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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
25 May 2023 (25.05.2023)

WIPO | PCT

(10) International Publication Number
WO 2023/091614 A3

(51) International Patent Classification:
A61K 39/395 (2006.01) *C07K 7/06* (2006.01)
A61K 38/08 (2019.01) *C07K 14/47* (2006.01)
A61K 38/17 (2006.01) *C07K 16/22* (2006.01)

(21) International Application Number:
PCT/US2022/050322

(22) International Filing Date:
17 November 2022 (17.11.2022)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

63/280,840	18 November 2021 (18.11.2021)	US
63/286,522	06 December 2021 (06.12.2021)	US
63/374,497	02 September 2022 (02.09.2022)	US
63/379,634	14 October 2022 (14.10.2022)	US

(71) Applicant: **TWIST BIOSCIENCE CORPORATION** [US/US]; 681 Gateway Boulevard, South San Francisco, California 94080 (US).

(72) Inventors: **SATO, Aaron**; 681 Gateway Boulevard, South San Francisco, California 94080 (US). **YUAN, Tom**; 681 Gateway Boulevard, South San Francisco, California 94080 (US). **WANG, Linya**; 681 Gateway Boulevard, South San Francisco, California 94080 (US). **AXELROD, Fumiko**; 681 Gateway Boulevard, South San Francisco, California 94080 (US).

(74) Agent: **SCARR, Rebecca, B.**; McNeill Baur PLLC, 125 Cambridge Park Drive, Suite 301, Cambridge, MA 02140 (US).

(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, CV, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IQ, IR, IS, IT, JM, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, 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, CV, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SC, 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,

(54) Title: DICKKOPF-1 VARIANT ANTIBODIES AND METHODS OF USE

(57) Abstract: Provided herein are methods and compositions relating to libraries of optimized antibodies having nucleic acids encoding for an antibody comprising modified sequences. Libraries described herein comprise nucleic acids encoding Dickkopf WNT signaling pathway inhibitor 1 (DKK1) antibodies. Further described herein are protein libraries generated when the nucleic acid libraries are translated. Further described herein are cell libraries expressing variegated nucleic acid libraries described herein.

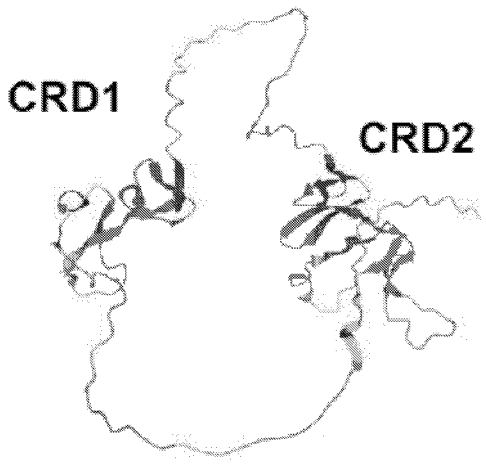


FIG. 17B

WO 2023/091614 A3

[Continued on next page]

LU, LV, MC, ME, 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).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

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))*

(88) Date of publication of the international search report:
02 November 2023 (02.11.2023)

DICKKOPF-1 VARIANT ANTIBODIES AND METHODS OF USE

CROSS REFERENCE

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/280,840, filed on November 18, 2021, U.S. Provisional Patent Application No. 63/286,522, filed on December 6, 2021, U.S. Provisional Patent Application No. 63/374,497, filed on September 2, 2022, and U.S. Provisional Patent Application No. 63/379,634, filed on October 14, 2022, which is each incorporated by reference in its entirety.

BACKGROUND

[0002] Dickkopf WNT signaling pathway inhibitor 1 (also known as dickkopf-1 or DKK1) is a secreted glycoprotein characterized by two cysteine-rich domains that mediate protein-protein interactions. DKK1 is involved in embryonic development of the heart, head, and forelimbs through its inhibition of the WNT signaling pathway. In adults, elevated expression of this gene has been observed in numerous human cancers, and this protein may promote proliferation, invasion, and growth in cancer cell lines. Given the role of DKK1 in various diseases and disorders, there is a need for improved therapeutics.

INCORPORATION BY REFERENCE

[0003] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF SUMMARY

[0004] Provided herein are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH), wherein the VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-98 or 919-1332; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 99-196 or 1333-1746; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 197-294 or 1747-2160. Further provided herein are antibodies or antibody fragments, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab′)2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a

fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. Further provided herein are antibodies or antibody fragments, wherein the antibody is a single domain antibody. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to DKK1.

[0005] Provided herein are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258, and wherein the VL comprises at least 90% sequence identity to any one of SEQ ID NOs 713-918. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to a spike glycoprotein. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to a receptor binding domain of the spike glycoprotein. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab′)2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. Further provided herein are antibodies or antibody fragments, wherein the antibody is a single domain antibody.

