDE-REIREIEEEARRILEHLEELARK(SEQ ID NO:101)X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-2_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGASPAAPAPASPAGGELEEQVMHVLD QVSELAHELLHKLTGEELERAAYFNWWATEMMLELI KSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 277	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)

2-2_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 278)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
3-1_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 279)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
3-1_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 280)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO:155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
2-1_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 281)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO:101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
2-1_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 282)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID NO:101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
3v2.3-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 283)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3
2-3v2.3-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 284)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3
2-2-2_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 285)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART (SEQ ID NO: 164)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 164)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 164)

1-1-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRG(SEQ ID NO: 286)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR (SEQ ID NO:125)
3v2.3-2-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 287)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 164)-X3
2-3v2.3-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR(SEQ ID NO: 288)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 164)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3
3v2.3-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 289)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS (SEQ ID NO: 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3v2.3-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 290)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
3v2.3-2-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 291)	X1-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 164)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3v2.3-1_PAS24_ompT	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAAPAPSAPAGG	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART(SEQ ID NO: 164)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ

	SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SE Q ID NO: 292)	ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3v2.3-1_PAS24_NHis-TEV	MEKKIHHHHHHSGENLYFQSGGSGSSGELEEQVMHV LDQVSELAHELLHKLTGEELERAAYFNWWATEMMLE LIKSDDEREIREIEEEARRILEHLEELARKGGASPA APAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALH FAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEE LKELLERILSGGASPAAPAPASPAAPAPSAPAGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEAERLLEEVKR(SEQ ID NO: 293)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3v2.3-1_PAS24_omptN-His-TEV	MEKKIHHHHHHSGENLYFQSGGSGSSGELEEQVMHV LDQVSELAHELLHKLTGEELERAAYFNWWATEMMLE LIKSDDEREIREIEEEAARILEHLEELARTGGASPA APAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALH FAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEE LKELLERILSGGASPAAPAPASPAAPAPSAPAGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEAERLLEEVKR(SEQ ID NO: 294)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART(SEQ ID NO: 164)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_PAS24_NTSF	MEKKIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSG GSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAH ELLHKLTGEELERAAYFNWWATEMMLELIKSDDERE IREIEEEARRILEHLEELARKGGASPAAPAPASPAA PAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQK HAFQLFEKATKAYKNKDKQKLEKVVEELKELLERIL SGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEA ERLLEEVKR(SEQ ID NO: 295)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_PAS24_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARKG GASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLI YEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLE KVVEELKELLERILSGGASPAAPAPASPAAPAPSAP AGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 296)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_PAS24_NTSM	MEKKIEQKLISEEDLGSGSSAWSHPQFEKGGGSGGG SGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSEL AHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEARRILEHLEELARKGGASPAAPAPASP AAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEF QKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLER ILSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLE EAERLLEEVKR(SEQ ID NO: 297)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS24-3-PAS16-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSH PQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARKG GASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLI YEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLE KVVEELKELLERILSGGASPAAPAPASPAGGDKENV LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE NLLEEAERLLEEVKR(SEQ ID NO: 298)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEK ATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)

2-PAS16-3-PAS16-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 299)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS11-3-PAS16-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 300)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS24-3-PAS11-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 301)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS16-3-PAS11-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 302)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS11-3-PAS11-1_NTS3F	MEKKIDYKDHDGDYKDHDIDYKDDDDKGSGSSAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 303)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-2_G4	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 304)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
2-2_G2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 305)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)

2-3_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 306)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)
2-3_PAS16	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 307)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)
2-3_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 308)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS(SEQ ID NO: 163)
1-2-1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 309)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS24-3-PAS24-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 310)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS24-3-PAS16-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 311)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS (SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS16-3-	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLE	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLE

PAS16-1_NTS	EHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 313)	ELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS11-3-PAS16-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 314)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS24-3-PAS11-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 315)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-PAS16-3-PAS11-1_NTS	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 316)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_PAS7	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 318)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_GS7	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVK	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-

	R(SEQ ID NO: 319)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_GS5	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSGGNLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKEL LERLLSGGSGGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 320)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_GS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSGGSGGSGGNLDELHMQMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLSGGSGGSGGSGGDKENVLQKIYEIM KELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER LLEEVKR(SEQ ID NO: 321)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-2-2_PAS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGASPAAPAGGELEEQVMHVLDQVSEL AHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEARRILEHLEELARKGGASPAAPAGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO: 322)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)
2-2-2_GS11	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSGGSGGSGGELEEQVMHVLDQVSEL AHELLHKLTGEELERAAYFNWWATEMMLELIKSDDE REIREIEEEARRILEHLEELARKGGSGGSGGSGGEL EEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO: 323)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)
2-2-2_GS8	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSGGELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKSDDEREIREI EEEARRILEHLEELARKGGSGGELEEQVMHVLDQVS ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEARRILEHLEELARK(SEQ ID NO: 324)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)
2-2-2_GS5	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRIL EHLEELARKGGSGGELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKSDDEREIREI EEEARRILEHLEELARKGGSGGELEEQVMHVLDQVS ELAHELLHKLTGEELERAAYFNWWATEMMLELIKSD DEREIREIEEEARRILEHLEELARK(SEQ ID NO: 325)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)

2-3-1_GGGGS15	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEHLEELARKGGSGGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 326)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_GGGGS12	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEHLEELARKGGSGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 327)	X1-E-LEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK (SEQ ID No: 101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_GGGGS9	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEHLEELARKGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 328)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
2-3-1_GGGGS7	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEHLEELARKGGGSGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 329)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLG(SEQ ID NO: 135)HAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
1-1_GGGGS25	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 330)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
1-1_GGGGS20	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 331)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
1-1_GGGGS15	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 332)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
1-1_GGG	MEKKIGGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO:

GS10	FMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 333)	135)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
2-1_GGGGS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 334)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
3-1_GGGGS10	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 335)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
2-3_GGGGS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEK(SEQ ID NO: 336)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
3-2_GGGGS10	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEK(SEQ ID NO: 337)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
2-3-1_GGGGS10	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEK(SEQ ID NO: 338)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
3-2-1_GGGGS10	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEK(SEQ ID NO: 339)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
2-3-1_GGGGS15	MEKKIGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 340)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
3-2-1_GGGGS15	MEKKIGGGNLDELHMQMTDLVYEALHFAKDEEFQKH	X1-

1_GGG GS15	VFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS GGSGGGGSGGGGSGGELEEQVMHVLDQVSELAHELL HKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSGGGGSGGDKE NVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTK DENLLEEAERLLEEVKRGGGSGGGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 341)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
LCB3- LCB1_ PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSG SAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 342)	X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
AHB2- LCB1_ PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEARRILE HLEELARKGGASPAAPAPGGDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLE EVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSH PQFEK(SEQ ID NO: 343)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
AHB2- LCB3_ PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEARRILE HLEELARKGGASPAAPAPGGNLDELHMQMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK(SEQ ID NO: 344)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
LCB3- AHB2_ PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDEREIREIEEEAR RILEHLEELARKGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK(SEQ ID NO: 345)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3
AHB2- LCB3- LCB1_ PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEARRILE HLEELARKGGASPAAPAPGGNLDELHMQMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLSGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE RLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 346)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X2- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
LCB3- AHB2- LCB1_ PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDEREIREIEEEAR RILEHLEELARKGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE RLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 347)	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
LCB3- AHB2- LCB1_ PAS24	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDD EREIREIEEEARRILEHLEELARKGGASPAAPAPAS PAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEA SMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSG SSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SE	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLE ELARK(SEQ ID NO:101)-X3- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF

	Q ID NO: 348)	MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
AHB2v 2-LCB1_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEAARILE HLEELARTGGASPAAPAPGGDKENVLQKIYEIMKEL ERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLE EVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSH PQFEK(SEQ ID NO: 349)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164)-X2-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X3
AHB2v 2-LCB3_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEAARILE HLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLSGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK(SEQ ID NO: 350)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART(SEQ ID NO: 164)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
LCB3-AHB2v2_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDEREIREIEEEAA RILEHLEELARTGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK(SEQ ID NO: 351)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART (SEQ ID NO: 164)-X3
AHB2v 2-LCB3-LCB1_PAS12	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELER AAYFNWWATEMMLELIKSDDEREIREIEEEAARILE HLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEA LHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLSGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE RLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 352)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART(SEQ ID NO: 164)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR (SEQ ID NO: 135)-X4
LCB3-AHB2v2-LCB1_PAS12	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDEREIREIEEEAA RILEHLEELARTGGASPAAPAPGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE RLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 353)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART(SEQ ID NO: 164)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X4
AHB2v 2-LCB3-LCB1_PAS24	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKG GSGSSGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEAARIL EHLEELARTGGASPAAPAPASPAAPAPSAPAGGNLD ELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKA YKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPA SPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SE Q ID NO: 354)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART(SEQ ID NO: 164)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
LCB3-AHB2v2-LCB1_PAS24	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGA SPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDD EREIREIEEEAARILEHLEELARTGGASPAAPAPAS PAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEA SMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSG SSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SE Q ID NO: 355)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEK ATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEAARILEHLE ELART(SEQ ID NO: 164)-X3-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO:

135)-X4

Table 8A

SEQ ID	Name	Sequence
51	1GS1	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGG GSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGD ERLLEEAERLLEEVER
52	1PRO1	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERA GSGGSGGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTP PTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGD ERLLEEAERLLEEVER
53	3GS3	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS GGGGSGGGGSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQL FEKATKAYKNKDRQKLEKVVEELKELLERLLS
54	3PRO3	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPS PSPVPSTPPTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQL FEKATKAYKNKDRQKLEKVVEELKELLERLLS
55	1GS3	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGG GSGGGGSGGGGSGGGGSNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAY KNKDRQKLEKVVEELKELLERLLS
56	3GS1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS GGGGSGGGGSGGGGSGGGGSGGGGSDKENILQKIYEIMKTLDQLGHAEASMQVSDLI YEFMKQGDERLLEEAERLLEEVER
58	1PRO3	DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERA GSGGSGGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPSPSPVPSTP PTPSPSTPPTPSPSASGNDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAY KNKDRQKLEKVVEELKELLERLLS
59	3PRO1	NDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSAGSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSPVPSTPPTPSPSTPPTPS PSPVPSTPPTPSPSTPPTPSPSASGDKENILQKIYEIMKTLDQLGHAEASMQVSDLI YEFMKQGDERLLEEAERLLEEVER
454	CSL-LCB1-GS15-LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG GGGSGGGGSGGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERL LEEAERLLEEVER
455	CSL-LCB3-GS15-LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFEL ADKAYKNNDRQKLEKVVEELKELLERLLS
456	CSL-LCB1-GS20-LCB1	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG GGGSGGGGSGGGGSGGGGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK GDERLLEEAERLLEEVER
457	CSL-LCB3-GS20-LCB3	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE LLERLLSGGGGSGGGGSGGGGSGGGGSNDDELHMLMTDLVYEALHFAKDEEIKKRVF QLFELADKAYKNNDRQKLEKVVEELKELLERLLS
458	CSL-LCB1-GS20-LCB1-	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG SSGSGSSGSGSSGSGSSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK GDERLLEEAERLLEEVERGSSSGGSSSGGSSSGGSSSGDKEWILQKIYEIMRLLDEL GHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER

	GS20-LCB1	
	CSL-LCB3-	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE
	GS20-	LLERLLSGSSGSGSSGSGSSGSGSSGSNDDELHMLMTDLVYEALHFAKDEEIKKRVF
	LCB3-	QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGGSSSGGSSSGGSSSGNDD
	GS20-	ELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE
459	LCB3	RLLS
	CSL-	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG
	LCB1-	SAGGSPAGSPTSTGTSTSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK
460	XTENx2	GDERLLEEAERLLEEVER
		DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG
	CSL-	SAGGSPAGSPTSTGTSGSGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK
	LCB1-	GDERLLEEAERLLEEVERGSAGGSPAGSPTSTGTSGSGDKEWILQKIYEIMRLLDEL
461	XTENx3	GHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
	CSL-	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE
	LCB3-	LLERLLSGSAGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVF
462	XTENx2	QLFELADKAYKNNDRQKLEKVVEELKELLERLLS
		NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE
		LLERLLSGSAGGSPAGSPTSTGTSGSGNDDELHMLMTDLVYEALHFAKDEEIKKRVF
	CSL-	QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSAGGSPAGSPTSTGTSGSGNDD
	LCB3-	ELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE
463	XTENx3	RLLS
	C-LCB1-	
	GS20-	
	LCB1-	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG
	GS20-	SSGSGSSGSGSSGSGSSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKK
	LCB1-	GDERLLEEAERLLEEVERGSSSGGSSSGGSSSGGSSSGDKEWILQKIYEIMRLLDEL
458	LS	GHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
	C-LCB3-	
	GS20-	NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE
	LCB3-	LLERLLSGSSGSGSSGSGSSGSGSSGSNDDELHMLMTDLVYEALHFAKDEEIKKRVF
	GS20-	QLFELADKAYKNNDRQKLEKVVEELKELLERLLSGSSSGGSSSGGSSSGGSSSGNDD
	LCB3-	ELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKELLE
459	LS	RLLS
	CSL-	DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERG
	LCB1-	GSSAGSPTSTGTSSATPSGSGTGGDKEWILQKIYEIMRLLDELGHAEASMRVSDLIY
	XTEN25	EFMKKGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKEWILQKI
464	x3	YEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER
		NDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEKVVEELKE
	CSL-	LLERLLSGGSSAGSPTSTGTSSATPSGSGTGGNDDELHMLMTDLVYEALHFAKDEEI
	LCB3-	KKRVFQLFELADKAYKNNDRQKLEKVVEELKELLERLLSGGSSAGSPTSTGTSSATP
	XTEN25	SGSGTGGNDDELHMLMTDLVYEALHFAKDEEIKKRVFQLFELADKAYKNNDRQKLEK
465	x3	VVEELKELLERLLS
	LCB1_v1.3_GS_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGGGSSGGGSSGGGSSGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVER
466		
	LCB1_v1.3_XTEN_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVER
467		
	LCB1_v1.3_EAAAK_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVER
468		
	LCB1_v1.3_Pro_2X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVS DLIYEFMKQGDERLLEEAERLLEEVER
469		
470	LCB1_v1.3_Ub	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGR

	_2X	TLSDYNIQKESTLHLVLRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVER
471	LCB1_v 1.3_XT EN_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSAGSPTSTGTSSATPSGSGTGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVERGGSSAGSPTSTGTSSATPSGSGTGGDKENILQKI YEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
472	LCB1_v 1.3_EA AAK_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGEAAAKEAAAKEAAAKGSSGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIY EFMKQGDERLLEEAERLLEEVERGGSSGEAAAKEAAAKEAAAKGSSGGDKENILQKI YEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
473	LCB1_v 1.3_Pr o_3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVS DLIYEFMKQGDERLLEEAERLLEEVERGGSSGPSTPPTPSPSTPPTPSPSPGGSSGD KENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
474	LCB1_v 1.3_Ub _3X	DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERG GSSGQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGR TLSDYNIQKESTLHLVLRLRGGGGSSGDKENILQKIYEIMKTLEQLGHAEASMQVSD LIYEFMKQGDERLLEEAERLLEEVERGGSSGQIFVKTLTGKTITLEVEPSDTIENVK AKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGGGGSSGDKE NILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER
475	1GS1_N TS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKR
476	1Pro1_ NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTKDENLLEEAERLLEEVKR
477	3GS3_N TS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
478	3Pro3_ NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
475	1GS1_C TS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKR
476	1Pro1_ CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTKDENLLEEAERLLEEVKR
477	3GS3_C TS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
478	3Pro3_ CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
479	1GS1GS 1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
480	1Pro1P ro1_NT S	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGD KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
481	3GS3GS 3_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGS SGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLS
482	3Pro3P ro3_NT	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK

	S	DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSP STPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKN KDRQKLEKVVEELKELLERLLS
479	1GS1GS 1_CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKRGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
480	1Pro1P ro1_CT S	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS DLIYEFMKTKDENLLEEAERLLEEVKRGGSSGPSTPPTPSPSTPPTPSPSPGGSSGD KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
481	3GS3GS 3_CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEF QKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGGGSSGGGSSGGGS SGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEK VVEELKELLERLLS
482	3Pro3P ro3_CT S	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAK DEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSSGPSTPPTPSP STPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKN KDRQKLEKVVEELKELLERLLS
483	1GS3_N TS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS
484	1Pro3_ NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
485	3GS1_N TS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTKDENLLEEAERLLEEVKR
486	3Pro1_ NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
483	1GS3_C TS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLF EKATKAYKNKDRQKLEKVVEELKELLERLLS
484	1Pro3_ CTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGPSTPPTPSPSTPPTPSPSPGGSSGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
485	3GS1_C TS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEAS MQVSDLIYEFMKTKDENLLEEAERLLEEVKR
486	3Pro1_ CTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGPSTPPTPSPSTPPTPSPSPGGSSGDKENVLQKIYEIMKELERLGH AEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
487	3- GS10- 1- L_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKD ENLLEEAERLLEEVKR
488	3- GS10- 1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKD ENLLEEAERLLEEVKR
489	3- GS15- 1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR
490	3- GS20- 1_NTS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKR

	1-GS10-1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE
491		RLLEEVKR
	1-GS15-1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENL
492		LEEAERLLEEVKR
	1-GS20-1_NTS	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT
493		KDENLLEEAERLLEEVKR
	2-1_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVS
494		DLIYEFMKTKDERLLEEAERLLEEVKR
	2-1_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEA
495		SMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
	2-1_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERL
496		GHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
	2-2-1_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEEL ERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGD
497		KENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
	2-2-1_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGG GSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDERLLEEAE
498		RLLEEVKR
	2-2-1_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHE LLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKG GSSGGGSSGGGSSGGGSSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT
499		KDERLLEEAERLLEEVKR
	2-2_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEEL
500		ERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
	2-2_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKL
501		TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
	2-2_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHE
502		LLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
	2-2-2_GS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEEL ERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGGGSSGE LEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREI
503		EEEARRILEHLEELARK
	2-2-2_GS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKL TGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSSGG GSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIK
504		SDDEREIREIEEEARRILEHLEELARK
	2-2-2_GS20	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHE LLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKG GSSGGGSSGGGSSGGGSSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW
505		ATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
	AHB2-AHB2_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE
506		LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL

		ARK
507	LCB3-LCB1_PAS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASM QVSDLIYEFMKTKDERLLEEAERLLEEVKR
508	AHB2-LCB1_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKE LERLGHAEASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
509	AHB2_3x_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
510	3-2-1_PAS	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE RLLEEAERLLEEVKR
511	2-3-1_PAS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYE ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE RLLEEAERLLEEVKR
512	1-1-1_PAS24	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE FMKTKDENLLEEAERLLEEVKRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
509	2-2-2_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
513	3-3-3_PAS24	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQ KHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPS APAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVV EELKELLERLLS
514	2-2-1_PAS24	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARKGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKR
515	2-2_PAS16	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAGGELEEQVMHVLDQVSELAHELLHK LTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
516	2-2_PAS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEE LERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
517	3-1_PAS16	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE FMKTKDERLLEEAERLLEEVKR
518	3-1_PAS11	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFFMKTK DERLLEEAERLLEEVKR
519	2-1_PAS16	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAGGDKENVLQKIYEIMKELERLGHAE ASMQVSDLIYEFMKTKDERLLEEAERLLEEVKR
520	2-1_PAS11	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAGGDKENVLQKIYEIMKELERLGHAEASMQV SDLIYEFMKTKDERLLEEAERLLEEVKR

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                NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
     3v2.3-     LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG
     2-         EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
521  4          RLLEEAERLLEEVKR

                ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     2-         IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
     3v2.3-     ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
522  4          RLLEEAERLLEEVKR

                ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
                IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSE
     2-2-       LAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEEL
     2_PAS2     ARTGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELE
523  4_ompT     RAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELART

                DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTRG
     1-1-       GASPAAPAPASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYE
     1_PAS2     FMKTKDENLLEEAERLLEEVTRGGASPAAPAPASPAAPAPSAPAGGDKENVLQKIYE
524  4_ompT     IMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVTR

                NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
     3v2.3-     LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG
     2-         EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
525  4_ompT     RLLEEAERLLEEVKR

                ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     2-         IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
     3v2.3-     ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
526  4_ompT     RLLEEAERLLEEVKR

                NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
     3v2.3-     LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG
     2-         EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
527  4          NLLEEAERLLEEVKR

                ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     2-         IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
     3v2.3-     ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
528  4          NLLEEAERLLEEVKR

                NIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKE
     3v2.3-     LLERILSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG
     2-         EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
529  4_ompT     NLLEEAERLLEEVKR

                ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     2-         IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
     3v2.3-     ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
     1_PAS2     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
530  4_ompT     NLLEEAERLLEEVKR

     2-
     3v2.3-     ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     1_PAS2     IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
     4_N-       ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
     His-       APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
538  TEV        NLLEEAERLLEEVKR

     2-
                ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     3v2.3-     IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
     1_PAS2     ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
     4_ompT     APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
530  _N-        NLLEEAERLLEEVKR
     His-
```

	TEV	
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	2-3-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2	APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
531	4_NTSF	NLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	1_PAS2	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	4_NTS3	APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
531	F	NLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	2-3-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_PAS2	APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
531	4_NTSM	NLLEEAERLLEEVKR
	2-	
	PAS24-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	PAS16-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_NTS3	APASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER
532	F	LLEEVKR
	2-	
	PAS16-	
	3-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS16-	IEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDE
	1_NTS3	EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGG
533	F	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	2-	
	PAS11-	
	3-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS16-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	1_NTS3	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAPASPAGGDKENV
534	F	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	2-	
	PAS24-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3-	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE
	PAS11-	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAP
	1_NTS3	AGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEV
535	F	KR
	2-	
	PAS16-	
	3-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS11-	IEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDE
	1_NTS3	EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENV
536	F	LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	2-	
	PAS11-	
	3-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	PAS11-	IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
	1_NTS3	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGASPAAPAGGDKENVLQKIY
537	F	EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF
538	2-2_G4	NWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW
539	2-2_G2	WATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
540	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	3_PAS2	IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNIDELLMQVTDLIYE

	4	ALHFAKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
	2-3_PAS1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAGGNIDELLMQVTDLIYEALHFAKDE
541	6	EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
	2-3_PAS1	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAGGNIDELLMQVTDLIYEALHFAKDEEFQKH
542	1	AFQLFEKATKAYKNKDKQKLEKVVEELKELLERILS
	1-2-1_PAS2	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAY FNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPASPAAP APSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER
543	4	LLEEVKR
	2-PAS24-3-PAS24-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYE ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
544		NLLEEAERLLEEVKR
	2-PAS24-3-PAS16-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYE ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP APASPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER
545		LLEEVKR
	2-PAS16-3-PAS24-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDE EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAP APSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAER
546		LLEEVKR
	2-PAS16-3-PAS16-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDE EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGG
547		DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	2-PAS11-3-PAS16-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKH VFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAGGDKENV
548		LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
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549		KR
	2-PAS16-3-PAS11-1_NTS	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPASPAGGNLDELHMQMTDLVYEALHFAKDE EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAGGDKENV
550		LQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
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551		EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	2-3-1_PAS7	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQL FEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASAGGDKENVLQKIYEIMKELER
552		LGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	2-3-1_GS7	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQ LFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGDKENVLQKIYEIMKEL
553		ERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFE
	2-3-	KATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGDKENVLQKIYEIMKELERLGHA
554	1_GS5	EASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGSGGSGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKH
	2-3-	VFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGSGGSGGDKENVLQKIY
555	1_GS11	EIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGASPAAPAGGELEEQVMHVLDQVSELAHELLHKLTGEE
	2-2-	LERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAG
	2_PAS1	GELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIR
556	1	EIEEEARRILEHLEELARK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
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	2-2-	GELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIR
557	2_GS11	EIEEEARRILEHLEELARK
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		AAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGSGGELEEQ
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558	2_GS8	RRILEHLEELARK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAY
		FNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGELEEQVMHVLD
	2-2-	QVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH
559	2_GS5	LEELARK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-3-	IEEEARRILEHLEELARKGGSGGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEE
	1_GGGG	FQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGDK
560	S15	ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-3-	IEEEARRILEHLEELARKGGSGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQK
	1_GGGG	HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGDKENVLQK
561	S12	IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-3-	IEEEARRILEHLEELARKGGGGSGGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVF
	1_GGGG	QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGGSGGGGDKENVLQKIYEIMK
562	S9	ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	2-3-	IEEEARRILEHLEELARKGGGSGGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQL
	1_GGGG	FEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGDKENVLQKIYEIMKELER
563	S7	LGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG
	1_GGGG	GSGGGGSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIY
564	S25	EFMKTKDENLLEEAERLLEEVKR
	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG
	1_GGGG	GSGGGGSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT
565	S20	KDENLLEEAERLLEEVKR
	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG
	1_GGGG	GSGGGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENL
566	S15	LEEAERLLEEVKR
	1-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG
	1_GGGG	GSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAE
567	S10	RLLEEVKR
	2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	1_GGGG	IEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVS
568	S10	DLIYEFMKTKDENLLEEAERLLEEVKR

	3-1_GGGGS10	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSGGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKD ENLLEEAERLLEEVKR
569		
	2-3_GGGGS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
570		
	3-2_GGGGS10	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSGGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARK
571		
	2-3-1_GGGGS10	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
572		
	3-2-1_GGGGS10	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSGGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGDKENVLQKIYEI MKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
573		
	2-3-1_GGGGS15	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGSGGGGSGGGGSGGNLDELHMQMTDLVYEALHFAKDEE FQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGSGGGGSGGGGSGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
560		
	3-2-1_GGGGS15	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGSGGGGSGGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSGGGGSGGDK ENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
574		
	LCB3-LCB1_PAS12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEAERLLEEVKR
575		
	AHB2-LCB1_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTKDENLLEEAERLLEEVKR
576		
	AHB2-LCB3_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQK HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
577		
	LCB3-AHB2_PAS12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
578		
	AHB2-LCB3-LCB1_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQK HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQK IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
579		
	LCB3-AHB2-LCB1_PAS12	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW ATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAPAPGGDKENVLQK IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR
580		
	LCB3-AHB2-LCB1_PAS24	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG EELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGASPAAP APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE NLLEEAERLLEEVKR
581		
	AHB2v2-LCB1_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEAARILEHLEELARTGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQ VSDLIYEFMKTKDENLLEEAERLLEEVKR
582		
	AHB2v2-LCB3_PAS12	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEAARILEHLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQK HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
583		

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     LCB3-    NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
     AHB2v2   LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW
584  _PAS12   ATEMMLELIKSDDEREIREIEEEAARILEHLEELART

     AHB2v2   ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     -LCB3-   IEEEAARILEHLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQK
     LCB1_P   HVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQK
585  AS12     IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

     LCB3-
     AHB2v2   NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
     -        LLERLLSGGASPAAPAPGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWW
     LCB1_P   ATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAPAPGGDKENVLQK
586  AS12     IYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR

              ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
     AHB2v2   IEEEAARILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYE
     -LCB3-   ALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAP
     LCB1_P   APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
587  AS24     NLLEEAERLLEEVKR

     LCB3-    NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
     AHB2v2   LLERLLSGGASPAAPAPASPAAPAPSAPAGGELEEQVMHVLDQVSELAHELLHKLTG
     -        EELERAAYFNWWATEMMLELIKSDDEREIREIEEEAARILEHLEELARTGGASPAAP
     LCB1_P   APASPAAPAPSAPAGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
588  AS24     NLLEEAERLLEEVKR
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In some embodiments, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a genus selected from those recited in the middle column of Table 8. In these embodiments, X1, X2, X3 (when recited in the genus), and X4 (when recited in the genus) may be present or absent, and when present may be any sequence of 1 or more amino acids. By way of example, the genus in the middle column, first row of sequences in Table 8 is X1-(SEQ ID NO:4)-X2-(SEQ ID NO:4). In this embodiment, X2 may be present or absent and, when present, may (for example) comprise an amino acid linker of any suitable length and amino acid composition as deemed appropriate. X1 may be present or absent, and when present may comprise any amino acid residue or residues as deemed appropriate, including but not limited to a leader sequence, a detectable tag, a purification tag, etc.

In another example, the genus in the middle column, last row of sequences in Table 8 is X1-(SEQ ID NO: 155)-X2-(SEQ ID NO: 164)-X3-(SEQ ID NO: 135)-X4. In this embodiment, X2 and X3 may be present or absent and, when present, may (for example) comprise an amino acid linker of any suitable length and amino acid composition as deemed appropriate. X1 and X4 may be present or absent, and when present may comprise any amino acid residue or residues as deemed appropriate, including but not limited to a leader sequence, a detectable tag, a purification tag, secretion signal etc.

In some embodiments, the optional domain that is present between monomer domains is present and may comprise an amino acid linker. Under this embodiment, (a) in the first example above X2 would be present and comprise an amino acid linker of any appropriate length and amino acid composition, and X1 may be present or absent; and (b) in the second example above one or both of X2 and X3 would be present and comprise an amino acid linker of any appropriate length and amino acid composition, and X1 and X4 may independently be present or absent.

In any embodiment or combination of embodiments of the polypeptides disclosed herein, the polypeptide may further comprise one or more additional functional peptide domain. Any such additional functional peptide domain may be used as appropriate for an intended purpose. In various non-limiting embodiments, the additional functional peptide domain may comprise, for example, a targeting domain, a detectable domain, a scaffold domain, a secretion signal, an Fc domain, or a further therapeutic peptide domain. In one embodiment, the additional functional domain comprises an Fc domain, including but not limited to an Fc domain comprising an amino acid sequence comprising the amino acid sequence of SEQ ID NO:64.

Fc domain:

EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:64)

In another embodiment, the added functional domain may comprise an oligomerization domain. Any oligomerization domain may be used as suitable to generate an oligomer as suitable for an intended purpose. In one non-limiting embodiment, the oligomerization domain may comprise a homotrimerization domain. Exemplary oligomerization domains may comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:179-189 and 589-594.

1rfo	GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 179)
1na0_int2-R3	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYY QKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 180)
1na0_int2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 181)
6msr	GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNA

	IIVENNRIIAAVLELIVRAIK(SEQ ID NO: 182)
1gcm	RMKQIEDKIEEILSKIYHIENEIARIKKLIGER (SEQ ID NO: 183)
pRO-2-noHis	GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNA IIVENNRIIAAVLELIVRAIK(SEQ ID NO: 184)
1na0_3	NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDP NNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 185)
4pn9	GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG(SEQ ID NO: 186)
SB175	SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLK(SEQ ID NO: 187)
SB175.1	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR IIAK(SEQ ID NO: 188)
SB175.2	SEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLR(SEQ ID NO: 189)
5L6HC3_1	SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREE IRKVKEESKRIVEEAEEEIRRAKEESRKIADESR (SEQ ID NO: 589)
3672 9.2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDP NNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL(SEQ ID NO: 590)
1na0_int2-R3v2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIYYQKALELDPNNAEAKQNLGNAKQKQ(SEQ ID NO: 591)
1na0_int2-R3v3	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG DYDEIEYYQKALELDPNNAEAKQNLGNAKQKQ(SEQ ID NO: 592)
1na0_int2 v2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPN NAEAKQNLGNKQKQ(SEQ ID NO: 593)
6msrv2	EYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEH NAIIVENRIIAAVLELIVRAIK(SEQ ID NO: 594)

In one embodiment, the polypeptide comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS 356-453 and 595-692 and a genus selected from those recited in the right hand column of Table 9 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids. In all embodiments, any N-terminal methionine residues may be present or absent in the polypeptide. In one embodiment, any N-terminal methionine residues are absent in the polypeptide.

Table 9. Homotrimer Designs

Name	Protein	**Annotated:** X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids
AHB2-6GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 356)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 179)-X3
AHB2-28GS-AHB2-6GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 357)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
AHB2-5GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 358)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X3
AHB2-4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 359)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X3
AHB2-3GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 360)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X3
AHB2-28GS-AHB2-3GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 361)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
AHB2-4GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSAWSHPQFEK(SEQ ID NO: 362)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR (SEQ ID NO: 589)

	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSEELRAVADLQRLNIELARKLLE AVARLQELNIDLVRKTSELTDEKTIRE EIRKVKEESKRIVEEAEEEIRRAKEES	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-
AHB2- 5GS- 5L6HC3_1	RKIADESRGGSGSSGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 363)	SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVR KTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAK EESRKIADESR (SEQ ID NO: 589)
	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSGSGSGSGSGSGSGSGS ELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDERE IREIEEEARRILEHLEELARKGSGSSE ELRAVADLQRLNIELARKLLEAVARLQ	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-
AHB2- 28GS- AHB2- 4GS- 5L6HC3_1	ELNIDLVRKTSELTDEKTIREEIRKVK EESKRIVEEAEEEIRRAKEESRKIADE SRGGSGSSGSAWSHPQFEKGGGSGGGS GGSAWSHPQFEK(SEQ ID NO: 364)	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X3
	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSGSGSGSGSGSGSGSGS ELEEQVMHVLDQVSELAHELLHKLTGE ELERAAYFNWWATEMMLELIKSDDERE IREIEEEARRILEHLEELARKGSGSGS EELRAVADLQRLNIELARKLLEAVARL	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-
AHB2- 28GS- AHB2- 5GS- 5L6HC3_1	QELNIDLVRKTSELTDEKTIREEIRKV KEESKRIVEEAEEEIRRAKEESRKIAD ESRGGSGSSGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK(SEQ ID NO: 365)	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X3
	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSGYIPEA PRDGQAYVRKDGEWVLLSTFLGGSGSS	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-
LCB3- 6GS-1rfo	GSAWSHPQFEKGGGSGGGSGGSAWSHP QFEK(SEQ ID NO: 366)	GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X3
	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGGYIPEAP RDGQAYVRKDGEWVLLSTFLGGSGSSG	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-
LCB3- 5GS-1rfo	SAWSHPQFEKGGGSGGGSGGSAWSHPQ FEK(SEQ ID NO: 367)	GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X3
	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGYIPEAPR DGQAYVRKDGEWVLLSTFLGGSGSSGS	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-
LCB3- 4GS-1rfo	AWSHPQFEKGGGSGGGSGGSAWSHPQF EK(SEQ ID NO: 368)	GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X3
	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSEELRAV ADLQRLNIELARKLLEAVARLQELNID LVRKTSELTDEKTIREEIRKVKEESKR	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-
LCB3- 5GS- 5L6HC3_1	IVEEAEEEIRRAKEESRKIADESRGGS GSSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK(SEQ ID NO: 369)	SEELRAVADLQRLNIELARKLLEAVARLQELNIDLVR KTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAK EESRKIADESR (SEQ ID NO: 589)
LCB3- 28GS- LCB3-	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSGSGS	X1- NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID

4GS-5L6HC3_1	GSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 370)	NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
LCB3-28GS-LCB3-5GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 371)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
36729.2_LCB1v2.2_6GS	MEKKIEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 372)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)
36729.2_LCB1v2.2_4GS	MEKKIEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 373)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)
36729.2_LCB1v2.2_2GS	MEKKIEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 374)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)
LCB3-PAS24-LCB3-4GS-5L6HC3_1	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 375)	-X1NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
LCB3-	MEKKINLDELHMQMTDLVYEALHFAKD	X1-

PAS24-LCB3-5GS-5L6HC3_1	EEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESRGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 376)	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
LCB1-10GS-AHB2-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEK(SEQ ID NO: 377)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
LCB1-28GS-AHB2-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 378)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
LCB3-10GS-AHB2-4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 379)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
LCB3-16GS-AHB2-4GS-1rfo	MEKKINLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 380)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
36729.2_6GS_LCB1-v2.2-28GS-LCB3	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 381)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
36729.2_6GS_LCB1	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGE	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK

v2.2-9GS-LCB3	LAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 382)	TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)
36729.2_6GS_LCB1v2.2-28GS-AHB2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 383)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
36729.2_6GS_LCB1v2.2-9GS-AHB2	MEKKISAWSHPQFEKGGGSGGGSGGSAWSHPQFEKGGSGSSGMEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO: 384)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)