[0006] Provided herein are nucleic acid compositions comprising: a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising complementarity determining regions CDRH1, CDRH2, and CDRH3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-98 or 919-1332; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 99-196 or 1333-1746; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 197-294 or 1747-2160; and an excipient.

[0007] Provided herein are nucleic acid compositions comprising: a) a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258; and an excipient.

[0008] Provided herein are antibodies or antibody fragments comprising a variable domain, light chain region (VL), wherein the VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 2259-2464; (b) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 2465-2521; and (c) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 2522-2727. Further provided herein are antibodies or antibody fragments, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. Further provided herein are antibodies or antibody fragments, wherein the antibody is a single domain antibody. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to DKK1.

[0009] Provided herein are antibodies or antibody fragments comprising a variable domain, light chain region (VL) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 713-918. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to a spike glycoprotein. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment binds to a receptor binding domain of the spike glycoprotein. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM. Further provided herein are antibodies or antibody fragments, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab′)2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. Further provided herein are antibodies or antibody fragments, wherein the antibody is a single domain antibody.

[0010] Provided herein are nucleic acid compositions comprising: : a first nucleic acid encoding a variable domain, light chain region (VL) comprising complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 2259-2464; (b) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 2465-2521; and (c) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 2522-2727; and an excipient.

[0011] Provided herein are nucleic acid compositions comprising: a) a first nucleic acid encoding a variable domain, light chain region (VL) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 713-918; and an excipient.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0013] **Figure 1A** depicts a first schematic of an immunoglobulin.

[0014] **Figure 1B** depicts a second schematic of an immunoglobulin.

[0015] **Figure 2** depicts a schematic of a motif for placement in an immunoglobulin.

[0016] **Figure 3** presents a diagram of steps demonstrating an exemplary process workflow for gene synthesis as disclosed herein.

[0017] **Figure 4** illustrates an example of a computer system.

[0018] **Figure 5** is a block diagram illustrating an architecture of a computer system.

[0019] **Figure 6** is a diagram demonstrating a network configured to incorporate a plurality of computer systems, a plurality of cell phones and personal data assistants, and Network Attached Storage (NAS).

[0020] **Figure 7** is a block diagram of a multiprocessor computer system using a shared virtual address memory space.

[0021] **Figure 8A** depicts a schematic of an immunoglobulin comprising a VH domain attached to a VL domain using a linker.

[0022] **Figure 8B** depicts a schematic of a full-domain architecture of an immunoglobulin comprising a VH domain attached to a VL domain using a linker, a leader sequence, and pIII sequence.

[0023] **Figure 8C** depicts a schematic of four framework elements (FW1, FW2, FW3, FW4) and the variable 3 CDR (L1, L2, L3) elements for a VL or VH domain.

[0024] **Figure 9A** depicts long read NGS sequencing of the eluted phage pool for antibody pool A. The top portion of the figure shows the cluster enrichment number, the number of instances the antibody appears, plotted against the cluster rank, which lists the antibody rank order of the antibodies by size cluster. The bottom portion of the figure shows the parallel histogram showing the distribution of the HCDR3 lengths among the top 95 antibody clusters.

[0025] **Figure 9B** depicts long read NGS sequencing of the eluted phage pool for antibody pool B. The top portion of the figure shows the cluster enrichment number, the number of instances the antibody appears, plotted against the cluster rank, which lists the antibody rank order of the antibodies by size cluster. The bottom portion of the figure shows the parallel histogram showing the distribution of the HCDR3 lengths among the top 95 antibody clusters.

[0026] **Figure 9C** depicts long read NGS sequencing of the eluted phage pool for antibody pool C. The top portion of the figure shows the cluster enrichment number, the number of instances the antibody appears, plotted against the cluster rank, which lists the antibody rank order of the antibodies by size cluster. The bottom portion of the figure shows the parallel histogram showing the distribution of the HCDR3 lengths among the top 95 antibody clusters.

[0027] **Figure 10A** depicts the distribution of antibody yields from 1.2 mL high-throughput antibody expression and purification among antibodies identified from the three library pools. Points are color-coded by whether the antibody was identified by phage ELISA screening (blue) or NGS enrichment data (green).

[0028] **Figure 10B** depicts the distribution of antibody binding affinity to DKK1 as measured by SPR (Carterra). Points are color-coded by whether the antibody was identified by phage ELISA screening (blue) or NGS enrichment data (green).

[0029] **Figure 10C** depicts the distribution of MFI ratio among antibodies identified from the three library pools. The MFI ratio is defined as the MFI measured of the antibody binding to HEK293 cells overexpressing DKK1 divided by the MFI measured of the antibody binding to HEK293 cells. Points are color-coded by whether the antibody was identified by phage ELISA screening (blue) or NGS enrichment data (green).

[0030] **Figure 11A** depicts the relationship between the MFI ratio and binding affinity to DKK1 as measured by SPR. The size of each dot corresponds to the antibody yield from 1.2 ml high-throughput antibody expression and purification. Points are color-coded by the library pool used during panning.

[0031] **Figure 11B** depicts the relationship between the MFI ratio and binding affinity to DKK1 as measured by SPR. The size of each dot corresponds to the antibody yield from 1.2 ml high-throughput antibody expression and purification. Points are color-coded by whether the antibody was identified by phage ELISA screening (blue) or NGS enrichment data (green).

[0032] **Figure 12A** depicts Carterra SPR kinetic graphs showing VHH-Fc hits identified from NGS sequencing binding with high affinity to DKK1. Antibody lawn (10 ug/mL), 0-500 nM antigen, HBSTE + 0.5 mg/mL BSA pH 7.4. **Figure 12B** depicts Carterra SPR kinetic graphs showing VHH-Fc hits identified from ELISA screening binding with high affinity to DKK1. **Figure 12C** depicts additional Carterra SPR kinetic graphs showing VHH-Fc hits identified from NGS sequencing binding with high affinity to DKK1. **Figure 12D** depicts additional Carterra SPR kinetic graphs showing VHH-Fc hits identified from NGS sequencing binding with high affinity to DKK1.

[0033] **Figure 13** depicts the results of a TCF/LEF reporter (Wnt signaling) assay. Wnt signaling activation is plotted with SPR binding affinity.

[0034] **Figures 14A-14D** depict *in vitro* primary immune cell activation. **Figure 14A** depicts an immune cell activation assay using peripheral blood mononuclear cells (PBMCs) and interferon gamma (IFN or IFN-γ). **Figure 14B** depicts an immune cell activation assay using PBMCs and granulocyte-macrophage colony-stimulating factor (GM-CSF). GM-CSF is the marker for NK cell activation. Human PBMC is treated with immune stimulator, mWnt3a, hDKK1, and Dkk1 leads from ML synthetic library (**Figure 14C**) **and ML from VHH library (Figure 14D**). Cytokine release of GM-CSF is measured by ELISA.

[0035] **Figure 15A** depicts the outcomes of a tumor killing assay. Activated immune cells kill PC3, while hDKK1 treatment inhibits cytotoxicity. **Figure 15B** depicts a graph of the results of a tumor killing assay. **Figure 15C** highlights specific hits from the tumor killing assay that were also found in the TCF/LEF reporter (Wnt signaling) assay. **Figure 15D** shows that ML synthetic library and ML from VHH library restore the cytotoxicity potency when DKK1 leads block the interaction of hDKK1 to the receptor. **Figure 15E** shows PC3 tumor cell viability results. **Figure 15F** shows top clones in a PC3 cytotoxicity assay. **Figure 15G** shows a subset of the top clones in a PC3 cytotoxicity assay.

[0036] **Figure 16** depicts antibody yield results from 1mL Expi293 cell culture.

[0037] **Figures 17A-C** show anti-DKK1 binding to hDKK1 by SPR analysis. **Figure 17A** shows two epitope binds (activation of Wnt signaling vs immune response) apparent among DKK1 leads. **Figure 17B** shows an example of a hDDK1 protein with CRD1 and CRD2 annotated. **Figure 17C** shows that DKK1 leads which bind to hDKK1 CRD1 and/or hDKK1 CRD2 result in different activation pathways.

[0038] **Figures 18A-18C** depict Wnt TCF/LEF reporter assay screening. Wnt TCF/LEF signaling is blocked by DKK1 binding to LRP5/6. DKK1 leads were screened from a VHH library (**Figure 18A**), a ML synthetic library (**Figure 18B**), and a ML from VHH library (**Figure 18C**).

[0039] **Figures 19A-19D** depict BsAb functional assays. DKK1-99 binds to DKK1 CRD1 and activates an immune response, while DKK1-100 binds to DKK1 CRD2 and activates Wnt signaling. A bispecific Ab of DKK1-99 and DKK1-100 (**Figure 19A**) shows the potency of activating both Wnt (**Figure 19B**) and immune response (**Figure 19C**). **Figure 19D** shows another graph of immune response activation.

[0040] **Figures 20A-20D** depict DKK1 leads in tumor regression. **Figure 20A** shows a schematic of mice inoculation with PC3 cells. Dosing was initiated at tumor volume average of approximately 100 mm^3 with 10 mg/kg via intraperitoneal injection once every 3 days for 8 cycles.