LCB1-10GS-LCB3-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSGGSGGSAWSHPQFEK(SEQ ID NO: 385)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
LCB1-28GS-LCB3-4GS-1rfo	MEKKIDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSGGSGGSAWSHPQFEK(SEQ ID NO: 386)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
AHB2-10GS-LCB3-4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWS	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155) -X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID

	HPQFEK(SEQ ID NO: 387)	NO: 179)-X4
AHB2-16GS-LCB3-4GS-1rfo	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSGSGSGSNLDELHMQMTDL VYEALHFAKDEEFQKHVFQLFEKATKA YKNKDRQKLEKVVEELKELLERLLSGS GSGYIPEAPRDGQAYVRKDGEWVLLST FLGGSGSSGSAWSHPQFEKGGGSGGGS GGSAWSHPQFEK(SEQ ID NO: 388)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3-GYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 179)-X4
LCB1-9GS-LCB3-5GS-5L6HC3_1	MEKKIDKENVLQKIYEIMKELERLGHA EASMQVSDLIYEFMKTKDENLLEEAER LLEEVKRGSGSGSGSGNLDELHMQMTD LVYEALHFAKDEEFQKHVFQLFEKATK AYKNKDRQKLEKVVEELKELLERLLSG SGSGSEELRAVADLQRLNIELARKLLE AVARLQELNIDLVRKTSELTDEKTIRE EIRKVKEESKRIVEEAEEEIRRAKEES RKIADESRGGSGSSGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 389)	X1-DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
AHB2-9GS-LCB3-5GS-5L6HC3_1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGNLDELHMQMTDLVYEALHF AKDEEFQKHVFQLFEKATKAYKNKDRQ KLEKVVEELKELLERLLSGSGSGSEEL RAVADLQRLNIELARKLLEAVARLQEL NIDLVRKTSELTDEKTIREEIRKVKEE SKRIVEEAEEEIRRAKEESRKIADESR GGSGSSGSAWSHPQFEKGGGSGGGSGG SAWSHPQFEK(SEQ ID NO: 390)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X3
AHB2-4GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSEEAELAYLLGELAYKLGEYRIAIR AYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIYYQKALELDPNNAEAKQNLGN AKQKQGGGSGSSGSAWSHPQFEKGGGS GGGSGGSAWSHPQFEK(SEQ ID NO: 391)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQ NLGNAKQKQ (SEQ ID NO: 591)
AHB2-6GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSEEAELAYLLGELAYKLGEYRIA IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEIEYYQKALELDPNNAEAKQNL GNAKQKQGGGSGSSGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 392)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEIEYYQKALELDPNNAEAKQ NLGNAKQKQ (SEQ ID NO: _592)
AHB2-4GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSEEAELAYLLGELAYKLGEYRIAIR AYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIYYQKALELDPNNAEAWYNLGN AYYKQGDYDEAIEYYQKALELDPNNAE AKQNLGNKQKQGGGSGSSGSAWSHPQF EKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 393)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLG NKQKQ (SEQ ID NO: 593)
AHB2-6GS-	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW

1na0_int 2	DDEREIREIEEEARRILEHLEELARKG SGSGSEEAELAYLLGELAYKLGEYRIA IRAYRIALKRDPNNAEAWYNLGNAYYK QGDYDEAIYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNN AEAKQNLGNKQKQGGGSGSSGSAWSHP QFEKGGGSGGGSGGSAWSHPQFEK(SE Q ID NO: 394)	WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLG NKQKQ (SEQ ID NO: 593)
AHB2-4GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSEYEIRKALEELKASTAELKRAT ASLRASTEELKKNPSEDALVENNRLIV EHNAIIVENRIIAAVLELIVRAIKGGS GSSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK(SEQ ID NO: 395)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EYEIRKALEELKASTAELKRATASLRASTEELKKNPS EDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK (SEQ ID NO: 594)
AHB2-6GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSEYEIRKALEELKASTAELKR ATASLRASTEELKKNPSEDALVENNRL IVEHNAIIVENRIIAAVLELIVRAIKG GSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 396)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EYEIRKALEELKASTAELKRATASLRASTEELKKNPS EDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK (SEQ ID NO: 594)
36729.2_LCB1v2.2_6GS	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGEEAELAYLLGEL AYKLGEYRIAIRAYRIALKRDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAWYNLGNAYYKQGD YDEAIEYYQKALELGSGSGSDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYE FMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 397)	X1- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
36729.2_LCB1v2.2_4GS	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGEEAELAYLLGEL AYKLGEYRIAIRAYRIALKRDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAWYNLGNAYYKQGD YDEAIEYYQKALELGSGSDKENVLQKI YEIMKELERLGHAEASMQVSDLIYEFM KTKDENLLEEAERLLEEVKR(SEQ ID NO: 398)	X1- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
36729.2_LCB1v2.2_2GS	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGEEAELAYLLGEL AYKLGEYRIAIRAYRIALKRDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAWYNLGNAYYKQGD YDEAIEYYQKALELGSGSDKENVLQKIYE IMKELERLGHAEASMQVSDLIYEFMKT KDENLLEEAERLLEEVKR (SEQ ID NO: 399)	X1- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALEL (SEQ ID NO: 590)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
AHB2-8GS-1na0_int 2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSEEAELAYLLGELAYKLGEYR IAIRAYRIALKRDPNNAEAWYNLGNAY YKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQGGGSGSSGSAWSHPQFE KGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 400)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQG (SEQ ID NO: 180)-X3

AHB2-8GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 401)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 181)-X3
AHB2-8GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 402)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(SEQ ID NO: 182)-X3
AHB2-10GS-6msr	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 403)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK(SEQ ID NO: 182)-X3
AHB2-10GS-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 404)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 180)-X3
AHB2-10GS-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 405)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 181)-X3
AHB2-4GS-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 406)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(SEQ ID NO: 183)-X3
AHB2-8GS-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 407)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(SEQ ID NO: 183)-X3
AHB2-4GS-pRO-	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKG	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELAR

2-noHis	SGSGSEYEIRKALEELKASTAELKRST ASLRASTEELKKNPSEDALVENNRLIV ENNAIIVENNRIIAAVLELIVRAIKGG SGSSGSAWSHPQFEKGGGSGGGSGGSA WSHPQFEK(SEQ ID NO: 408)	K(SEQ ID NO:101)-X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK(SEQ ID NO: 184)-X3
AHB2-8GS-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSEYEIRKALEELKASTAEL KRSTASLRASTEELKKNPSEDALVENN RLIVENNAIIVENNRIIAAVLELIVRA IKGGSGSSGSAWSHPQFEKGGGSGGGS GGSAWSHPQFEK(SEQ ID NO: 409)	X1ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYF NWWATEMMLELIKSDDEREIREIEEEARRILEHLEEL ARK(SEQ ID NO:101)-X2- GSEYEIRKALEELKASTAELKRSTASLRASTEELKKN PSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRA IK(SEQ ID NO: 184)-X3
AHB2-6GS-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSNLAEKMYKAGNAMYRKGQYTIA IIAYTLALLKDPNNAEAWYNLGNAAYK KGEYDEAIEAYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYQKALELDPN NAEAKQNLGNAKQKQGGGSGSSGSAWS HPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 410)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNA EAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 185)-X3
AHB2-10GS-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSNLAEKMYKAGNAMYRKGQ YTIAIIAYTLALLKDPNNAEAWYNLGN AAYKKGEYDEAIEAYQKALELDPNNAE AWYNLGNAYYKQGDYDEAIEYYQKALE LDPNNAEAKQNLGNAKQKQGGGSGSSG SAWSHPQFEKGGGSGGGSGGSAWSHPQ FEK(SEQ ID NO: 411)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNA EAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 185)-X3
AHB2-6GS-4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGEIAKSLKEIAKSLKEIAWSLK EIAKSLKGGGSGSSGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 412)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG(SEQ ID NO: 186)-X3
AHB2-10GS-4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG SGSGSGSGSGEIAKSLKEIAKSLKEIA WSLKEIAKSLKGGGSGSSGSAWSHPQF EKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 413)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG(SEQ ID NO: 186)-X3
AHB2-GGGGS5-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGEEAELAYLLGELAYKLGEYRIAI RAYRIALKRDPNNAEAWYNLGNAYYKQ GDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQGGGSGSSGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 414)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQG(SEQ ID NO: 180)-X3
AHB2-GGGGS7-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGEEAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYY KQGDYDEAIEYYQKALELDPNNAEAKQ NLGNAKQKQGGGSGSSGSAWSHPQFEK	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK

	GGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 415)	QNLGNAKQKQG(SEQ ID NO: 180)-X3
AHB2-GGGGS9-1na0_int2-R3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGGGGEEAELAYLLGELAYKLGEY RIAIRAYRIALKRDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELDPNNAEA KQNLGNAKQKQGGGSGSSGSAWSHPQF EKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 416)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAK QNLGNAKQKQG(SEQ ID NO: 180)-X3
AHB2-GGGGS5-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGEEAELAYLLGELAYKLGEYRIAI RAYRIALKRDPNNAEAWYNLGNAYYKQ GDYDEAIEYYQKALELDPNNAEAWYNL GNAYYKQGDYDEAIEYYQKALELDPNN AEAKQNLGNAKQKQGGGSGSSGSAWSH PQFEKGGGSGGGSGGSAWSHPQFEK(S EQ ID NO: 417)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 181)-X3
AHB2-GGGGS7-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGEEAELAYLLGELAYKLGEYRI AIRAYRIALKRDPNNAEAWYNLGNAYY KQGDYDEAIEYYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNAKQKQGGGSGSSGSAW SHPQFEKGGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 418)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 181)-X3
AHB2-GGGGS9-1na0_int2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGGGGEEAELAYLLGELAYKLGEY RIAIRAYRIALKRDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAKQNLGNAKQKQGGGSGSSGS AWSHPQFEKGGGSGGGSGGSAWSHPQF EK(SEQ ID NO: 419)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNA EAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 181)-X3
AHB2-GGGGS5-6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGSEYEIRKALEELKASTAELKRA TASLRASTEELKKNPSEDALVENNRLI VEHNAIIVENNRIIAAVLELIVRAIKG GSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 420)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA IK(SEQ ID NO: 182)-X3
AHB2-GGGGS7-6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGSEYEIRKALEELKASTAELK RATASLRASTEELKKNPSEDALVENNR LIVEHNAIIVENNRIIAAVLELIVRAI KGGSGSSGSAWSHPQFEKGGGSGGGSG GSAWSHPQFEK(SEQ ID NO: 421)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA IK(SEQ ID NO: 182)-X3
AHB2-GGGGS9-6msr	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGGGGGSEYEIRKALEELKASTAE LKRATASLRASTEELKKNPSEDALVEN NRLIVEHNAIIVENNRIIAAVLELIVR AIKGGSGSSGSAWSHPQFEKGGGSGGG	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRATASLRASTEELKKN PSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRA

	SGGSAWSHPQFEK(SEQ ID NO: 422)	IK(SEQ ID NO: 182)-X3
AHB2-GGGGS5-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 423)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(SEQ ID NO: 183)-X3
AHB2-GGGGS7-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 424)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(SEQ ID NO: 183)-X3
AHB2-GGGGS9-1gcm	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGERGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 425)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-RMKQIEDKIEEILSKIYHIENEIARIKKLIGER(SEQ ID NO: 183)-X3
AHB2-GGGGS5-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 426)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(SEQ ID NO: 184)-X3
AHB2-GGGGS7-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 427)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(SEQ ID NO: 184)-X3
AHB2-GGGGS9-pRO-2-noHis	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGGSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIKGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 428)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-GSEYEIRKALEELKASTAELKRSTASLRASTEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK(SEQ ID NO: 184)-X3
AHB2-GGGGS5-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAAYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQGGGSGSSGSAWSHPQFEKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 429)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAAYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG(SEQ ID NO: 185)-X3
AHB2-GGGGS7-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGSGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAY	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK(SEQ ID NO:101)-X2-NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNA

	KKGEYDEAIEAYQKALELDPNNAEAWY NLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNAKQKQGGGSGSSGSAW SHPQFEKGGGSGGGSGGSAWSHPQFEK (SEQ ID NO: 430)	EAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 185)-X3
AHB2-GGGGS9-1na0_3	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGGGGNLAEKMYKAGNAMYRKGQY TIAIIAYTLALLKDPNNAEAWYNLGNA AYKKGEYDEAIEAYQKALELDPNNAEA WYNLGNAYYKQGDYDEAIEYYQKALEL DPNNAEAKQNLGNAKQKQGGGSGSSGS AWSHPQFEKGGGSGGGSGGSAWSHPQF EK(SEQ ID NO: 431)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- NLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNA EAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAW YNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNL GNAKQKQG(SEQ ID NO: 185)-X3
AHB2-GGGGS5-4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSGGGEIAKSLKEIAKSLKEIAWSLKE IAKSLKGGGSGSSGSAWSHPQFEKGGG SGGGSGGSAWSHPQFEK(SEQ ID NO: 432)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG(SEQ ID NO: 186)-X3
AHB2-GGGGS7-4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSGGGGEIAKSLKEIAKSLKEIAWSL KEIAKSLKGGGSGSSGSAWSHPQFEKG GGSGGGSGGSAWSHPQFEK(SEQ ID NO: 433)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG (SEQ ID NO: 186)-X3
AHB2-GGGGS9-4pn9	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGGGGGEIAKSLKEIAKSLKEIAW SLKEIAKSLKGGGSGSSGSAWSHPQFE KGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 434)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- GEIAKSLKEIAKSLKEIAWSLKEIAKSLKG(SEQ ID NO: 186)-X3
AHB2-2GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSEALEELEKALRELKKSTDELERSTE ELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLKGGSGSSGSAWSHPQFEK GGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 435)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK (SEQ ID NO:187)-X3
AHB2-4GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSSEALEELEKALRELKKSTDELERS TEELEKNPSEDALVENNRLIVENNKII VEVLRIIAKVLKGGSGSSGSAWSHPQF EKGGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 436)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
AHB2-6GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGSEALEELEKALRELKKSTDELE RSTEELEKNPSEDALVENNRLIVENNK IIVEVLRIIAKVLKGGSGSSGSAWSHP QFEKGGGSGGGSGGSAWSHPQFEK(SE Q ID NO: 437)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
AHB2-2GS-	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW

SB175.1	DDEREIREIEEEARRILEHLEELARKG GSPELEKALRELKKSTDELERSTEELE KNGSPEALVENNRLIVENNKIIVEVLR IIAKGGSGSSGSAWSHPQFEKGGGSGG GSGGSAWSHPQFEK(SEQ ID NO: 438)	WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK(SEQ ID NO: 188)- X3
AHB2-4GS-SB175.1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSSPELEKALRELKKSTDELERSTEE LEKNGSPEALVENNRLIVENNKIIVEV LRIIAKGGSGSSGSAWSHPQFEKGGGS GGGSGGSAWSHPQFEK(SEQ ID NO: 439)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK(SEQ ID NO: 188)- X3
AHB2-6GS-SB175.1	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGSPELEKALRELKKSTDELERST EELEKNGSPEALVENNRLIVENNKIIV EVLRIIAKGGSGSSGSAWSHPQFEKGG GSGGGSGGSAWSHPQFEK(SEQ ID NO: 440)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK(SEQ ID NO: 188)- X3
AHB2-2GS-SB175.2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSEKALRELKKSTDELERSTEELEKNG SPEALVENNRLIVENNKIIVEVLRGGS GSSGSAWSHPQFEKGGGSGGGSGGSAW SHPQFEK(SEQ ID NO: 441)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVLR(SEQ ID NO: 189)-X3
AHB2-4GS-SB175.2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGSSEKALRELKKSTDELERSTEELEK NGSPEALVENNRLIVENNKIIVEVLRG GSGSSGSAWSHPQFEKGGGSGGGSGGS AWSHPQFEK(SEQ ID NO: 442)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2- SEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVLR(SEQ ID NO: 189)-X3
AHB2-6GS-SB175.2	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GGGSGSEKALRELKKSTDELERSTEEL EKNGSPEALVENNRLIVENNKIIVEVL RGGSGSSGSAWSHPQFEKGGGSGGGSG GSAWSHPQFEK(SEQ ID NO: 443)	X1- ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K-X2- SEKALRELKKSTDELERSTEELEKNGSPEALVENNRL IVENNKIIVEVLR(SEQ ID NO: 189)-X3
SB175-6GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGSEALEELEKALR ELKKSTDELERSTEELEKNPSEDALVE NNRLIVENNKIIVEVLRIIAKVLKGGG GSGDKENVLQKIYEIMKELERLGHAEA SMQVSDLIYEFMKTKDENLLEEAERLL EEVKR(SEQ ID NO: 444)	X1- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
SB175-10GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGSEALEELEKALR ELKKSTDELERSTEELEKNPSEDALVE NNRLIVENNKIIVEVLRIIAKVLKGGG GSGGGGSDKENVLQKIYEIMKELERLG HAEASMQVSDLIYEFMKTKDENLLEEA ERLLEEVKR(SEQ ID NO: 445)	X1- SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X2- DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
SB175.1-6GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGSPELEKALRELK KSTDELERSTEELEKNGSPEALVENNR LIVENNKIIVEVLRIIAKGGGGSGDKE	X1- SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK(SEQ ID NO: 188)- X2-

	NVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 446)	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
SB175.1-10GS-LCB1v2.2	MEKKISAWSHPQFEKGGGSGGGSGGSA WSHPQFEKGGSGSSGSPELEKALRELK KSTDELERSTEELEKNGSPEALVENNR LIVENNKIIVEVLRIIAKGGGGSGGGG SDKENVLQKIYEIMKELERLGHAEASM QVSDLIYEFMKTKDENLLEEAERLLEE VKR(SEQ ID NO: 447)	X1-SPELEKALRELKKSTDELERSTEELEKNGSPEALVEN NRLIVENNKIIVEVLRIIAK(SEQ ID NO: 188)-X2 DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMK TKDENLLEEAERLLEEVKR(SEQ ID NO: 135)
LCB3-8GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGGGGSGGGSEAL EELEKALRELKKSTDELERSTEELEKN PSEDALVENNRLIVENNKIIVEVLRII AKVLKGGASPAAPAGGSAWSHPQFEKG GGSGGGSGGSAWSHPQFEK(SEQ ID NO: 448)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
LCB3-6GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGGGGSGSEALEE LEKALRELKKSTDELERSTEELEKNPS EDALVENNRLIVENNKIIVEVLRIIAK VLKGGASPAAPAGGSAWSHPQFEKGGG SGGGSGGSAWSHPQFEK(SEQ ID NO: 449)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
LCB3-4GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGGGSSEALEELE KALRELKKSTDELERSTEELEKNPSED ALVENNRLIVENNKIIVEVLRIIAKVL KGGASPAAPAGGSAWSHPQFEKGGGSG GGSGGSAWSHPQFEK(SEQ ID NO: 450)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
LCB3-2GS-SB175	MEKKINLDELHMQMTDLVYEALHFAKD EEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGGSEALEELEKA LRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLKG GASPAAPAGGSAWSHPQFEKGGGSGGG SGGSAWSHPQFEK(SEQ ID NO: 451)	X1-NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKAT KAYKNKDRQKLEKVVEELKELLERLLS(SEQ ID NO: 155)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
AHB2v1-2GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEARRILEHLEELARKG GSEALEELEKALRELKKSTDELERSTE ELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLKGGSGSSGSAWSHPQFEK GGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 452)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEARRILEHLEELAR K(SEQ ID NO:101)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187)-X3
AHB2v2-2GS-SB175	MEKKIELEEQVMHVLDQVSELAHELLH KLTGEELERAAYFNWWATEMMLELIKS DDEREIREIEEEAARILEHLEELARTG GSEALEELEKALRELKKSTDELERSTE ELEKNPSEDALVENNRLIVENNKIIVE VLRIIAKVLKGGSGSSGSAWSHPQFEK GGGSGGGSGGSAWSHPQFEK(SEQ ID NO: 453)	X1-ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNW WATEMMLELIKSDDEREIREIEEEAARILEHLEELAR T(SEQ ID NO: 164)-X2-SEALEELEKALRELKKSTDELERSTEELEKNPSEDAL VENNRLIVENNKIIVEVLRIIAKVLK(SEQ ID NO:187) -X3

Table 9A

SEQ	Name	Sequence

ID		
	AHB2-6GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
595	1rfo	IEEEARRILEHLEELARKGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-28GS-	IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD
	AHB2-6GS-	QVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH
596	1rfo	LEELARKGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
	AHB2-5GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
597	1rfo	IEEEARRILEHLEELARKGSGSGGYIPEAPRDGQAYVRKDGEWVLLSTFL
	AHB2-4GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
598	1rfo	IEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
	AHB2-3GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
599	1rfo	IEEEARRILEHLEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFL
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-28GS-	IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD
	AHB2-3GS-	QVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH
600	1rfo	LEELARKGSGGYIPEAPRDGQAYVRKDGEWVLLSTFL
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-4GS-	IEEEARRILEHLEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDL
601	5L6HC3_1	VRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-5GS-	IEEEARRILEHLEELARKGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNID
602	5L6HC3_1	LVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD
	AHB2-28GS-	QVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH
	AHB2-4GS-	LEELARKGSGSSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDEK
603	5L6HC3_1	TIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLD
	AHB2-28GS-	QVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEH
	AHB2-5GS-	LEELARKGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDE
604	5L6HC3_1	KTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
	LCB3-6GS-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
605	1rfo	LLERLLSGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
	LCB3-5GS-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
606	1rfo	LLERLLSGSGSGGYIPEAPRDGQAYVRKDGEWVLLSTFL
	LCB3-4GS-	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
607	1rfo	LLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	LCB3-5GS-	LLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVRKTSELTDE
608	5L6HC3_1	KTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
		LLERLLSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKD
	LCB3-28GS-	EEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQ
	LCB3-4GS-	RLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEE
609	5L6HC3_1	EIRRAKEESRKIADESR
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
		LLERLLSGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKD
	LCB3-28GS-	EEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADL
	LCB3-5GS-	QRLNIELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAE
610	5L6HC3_1	EEIRRAKEESRKIADESR
		EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI
		EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA
	36729.2_LCB	YYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL
611	1v2.2_6GS	IYEFMKTKDENLLEEAERLLEEVKR
612		
	36729.2_LCB	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI

	1v2.2_4GS	EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKR
613	36729.2_LCB 1v2.2_2GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR
614	LCB3-PAS24- LCB3-4GS- 5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQ KHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSSEELRAVADLQRLNI ELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRR AKEESRKIADESR
615	LCB3-PAS24- LCB3-5GS- 5L6HC3_1	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQ KHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLN IELARKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIR RAKEESRKIADESR
616	LCB1-10GS- AHB2-4GS- 1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIK SDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTF L
617	LCB1-28GS- AHB2-4GS- 1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG SGSGSGSGSGSGSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPR DGQAYVRKDGEWVLLSTFL
618	LCB3-10GS- AHB2-4GS- 1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGGGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWAT EMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQAYVRKDG EWVLLSTFL
619	LCB3-16GS- AHB2-4GS- 1rfo	NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE LLERLLSGSGSGSGSGSGSGSELEEQVMHVLDQVSELAHELLHKLTGEELERAAY FNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGSGSGYIPEAPRDGQA YVRKDGEWVLLSTFL
620	36729.2_6GS _LCB1v2.2- 28GS-LCB3	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSNLDE LHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLER LLS
621	36729.2_6GS _LCB1v2.2- 9GS-LCB3	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGNLDELHMQMTDLVYEALHFAKDE EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLS
622	36729.2_6GS _LCB1v2.2- 28GS-AHB2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGSGSGSGSGSGSGSGSGSELEE QVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEE ARRILEHLEELARK
623	36729.2_6GS _LCB1v2.2- 9GS-AHB2	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKRGSGSGSGSGELEEQVMHVLDQVSELAHELLHK LTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARK
624	LCB1-10GS- LCB3-4GS- 1rfo	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG GGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKL EKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL
625	LCB1-28GS- LCB3-4GS-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG SGSGSGSGSGSGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDEEFQKHVF

	1rfo	QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDGE WVLLSTFL
	AHB2-10GS- LCB3-4GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHV FQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQAYVRKDG
626	1rfo	EWVLLSTFL
	AHB2-16GS- LCB3-4GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSGSGSGSGSNLDELHMQMTDLVYEALHFAKDE EFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGYIPEAPRDGQA
627	1rfo	YVRKDGEWVLLSTFL
	LCB1-9GS- LCB3-5GS-	DKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRG SGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLE KVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELARKLLEAVARLQELNIDLVR
628	5L6HC3_1	KTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKEESRKIADESR
	AHB2-9GS- LCB3-5GS-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGSGSGSEELRAVADLQRLNIELA RKLLEAVARLQELNIDLVRKTSELTDEKTIREEIRKVKEESKRIVEEAEEEIRRAKE
629	5L6HC3_1	ESRKIADESR
	AHB2-4GS- lna0_int2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPN
630	R3	NAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAKQNLGNAKQKQ
	AHB2-6GS- lna0_int2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRD
631	R3	PNNAEAWYNLGNAYYKQGDYDEIEYYQKALELDPNNAEAKQNLGNAKQKQ
	AHB2-4GS- lna0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPN NAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEY YQKALELDPNNAEAKQNLGNKQKQ
	AHB2-6GS- lna0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALKRD PNNAEAWYNLGNAYYKQGDYDEAIYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAKQNLGNKQKQ
	AHB2-4GS- 6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSEYEIRKALEELKASTAELKRATASLRASTEELK KNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK
	AHB2-6GS- 6msr	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSEYEIRKALEELKASTAELKRATASLRASTEE LKKNPSEDALVENNRLIVEHNAIIVENRIIAAVLELIVRAIK
	36729.2_LCB 1v2.2_6GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKR
	36729.2_LCB 1v2.2_4GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIY EFMKTKDENLLEEAERLLEEVKR
	36729.2_LCB 1v2.2_2GS	EEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNA YYKQGDYDEAIEYYQKALELGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR
	AHB2-8GS- lna0_int2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALK
639	R3	RDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
	AHB2-8GS- lna0_int2	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE IEEEARRILEHLEELARKGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIALK RDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYD EAIEYYQKALELDPNNAEAKQNLGNAKQKQG

		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-8GS-6msr	IEEEARRILEHLEELARKGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRAST
641		EELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-10GS-6msr	IEEEARRILEHLEELARKGSGSGSGSGSGSEYEIRKALEELKASTAELKRATASLRA
642		STEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
	AHB2-10GS-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGSGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIA
643		LKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGSGSGSGSGSEEAELAYLLGELAYKLGEYRIAIRAYRIA
	AHB2-10GS-1na0_int2	LKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGD
644		YDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
	AHB2-4GS-1gcm	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
645		IEEEARRILEHLEELARKGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-8GS-1gcm	IEEEARRILEHLEELARKGSGSGSGSRMKQIEDKIEEILSKIYHIENEIARIKKLIG
646		ER
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-4GS-pRO-2-noHis	IEEEARRILEHLEELARKGSGSGSEYEIRKALEELKASTAELKRSTASLRASTEELK
647		KNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-8GS-pRO-2-noHis	IEEEARRILEHLEELARKGSGSGSGSGSEYEIRKALEELKASTAELKRSTASLRAST
648		EELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGSGSGSNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKD
	AHB2-6GS-1na0_3	PNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEA
649		IEYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGSGSGSGSGSNLAEKMYKAGNAMYRKGQYTIAIIAYTLA
	AHB2-10GS-1na0_3	LLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGD
650		YDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
	AHB2-6GS-4pn9	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
651		IEEEARRILEHLEELARKGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-10GS-4pn9	IEEEARRILEHLEELARKGSGSGSGSGSGEIAKSLKEIAKSLKEIAWSLKEIAKSLK
652		G
	AHB2-GGGGS5-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDP
653		NNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
	AHB2-GGGGS7-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGGSGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKR
654		DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
	AHB2-GGGGS9-1na0_int2-R3	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
		IEEEARRILEHLEELARKGGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIAL
655		KRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-GGGGS5-1na0_int2	IEEEARRILEHLEELARKGGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDP
		NNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAI
656		EYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-GGGGS7-1na0_int2	IEEEARRILEHLEELARKGGGSGGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKR
		DPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDE
657		AIEYYQKALELDPNNAEAKQNLGNAKQKQG

		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGGSGGGGEEAELAYLLGELAYKLGEYRIAIRAYRIAL
	GGGGS9-	KRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDY
658	1na0_int2	DEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGSGGGSEYEIRKALEELKASTAELKRATASLRASTEEL
659	GGGGS5-6msr	KKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGSGGGGSEYEIRKALEELKASTAELKRATASLRASTE
660	GGGGS7-6msr	ELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGGSGGGGGSEYEIRKALEELKASTAELKRATASLRAS
661	GGGGS9-6msr	TEELKKNPSEDALVENNRLIVEHNAIIVENNRIIAAVLELIVRAIK
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
662	GGGGS5-1gcm	IEEEARRILEHLEELARKGGSGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGER
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGSGGGRMKQIEDKIEEILSKIYHIENEIARIKKLIGE
663	GGGGS7-1gcm	R
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGGSGGGGRMKQIEDKIEEILSKIYHIENEIARIKKLI
664	GGGGS9-1gcm	GER
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	GGGGS5-pRO-	IEEEARRILEHLEELARKGGSGGGSEYEIRKALEELKASTAELKRSTASLRASTEEL
665	2-noHis	KKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	GGGGS7-pRO-	IEEEARRILEHLEELARKGGGSGGGGSEYEIRKALEELKASTAELKRSTASLRASTE
666	2-noHis	ELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	GGGGS9-pRO-	IEEEARRILEHLEELARKGGGGSGGGGGSEYEIRKALEELKASTAELKRSTASLRAS
667	2-noHis	TEELKKNPSEDALVENNRLIVENNAIIVENNRIIAAVLELIVRAIK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGSGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDP
	GGGGS5-	NNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAI
668	1na0_3	EYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGSGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLK
	GGGGS7-	DPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDE
669	1na0_3	AIEYYQKALELDPNNAEAKQNLGNAKQKQG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-	IEEEARRILEHLEELARKGGGGSGGGGNLAEKMYKAGNAMYRKGQYTIAIIAYTLAL
	GGGGS9-	LKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDY
670	1na0_3	DEAIEYYQKALELDPNNAEAKQNLGNAKQKQG
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
671	GGGGS5-4pn9	IEEEARRILEHLEELARKGGSGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
672	GGGGS7-4pn9	IEEEARRILEHLEELARKGGGSGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
	AHB2-	ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
673	GGGGS9-4pn9	IEEEARRILEHLEELARKGGGGSGGGGGEIAKSLKEIAKSLKEIAWSLKEIAKSLKG
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-2GS-	IEEEARRILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDAL
674	SB175	VENNRLIVENNKIIVEVLRIIAKVLK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-4GS-	IEEEARRILEHLEELARKGGGSSEALEELEKALRELKKSTDELERSTEELEKNPSED
675	SB175	ALVENNRLIVENNKIIVEVLRIIAKVLK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-6GS-	IEEEARRILEHLEELARKGGGGSGSEALEELEKALRELKKSTDELERSTEELEKNPS
676	SB175	EDALVENNRLIVENNKIIVEVLRIIAKVLK

		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-2GS-	IEEEARRILEHLEELARKGGSPELEKALRELKKSTDELERSTEELEKNGSPEALVEN
677	SB175.1	NRLIVENNKIIVEVLRIIAK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-4GS-	IEEEARRILEHLEELARKGGGSSPELEKALRELKKSTDELERSTEELEKNGSPEALV
678	SB175.1	ENNRLIVENNKIIVEVLRIIAK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-6GS-	IEEEARRILEHLEELARKGGGGSGSPELEKALRELKKSTDELERSTEELEKNGSPEA
679	SB175.1	LVENNRLIVENNKIIVEVLRIIAK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
680	AHB2-2GS-	IEEEARRILEHLEELARKGGSEKALRELKKSTDELERSTEELEKNGSPEALVENNRL
41	SB175.2	IVENNKIIVEVLR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-4GS-	IEEEARRILEHLEELARKGGGSSEKALRELKKSTDELERSTEELEKNGSPEALVENN
681	SB175.2	RLIVENNKIIVEVLR
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2-6GS-	IEEEARRILEHLEELARKGGGGSGSEKALRELKKSTDELERSTEELEKNGSPEALVE
682	SB175.2	NNRLIVENNKIIVEVLR
		SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRI
	SB175-6GS-	IAKVLKGGGGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLE
683	LCB1v2.2	EAERLLEEVKR
		SEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIVEVLRI
	SB175-10GS-	IAKVLKGGGGSGGGGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDE
684	LCB1v2.2	NLLEEAERLLEEVKR
	SB175.1-	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK
	6GS-	GGGGSGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLL
685	LCB1v2.2	EEVKR
	SB175.1-	SPELEKALRELKKSTDELERSTEELEKNGSPEALVENNRLIVENNKIIVEVLRIIAK
	10GS-	GGGGSGGGGSDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEA
686	LCB1v2.2	ERLLEEVKR
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	LCB3-8GS-	LLERLLSGGGGSGGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNR
687	SB175	LIVENNKIIVEVLRIIAKVLK
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	LCB3-6GS-	LLERLLSGGGGSGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLI
688	SB175	VENNKIIVEVLRIIAKVLK
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	LCB3-4GS-	LLERLLSGGGSSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVE
689	SB175	NNKIIVEVLRIIAKVLK
		NLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKDRQKLEKVVEELKE
	LCB3-2GS-	LLERLLSGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENN
690	SB175	KIIVEVLRIIAKVLK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2v1-2GS-	IEEEARRILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDAL
691	SB175	VENNRLIVENNKIIVEVLRIIAKVLK
		ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIRE
	AHB2v2-2GS-	IEEEAARILEHLEELARTGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDAL
692	SB175	VENNRLIVENNKIIVEVLRIIAKVLK

In some embodiments, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of a genus selected from those recited in the middle column of Table 9. In these embodiments, X1, X2, X3 (when recited in

the genus), and X4 (when recited in the genus) may be present or absent, and when present may be any sequence of 1 or more amino acids, as described above for embodiments listed in Table 8. In some embodiments, the optional domain that is present between monomer domains is present and may comprise an amino acid linker, as described above for embodiments listed in Table 8.

In another embodiment, the polypeptides comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence comprising the amino acid sequence selected from the group consisting of SEQ ID NOS:693 to 701, wherein any N-terminal methionine residue may be absent or present, and wherein residues in parentheses may be present or absent (preferably absent) and are not considered in determining percent identity. In one embodiment, the N-terminal methionine residue is absent and the optional residues are absent.

Table 9B

Name	Sequence
C389_AHB2v1_2GS-SB175	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKIIV EVLRIIAKVLK (SEQ ID NO: 693)
AHB2v2_12PAS_LCB3v2.2_12PAS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAAR ILEHLEELARTGGASPAAPAPGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKN KDRQKLEKVVEELKELLERLLSGGASPAAPAPGGDKENVLQKIYEIMKELERLGHAEASMQVSDL IYEFMKTKDENLLEEAERLLEEVKR (SEQ ID NO: 694)
AHB2v2_24PAS_LCB3v2.2_24PAS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEAAR ILEHLEELARTGGASPAAPAPASPAAPAPSAPAGGNLDELHMQMTDLVYEALHFAKDEEFQKHVF QLFEKATKAYKNKDRQKLEKVVEELKELLERLLSGGASPAAPAPASPAAPAPSAPAGGDKENVLQ KIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 695)
C398_SB175_6GS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGGSSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKI IVEVLRIIAKVLK(SEQ ID NO: 696)
AHB2v1_10GS_LCB3v2.2_10GS_LCB1v2.2	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGGSGGGSGGNLDELHMQMTDLVYEALHFAKDEEFQKHVFQLFEKATKAYKNKD RQKLEKVVEELKELLERLLSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSDLIYEF MKTKDENLLEEAERLLEEVKR(SEQ ID NO: 697)
C390-AHB2v1-4GS-SB175	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGGGSSEALEELEKALRELKKSTDELERSTEELEKNPSEDALVENNRLIVENNKI IVEVLRIIAKVLK(SEQ ID NO: 696)
C326-AHB2v1-4GS-1rfo	MELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMMLELIKSDDEREIREIEEEARR ILEHLEELARKGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFL(SEQ ID NO: 698)
AHB2v1-10GS-LCB3_v2.3-10GS-LCB1_v2.2 with His Tev tag	(MSHHHHHHHHSENLYFQSGG)ELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGSGGNIDELLMQVTDLIYEALHFAKDE EFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMK ELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKR(SEQ ID NO: 699)

LCB1v3 with His Tev tag (MSHHHHHHHHSENLYFQSGGG)DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDER LLEEAERLLEEVER(SEQ ID NO: 700)

LCB1-Fc9 With signal sequence leader removed DKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSGSGSG GSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK(SEQ ID NO: 701)

The polypeptide of any embodiment or combination of embodiments described here may further be linked to a stabilization domain to promote increased residency time upon administration to a subject. Any suitable stabilization domain may be used for an intended purpose. Exemplary stabilization domains include, but are not limited to, polyethylene glycol (PEG), albumin, hydroxyethyl starch (HES), conformationally disordered polypeptide sequence composed of the amino acids Pro, Ala, and/or Ser ('PASylation'), and/or a mucin diffusivity polypeptide composed of amino acids Lys and Ala, with or without Glu. Non-limiting embodiments of such mucin diffusivity polypeptides include, but are not limited to:

Mucin domain: AKAKAKAKAKAKAKAKAKAKGG (SEQ ID NO:61); GGAKAKAKAKAKAKAKAKAK (SEQ ID NO:62)

Exemplary polypeptides of these embodiments may, for example, comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 65-96, wherein in embodiments where a secretion signal is present (MARAWIFFLLCLAGRALA; SEQ ID NO:63) it can be replaced with any other secretion signal.

>Mucin_LCB1_v1.1_Cys_
AKAKAKAKAKAKAKAKAKAKGGDKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERC (SEQ ID NO:65)

>Mucin_LCB1_v1.3
AKAKAKAKAKAKAKAKAKAKGGDKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:66)

>LCB1_v1.3_Mucin
DKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGAKAKAKAKAKAKAKAKAK SEQ ID NO:67)

FC Fusions (**Bold = Secretion Signal**, underline = LCB, Yellow is the GS Linker, Green is Fc)

>LCB1-Fc1 (BM40-LCB1-GS4-Fc-Opt-WT) (The LCB1 sequences = **LCB1-1** of first provisional)
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGSGSEPKSS
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:68)

> LCB1-Fc2 (BM40-LCB1-GS15-Fc-Opt-WT)(The LCB1 sequence = **LCB1-1** of first provisional)
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:69)

>LCB1-Fc3 (BM40-Fc-Opt- GS15-2-LCB1-WT) (The LCB1 sequence = **LCB1-1** of first provisional)
MARAWIFFLLCLAGRALAEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
KSGGSGSGSGGSGSGS DKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO: 70)

>LCB1-Fc4 (BM40-LCB1-GS15-Fc-Opt-GS15-2-LCB1-WT) (The LCB1 sequences = **LCB1-1** of first provisional)
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGSGSGSGGS
GSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKKGDERLLEEAERLLEEVER (SEQ ID NO:71)

>LCB1-Fc5 (BM40-LCB1-GS4-Fc-Opt-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVERGSGSEPKSS
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:72)

>LCB1-Fc6 (BM40-LCB1-GS15-Fc-Opt-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:73)

>LCB1-Fc7 (BM40-Fc-Opt-GS15-2-LCB1-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)
MARAWIFFLLCLAGRALAEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
KSGGSGSGSGGSGSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:74)

>LCB1-Fc8 (BM40-LCB1-Q38-GS15-Fc-Opt-GS15-2-LCB1-Q38)(The LCB1 sequences = **LCB1-3** of first provisional)
MARAWIFFLLCLAGRALADKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR

EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGSGSGSGGS
GSGSDKEWILQKIYEIMRLLDELGHAEASMRVSDLIYEFMKQGDERLLEEAERLLEEVER (SEQ ID NO:75)

> LCB1-6M-Fc9 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS15-Fc-Opt)
(The LCB1 sequence = **LCB1_v1.1 of this provisional**)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:76)

> LCB1-6M-Ngly-Fc10 (BM40-LCB1-6M-Ngly -4N,14K,15T,18Q,**27N**,38Q -GS15-Fc-Opt) (The
LCB1 sequence = **LCB1-5 of the original provisional =** LCB1_v1.1 = LCB1-4 with N-link
Glycosylation)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLDQLGHAEASM**N**VSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:77)

> LCB3-6M-Fc11 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS15-Fc-Opt)
(LCB sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSG
GSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO:78)

> LCB3-6M-NGly-Fc12 (BM40-LCB3-6M-Ngly -8Q,26Q,28H,35N,37T,43K -GS15-Fc-Opt) (LCB
sequence is the same as **LCB3-4** of First Provisional which is LCB3-3 with N-link
Glycosylation)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFENATKAYKNKDRQKLEKVVEELKELLERLLSG
GSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO:79)

> LCB1-6M-GPGcP-Fc13 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GPGcP-Fc-Opt) (LCB
sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGS
GGSPVPSTPPTPSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSASEPKSSDKTHTCPPCPAPELLGGPSVF
LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:80)

> LCB3-6M-GPGcP-Fc14 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GPGcP-Fc-Opt) (LCB
sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSA
GSGGSGGSGGSPVPSTPPTPSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSASEPKSSDKTHTCPPCPAPE
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:81)

> LCB1-6M-GS30-Fc15 (BM40-LCB1-6M -4N,14K,15T,18Q,27Q,38Q -GS30-Fc-Opt)LCB1-4
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLDQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGSGGGGS
GGGGSGGGGSGGGGSGGGGSGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK (SEQ ID NO:82)

> LCB3-6M-GS30-Fc16 (BM40-LCB3-6M -8Q,26Q,28H,35K,37T,43K -GS30-Fc-Opt) (LCB sequence is the same as **LCB3-3** of First Provisional)
MARAWIFFLLCLAGRALANDDELHMQMTDLVYEALHFAKDEEIQKHVFQLFEKATKAYKNKDRQKLEKVVEELKELLERLLSG
GGSGGGGSGGGGSGGGGSGGGGSGGGGSGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPGK (SEQ ID NO:83)

> LCB1-v1.3-Fc17 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27Q,38Q -GS15-Fc-Opt)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:84)

> LCB1-v1.3-Ngly-Fc18 (BM40-LCB1-v1.3 Ngly -4N,14K,15T,17E,18Q,27N,38Q -GS15-Fc-Opt) (>LCB1_v1.5 (= LCB1_v1.3 with N-link Glycosylation)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMNVSDLIYEFMKQGDERLLEEAERLLEEVERGGSGSGGSG
SGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID
NO:85)

> LCB1-v1.3-GPGcP-Fc19 (BM40-LCB1-v1.3-Fc19 -4N,14K,15T,17E,18Q,27Q,38Q—GPGcP-Fc-Opt)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERAGSGGSGGS
GGSPVPSTPPTPSPSTPPTPSPSGGSGNSSGSGGSPVPSTPPTPSPSTPPTPSPSASEPKSSDKTHTCPPCPAPELLGGPSVF
LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:86)

> LCB1-v1.3-GS30-Fc20 (BM40-LCB1-v1.3 -4N,14K,15T,17E,18Q,27Q,38Q -GS30-Fc-Opt)
MARAWIFFLLCLAGRALADKENILQKIYEIMKTLEQLGHAEASMQVSDLIYEFMKQGDERLLEEAERLLEEVERGGGSGGGGS
GGGGSGGGGSGGGGSGGGGSGEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK (SEQ ID NO:87)

Fc21-LCB1v2.2-FcIgG1_WT

MARAWIFFLLCLAGRALADKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENL
LEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK (SEQ ID NO: 88)

Fc22-LCB1v2.2-FcIgG3_WT

MARAWIFFLLCLAGRALADKENVLQKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENL
LEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPRCPAPELLGGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEA

LHNRFTQKSLSLSPGK (SEQ ID NO: 89)

Fc23_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_WT

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 90)

Fc24_AHB2-10GS-LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_WT

MARAWIFFLLCLAGRALAELEEQVMHVLDQVSELAHELLHKLTGEELERAAYFNWWATEMM LELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGSGGNIDELLMQVTDLIYEALHF AKDEEFQKHAFQLFEKATKAYKNKDKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVL QKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSG SGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(SEQ ID NO: 91)

Fc25_LCB3_v2.3-10GS-AHB2-10GS-LCB1_v2.2_FcIgG1_WT

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK DKQKLEKVVEELKELLERILSGGGSGGGSGGELEEQVMHVLDQVSELAHELLHKLTGEELE RAAYFNWWATEMMLELIKSDDEREIREIEEEARRILEHLEELARKGGGSGGGSGGDKENVL QKIYEIMKELERLGHAEASMQVSDLIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSG SGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK(SEQ ID NO: 92)

Fc26_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GA

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELL AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK(SEQ ID NO: 93)

Fc27_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GRLR

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELL RGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKARPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK(SEQ ID NO: 94)

Fc28_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GAALIE

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELL AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPLPEEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK(SEQ ID NO: 95)

Fc29_LCB3_v2.3-10GS-LCB1_v2.2_FcIgG1_GAALIELS

MARAWIFFLLCLAGRALANIDELLMQVTDLIYEALHFAKDEEFQKHAFQLFEKATKAYKNK DKQKLEKVVEELKELLERILSGGGSGGGSGGDKENVLQKIYEIMKELERLGHAEASMQVSD LIYEFMKTKDENLLEEAERLLEEVKRGGSGSGGSGSGSGGSEPKSSDKTHTCPPCPAPELL AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPLPEEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVLHEALHSHYTQKSLSLSPGK(SEQ ID NO: 96)

The disclosure further provides oligomers of the polypeptide of any embodiment or combination of embodiments herein. In one embodiment, the oligomers are oligomers of polypeptides disclosed herein that comprise oligomerization domains. In one embodiment, the oligomer comprises a trimer, including but not limited to a homotrimer.

In another embodiment, the disclosure provides compositions, comprising 2, 3, 4, or more copies of the polypeptide of any embodiment or combination of embodiments herein attached to a support, including but not limited to a polypeptide particle support, such as a nanoparticle or virus like particle.

As disclosed herein, the polypeptides bind to the SARS-CoV-2 Spike glycoprotein, and thus are useful (for example), as therapeutics to treat SARS-CoV-2 infection. In one embodiment, the polypeptides bind to the SARS-CoV-2 Spike glycoprotein with an affinity of at least 10 nM, measured as described in the attached examples.

In another aspect, the disclosure provides nucleic acids encoding a polypeptide of the disclosure. The nucleic acid sequence may comprise RNA (such as mRNA) or DNA. Such nucleic acid sequences may comprise additional sequences useful for promoting expression and/or purification of the encoded protein, including but not limited to polyA sequences, modified Kozak sequences, and sequences encoding epitope tags, export signals, and secretory signals, nuclear localization signals, and plasma membrane localization signals. It will be apparent to those of skill in the art, based on the teachings herein, what nucleic acid sequences will encode the proteins of the invention.

In another aspect, the disclosure provides expression vectors comprising the nucleic acid of any embodiment or combination of embodiments of the disclosure operatively linked to a suitable control sequence. "Expression vector" includes vectors that operatively link a nucleic acid coding region or gene to any control sequences capable of effecting expression of the gene product. "Control sequences" operably linked to the nucleic acid sequences of the disclosure are nucleic acid sequences capable of effecting the expression of the nucleic acid molecules. The control sequences need not be contiguous with the nucleic acid sequences, so long as they function to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between a promoter sequence and the nucleic acid sequences and the promoter sequence can still be considered "operably linked" to the coding sequence. Other such control sequences include, but are not limited to, polyadenylation signals, termination signals, and ribosome binding sites. Such expression vectors can be of any type known in the art, including but not limited to plasmid and viral-based expression vectors. The control sequence used to drive expression of the disclosed

nucleic acid sequences in a mammalian system may be constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of inducible promoters including, but not limited to, tetracycline, ecdysone, steroid-responsive).

In one aspect, the present disclosure provides cells comprising the polypeptide, the composition, the nucleic acid, and/or the expression vector of any embodiment or combination of embodiments of the disclosure, wherein the cells can be either prokaryotic or eukaryotic, such as mammalian cells. In one embodiment the cells may be transiently or stably transfected with the nucleic acids or expression vectors of the disclosure. Such transfection of expression vectors into prokaryotic and eukaryotic cells can be accomplished via any technique known in the art. A method of producing a polypeptide according to the invention is an additional part of the invention. The method comprises the steps of (a) culturing a host according to this aspect of the invention under conditions conducive to the expression of the polypeptide, and (b) optionally, recovering the expressed polypeptide. In other embodiments, the polypeptides may be produced via any other suitable technique, including but not limited to using cell-free protein synthesis (or in vitro transcription and translation).

In another aspect, the disclosure provides pharmaceutical compositions/vaccines comprising

(a) the polypeptide, the nucleic acid, the expression vector, and/or the host cell of any embodiment or combination of embodiments herein; and

(b) a pharmaceutically acceptable carrier.

The compositions may further comprise (a) a lyoprotectant; (b) a surfactant; (c) a bulking agent; (d) a tonicity adjusting agent; (e) a stabilizer; (f) a preservative and/or (g) a buffer. In some embodiments, the buffer in the pharmaceutical composition is a Tris buffer, a histidine buffer, a phosphate buffer, a citrate buffer or an acetate buffer. The composition may also include a lyoprotectant, e.g. sucrose, sorbitol or trehalose. In certain embodiments, the composition includes a preservative e.g. benzalkonium chloride, benzethonium, chlorohexidine, phenol, m-cresol, benzyl alcohol, methylparaben, propylparaben, chlorobutanol, o-cresol, p-cresol, chlorocresol, phenylmercuric nitrate, thimerosal, benzoic acid, and various mixtures thereof. In other embodiments, the composition includes a bulking agent, like glycine. In yet other embodiments, the composition includes a surfactant e.g., polysorbate-20, polysorbate-40, polysorbate- 60, polysorbate-65, polysorbate-80 polysorbate-85, poloxamer-188, sorbitan monolaurate, sorbitan monopalmitate, sorbitan monostearate,

sorbitan monooleate, sorbitan trilaurate, sorbitan tristearate, sorbitan trioleaste, or a combination thereof. The composition may also include a tonicity adjusting agent, e.g., a compound that renders the formulation substantially isotonic or isoosmotic with human blood. Exemplary tonicity adjusting agents include sucrose, sorbitol, glycine, methionine, mannitol, dextrose, inositol, sodium chloride, arginine and arginine hydrochloride. In other embodiments, the composition additionally includes a stabilizer, e.g., a molecule which substantially prevents or reduces chemical and/or physical instability of the nanostructure, in lyophilized or liquid form. Exemplary stabilizers include sucrose, sorbitol, glycine, inositol, sodium chloride, methionine, arginine, and arginine hydrochloride.

The polypeptide, the nucleic acid, the expression vector, and/or the host cell may be the sole active agent in the composition, or the composition may further comprise one or more other agents suitable for an intended use.

In a further aspect, the disclosure provides methods for treating a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection. In one embodiment, the SARS coronavirus comprises SARS-CoV-2.

In another aspect, the disclosure provides methods for limiting development of a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection. In one embodiment, the SARS coronavirus comprises SARS-CoV-2.

The polypeptide, the nucleic acid, the expression vector, the host cell, and/or the pharmaceutical composition may be administered via any suitable administrative route as deemed appropriate by attending medical personnel. In one embodiment, the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered intra-nasally. In another embodiment, the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered systemically.

When the method comprises treating a SARS coronavirus infection, the one or more polypeptides, nucleic acids, expression vectors, host cells, and/or pharmaceutical compositions are administered to a subject that has already been diagnosed as having a SARS

coronavirus infection. As used herein, "treat" or "treating" means accomplishing one or more of the following: (a) reducing severity of symptoms of the infection in the subject; (b) limiting increase in symptoms in the subject; (c) increasing survival; (d) decreasing the duration of symptoms; (e) limiting or preventing development of symptoms; and (f) decreasing the need for hospitalization and/or the length of hospitalization for treating the infection.

When the method comprises limiting development of SARS coronavirus infection, the one or more polypeptides, nucleic acids, expression vectors, host cells, and/or pharmaceutical compositions are administered prophylactically to a subject that is not known to have a SARS coronavirus infection, but may be at risk of such an infection. As used herein, “limiting” means to limit development of a SARS coronavirus infection in subjects at risk of such infection, which may be any subject.

The subject may be any subject, such as a human subject

Exemplary symptoms of SARS-CoV-2 infection include, but are not limited to, fever, fatigue, cough, shortness of breath, chest pressure and/or pain, loss or diminution of the sense of smell, loss or diminution of the sense of taste, and respiratory issues including but not limited to pneumonia, bronchitis, severe acute respiratory syndrome (SARS), and upper and lower respiratory tract infections.

As used herein, an “effective amount” refers to an amount of the composition that is effective for treating and/or limiting SARS-CoV-2 infection. The polypeptide, composition, nucleic acid, or composition of any embodiment herein are typically formulated as a pharmaceutical composition, such as those disclosed above, and can be administered via any suitable route, including orally, parentally, by inhalation spray, rectally, or topically in dosage unit formulations containing conventional pharmaceutically acceptable carriers, adjuvants, and vehicles. The term parenteral as used herein includes, subcutaneous, intravenous, intra-arterial, intramuscular, intrasternal, intratendinous, intraspinal, intracranial, intrathoracic, infusion techniques or intraperitoneally. Polypeptide compositions may also be administered via microspheres, liposomes, immune-stimulating complexes (ISCOMs), or other microparticulate delivery systems or sustained release formulations introduced into suitable tissues (such as blood). Dosage regimens can be adjusted to provide the optimum desired response (e.g., a therapeutic or prophylactic response). A suitable dosage range may, for instance, be 0.1 μg/kg-100 mg/kg body weight of the polypeptide or nanoparticle thereof. The composition can be delivered in a single bolus, or may be administered more than once (e.g., 2, 3, 4, 5, or more times) as determined by attending medical personnel.

The disclosure also provides methods for designing polypeptides that bind to the receptor binding site (RBD) of SARS-Cov-2, wherein the methods comprise steps as described in the examples that follow. Such methods may comprise the steps of polypeptide design (as described in any embodiment or combination of embodiments in the examples), cell-free synthesis, and evaluation for SARS-Cov-2 RBD binding using any suitable technique.

Examples

Summary

Effective therapeutics for SARS-CoV-2 are needed. We sought to use computational protein design to generate high affinity binders to the receptor binding site (RBD) of SARS-Cov-2 that block the interaction with the Ace2 receptor required for cell entry. We generated small protein scaffolds with shape complementary to the Ace2 binding site on the RBD using two strategies: first, scaffolds were built around the helix in Ace2 that makes the majority of the interactions with the RBD, and second, diverse de novo designed scaffolds less than 65 residues in length were docked against this region. In both cases, the scaffold residues at the RBD interface were then optimized for high affinity binding and those in the remainder of the protein, for folding to the target structure and stability. The 50,000 designs predicted to bind most strongly to the virus were encoded in large oligonucleotide arrays, and screened using yeast surface display for binding to the RBD with fluorescence activated cell sorting; deep sequencing of the population before and after sorting identified hundreds of designs that bind the target. The binding modes of the highest affinity (most enriched by sorting) binders were confirmed by high resolution sequence mapping, and the affinities were further increased by combining 1-4 beneficial substitutions. Eight of the optimized designs with different binding sites surrounding the Ace2 interface on the RBD, and completely different sequences, were found to express at high levels in E coli, and to bind the RBD with Kd's ranging from 100pM to 10nM. The designs blocked infection of vero-6 cells by live virus with IC50's ranging from 10nM to 20pM. The polypeptides are thus useful, for example, in both intra-nasal and systemic SARS-CoV-2 therapeutics, and, more generally, our results demonstrate the power of computational protein design for rapidly generating potential therapeutic candidates against pandemic threats.

SARS -CoV-2 infection is thought to often start in the nose, with virus replicating there for several before spreading to the broader respiratory system. Delivery of a high concentration of a viral inhibitor into the nose and into the respiratory system generally could

therefore potentially provide prophylactic protection, and therapeutic efficacy early in infection, and could be particularly useful for health care workers and others coming into frequent contact with infected individuals. A number of monoclonal antibodies are in development as systemic SARS-CoV-2 therapeutics, but these compounds are not ideal for intranasal delivery as antibodies are large and often not extremely stable molecules, and the density of binding sites is low (two per 150Kd antibody); the Fc domain provides little added benefit. More desirable would be protein inhibitory with the very high affinity for the virus of the monoclonals, but with higher stability and very much smaller size to maximize the density of inhibitory domains and enable direct delivery into the respiratory system through nebulization.

We set out to *de novo* design high affinity binders to the RBD that compete with Ace2 binding. We explored two strategies: first we attempted to scaffold the alpha helix in Ace2 that makes the majority of the interactions with the RBD in a small designed protein that makes additional interactions with the RBD to attain higher affinity, and second, we sought to design binders completely from scratch that do not incorporate any known binding interaction with the RBD. An advantage of the second approach is that the range of possibilities for design is much larger, and so potentially higher affinity binding modes can be identified. For the first approach, we used the Rosetta™ blue print builder to generate small proteins which incorporate the Ace2 helix and for the second approach, RIF docking and design using large miniprotein libraries. The designs interact with distinct regions of the RBD surface surrounding the Ace2 binding sites (**Figure 1**). Designs for approach 1, and approach 2, were encoded in long oligonucleotides, and screened for binding to fluorescently tagged RBD on the yeast cell surface. Deep sequencing identified 3 Ace2 helix scaffolded designs (approach 1), and 150 de novo interface designs (approach 2) that were clearly enriched following FACS sorting for RBD binding. Designs were expressed in *E. coli* and purified, and many were found to be have soluble expression and to bind RBD in biolayer interferometry experiments and could effectively compete with ACE-2 for binding to RBD (example shown in Figure 2). Based on BLI data (e.g. See **Figure 2**) the RBD binding affinities of minibinders are: LCB1 <1nM, LCB3 <1nM. The affinities of LCB2, LCB4, LCB5, LCB6, LCB7, LCB8 range from 1~20nM, with relative strength of different binders being LCB4 > LCB2 > LCB9 = LCB5 > LCB6 > LCB7.

To determine whether the designs binding the RBD through the designed interfaces, site saturation libraries in which every residue in each design was substituted with each of the 20 amino acids one at a time were constructed, and subjected to FACS sorting for RBD

binding. Deep sequencing showed that the binding interface residues and protein core residues were conserved in many of the designs for which such site saturation libraries (SSM's) were constructed (SSMs were used to define allowable positions for amino acid changes in **Table 1**). For most of the designs, a small number of substitutions were enriched in the FACS sorting, suggesting they increase binding affinity for RBD. For the highest affinity of the approach 1 designs, and 8 of the approach 2 designs, combinatorial libraries incorporating these substitutions were constructed and again screened for binding with FACS; because of the very high binding affinity the concentrations used in the sorting were as low as 20pM. Each library converged on a small number of closely related sequences, and for each design, one of the optimized variants was expressed in *E. coli* and purified.

The binding of the 8 optimized designs with different binding modes to RBD (Figure1) was investigated by biolayer interferometry. For a number of the designs, the Kd's ranged from 1-20nM, and for the remainder, the Kd's were below 1nM, too strong to measure reliably with this technique (See Figure 2). Circular dichroism spectra of the designs were consistent with the design models, and the designs retained full binding activity after a number of days at room temperature (**Figure 3**).

We investigated the ability of the designs to block infection of human cells by live virus. 100 FFU of SARS-CoV-2 was added to 2.5-3x10^4 vero cells in the presence of varying amounts of the designed binders. Details are provided in the legend to **Figure 4.** We observed potent inhibition of infection for all of the designs with IC50's ranging from 1 nM to 0.02 nM.

Details on specific designs are provided in Table 10.

Table 10

Construct Name	Seq ID	Expression Host	Vector	Expression Method	Estimated Level of Soluble Production (mg / L)	Estimated Kd for RBD (nM)	Estimated Kd for Spike (nM) Avidity	SARS-CoV-2 Neutralization IC50 (nM)
LCB1-1	(SEQ ID NO:1)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-2	(SEQ ID NO:2)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-3	(SEQ ID NO:3)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-4	(SEQ ID NO:4)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-5	(SEQ ID NO:5)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01

LCB1_v1.1_Cys	(SEQ ID NO:6)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.2	(SEQ ID NO:7)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.3	(SEQ ID NO:8)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.4	(SEQ ID NO:9)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.5 (LCB1_v1.3 with N-link Glycosylation)	(SEQ ID NO:10)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB2-1	(SEQ ID NO:11)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB2-2	(SEQ ID NO:12)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-1	(SEQ ID NO:13)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-2	(SEQ ID NO:14)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-3	(SEQ ID NO:15)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-4	(SEQ ID NO:16)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.1	(SEQ ID NO:17)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2	(SEQ ID NO:15)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.3	(SEQ ID NO:19)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.4	(SEQ ID NO:20)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.5	(SEQ ID NO:21)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3-4	(SEQ ID NO:16)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB4-1	(SEQ ID NO:23)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB4-2	(SEQ ID NO:24)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB5-1	(SEQ ID NO:25)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB5-2	(SEQ ID NO:26)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB6-1	(SEQ ID NO:27)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB6-2	(SEQ ID NO:28)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB7-1	(SEQ ID NO:29)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB7-2	(SEQ ID NO:30)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB8-1	(SEQ ID NO:31)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB8-2	(SEQ ID NO:32)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB1-1	(SEQ ID NO:33)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB1-2	(SEQ ID NO:34)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB2-1	(SEQ ID NO:100)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
AHB2-2	(SEQ ID	E. coli	pET	Autoinduction	10	0.2	0.1	0.01

	NO:101)			37 C				
LCB1-6GS-LCB1	(SEQ ID NO:47)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-12GS-LCB1	(SEQ ID NO:48)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-24GS-LCB1	(SEQ ID NO:49)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-36GS-LCB1	(SEQ ID NO:50)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.1-GSLCB1_v1.1(1GS1)	(SEQ ID NO:51)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.1-PRO-LCB1_v1.1(1PRO1)	(SEQ ID NO:52)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2-GS3-LCB3_v1.2(3GS3)	(SEQ ID NO:53)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2-PRO-LCB3_v1.2(3PRO3)	(SEQ ID NO:54)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.1-GS-LCB3_v1.2(1GS3)	(SEQ ID NO:55)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2-GS-LCB1_v1.1(3GS1)	(SEQ ID NO:56)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2-10GS-LCB1_v1.1(LCB3-GS10-LCB1)	(SEQ ID NO:57)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.1-PRO-LCB3_v1.2(1PRO3)	(SEQ ID NO:58)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB3_v1.2-PRO-LCB1_v1.1(3PRO1)	(SEQ ID NO:59)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
(5_LCB1_linker14)	(SEQ ID NO:60)	E. coli	pET	Autoinduction 37 C	20.38	0.2	0.1	0.01141
Mucin_LCB1_v1.1_Cys	(SEQ ID NO:65)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
Mucin_LCB1_v1.3	(SEQ ID NO:66)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1_v1.3_Mucin	(SEQ ID NO:67)	E. coli	pET	Autoinduction 37 C	10	0.2	0.1	0.01
LCB1-Fc1 (BM40-LCB1-GS4-Fc-Opt-WT) (The LCB1 sequences = LCB1-1 of first provisional)	(SEQ ID NO:68)	Human 293 cells	pCMVR	Transient Transfection 37 C	12	0.2	0.1	0.01
LCB1-Fc2 (BM40-LCB1-	(SEQ ID NO:69)	Human 293	pCMVR	Transient Transfection	12	0.2	0.1	0.01

GS15-Fc-Opt-WT)(The LCB1 sequence = LCB1-1 of first provisional)		cells		37 C				
LCB1-Fc3 (BM40-Fc-Opt- GS15-2-LCB1-WT) (The LCB1 sequence = LCB1-1 of first provisional)	(SEQ ID NO: 70)	Human 293 cells	pCMVR	Transient Transfection 37 C	12	0.2	0.1	0.01
LCB1-Fc4 (BM40-LCB1-GS15-Fc-Opt-GS15-2-LCB1-WT) (The LCB1 sequences = **LCB1-1** of first provisional)	(SEQ ID NO:71)	Human 293 cells	pCMVR	Transient Transfection 37 C	2	0.2	0.1	0.01
LCB1-Fc5 (BM40-LCB1-GS4-Fc-Opt-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)	(SEQ ID NO:72)	Human 293 cells	pCMVR	Transient Transfection 37 C	6	0.2	0.1	0.01
LCB1-Fc6 (BM40-LCB1-GS15-Fc-Opt-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)	(SEQ ID NO:73)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-Fc7 (BM40-Fc-Opt-GS15-2-LCB1-Q38) (The LCB1 sequence = **LCB1-3** of first provisional)	(SEQ ID NO:74)	Human 293 cells	pCMVR	Transient Transfection 37 C	10	0.2	0.1	0.01
LCB1-Fc8 (BM40-LCB1-Q38-GS15-Fc-Opt-GS15-2-LCB1-Q38)(The LCB1 sequences = **LCB1-3** of first provisional)	(SEQ ID NO:75)	Human 293 cells	pCMVR	Transient Transfection 37 C	1	0.2	0.1	0.01
LCB1-6M-Fc9 (BM40-LCB1-6M -	(SEQ ID NO:76)	Human 293 cells	pCMVR	Transient Transfection 37 C	20	0.2	0.1	0.01

4N,14K,15T,18Q,27Q,38Q - GS15-Fc-Opt)								
LCB1-6M-Ngly-Fc10 (BM40-LCB1-6M-Ngly - 4N,14K,15T,18Q,**27N**,38Q - GS15-Fc-Opt) (The LCB1 sequence = **LCB1-5 of the original provisional** = LCB1_v1.1 = LCB1-4 with N-link Glycosylation)	(SEQ ID NO:77)	Human 293 cells	pCMVR	Transient Transfection 37 C	20	0.2	0.1	0.01
LCB3-6M-Fc11 (BM40-LCB3-6M - 8Q,26Q,28H,35K,37T,43K - GS15-Fc-Opt) (LCB sequence is the same as LCB3-3 of First Provisional)	(SEQ ID NO:78)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB3-6M-NGly-Fc12 (BM40-LCB3-6M-Ngly - 8Q,26Q,28H,35N,37T,43K - GS15-Fc-Opt) (LCB sequence is the same as **LCB3-4** of First Provisional which is LCB3-3 with N-link Glycosylation)	(SEQ ID NO:79)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-6M-GPGcP-Fc13 (BM40-LCB1-6M - 4N,14K,15T,18Q,27Q,38Q - GPGcP-Fc-Opt) (LCB sequence is the same as **LCB3-3** of First Provisional)	(SEQ ID NO:80)	Human 293 cells	pCMVR	Transient Transfection 37 C	2	0.2	0.1	0.01
LCB3-6M-GPGcP-Fc14 (BM40-LCB3-	(SEQ ID NO:81)	Human 293 cells	pCMVR	Transient Transfection 37 C	2	0.2	0.1	0.01

6M - 8Q,26Q,28H,35K,37T,43K - GPGcP-Fc-Opt) (LCB sequence is the same as **LCB3-3** of First Provisional)								
LCB1-6M-GS30-Fc15 (BM40-LCB1-6M - 4N,14K,15T,18Q,27Q,38Q - GS30-Fc-Opt)LCB1-4	(SEQ ID NO:82)	Human 293 cells	pCMVR	Transient Transfection 37 C	1	0.2	0.1	0.01
LCB3-6M-GS30-Fc16 (BM40-LCB3-6M - 8Q,26Q,28H,35K,37T,43K - GS30-Fc-Opt) (LCB sequence is the same as **LCB3-3** of First Provisional)	(SEQ ID NO:83)	Human 293 cells	pCMVR	Transient Transfection 37 C	1	0.2	0.1	0.01
LCB1-v1.3-Fc17 (BM40-LCB1-v1.3 - 4N,14K,15T,17E,18Q,27Q,38Q -GS15-Fc-Opt)	(SEQ ID NO:84)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-v1.3-Ngly-Fc18 (BM40-LCB1-v1.3 Ngly - 4N,14K,15T,17E,18Q,27N,38Q -GS15-Fc-Opt) (>LCB1_v1.5 (= LCB1_v1.3 with N-link Glycosylation)	(SEQ ID NO:85)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-v1.3-GPGcP-Fc19 (BM40-LCB1-v1.3-Fc19 - 4N,14K,15T,17E,18Q,27Q,38Q-GPGcP-Fc-Opt)	(SEQ ID NO:86)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01
LCB1-v1.3-GS30-Fc20 (BM40-LCB1-v1.3 - 4N,14K,15T,17E,18Q,27Q,38Q -GS30-Fc-	(SEQ ID NO:87)	Human 293 cells	pCMVR	Transient Transfection 37 C	5	0.2	0.1	0.01

Opt)								

The designed binders have several advantages over antibodies as potential therapeutics. Together, they span a range of binding modes, and in combination viral escape would be quite unlikely. The retention of activity after extended time at elevated temperatures suggests they would not require a cold chain. The designs are 20 fold smaller than a full antibody molecule, and hence in an equal mass have 20 fold more potential neutralizing sites, increasing the potential efficacy of a locally administered drug. The cost of goods and the ability to scale to very high production should be lower for the much simpler miniproteins, which unlike antibodies, do not require expression in mammalian cells for proper folding. The small size and high stability should make them amenable to direct delivery into the respiratory system by nebulization. Immunogenicity is a potential problem with any foreign molecule, but for previously characterized small de novo designed proteins little or no immune response has been observed, perhaps because the high solubility and stability together with the small size makes presentation on dendritic cells less likely.

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Ultrapotent miniproteins targeting the receptor-binding domain protect against SARS-CoV-2 infection and disease

Despite the introduction of public health measures and spike protein-based vaccines to mitigate the COVID-19 pandemic, SARS-CoV-2 infections and deaths continue to rise.. Here, we investigated the capacity of modified versions of one lead binder, LCB1, to protect against SARS-CoV-2-mediated lung disease in human ACE2-expressing transgenic mice. Systemic administration of LCB1-Fc reduced viral burden, diminished immune cell infiltration and inflammation, and completely prevented lung disease and pathology. A single

intranasal dose of LCB1v1.3 reduced SARS-CoV-2 infection in the lung even when given as many as five days before or two days after virus inoculation. Importantly, LCB1v1.3 protected *in vivo* against a historical strain (WA1/2020), an emerging B.1.1.7 strain, and a strain encoding key E484K and N501Y spike protein substitutions. These data support the use of LCB1v1.3 for prevention or treatment of SARS-CoV-2 infection.

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the cause of the Coronavirus Disease 2019 (COVID-19) pandemic, has resulted in global disease, suffering, and economic hardship. Despite implementation of public health measures, SARS-CoV-2 transmission persists principally through human-to-human spread (Day, 2020; Li et al., 2020; Standl et al., 2020). SARS-CoV-2-induced clinical manifestations range from asymptomatic infection to severe pneumonia, multi-organ failure, and death. Although the underlying mechanisms that dictate disease severity are poorly understood, the immunocompromised, the elderly, and those with specific comorbidities (*e.g.*, history of cardiovascular disease, diabetes, or obesity) are at increased risk for poor outcome (Zhou et al., 2020).

Here, using a stringent model of SARS-CoV-2 disease pathogenesis in human ACE2 (hACE2)-expressing transgenic mice (Golden et al., 2020; Winkler et al., 2020a), we evaluated the efficacy *in vivo* of exemplary miniprotein binder, LCB1. For our *in vivo* experiments, we evaluated two versions of LCB1: (a) an Fc-modified bivalent form, LCB1-hIgG-Fc9 (LCB1-Fc) that should extend half-life *in vivo* and engage effector arms of the immune system; and (b) a further optimized, monomeric form of LCB1 lacking an Fc domain, LCB1v1.3. Intraperitoneal administration of LCB1-Fc at one day pre- or post SARS-CoV-2 exposure conferred substantial protection including an absence of weight loss, reductions in viral burden approaching the limit of detection, and inhibition of lung inflammation and pathology. Intranasal delivery of LCB1v1.3 conferred protection as many as five days before or two days after SARS-CoV-2 inoculation. Dosing experiments revealed that LCB1v1.3 retained efficacy at pharmacologically attainable concentrations and was weakly immunogenic. Most importantly, LCB1v1.3 protected animals against the currently emerging B.1.1.7 United Kingdom variant and a SARS-CoV-2 strain encoding key spike substitutions E484K and N501Y present in both the South Africa (B.1.351) and Brazil (B.1.1.248) variants of concern. Overall, these studies establish LCB1-Fc and LCB1v1.3 as possible treatments to prevent or mitigate SARS-CoV-2 disease.

RESULTS

LCB1v1.3 prophylaxis limits viral burden and clinical disease. We modified LCB1 to generate two versions for *in vivo* testing: (a) we introduced polar mutations into

LCB1 to increase expression yield and solubility without altering RBD binding (LCB1v1.3) and (b) we modified LCB1 by fusing it to a human IgG1 Fc domain (LCB1-Fc) to enhance bioavailability. LCB1v1.3 and LCB1-Fc bound avidly to a single RBD within the S trimer (**Fig 5A**) with dissociation constants (K_D) of less than 625 and 156 pM, respectively (**Fig 5B**). LCB1v1.3 and LCB1-Fc also potently neutralized an authentic SARS-CoV-2 isolate (2019n-CoV/USA_WA1/2020 [WA1/2020]) (EC_{50} of 14.4 and 71.8 pM, respectively; **Fig 5C**).

To determine the protective potential of these miniproteins against SARS-CoV-2, we utilized K18 human hACE2-expressing transgenic mice, which develop severe lung infection and disease after intranasal inoculation of SARS-CoV-2 (Golden et al., 2020; Winkler et al., 2020a). In prophylaxis studies, a single 250 μg (10 mg/kg) dose of LCB1-Fc administered by intraperitoneal injection (i.p.) one day prior to intranasal (i.n.) inoculation with 10^3 PFU of SARS-CoV-2 WA1/2020 prevented weight loss compared to animals given a control protein (influenza A virus hemagglutinin minibinder) designed using similar computational methods (**Fig 5D**). After LCB1-Fc prophylaxis, infectious virus was not detected in the lungs at 4- or 7-days post-infection (dpi), whereas high levels were observed in animals administered control protein (**Fig 5E,** *top and bottom*). Similarly, viral RNA levels in the lung, heart, spleen, and brain of LCB1-Fc treated animals were at or near the limit of detection of the assay at 4 or 7 dpi (**Fig 5F-I**). LCB1-Fc treatment had no effect on viral RNA levels in nasal wash samples obtained at 4 dpi (**Fig 5J**), results that are similar to a recent study of a neutralizing human antibody in hamsters (Zhou et al., 2021). However, viral RNA levels were reduced at 7 dpi, suggesting that LCB1-Fc treatment accelerated viral clearance or prevented spread in the upper respiratory tract.

Diffuse alveolar damage, inflammation, and pneumonia are manifestations of COVID-19 lung disease, culminating in respiratory failure and a requirement for mechanical ventilation (Johnson et al., 2020; Kordzadeh-Kermani et al., 2020). We evaluated the capacity of LCB1-Fc to prevent the compromised lung function seen after SARS-CoV-2 infection of K18-hACE2 mice (Winkler et al., 2020a). At 7 dpi, mechanical ventilation tests of lung biomechanics in animals treated with LCB1-Fc showed no difference from naïve animals (**Fig 6A**), whereas mice receiving the control binder protein showed decreased inspiratory capacity and lung compliance as well as increased pulmonary resistance, elastance, and tissue damping, all consistent with compromised lung function. These biophysical properties resulted in disparate pressure-volume loops between control binder

and LCB1-Fc treated or naïve animals. We also assessed the effect of LCB1-Fc treatment on SARS-CoV-2-induced lung pathology. Lung sections of animals collected at 7 dpi with SARS-CoV-2 showed widespread inflammation characterized by a cellular infiltrate and airspace consolidation in control protein-treated but not LCB1-Fc treated or naïve mice (**Fig 6B**). At 4 dpi, inflammatory cytokine and chemokine RNA signatures in the lung were absent in LCB1-Fc treated but not control binder treated animals, suggesting that LCB1-Fc treatment prevents virus infection and inflammation in the lung (**Fig 6C and 11**).

Post-exposure therapy with anti-RBD binders reduces viral burden. To evaluate its efficacy in a post-exposure setting, we administered LCB1-Fc by i.p. injection at 1 dpi. Therapy with LCB1-Fc prevented weight loss (**Fig 7A**) and reduced viral burden in all tested tissues at 4 and 7 dpi (**Fig 7B-G**). Infectious virus was not recovered from the lungs of LCB1-Fc treated animals collected at either timepoint. Lung sections confirmed that therapy with LCB1-Fc improved pathological outcome (**Fig 7H**). At 7 dpi, immune cell infiltrates were absent in the lung sections of LCB1-Fc treated but not control binder-treated animals.

We next tested the efficacy of LCB1v1.3 as an i.n.-delivered post-exposure therapy. I.n. delivery, might enable self-administration of an anti-SARS-CoV-2 biological drug. Indeed, miniprotein inhibitors against influenza virus have shown efficacy as a nasal mist (Chevalier et al., 2017). For these studies, we used LCB1v1.3 because it can bind an increased number of RBD molecules for a given mass dose, resulting in increased neutralization activity (**Fig 5C**). Whereas high levels of SARS-CoV-2 RNA were detected in the lungs and other peripheral tissues of control binder-treated animals at 7 dpi, infection was reduced in animals receiving LCB1v1.3 by i.n. administration at D+1 or D+2 after inoculation with SARS-CoV-2 (**Fig 7I and12**). Levels of viral RNA were reduced in the nasal washes of animals receiving LCB1v1.3 after treatment at D+1 but not D+2 compared to control binder-treated animals (**Fig 7J**).

Intranasal delivery of LCB1v1.3 confers protection against SARS-CoV-2 when administered up to 5 days before infection. We next evaluated the durability of LCB1v1.3 administered via i.n. prophylaxis. At 5 days, 3 days, 1 day, or 6 hours prior to inoculation with 10^3 PFU of SARS-CoV-2, K18-hACE2 transgenic mice received a single 50 μg i.n. dose of LCB1v1.3 or the control binder. At 4 or 7 dpi, viral burden in tissues was determined by RT-qPCR. As expected, protection by LCB1v1.3 was better when administered closer to the time of SARS-CoV-2 exposure, as reflected by greater reductions in viral load and weight loss (**Fig 8A-D and S3**). However, even mice receiving LCB1v1.3 five days prior to

inoculation and collected at 7 dpi showed reduced viral RNA levels in the lung compared to control binder treated animals. Regardless of the collection timepoint, lung viral RNA levels were reduced in animals receiving LCB1v1.3 three days prior to inoculation with SARS-CoV-2.

We tested a range of i.n. doses LCB1v1.3 for efficacy (**Fig 8E-J**). Treatment with as little as 2 μg (0.1 mg/kg) of LCB1v1.3 prevented SARS-CoV-2-induced weight loss. Doses between 2 and 10 μg (0.1 to 0.5 mg/kg) of LCB1v1.3 reduced viral RNA levels in the lung, heart, and spleen at 7 dpi relative to control binder-treated animals. Moreover, animals receiving a 50 μg dose of LCB1v1.3 showed minimal, if any, lung inflammation (**Fig 8K**). Collectively, these results indicate that even low doses of LCB1v1.3, when administered via an i.n. route prior to exposure, can limit SARS-CoV-2 infection and disease in the stringent K18-hACE transgenic mouse model of pathogenesis.

LCB1v1.3 is weakly immunogenic and retains protective activity after repeated dosing. We treated K18-hACE2 transgenic mice with 50 μg of control binder or LCB1v1.3 every three days for a total of 18 days (**Fig 9A**). At this time, we collected sera and assessed the presence of anti-LCB1v1.3 antibodies. Only 1 of 10 mice developed IgG antibodies against LCB1v1.3 (**Fig 9B**). To determine if repeated dosing affected LCB1v1.3-mediated protection, we challenged the cohort with 10^3 PFU of SARS-CoV-2. Again, substantial protection against weight loss (**Fig 9C**) and viral infection in the lung and other organs was observed in all animals receiving LCB1v1.3 (**Fig 9D-H**).

LCB1v1.3 protects against emerging SARS-CoV-2 variants. We evaluated the activity of LCB1v1.3 against a B.1.1.7 isolate containing deletions at 69-70 and 144-145, and substitutions at N501Y, A570D, D614G, and P681H, and against a recombinant WA1/2020 strain containing key substitutions present in the B.1.351 and B.1.248 variant strains at residues E484K, N501Y, and D614G (Xie et al., 2021a). Although the neutralizing activity of LCB1v1.3 against the B.1.1.7 and E484K/N501Y/D614G strains was approximately 45 to 50-fold lower than for the WA1/2020 strain, the EC_{50} values still were ~800 pM and 667 pM, respectively (**Fig 10A**). To determine whether LCB1v1.3 could protect *in vivo* against SARS-CoV-2 strains with concerning spike protein substitutions, we treated K18-hACE2 transgenic mice with a single i.n. 50 μg dose of LCB1v1.3 or control binder one day prior to inoculation with 10^3 PFU of B.1.1.7 or E484K/N501/D614G SARS-CoV-2. Notably, LCB1v1.3 treatment before challenge with either variant strain protected against weight loss (**Fig 10B**

and 10H) and viral infection in all tissues collected at 6 dpi (**Fig 10C-G and 10I-M**). Thus, LCB1v1.3 is effective against both circulating and emerging strains of SARS-CoV-2.

DISCUSSION

Here, using the stringent K18-hACE2 mouse model of SARS-CoV-2 pathogenesis, we show that LCB1-Fc prevented SARS-CoV-2 infection and disease when administered one day before or after virus inoculation. Lung biomechanics of mice treated with LCB1-Fc mirrored those of naïve animals in all parameters tested.

We also evaluated the efficacy of LCB1v1.3, an optimized, monomeric form of LCB1 without an Fc domain. A single i.n. dose of LCB1v1.3 reduced viral burden when administered as many as five days before or two days after SARS-CoV-2 infection. Our i.n. delivery approach is unique. I.n. therapy of SARS-CoV-2 has been reported only with type I interferon in a hamster model of disease (Hoagland et al., 2021) and efficacy was limited. The K18-hACE2 mouse model recapitulates several aspects of severe COVID-19, including lung inflammation and reduced pulmonary function (Golden et al., 2020; Winkler et al., 2020a). Since K18-hACE2 mice are highly vulnerable to infection, the therapeutic window of treatment is limited (Winkler et al., 2020b) and for our miniproteins, might only curb viral infection. Importantly, our data demonstrate that LCB1v1.3 binder treatment before or after infection limited immune cell infiltration and lung inflammation, which prevented tissue damage and compromise of respiratory function. As part of our proof-of-principle studies for a nasal prophylaxis, we observed little immunogenicity of LCB1v1.3, suggesting that repeated dosing may be possible.

Although several antibody-based therapies demonstrate promise against SARS-CoV-2, and a few have been granted EUA status, viral evolution could jeopardize these interventions as evidenced by the emerging variants in the United Kingdom (B.1.1.7), South Africa (B.1.351), Brazil (B.1.248), and elsewhere. Indeed, we and others have observed that many monoclonal and polyclonal antibodies showed reduced neutralization activity against several of these variant strains (Chen et al., 2021; Wang et al., 2021a; Wang et al., 2021b; Wibmer et al., 2021; Xie et al., 2021b). In comparison, LCB1v1.3 showed efficacy against historical (WA1/2020) and emerging (B.1.1.7 and E484K/N501Y/D614G) SARS-CoV-2 strains. Based on the cryo-EM structure of the parent LCB1 binder in complex with SARS-CoV-2 RBD (Cao et al., 2020), only the N501Y mutation is expected to affect binding. While we observed a decrease in the neutralizing activity of LCB1v1.3 against the emerging variants, EC_{50} values were still less than 800 pM, suggesting substantial potency was retained.

Compared to other potential SARS-CoV-2 antibody-based treatments, miniproteins have several benefits: (a) due to their smaller size, they can bind each protomer of a single trimeric spike, resulting in greater potency for a given dose; (b) they can be manufactured cost-effectively; and (c) they can be mixed using linker proteins to generate multimerized constructs that limit resistance.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Cells and viruses. Vero E6 (CRL-1586, American Type Culture Collection (ATCC), Vero CCL81 (ATCC), Vero-furin (Mukherjee et al., 2016), and Vero-hACE2-TMPRSS2 (a gift of A. Creanga and B. Graham, NIH) were cultured at 37°C in Dulbecco's Modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 10 mM HEPES pH 7.3, 1 mM sodium pyruvate, 1× non-essential amino acids, and 100 U/ml of penicillin–streptomycin. Additionally, Vero-hACE2-TMPRSS2 cells were cultured in the presence of 5 μg/mL puromycin. The WA1/202 (2019n-CoV/USA_WA1/2020) isolate of SARS-CoV-2 was obtained from the US Centers for Disease Control (CDC). The B.1.1.7 and WA1/2020 E484K/N501Y/D614G viruses have been described previously (Chen et al., 2021; Xie et al., 2021a). Infectious stocks were propagated by inoculating Vero CCL81 or Vero-hACE2-TMPRSS2 cells. Supernatant was collected, aliquoted, and stored at -80°C. All work with infectious SARS-CoV-2 was performed in Institutional Biosafety Committee-approved BSL3 and A-BSL3 facilities at Washington University School of Medicine using positive pressure air respirators and protective equipment.

Mouse experiments. Animal studies were carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocols were approved by the Institutional Animal Care and Use Committee at the Washington University School of Medicine (assurance number A3381–01). Virus inoculations were performed under anesthesia that was induced and maintained with ketamine hydrochloride and xylazine, and all efforts were made to minimize animal suffering.

Heterozygous K18-hACE c57BL/6J mice (strain: 2B6.Cg-Tg(K18-ACE2)2Prlmn/J) were obtained from The Jackson Laboratory. Animals were housed in groups and fed standard chow diets. Mice of different ages and both sexes were administered 10^3 PFU of SARS-CoV-2 via intranasal administration.

METHOD DETAILS

Miniprotein production. LCB1-Fc was synthesized and cloned by GenScript into pCMVR plasmid, with kanamycin resistance. Plasmids were transformed into the NEB 5-alpha strain of *E. coli* (New England Biolabs) to recover DNA for transient transfection into Expi293F mammalian cells. Expi293F cells were grown in suspension using Expi293F expression medium (Life Technologies) at 33°C, 70% humidity, and 8% CO_2 rotating at 150 rpm. The cultures were transfected using PEI-MAX (Polyscience) with cells grown to a density of 3 x 10^6 cells per mL and cultivated for 3 days. Supernatants were clarified by centrifugation (5 min at 4000 x *g*, addition of PDADMAC solution to a final concentration of 0.0375% (Sigma Aldrich, #409014), and a second spin (5 min at 4000 x *g*). Clarified supernatants were purified using a MabSelect PrismA™ 2.6×5 cm column (Cytiva) on an AKTA Avant150 FPLC (Cytiva). Bound protein was washed with five column volumes of 20 mM $NaPO_4$ and 150 mM NaCl pH 7.2, then five column volumes of 20 mM $NaPO_4$ and 1 M NaCl pH 7.4, and eluted with three column volumes of 100 mM glycine at pH 3.0. The eluate was neutralized with 2 M Tris base to a final concentration of 50 mM. SDS-PAGE was used to assess protein purity. The protein was passed through a 0.22 μm filter and stored at 4°C until use.

LCB1v1.3 with polar mutations (4N, 14K, 15T, 17E, 18Q, 27Q, 38Q) relative to the original LCB1 was cloned into a pet29b vector. LCB1v1.3 was expressed in Lemo21(DE3) (NEB) in terrific broth media and grown in 2 L baffled shake flasks. Bacteria were propagated at 37°C to an O.D.600 of ~0.8, and then induced with 1 mM IPTG. Expression temperature was reduced to 18°C, and the cells were shaken for ~16 h. The cells were harvested and lysed using heat treatment and incubated at 80°C for 10 min with stirring. Lysates were clarified by centrifugation at 24,000 × *g* for 30 min and applied to a 2.6×10 cm Ni Sepharose™ 6 FF column (Cytiva) for purification by IMAC on an AKTA Avant150 FPLC system (Cytiva). Proteins were eluted over a linear gradient of 30 mM to 500 mM imidazole in a buffer of 50 mM Tris pH 8.0 and 500 mM NaCl. Peak fractions were pooled, concentrated in 10 kDa MWCO centrifugal filters (Millipore), sterile filtered (0.22 μm) and applied to either a Superdex™ 200 Increase 10/300, or HiLoad S200 pg GL SEC column (Cytiva) using 50 mM phosphate pH 7.4, 150 mM NaCl buffer. After size exclusion chromatography, bacterial-derived components were tested to confirm low levels of endotoxin.

Biolayer interferometry. Biolayer interferometry data were collected using an Octet™ RED96 (ForteBio) and processed using the instrument's integrated software. Briefly, biotinylated RBD (Acro Biosystems) was loaded onto streptavidin-coated biosensors (SA

ForteBio) at 20 nM in binding buffer (10 mM HEPES (pH 7.4), 150 mM NaCl, 3 mM EDTA, 0.05% surfactant P20, and 0.5% non-fat dry milk) for 360 s. Analyte proteins (LCB1v1.3 or LCB1-Fc) were diluted from concentrated stocks into binding buffer. After baseline measurement in the binding buffer alone, the binding kinetics were monitored by dipping the biosensors in wells containing the target protein at the indicated concentration (association step) for 3,600 s and then dipping the sensors back into baseline/buffer (dissociation) for 7,200 s.

Plaque assay. Vero-furin cells (Mukherjee et al., 2016) were seeded at a density of 2.5×10^5 cells per well in flat-bottom 12-well tissue culture plates. The following day, medium was removed and replaced with 200 µL of 10-fold serial dilutions of the material to be titrated, diluted in DMEM+2% FBS, and plates incubated at 37°C with rocking at regular intervals. One hour later, 1 mL of methylcellulose overlay was added. Plates were incubated at 37°C for 72 h, then fixed with 4% paraformaldehyde (final concentration) in PBS for 20 min. Fixed cell monolayers were stained with 0.05% (w/v) crystal violet in 20% methanol and washed twice with distilled, deionized water.

Measurement of viral burden. Tissues were weighed and homogenized with zirconia beads in a MagNA Lyser™ instrument (Roche Life Science) in 1,000 µL of DMEM media supplemented with 2% heat-inactivated FBS. Tissue homogenates were clarified by centrifugation at 10,000 rpm for 5 min and stored at −80°C. RNA was extracted using the MagMax mirVana™ Total RNA isolation kit (Thermo Scientific) on a Kingfisher Flex extraction robot (Thermo Scientific). RNA was reverse transcribed and amplified using the TaqMan™ RNA-to-CT 1-Step Kit (ThermoFisher). Reverse transcription was carried out at 48°C for 15 min followed by 2 min at 95°C. Amplification was accomplished over 50 cycles as follows: 95°C for 15 s and 60°C for 1 min. Copies of SARS-CoV-2 N gene RNA in samples were determined using a previously published assay (Case et al., 2020; Hassan et al., 2020). Briefly, a TaqMan™ assay was designed to target a highly conserved region of the N gene (Forward primer: ATGCTGCAATCGTGCTACAA (SEQ ID NO: 190); Reverse primer: GACTGCCGCCTCTGCTC (SEQ ID NO: 191); Probe: /56-FAM/TCAAGGAAC/ZEN/AACATTGCCAA/3IABkFQ/) (SEQ ID NO: 192). This region was included in an RNA standard to allow for copy number determination down to 10 copies per reaction. The reaction mixture contained final concentrations of primers and probe of 500 and 100 nM, respectively.

Cytokine and chemokine mRNA measurements. RNA was isolated from lung homogenates as described above. cDNA was synthesized from DNAse-treated RNA using

the High-Capacity cDNA Reverse Transcription kit (Thermo Scientific) with the addition of RNase inhibitor following the manufacturer's protocol. Cytokine and chemokine expression was determined using TaqMan™ Fast Universal PCR master mix (Thermo Scientific) with commercial primers/probe sets specific for *IFN-g* (IDT: Mm.PT.58.41769240), *IL-6* (Mm.PT.58.10005566), *IL-1b* (Mm.PT.58.41616450), *Tnfa* (Mm.PT.58.12575861), *CXCL10* (Mm.PT.58.43575827), *CCL2* (Mm.PT.58.42151692), *CCL5* (Mm.PT.58.43548565), *CXCL11* (Mm.PT.58.10773148.g), *Ifnb* (Mm.PT.58.30132453.g), *CXCL1* (Mm.PT.58.42076891) and results were normalized to *GAPDH* (Mm.PT.39a.1) levels. Fold change was determined using the $2^{-\Delta\Delta Ct}$ method comparing treated mice to naïve controls.

Lung Pathology. Animals were euthanized before harvest and fixation of tissues. The left lung was first tied off at the left main bronchus and collected for viral RNA analysis. The right lung was inflated with approximately 1.2 mL of 10% neutral buffered formalin using a 3-mL syringe and catheter inserted into the trachea. Tissues were embedded in paraffin, and sections were stained with hematoxylin and eosin. Slides were scanned using a Hamamatsu NanoZoomer™ slide scanning system, and images were viewed using NDP view software (ver.1.2.46).

Respiratory mechanics. Mice were anesthetized with ketamine/xylazine (100 mg/kg and 10 mg/kg, i.p., respectively). The trachea was isolated via dissection of the neck area and cannulated using an 18-gauge blunt metal cannula (typical resistance of 0.18 $cmH_2O.s/mL$), which was secured in place with a nylon suture. The mouse then was connected to the flexiVent™ computer-controlled piston ventilator (SCIREQ Inc.) via the cannula, which was attached to the FX adaptor Y-tubing. Mechanical ventilation was initiated, and mice were given an additional 100 mg/kg of ketamine and 0.1 mg/mouse of the paralytic pancuronium bromide via intraperitoneal route to prevent breathing against the ventilator and during measurements. Mice were ventilated using default settings for mice, which consisted in a positive end expiratory pressure at 3 cm H_2O, a 10 mL/kg tidal volume (Vt), a respiratory rate at 150 breaths per minute (bpm), and a fraction of inspired oxygen (FiO_2) of 0.21 (*i.e.*, room air). Respiratory mechanics were assessed using the forced oscillation technique, as previously described (McGovern et al., 2013), using the latest version of the flexiVent™ operating software (flexiWare v8.1.3). Pressure-volume loops and measurements of inspiratory capacity also were performed.

Neutralization assay. Serial dilutions of binder proteins were incubated with 10^2 focus-forming units (FFU) of SARS-CoV-2 for 1 h at 37°C. Binder-virus complexes were

added to Vero E6 (WA1/2020) or Vero-hACE2-TMPRSS2 (B.1.1.7 and WA1/2020 E484K/N501Y/D614G) cell monolayers in 96-well plates and incubated at 37°C for 1 h. Subsequently, cells were overlaid with 1% (w/v) methylcellulose in MEM supplemented with 2% FBS. Plates were harvested 24-30 h later by removing overlays and fixed with 4% PFA in PBS for 20 min at room temperature. Plates were washed and sequentially incubated with an oligoclonal pool of SARS2-2, SARS2-11, SARS2-16, SARS2-31, SARS2-38, SARS2-57, and SARS2-71 anti-spike protein antibodies (Zhou et al., 2021) and HRP-conjugated goat anti-mouse IgG in PBS supplemented with 0.1% saponin and 0.1% bovine serum albumin. SARS-CoV-2-infected cell foci were visualized using TrueBlue™ peroxidase substrate (KPL) and quantitated on an ImmunoSpot™ microanalyzer (Cellular Technologies). Data were processed using Prism™ software (GraphPad Prism™ 8.0).

ELISA. C-terminal biotinylated LCB1.1v3 was immobilized on streptavidin-coated plates (RayBiotech #7C-SCP-1) at 2.5 μg/mL in 100 μL total volume per well and incubated at 4°C overnight. Plates were washed with wash buffer (TBS + 0.1% (w/v) BSA + 0.05% (v/v) Tween20) and blocked with 200 μL/well blocking buffer (TBS + 2% (w/v) BSA + 0.05% (v/v) Tween20) for 1 h at room temperature. Plates were rinsed with wash buffer using 200 μL/well, and 100 μL of 1:100 diluted sera samples in blocking buffer were added to respective wells. For a positive control, Fc-RBD was serially diluted 1:5 starting at 240 ng/mL in 100 μL of blocking buffer. All samples were incubated for 1 h at room temperature. Plates were washed using 200 μL/well of wash buffer. For the serum samples, HRP-conjugated horse anti-mouse IgG antibody (Vector Laboratories #PI-2000-1) was diluted 1:200 in blocking buffer, and 100 μL was incubated in each well at room temperature for 30 min. For the positive control, HRP-conjugated mouse anti-human IgG antibody (Invitrogen #05-4220) was diluted 1:500 in blocking buffer, and 100 μL was incubated in each well at room temperature for 30 min. Plates were rinsed with wash buffer, and 100 μL of TMB (SeraCare) was added to each well for 2 min. The reaction was quenched by adding 100 μL of 1N HCl. Optical densities were determined at 450nm on a Synergy Neo2™ plate reader (BioTek Instruments).

QUANTIFICATION AND STATISTICAL ANALYSIS

Statistical significance was assigned when P values were < 0.05 using Prism™ Version 8 (GraphPad). Tests, number of animals, median values, and statistical comparison groups are indicated in each of the Figure legends. Analysis of weight change was determined by two-way ANOVA. Changes in functional parameters or immune parameters

were compared to control binder-treated animals and analyzed by one-way ANOVA with multiple comparisons tests. Statistical analyses of viral burden between two groups were determined by Mann-Whitney test.

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Multivalent Designs

Escape variants of SARS-CoV-2 are threatening to considerably prolong the COVID-19 pandemic. Here we develop multivalent minibinders as potential prophylactic and therapeutic agents to address this problem. We designed multivalent minibinders containing three copies of a minibinder (self-assembled homotrimer), or three linked distinct minibinders (multi-domain fusion) targeting different sites, geometrically matched to the spike trimer and optimized their composition using a rapid cell-free expression and evaluation workflow. The optimized designs have greatly slowed dissociation rates from the SARS-CoV-2-S-glycoprotein with complex half-lives of more than two weeks. Cryo-EM of the structures reveal that both homotrimer and fusion minibinder constructs can engage all three RBDs on a single spike protein. The top trimeric and fusion candidates neutralize the wild-type SARS-CoV-2 virus in addition to the B.1.1.7, B.1.351, B.1.1.28 variants of concern with IC50s in the low pM range. Additionally, the top homotrimer candidate provided prophylactic protection in a human ACE2-expressing transgenic mice against the same variant strains. Our approach highlights the utility of computational protein design coupled to rapid experimental prototyping to design potent multivalent inhibitors that can broadly neutralize widely circulating variants of concern.

We sought to develop multivalent versions of our computationally designed miniproteins that block the SARS-CoV-2 receptor binding domain (RBD) interaction with its host receptor ACE2. In principle, the small size of the designed minibinders enables simultaneous engagement of multiple RBDs within a single spike protein trimer. We

hypothesized that this multivalent binding would lead to ultra-high affinity inhibitors that are more resistant to escape mutations than their monomeric counterparts. The resulting avidity from these multivalent interactions could ameliorate the effects of mutations that would escape individual domains. Additionally, single proteins containing domains targeting multiple distinct epitopes or containing different sets of contacts with the target epitope could further increase the robustness of the designs to mutational escape. Starting with the LCB1, AHB2, and LCB3 minibinders (hereafter referred to as M1, M2, and M3 respectively; Table 11) and their known binding modes we pursued two parallel strategies for designing multivalent inhibitors, self-assembled homotrimers and multi-domain fusions.

ID	Protein
M1	LCB1_v2.2
M2	AHB2
M3	LCB3_v2.2
F23-P12	AHB2_v2-PAS12-LCB3_v2.2
F31-P12	LCB3_v2.2-PAS12-LCB1_v2.2
F231-P12	AHB2_v2-PAS12-LCB3_v2.2-PAS12-LCB1_v2.2
F231-P24	AHB2_v2-PAS24-LCB3_v2.2-PAS24-LCB1_v2.2
F23-G10	AHB2_v2-GS10-LCB3_v2.2
F31-F10	LCB3_v2.2-GS10-LCB1_v2.2
F231-G10	AHB2_v2-GS10-LCB3_v2.2-GS10-LCB1_v2.2
H1-1	SB175-6GS-LCB1_v2.2
H2-0	AHB2-4GS-1rfo
H2-1	AHB2-2GS-SB175
H3-1	LCB3_v2.2-6GS-SB175

Table 11. List of abbreviations used to describe multivalent minibinders

To enable rapid prototyping of the designed proteins, we developed a cell-free DNA assembly and protein expression workflow enabling a greatly shortened design-build-test cycle better matched to the urgency of a pandemic. The workflow combines a cell-free DNA assembly step utilizing Gibson assembly followed by PCR to generate linear expression templates that are used to drive cell-free protein synthesis (CFPS). The developed workflow allows us to translate synthetic DNA to purified protein in as little as 6 hours, is easily scaled

to high-throughput formats (e.g., 96- or 384-well plates), and is amenable to automated liquid handling. Furthermore, we coupled this cell-free workflow to an AlphaLISA™ protein-protein interaction (PPI) competition assay to enable comparison of dissociation rates of the designed proteins against either the monomeric RBD or the trimeric hexapro SARS-CoV-2-S-glycoprotein (S6P). Because multivalency largely only impacts the dissociation rate constant of the interaction, we reasoned that an in-solution off-rate screen would enable us to distinguish mono- from multi-valent binding. The resulting workflow can evaluate hundreds of candidate multivalent proteins per week.

Design and validation of multivalent binders

In the first strategy, we designed self-assembling trimeric versions of the M1, M2, and M3 miniproteins geometrically matched to the three RBDs in the spike trimer (hereafter referred to as H[binding domain #]-[homotrimer#]; for example, H1-1 represents a homotrimer of M1 with homotrimerization domain 1, Table 11). We designed, expressed, and evaluated more than one hundred different proteins containing various homotrimerization domains and linker lengths using our cell-free expression and multivalency screen workflow. We identified versions of each homotrimer that showed slow dissociation rates potentially indicating multivalent binding (Fig.14).

In the second strategy, we generated two- and three-domain fusions of the M1, M2 and M3 binding domains separated by flexible linkers (hereafter referred to as F[binding domain #s]-[linker]; for example, F231-P12 represents a fusion of M2 to M3 to M1 all separated by a PAS12 linker, Table 11). We evaluated a range of linker lengths chosen to span the distances between the termini of the domains when bound to the "open" and "closed" states of the RBD. We again expressed and evaluated more than one hundred different designs varying binding domain connectivity and linker length to optimize multivalency. Several identified two- and three-domain fusions show slow dissociation rates comparable to the homo-trimeric constructs described above (Fig.14).

The best candidates from each strategy showed little to no dissociation after 14 days of with competitor, with further measurements being limited by the stability of S6P. From these data we estimate the complex has a dissociation rate constant of slower than $1x10^{-7}$ s^{-1}. To our knowledge, these are the slowest measured dissociation rate constant for a synthetic protein-protein interactions ever reported.

We next used single particle cryo-electron microscopy (cryo-EM) to characterize the complex between S6P and the top candidate minibinders constructs (Fig. 15). The Cryo-EM

structures of the H2-1, F31-G10, and the F231-P24 constructs were determined at resolutions of 2.6, 4.5, and 3.9 Å respectively. H2-1 was found to simultaneously engage all three RBDs, causing all three RBDs to adopt the open state. The design model accurately closely matches the observed structure. F31-G10 bound to two RBDs, both appearing to adopt the open conformation upon binding. The structure indicates this linker length enabled simultaneous binding of two RBDs in their native state. The third free RBD adopted either the open or closed conformation in the structure. F231-P24 bound to three RBDs, with M1 binding a closed conformation RBD and M2 and M3 binding to open conformation RBDs. This suggests the linker length is sufficiently long enough to enable all three binding domains to simultaneously engage all three RBDs without significant distortion of the native state. In both F31-G10 and F231-P24 the maps are highly suggestive of multivalent binding, though the flexible linkers yield no density in the EM map to confirm linkage of the domains.

Multivalent minibinders neutralize widely circulating SARS-CoV-2 variants

We next sought to determine ability of the multivalent constructs to neutralize SARS-CoV-2 variants. We screened the off rate of the best multivalent minibinders against a panel of mutant spike proteins (Fig. 16). The homotrimers showed the most mutational resistance, with the H2 homotrimers showing little dissociation after 24 hours against any of the mutant spikes. The two-domain fusions showed little increased resilience to the tested point mutants. The three-domain fusions showed considerably more consistent binding to the tested point mutants, though some still impacted binding.

We additionally evaluated the potency of these proteins via neutralization assays against both a SARS-CoV-2 HIV pseudovirus in addition to authentic SARS-CoV-2 isolates (Fig. 16). The H2-0 and H2-1 homotrimers consistently performed the best across all constructs tested, with IC_{50}s in the low pM range. The three-domain fusions also performed well, with IC_{50}s in the sub nM range for all tested variants. The greater neutralization breadth of the H2 homotrimers likely reflects the closer mimicking if the ACE2 binding site by the M2 monomer, a unique advantage enabled by protein design.

Multivalent minibinders resist viral escape

In addition to evaluating the top candidate's ability to neutralize currently circulating SARS-CoV-2 mutants, we also tested the ability of the inhibitors to resist escape viral escape (Fig. 17). To do this, plaque assays were performed with a VSV-SARS-CoV-2 chimera virus were replicated on Vero E6 cells. To select mutants that were resistant to the inhibitor, the

inhibitor was included in the overlay to halt replication of non-resistant viruses. In positive control neutralizing antibody (2B04), multiple escape mutants were selected per plate. For both F231-P12 and H2-1 no escape mutants were isolated in 35 replicate wells of each inhibitor.

H2-0 provides prophylactic protection in human ACE2-expressing transgenic mice

To determine the ability of our multivalent minibinders to protect in an in vivo model, we evaluated them as a pre-exposure prophylactic treatment in human ACE2-expressing transgenic mice (Fig. 17). A single 50 μg dose of H2-0 was administered intranasally (i.n.) one day prior to inoculation with 10^3 focus forming units of SARS-CoV-2 Variants B.1.1.7, B1.351, B.1.1.24. In all cases, i.n. administration of H2-0 protected the mice against SARS-CoV-2-induced weight loss. At 6 days post infection viral burden was determined via RT-qPCR in a variety in tissues. Notably, viral loads in the lungs were reduced in all cases. These results indicate that H2-0 given via i.n. administration can provide prophylactic protection against SARS-CoV-2 infection in a relevant mouse model.

Conclusions

We anticipate that the cell-free protein expression and evaluation workflow will find utility in many different applications where the evaluation of individual protein variants is the limiting process step. In addition, our developed multivalency screen will accelerate the ability of researchers to develop multivalent protein therapeutics.

The designed protein constructs could have a number of advantages over monoclonal antibodies for preventing and treating COVID-19 infection. 1) direct administration into respiratory system, 2) low cost of goods and amenability to very large-scale production, 3) high stability and lack of need for cold chain, and 4) very broad resistance to escape mutants in single compounds. More generally, designed high affinity multivalent minibinders could provide a powerful platform for combating viral pandemics.

We claim

1. A polypeptide comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101, wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

2. The polypeptide of claim 1, wherein amino acid substitutions relative to the reference polypeptide amino acid sequence are selected from the exemplary amino acid substitutions provided in Table 1.

3. The polypeptide of claim 1 or 2, wherein interface residues are identical to those in the reference polypeptide or are conservatively substituted relative to interface residues in the reference polypeptide.

4. The polypeptide of any one of claims 1-3, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10, 13-17, 19-21, 33-34, and 100-101.

5. The polypeptide of any one of claims 1-4, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:1-10 and 102-136.

6. The polypeptide of claim 5, wherein the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:1 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or all 18 residues selected from the group consisting of 2, 4, 5, 14, 15, 17, 18, 27, 28, 32, 37, 38, 39, 41, 42, 49, 52, and 55.

7. The polypeptide of claim 6, wherein the substitutions are selected from the substitutions listed in Table 4, either individually or in combinations in a given row.

8. The polypeptide of any one of claims 1-4, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

9. The polypeptide of claim 8, wherein the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:13 at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or all 20 residues selected from the group consisting 2, 6, 8, 9, 13, 14, 19, 22, 25, 26, 28, 29, 34, 35, 37, 40, 43, 45, 49, and 62.

10. The polypeptide of claim 6, wherein the substitutions are selected from the substitutions listed in Table 6, either individually or in combinations in a given row.

11. The polypeptide of any one of claims 1-4, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:33-34 and 100-101 and 164.

12. The polypeptide of claim 11, wherein the polypeptide comprises an amino acid substitution relative to the amino acid sequence of SEQ ID NO:101 at or both residues selected from the group consisting 63 and 75.

13. The polypeptide of claim 12, wherein the substitutions comprise R63A and/or K75T.

14. The polypeptide of any one of claims 1-13, further comprising one or more added cysteine residues at the N-terminus and/or C-terminus.

15. The polypeptide of any one of claims 1-14, comprising an N-linked glycosylation site (i.e.: NX(S/T), where X is any amino acid).

16. The polypeptide of any one of claims 1-15, comprising two or more copies of the amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-101.

17. The polypeptide of claim 16, wherein the two or more copies of the polypeptide are all identical.

18. The polypeptide of claim 16, wherein the two or more copies of the polypeptide are not all identical.

19. The polypeptide of any one of claims 16-18, wherein the two or more copies of the polypeptide are separated by amino acid linker sequences.

20. The polypeptide of claim 9, wherein amino acid linker sequences comprise Gly-Ser rich (at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% Gly-Ser residues) amino acid linkers.

21. The polypeptide of claim 20, wherein the Gly-Ser rich linkers comprise an amino acid sequence selected from the group consisting of GG and SEQ ID NOs:35-46 and 165-171

22. The polypeptide of claim 19, wherein amino acid linker sequences comprise Pro-rich (at least 15%, 20%, 25%, or greater Pro residues) amino acid linkers.

23. The polypeptide of claim 22, wherein the Pro-rich amino acid linkers comprise an amino acid sequence selected from the group consisting of SEQ ID NOs:97-98 and 172-176.

24. The polypeptide of claim 19, wherein the amino acid linker comprises the amino acid sequence selected from the group consisting of SEQ ID NOS:99 and 177-178.

25. The polypeptide of any one of claims 19-24, wherein the amino acid linkers are independently between 2-100 amino acids in length.

26. The polypeptide of any one of claims 16-25, wherein the polypeptide comprises the formula Z1-Z2-Z3, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the

amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Z2 comprises an optional amino acid linker; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164;

Wherein Z1 and Z3 may be identical or different.

27. The polypeptide of claim 26, wherein Z1 and Z3 are identical.

28. The polypeptide of claim 26 wherein Z1 and Z3 are different.

29. The polypeptide of any one of claims 26-28, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

30. The polypeptide of any one of claims 26-28, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

31. The polypeptide of any one of claims 26-28, wherein:

Z1 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164; and

Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

32. The polypeptide of any one of claims 26-28, wherein:

one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

33. The polypeptide of any one of claims 26-28, wherein:

one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

34. The polypeptide of any one of claims 26-28, wherein:

one of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163; and

the other of Z1 and Z3 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-100, and 164.

35. The polypeptide of any one of claims 26-34, wherein the polypeptide comprises the formula B1-B2-Z1-Z2-Z3-B3-B4, wherein:

Z1, Z2, and Z3 are as defined in any one of claims 26-34;

B2 and B3 comprise optional amino acid linkers; and

one or both of B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164, wherein one of B1 and B4 may be absent.

36. The polypeptide of claim 35, wherein one of B1 and B4 is absent.

37. The polypeptide of claim 35, wherein B1 and B4 independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-17, 19-21, 23-34 and 100-164.

38. The polypeptide of claim 37, wherein B1 and B4 are identical.

39. The polypeptide of claim 37, wherein B1 and B4 are not identical.

40. The polypeptide of any one of claims 35-39, wherein B1 when present and B4 when present, are identical to one or both of Z1 and Z3, or wherein B1 when present and B4 when present, are not identical to either of Z1 and Z3.

41. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10, 13-17, 19-21, 33-34, and 100-164.

42. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136.

43. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163.

44. The polypeptide of any one of claims 35-40, wherein B1 when present, and B4 when present, independently comprise an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

45. The polypeptide of any one of claims 35-40, wherein both B1 and B4 are present, and wherein

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163;
- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 1-10 and 102-136, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164, or

- one of B1 and B4 comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 13-17, 19-21 and 137-163, and the other comprises an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 33-34, 100-101, and 164.

46. The polypeptide of any one of claims 1-45, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:47-60,193-355, and 454-588 and a genus selected from those recited in the right hand column of Table 8 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids and wherein any N-terminal methionine residues may be present or absent in the polypeptide, preferably wherein the polypeptide comprises and amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 454-588 and most preferably wherein the polypeptide comprises and amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS:693-701 wherein any N-terminal methionine residue may be absent or present, and wherein residues in parentheses may be present or absent (preferably absent) and are not considered in determining percent identity.

47. The polypeptide of any one of claims 1-46, further comprising an additional functional peptide domain.

48. The polypeptide of claim 47, wherein the additional functional peptide domain comprises a targeting domain, a detectable domain, a scaffold domain, a secretion signal, an Fc domain, or a further therapeutic peptide domain.

49. The polypeptide of claim 48, wherein the additional functional domain comprises an Fc domain, including but not limited to an Fc domain comprising an amino acid sequence comprising the amino acid sequence of SEQ ID NO:64.

50. The polypeptide of any one of claims 47-49, wherein the added functional domain comprises an oligomerization domain.

51. The polypeptide of claim 50, wherein the oligomerization domain comprises a homotrimerization domain.

52. The polypeptide of claim 50 or 51, wherein the oligomerization domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:179-189 and 589-594.

53. The polypeptide of any one of claims 50-52, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 356-453 and 595-692, and a genus selected from those recited in the right hand column of Table 9 wherein genus positions X1, X2, X3, and X4 may be present or absent, and when present may be any sequence of 1 or more amino acids and wherein any N-terminal methionine residues may be present or absent in the polypeptide,, preferably wherein the polypeptide comprises and amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 595-692.

54. The polypeptide of any one of claims 1-53, wherein the polypeptide is linked to a stabilization domain, including but not limited to polyethylene glycol (PEG), albumin, hydroxyethyl starch (HES), conformationally disordered polypeptide sequence composed of the amino acids Pro, Ala, and/or Ser ('PASylation'), and/or a mucin diffusivity polypeptide composed of amino acids Lys and Ala, with or without Glu.

55 The polypeptide of any one of claims 1-54, comprising an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOS: 65-96, wherein in embodiments where a secretion signal is present (MARAWIFFLLCLAGRALA; SEQ ID NO:63) it can be replaced with any other secretion signal.

56. The polypeptide of any one of claims 1-55, wherein the polypeptide binds to the SARS-CoV-2 Spike glycoprotein with an affinity of at least 10 nM, measured as described in the attached examples.

57. A nucleic acid encoding the polypeptide of any one of claims 1-56.

58. An expression vector comprising the nucleic acid of claim 57 operatively linked to a promoter.

59. A host cell comprising the polypeptide, the nucleic acid, and/or the expression vector of any preceding claim.

60. An oligomer of the polypeptide of any one of claims 1-56.

61. The oligomer of claim 60, wherein the oligomer comprises a trimer, including but not limited to a homotrimer.

62. A composition, comprising 2, 3, 4, or more copies of the polypeptide of any one of claims 1-56 attached to a support, including but not limited to a polypeptide particle support.

63. A pharmaceutical composition, comprising the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, and/or the composition of any of the preceding claims, and a pharmaceutically acceptable carrier.

64. A method for treating a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host

cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection.

65. The method of claim 64, wherein the SARS coronavirus comprises SARS-CoV-2.

66. A method for limiting development of a severe acute respiratory syndrome (SARS) coronavirus infection (including SARS-Co-V and SARS-CoV-2), comprising administering to a subject in need thereof an amount of the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition of any of the preceding claims, effective to treat the infection.

67. The method of claim 66, wherein the SARS coronavirus comprises SARS-CoV-2.

68. The method of any one of claims 64-67, wherein the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered intra-nasally.

69. The method of any one of claims 64-67, wherein the polypeptide, the nucleic acid, the expression vector, the host cell, the oligomer, the composition, and/or the pharmaceutical composition is administered systemically.

70. A method for designing polypeptides that bind to the receptor binding site (RBD) of SARS-Cov-2, wherein the methods comprise steps as described in any embodiment or combination of embodiments disclosed herein.

71. The method of claim 70, further comprising cell-free synthesis of the designed polypeptides, and evaluation of the synthesized polypeptides for SARS-Cov-2 RBD binding using any suitable technique.

72. A cell-free system comprising the polypeptide, the nucleic acid, and/or the expression vector of any preceding claim.

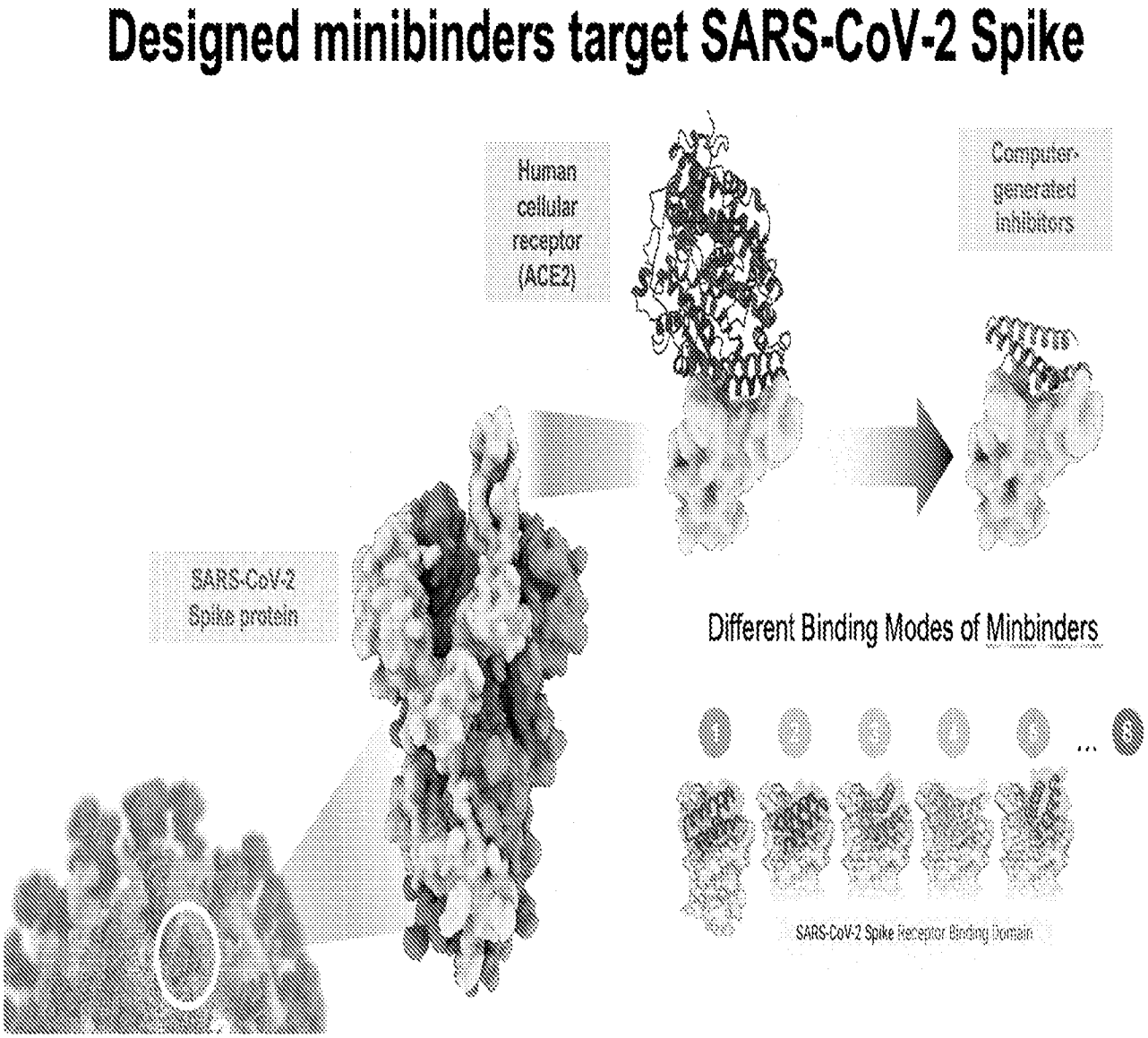
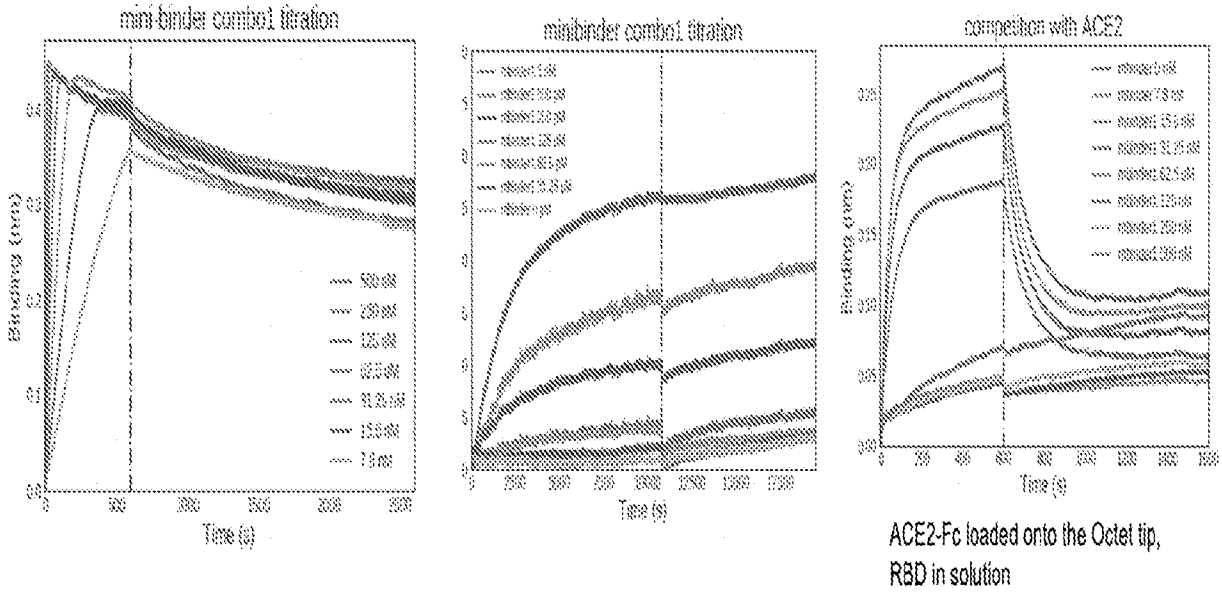

Designed minibinders target SARS-CoV-2 Spike
Human cellular receptor (ACE2)
Computer-generated inhibitors
SARS-CoV-2 Spike protein
Different Binding Modes of Minbinders
SARS-CoV-2 Spike Receptor Binding Domain

Figure 1

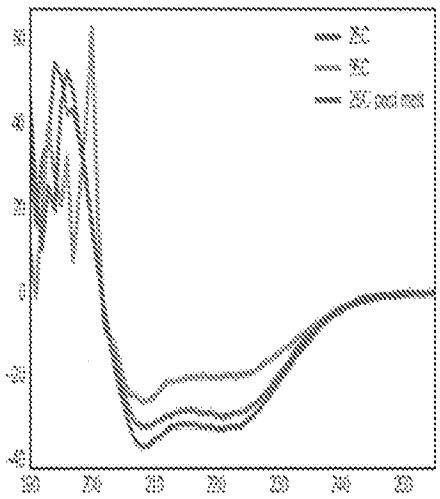
55 residue design binds RBD with ~300pM affinity and competes for binding with ACE2



Biolayer interferometry (BLI) data for combo 1 minibinder demonstrates ~300 pM affinity for Spike RBD and competes for binding to RBD by ACE-2.

Figure 2

55 residue Spike RBD minibinder has high thermal stability



Circular Dichroism (CD) spectrum for combo 1 minibinder demonstrates extreme heat stability up to 95C

Figure 3

Minibinders potently neutralize live coronavirus

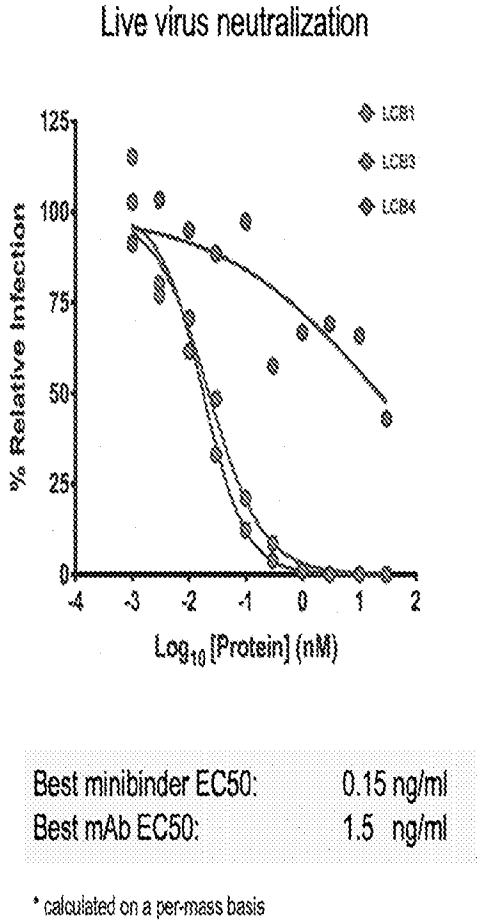
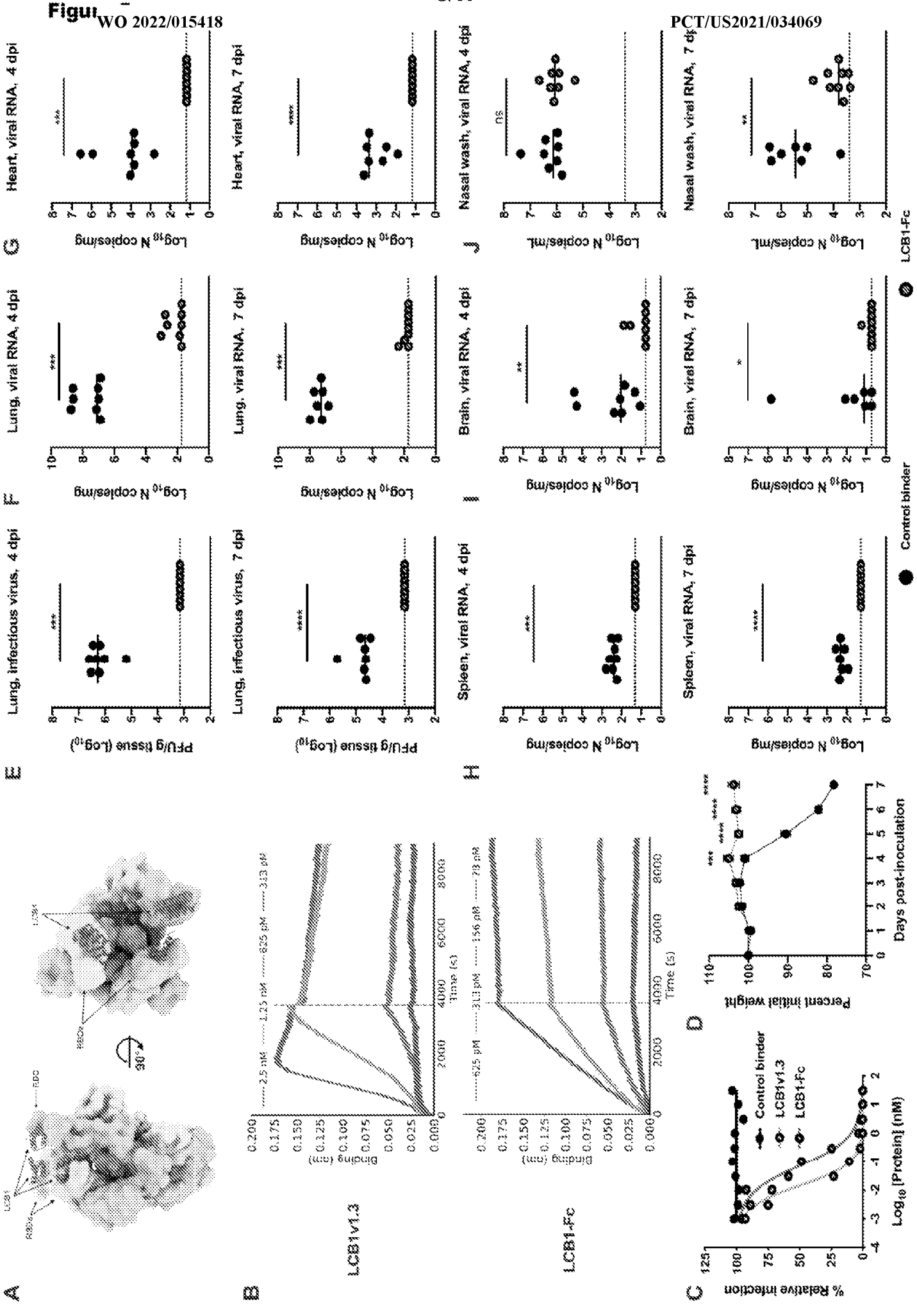
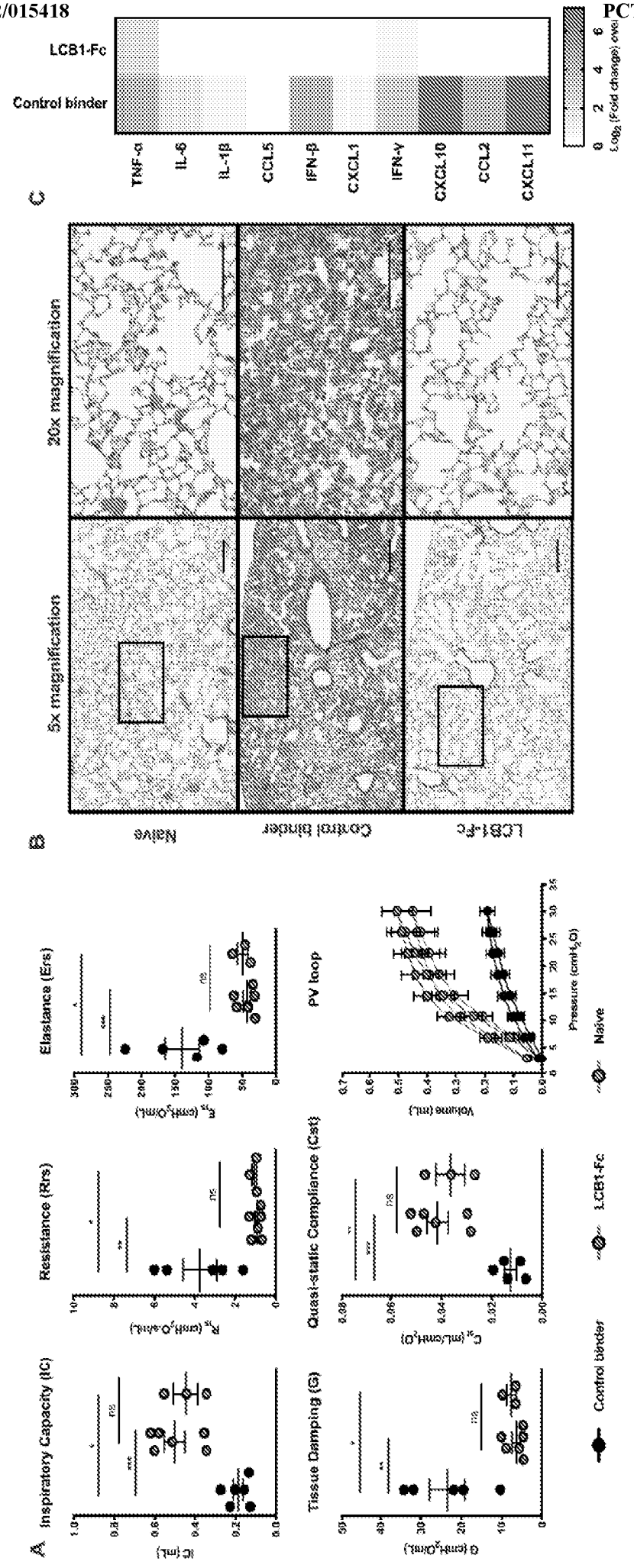
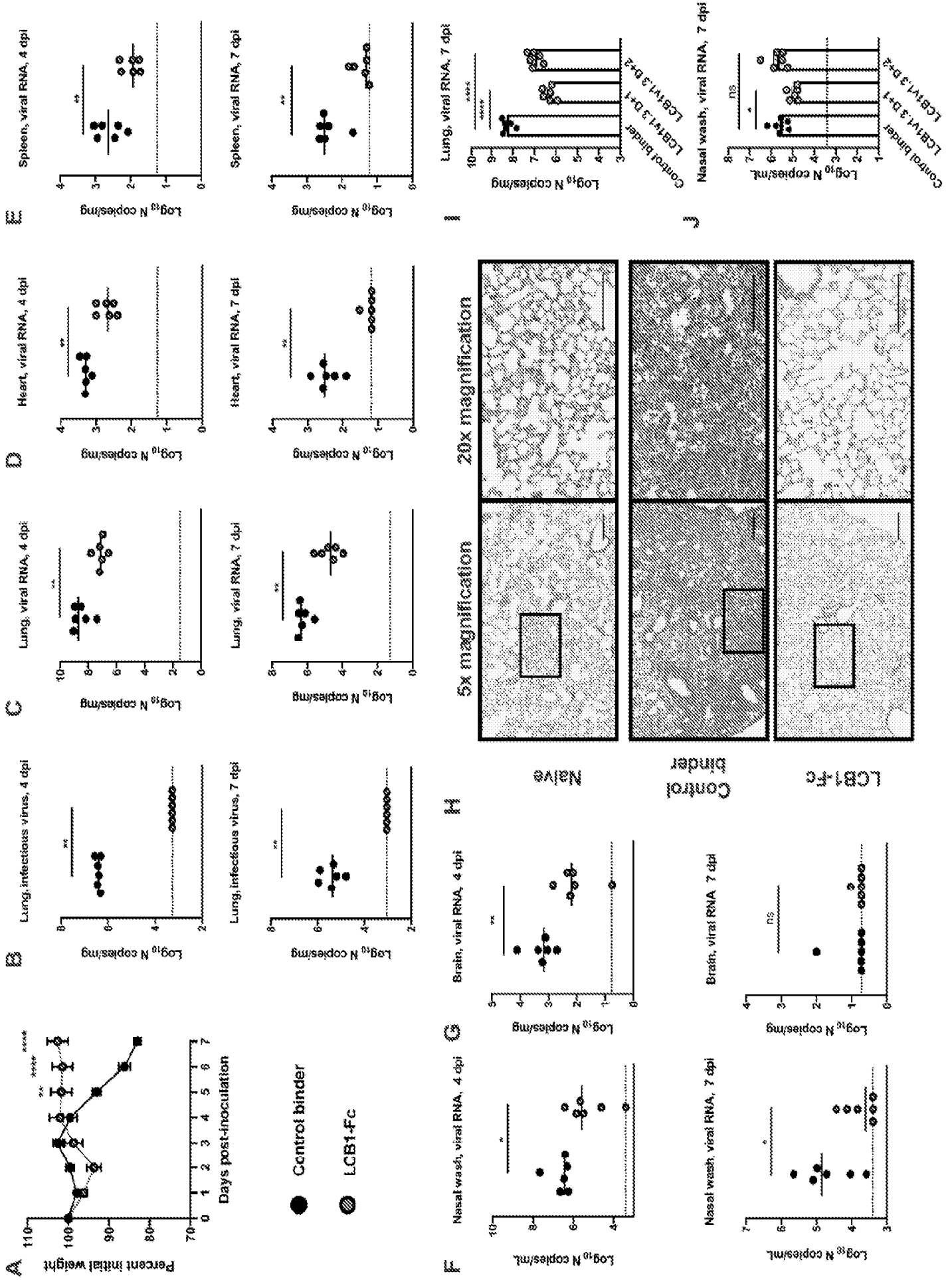


Figure 4

Figur


A
B
C
D
E
F
G
H
I
J
LCB1v1.3
LCB1-Fc
Control binder
% Relative infection
Log10 [Protein] (nM)
Percent initial weight
Days past-inoculation
Lung, infectious virus, 4 dpi
Lung, viral RNA, 4 dpi
Heart, viral RNA, 4 dpi
Spleen, viral RNA, 4 dpi
Brain, viral RNA, 4 dpi
Nasal wash, viral RNA, 4 dpi
Lung, infectious virus, 7 dpi
Lung, viral RNA, 7 dpi
Heart, viral RNA, 7 dpi
Spleen, viral RNA, 7 dpi
Brain, viral RNA, 7 dpi
Nasal wash, viral RNA, 7 dpi
PFU/g tissue (Log10)
Log10 N copies/mg
Log10 N copies/mL
Binding (nm)
Time (s)
ns
LCB1-Fc


C
LCB1-Fc
Control binder
TNF-α
IL-6
IL-1β
CCL5
IFN-β
CXCL1
IFN-γ
CXCL10
CCL2
CXCL11
Log2 (Fold change) over
B
5x magnification
20x magnification
Naive
Control binder
LCB1-Fc
A
Inspiratory Capacity (IC)
Tissue Damping (G)
Resistance (Rrs)
Quasi-static Compliance (Cst)
Elastance (Ers)
PV loop
Volume (mL)
Pressure (cmH2O)
Control binder
LCB1-Fc
Naive


A
Percent initial weight
Days post-inoculation
Control binder
LCB1-Fc
B
Lung, infectious virus, 4 dpi
Lung, infectious virus, 7 dpi
C
Lung, viral RNA, 4 dpi
Lung, viral RNA, 7 dpi
D
Heart, viral RNA, 4 dpi
Heart, viral RNA, 7 dpi
E
Spleen, viral RNA, 4 dpi
Spleen, viral RNA, 7 dpi
F
Nasal wash, viral RNA, 4 dpi
Nasal wash, viral RNA, 7 dpi
G
Brain, viral RNA, 4 dpi
Brain, viral RNA 7 dpi
H
5x magnification
20x magnification
Naive
Control binder
LCB1-Fc
I
Lung, viral RNA, 7 dpi
Control binder
LCB1v1.3 D+1
LCB1v1.3 D+2
J
Nasal wash, viral RNA, 7 dpi
Control binder
LCB1v1.3 D+1
LCB1v1.3 D+2

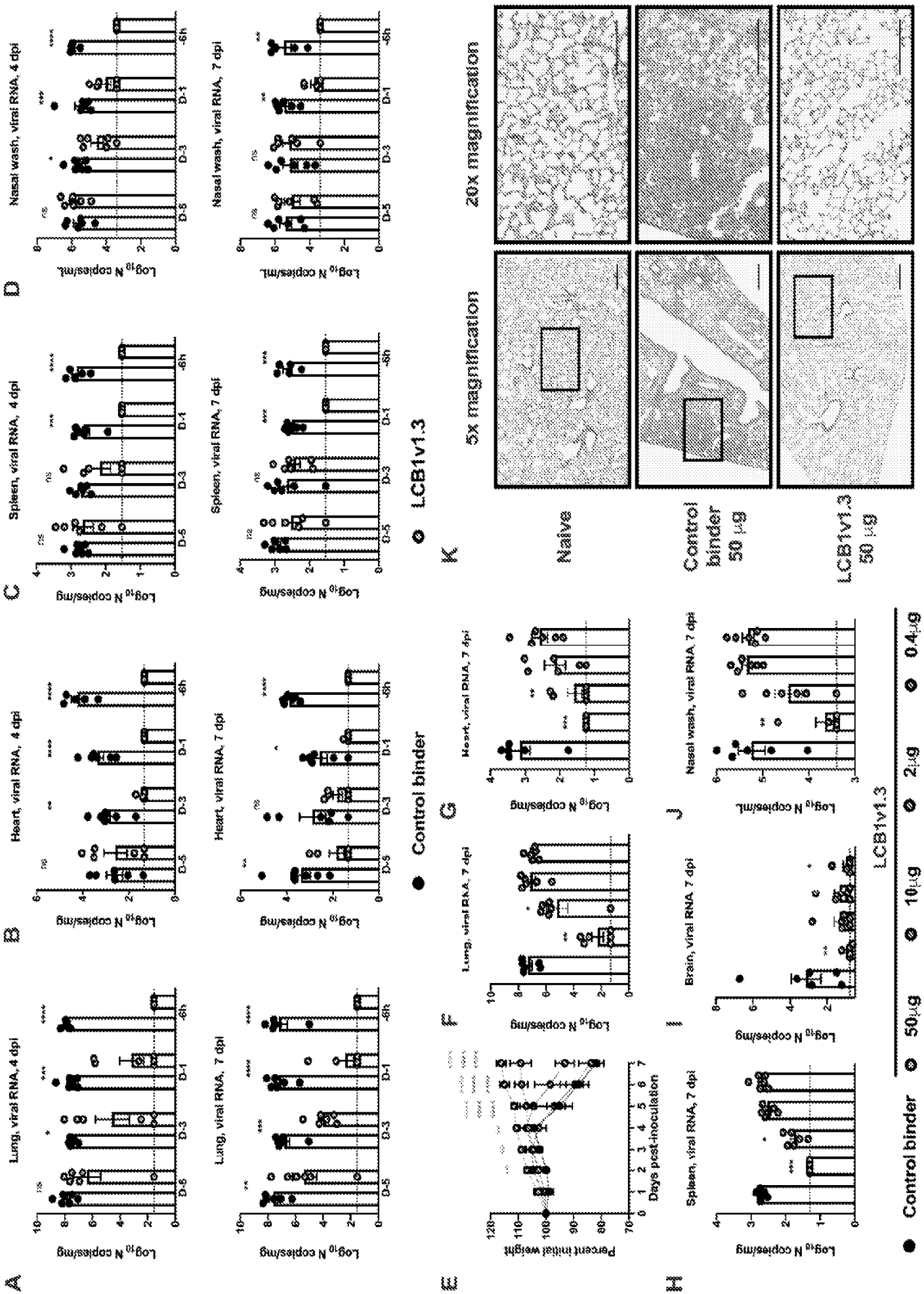

A
Lung, viral RNA, 4 dpi
Lung, viral RNA, 7 dpi
B
Heart, viral RNA, 4 dpi
Heart, viral RNA, 7 dpi
C
Spleen, viral RNA, 4 dpi
Spleen, viral RNA, 7 dpi
D
Nasal wash, viral RNA, 4 dpi
Nasal wash, viral RNA, 7 dpi
Log10 N copies/mg
Log10 N copies/mL
D-5
D-3
D-1
-6h
Control binder
LCB1v1.3
E
Percent initial weight
Days post-inoculation
F
Lung, viral RNA, 7 dpi
G
Heart, viral RNA, 7 dpi
H
Spleen, viral RNA, 7 dpi
I
Brain, viral RNA, 7 dpi
J
Nasal wash, viral RNA, 7 dpi
Control binder
50μg
10μg
2μg
0.4μg
LCB1v1.3
K
5x magnification
20x magnification
Naive
Control binder 50 μg
LCB1v1.3 50 μg

Figure 5

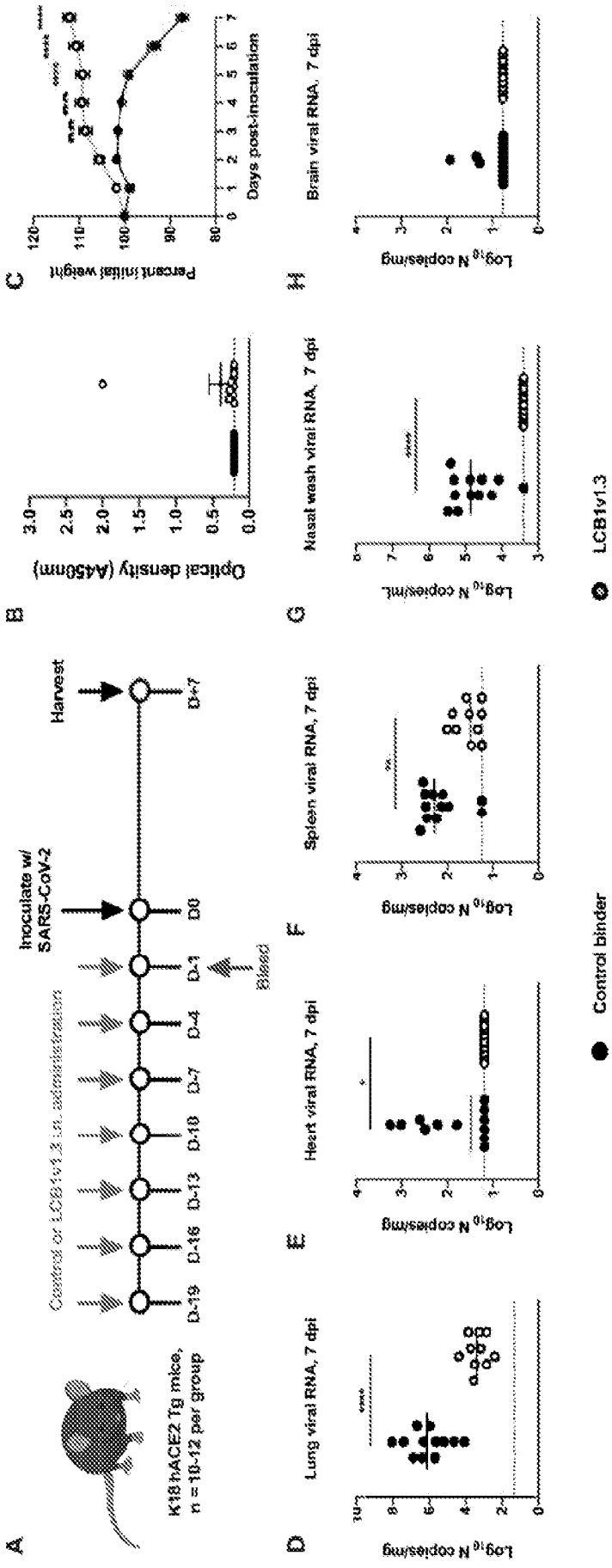

A
K18 hACE2 Tg mice, n = 10-12 per group
Control or LCB1v1.3 i.n. administration
D-19
D-16
D-13
D-10
D-7
D-4
D-1
D0
D+7
Inoculate w/ SARS-CoV-2
Harvest
Bleed
B
Optical density (A450nm)
C
Percent initial weight
Days post-inoculation
D
Lung viral RNA, 7 dpi
E
Heart viral RNA, 7 dpi
F
Spleen viral RNA, 7 dpi
G
Nasal wash viral RNA, 7 dpi
H
Brain viral RNA, 7 dpi
Log10 N copies/mg
Log10 N copies/mL
Control binder
LCB1v1.3

Figure 10

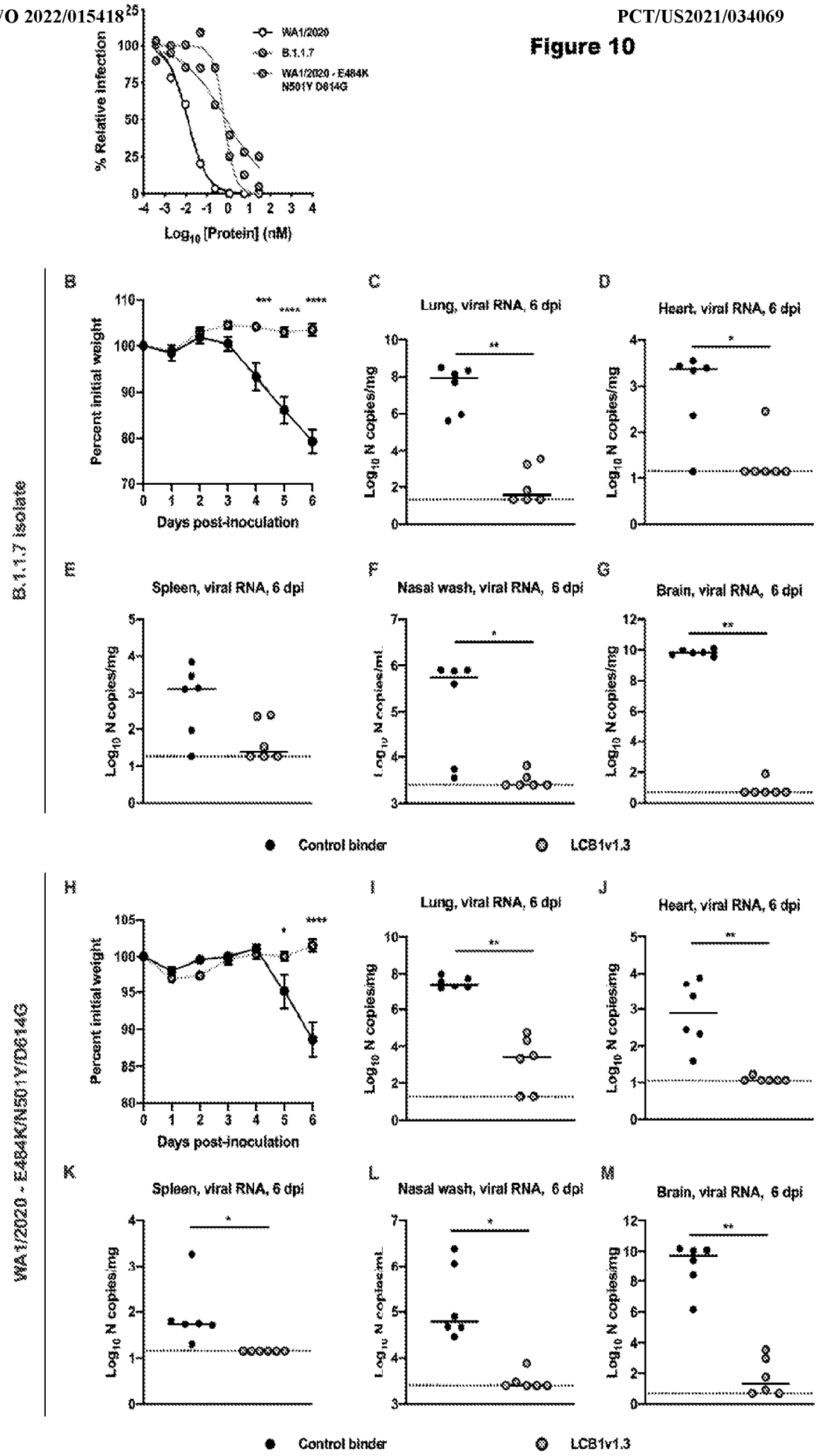

A
% Relative infection
WA1/2020
B.1.1.7
WA1/2020 + E484K N501Y D614G
Log10 [Protein] (nM)
B.1.1.7 isolate
B
Percent initial weight
Days post-inoculation
C
Lung, viral RNA, 6 dpi
Log10 N copies/mg
D
Heart, viral RNA, 6 dpi
Log10 N copies/mg
E
Spleen, viral RNA, 6 dpi
Log10 N copies/mg
F
Nasal wash, viral RNA, 6 dpi
Log10 N copies/mL
G
Brain, viral RNA, 6 dpi
Log10 N copies/mg
Control binder
LCB1v1.3
WA1/2020 + E484K/N501Y/D614G
H
Percent initial weight
Days post-inoculation
I
Lung, viral RNA, 6 dpi
Log10 N copies/mg
J
Heart, viral RNA, 6 dpi
Log10 N copies/mg
K
Spleen, viral RNA, 6 dpi
Log10 N copies/mg
L
Nasal wash, viral RNA, 6 dpi
Log10 N copies/mL
M
Brain, viral RNA, 6 dpi
Log10 N copies/mg
Control binder
LCB1v1.3

Figure 11

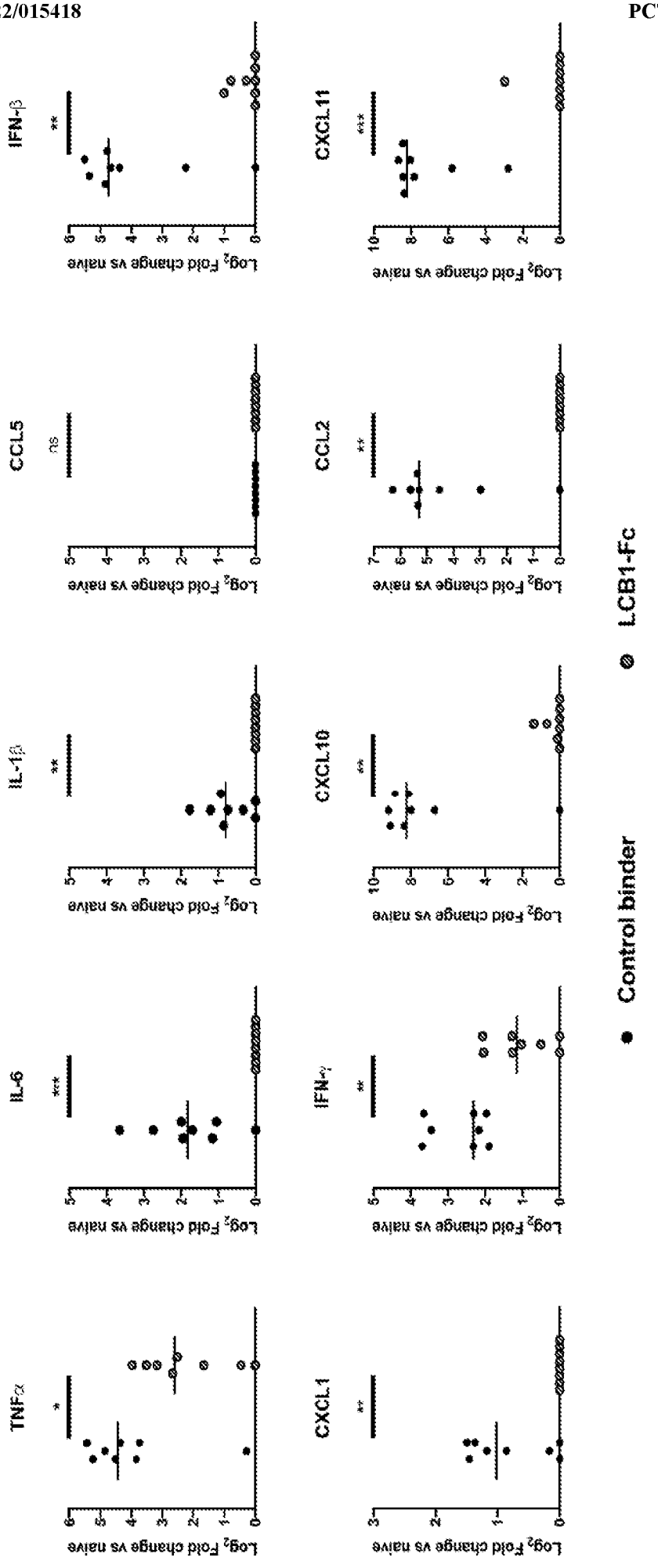
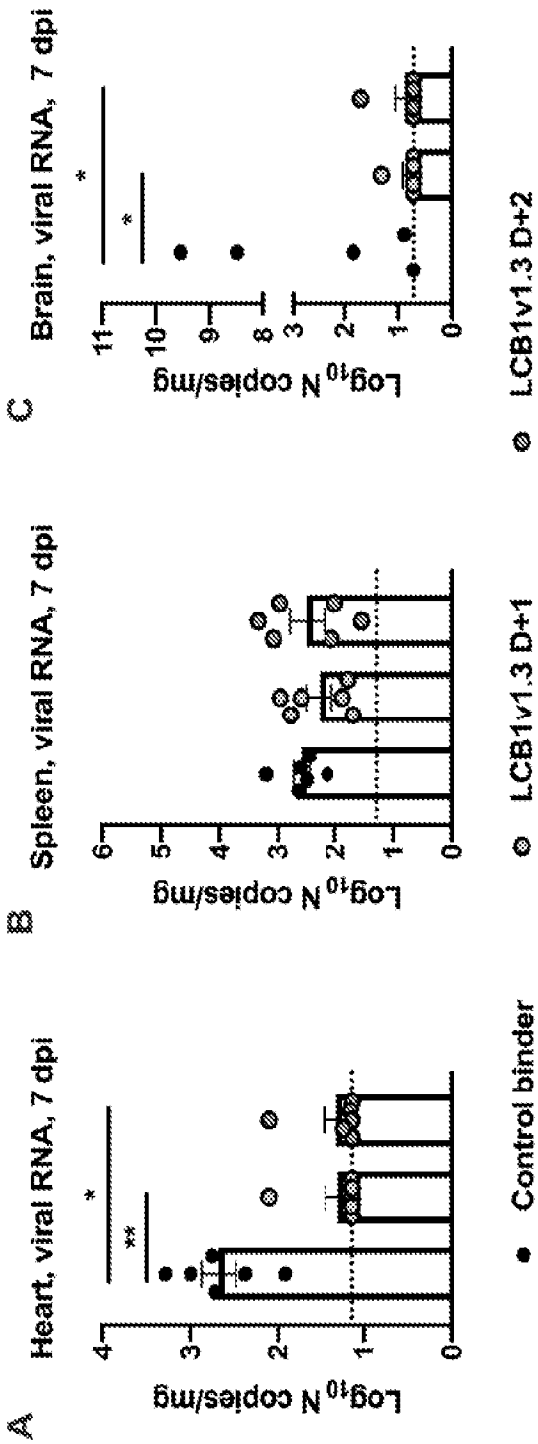
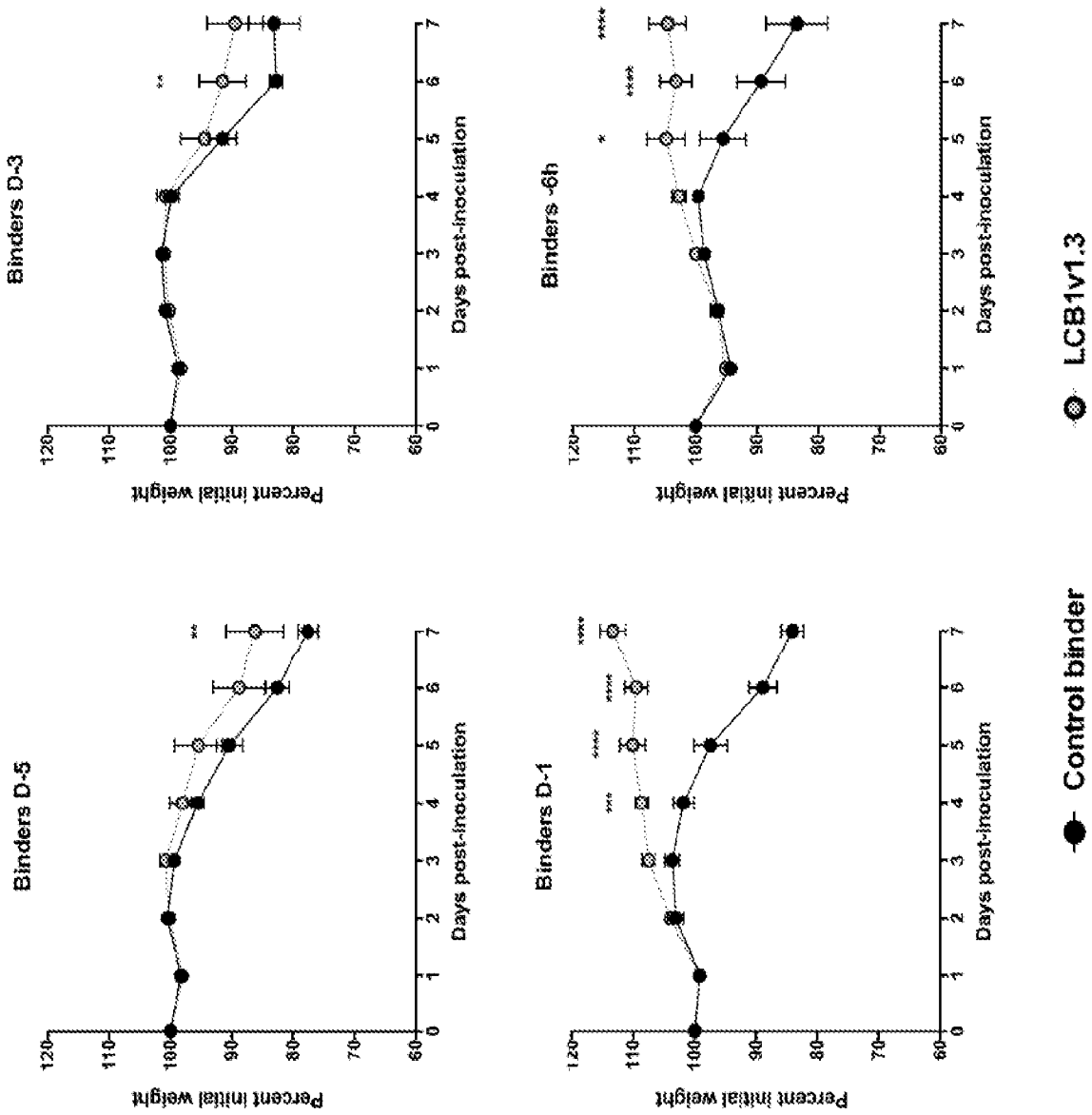

TNFα
IL-6
IL-1β
CCL5
IFN-β
CXCL1
IFNγ
CXCL10
CCL2
CXCL11
Log2 Fold change vs naive
Control binder
LCB1-Fc

Figure 12


A
Heart, viral RNA, 7 dpi
B
Spleen, viral RNA, 7 dpi
C
Brain, viral RNA, 7 dpi
Log10 N copies/mg
Control binder
LCB1v1.3 D+1
LCB1v1.3 D+2


Binders D-3
Binders -6h
Binders D-5
Binders D-1
Percent initial weight
Days post-inoculation
Control binder
LCB1v1.3

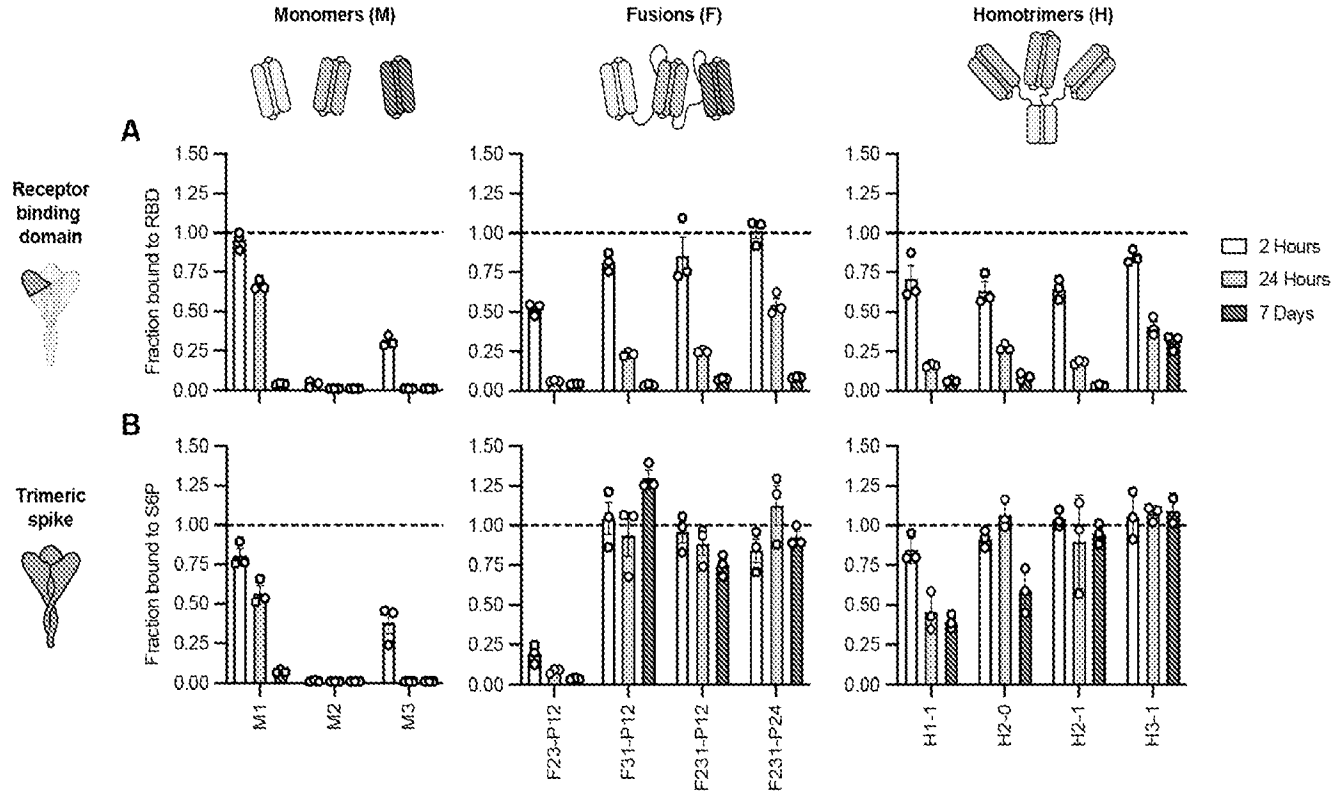

Monomers (M)
Fusions (F)
Homotrimers (H)
A
B
Receptor binding domain
Trimeric spike
Fraction bound to RBD
Fraction bound to S6P
1.50
1.25
1.00
0.75
0.50
0.25
0.00
2 Hours
24 Hours
7 Days
M1
M2
M3
F23-P12
F31-P12
F231-P12
F231-P24
H1-1
H2-0
H2-1
H3-1

Figure 14

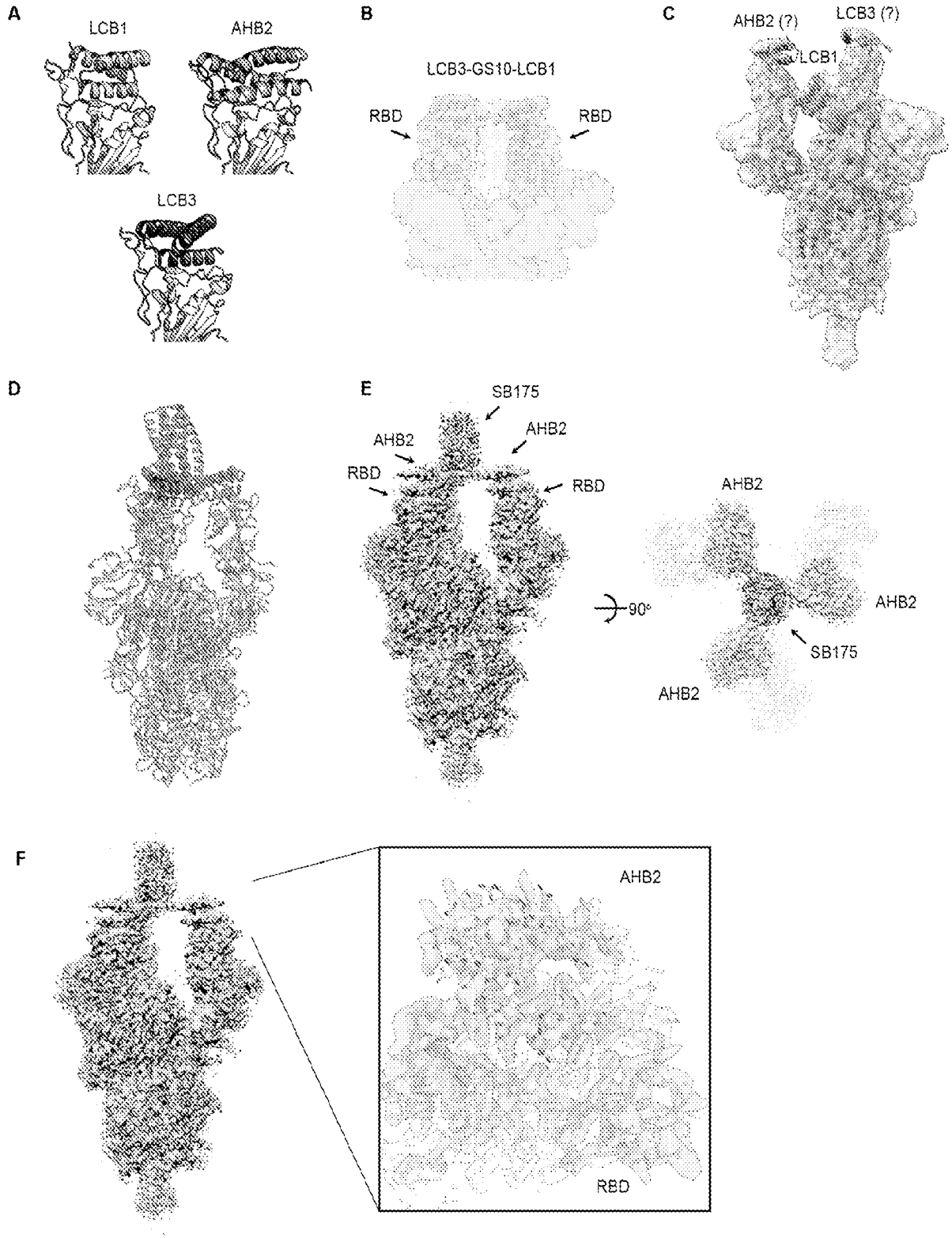
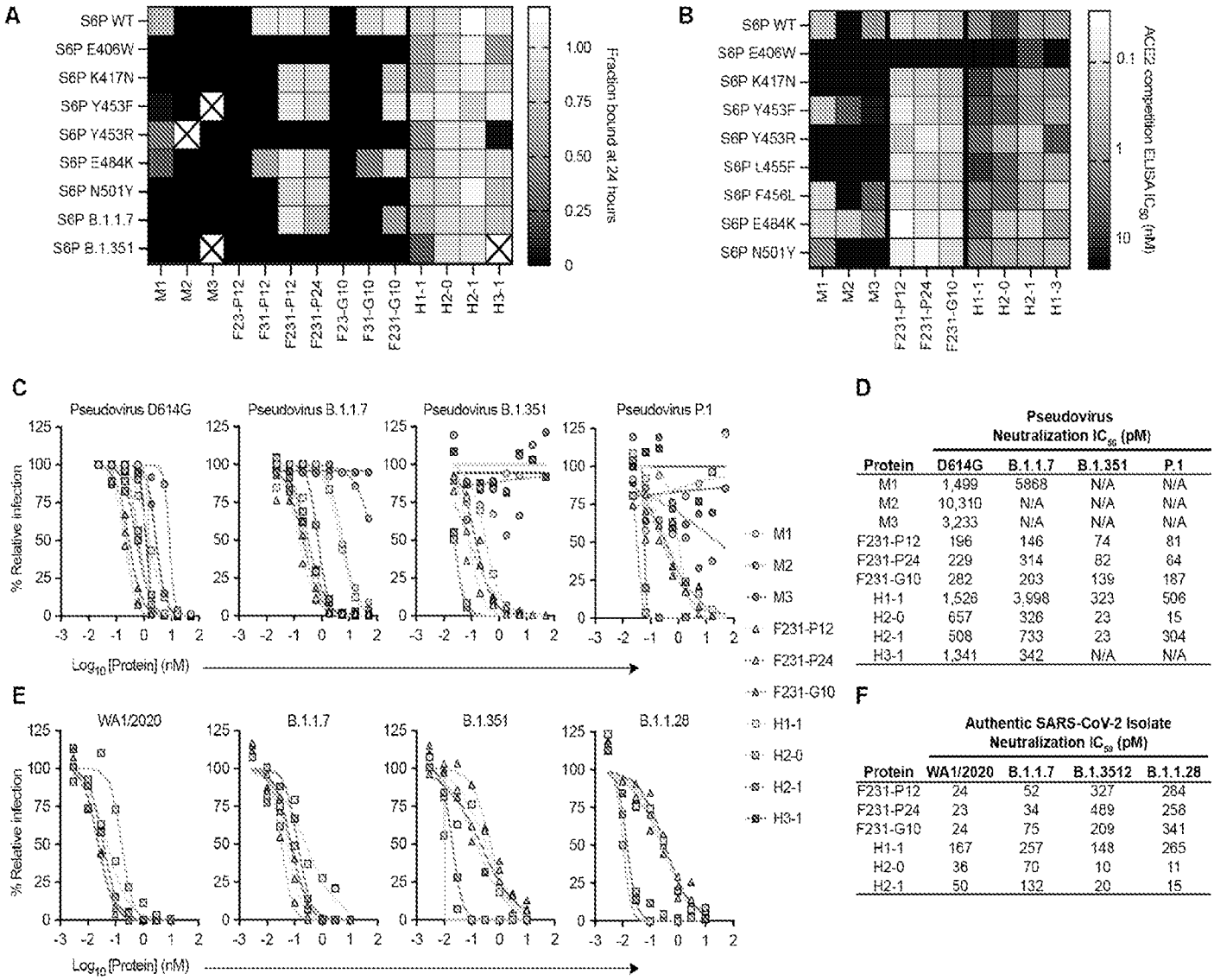

A
LCB1
AHB2
LCB3
B
LCB3-GS10-LCB1
RBD
RBD
C
AHB2 (?)
LCB3 (?)
LCB1
D
E
SB175
AHB2
AHB2
RBD
RBD
90°
AHB2
AHB2
SB175
AHB2
F
AHB2
RBD

Figure 15



D

	Pseudovirus Neutralization IC_{50} (pM)			
Protein	D614G	B.1.1.7	B.1.351	P.1
M1	1,499	5868	N/A	N/A
M2	10,310	N/A	N/A	N/A
M3	3,233	N/A	N/A	N/A
F231-P12	196	146	74	81
F231-P24	229	314	82	84
F231-G10	282	203	139	187
H1-1	1,526	3,998	323	506
H2-0	657	326	23	15
H2-1	508	733	23	304
H3-1	1,341	342	N/A	N/A

F

	Authentic SARS-CoV-2 Isolate Neutralization IC_{50} (pM)			
Protein	WA1/2020	B.1.1.7	B.1.3512	B.1.1.28
F231-P12	24	52	327	284
F231-P24	23	34	489	258
F231-G10	24	75	209	341
H1-1	167	257	148	265
H2-0	36	70	10	11
H2-1	50	132	20	15

Figure 16

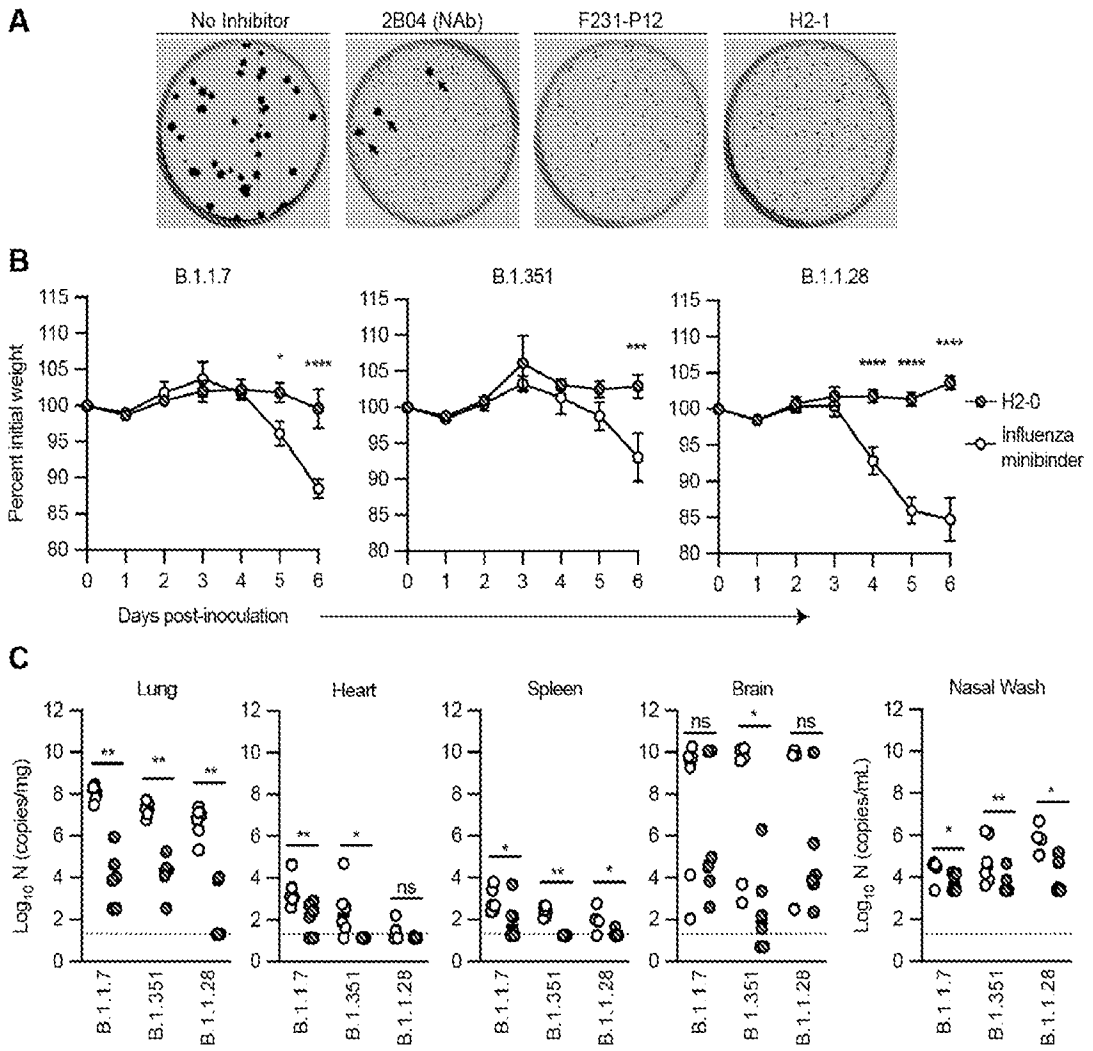

A
No Inhibitor
2B04 (NAb)
F231-P12
H2-1
B
B.1.1.7
B.1.351
B.1.1.28
Percent initial weight
Days post-inoculation
H2-0
Influenza minibinder
C
Lung
Heart
Spleen
Brain
Nasal Wash
Log10 N (copies/mg)
Log10 N (copies/mL)
ns

Figure 17

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2021/034069

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61P31/14 C07K14/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61P C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, Sequence Search, EMBASE, FSTA, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	G. Zhang ET AL: "The first-in-class peptide binder to the SARS-CoV-2 spike protein", bioRxiv, 30 March 2020 (2020-03-30), XP055759391, DOI: 10.1101/2020.03.19.999318 Retrieved from the Internet: URL:https://www.biorxiv.org/content/10.1101/2020.03.19.999318v1.full.pdf [retrieved on 2020-12-11] abstract; Fig. 1, 2 ----- -/--	1-7,10, 14-29, 32,33, 35-42, 45-69,72

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
2 September 2021	15/11/2021

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Behrens, Joyce

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Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2021/034069

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	DATABASE CAS [Online] 29 April 2021 (2021-04-29), Anonymous: "Hit details for CAS:2021_512700_2639510022_1", XP055836719, retrieved from EBI accession no. CAS:2021_512700_2639510022_1 Database accession no. 2021:512700-2639510-02-2 abstract -----	1-5
A	Lupala Cecylia S. ET AL: "Computational analysis on the ACE2-derived peptides for neutralizing the ACE2 binding to the spike protein of SARS-CoV-2", bioRxiv, 4 May 2020 (2020-05-04), pages 1-27, XP055799136, DOI: 10.1101/2020.05.03.075473 Retrieved from the Internet: URL:https://www.biorxiv.org/content/10.1101/2020.05.03.075473v1.full.pdf [retrieved on 2021-04-27] abstract; Fig. 2 -----	1-7,10, 14-29, 32,33, 35-42, 45-69,72
A	Walter Justin D ET AL: "Sybodies targeting the SARS-CoV-2 receptor-binding domain", bioRxiv, 16 May 2020 (2020-05-16), XP055795467, DOI: 10.1101/2020.04.16.045419 Retrieved from the Internet: URL:https://doi.org/10.1101/2020.04.16.045419 [retrieved on 2021-04-15] abstract; Table 2; Fig. 7, 8 -----	1-7,10, 14-29, 32,33, 35-42, 45-69,72
A	WO 02/098448 A1 (HUMAN GENOME SCIENCES INC [US]; PARRY TOM J [US] ET AL.) 12 December 2002 (2002-12-12) par 5, 50 -----	1-7,10, 14-29, 32,33, 35-42, 45-69,72

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2021/034069

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. [X] forming part of the international application as filed:

      [X] in the form of an Annex C/ST.25 text file.

      [ ] on paper or in the form of an image file.

   b. [ ] furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. [ ] furnished subsequent to the international filing date for the purposes of international search only:

      [ ] in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      [ ] on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. [ ] In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2021/034069

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

5-7, 10, 29, 42(completely); 1-4, 14-28, 32, 33, 35-41, 45-69
72(partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 5-7, 10, 29, 42(completely); 1-4, 14-28, 32, 33, 35-41, 45-69, 72(partially)

   A polypeptide comprising an amino acid sequence of SEQ ID NO: 1-10 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

   ---

2. claims: 1-4, 14-28, 35-41, 46-69, 72(all partially)

   A polypeptide comprising an amino acid sequence of SEQ ID NO: 11, 12 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

   ---

3. claims: 8, 9, 30, 43(completely); 1-4, 14-28, 32, 34-41, 45-69, 72(partially)

   A polypeptide comprising an amino acid sequence of SEQ ID NO: 13-17, 19-21 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

   ---

4. claims: 1-4, 14-28, 35-41, 46-69, 72(all partially)

   A polypeptide comprising an amino acid sequence of SEQ ID NO: 23, 24 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

   ---

5. claims: 1-4, 14-28, 35-41, 46-69, 72(all partially)

   A polypeptide comprising an amino acid sequence of SEQ ID NO: 25, 26 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

   ---

6. claims: 1-4, 14-28, 35-41, 46-69, 72(all partially)

   A polypeptide comprising an amino acid sequence of SEQ ID NO: 27, 28 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

   ---

7. claims: 1-4, 14-28, 35-41, 46-69, 72(all partially)

A polypeptide comprising an amino acid sequence of SEQ ID NO: 29, 30 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

---

8. claims: 1-4, 14-28, 35-41, 46-69, 72(all partially)

A polypeptide comprising an amino acid sequence of SEQ ID NO: 31, 32 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

---

9. claims: 1-4, 11, 14-28, 31, 33-41, 44-69, 72(all partially)

A polypeptide comprising an amino acid sequence of SEQ ID NO: 33, 34 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

---

10. claims: 12, 13(completely); 1-4, 11, 14-28, 31, 33-41, 44-69, 72(partially)

A polypeptide comprising an amino acid sequence of SEQ ID NO: 100, 101 (or a variant of thereof), wherein the polypeptide binds to SARS-CoV-2 Spike glycoprotein receptor binding domain (RBD).

---

11. claims: 70, 71(completely); 72(partially)

A method for designing polypeptides that bind to the receptor binding site (RBD) of SARS-Cov-2.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2021/034069

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 02098448 A1	12-12-2002	US 2003138894 A1	24-07-2003
		WO 02098448 A1	12-12-2002