Tumor sizes were measured 3 times a week. **Figure 20B** shows that anti-DKK1 treatment downregulates tumor growth, showing its efficacy in tumor suppression. **Figure 20C** shows that anti-DKK1 treatment downregulates tumor growth, showing efficacy in tumor suppression in days 1-7 of the study. **Figure 20D** shows the mean tumor volume across days 1-7 of the study.

[0041] **Figure 21** depicts a schematic of the panning rounds for DKK1 antibody production.

[0042] **Figures 22A-22C** show that antagonism of DKK1 inhibition of WNT in TCF/LEF assays is biphasic. **Figure 22A** shows a control DKN-01 antibody. **Figure 22B** shows the results for DKK1-28. **Figure 22C** shows the results for DKK1-100.

[0043] **Figure 23A** shows that transient and cell line TCF/LEF reporter rankings match in functional assays. **Figure 23B** shows a subset of the results of **Figure 23A**.

[0044] **Figure 24** shows the development of a DKK1/LRP6 binding assay.

[0045] **Figures 25A-25C** show that functional antagonists DKN-01 (**Figure 25A**), DKK1-100 (**Figure 25B**), and DKK1-28 (**Figure 25C**) enhance DKK1 binding to LRP6.

[0046] **Figures 26A-26B** show the results of primary immune cell reactivation assays. **Figure 26A** shows results using the IFN-gamma marker of immune cell activation. **Figure 26B** shows results using the GM-CSF marker for immune cell activation.

[0047] **Figure 27A** shows the results for primary NK cell activation. **Figure 27B** shows immune cell activation assay results for top clones. **Figure 27C** shows a subset of the results of **Figure 27B**.

[0048] **Figure 28A-28D** show the identification of antagonists DKK1-473 (**Figure 28A**), DKK1-478 (**Figure 28B**), DKK1-477 (**Figure 28C**), and DKK1-448 (**Figure 28D**) through signaling titration assays.

[0049] **Figure 29A** shows the results of an immune assay. **Figure 29B** shows a subset of the results of **Figure 29A**.

[0050] **Figure 30** depicts lung tumor organoid killing by immune cells with DKK1 inhibition.

DETAILED DESCRIPTION

[0051] The present disclosure employs, unless otherwise indicated, conventional molecular biology techniques, which are within the skill of the art. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of ordinary skill in the art.

[0052] **Definitions**

[0053] Throughout this disclosure, various embodiments are presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and

should not be construed as an inflexible limitation on the scope of any embodiments. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range to the tenth of the unit of the lower limit unless the context clearly dictates otherwise. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual values within that range, for example, 1.1, 2, 2.3, 5, and 5.9. This applies regardless of the breadth of the range. The upper and lower limits of these intervening ranges may independently be included in the smaller ranges, and are also encompassed within the disclosure, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the disclosure, unless the context clearly dictates otherwise.

[0054] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting of any embodiment. As used herein, the singular forms "a," "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. It will be further understood that the terms "comprises" and/or "comprising," when used in this specification, specify the presence of stated features, integers, steps, operations, elements, components, and/or groups, but do not preclude the presence or addition of one or more other features, integers, steps, operations, elements, components, and/or groups thereof. As used herein, the term "and/or" includes any and all combinations of one or more of the associated listed items.

[0055] Unless specifically stated or obvious from context, as used herein, the term "about" in reference to a number or range of numbers is understood to mean the stated number and numbers +/- 10% thereof, or 10% below the lower listed limit and 10% above the higher listed limit for the values listed for a range.

[0056] Unless specifically stated, as used herein, the term "nucleic acid" encompasses double- or triple-stranded nucleic acids, as well as single-stranded molecules. In double- or triple-stranded nucleic acids, the nucleic acid strands need not be coextensive (i.e., a double-stranded nucleic acid need not be double-stranded along the entire length of both strands). Nucleic acid sequences, when provided, are listed in the 5' to 3' direction, unless stated otherwise. Methods described herein provide for the generation of isolated nucleic acids. Methods described herein additionally provide for the generation of isolated and purified nucleic acids. A "nucleic acid" as referred to herein can comprise at least 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, or more bases in length. Moreover, provided herein are methods for

the synthesis of any number of polypeptide-segments encoding nucleotide sequences, including sequences encoding non-ribosomal peptides (NRPs), sequences encoding non-ribosomal peptide-synthetase (NRPS) modules and synthetic variants, polypeptide segments of other modular proteins, such as antibodies, polypeptide segments from other protein families, including non-coding DNA or RNA, such as regulatory sequences e.g. promoters, transcription factors, enhancers, siRNA, shRNA, RNAi, miRNA, small nucleolar RNA derived from microRNA, or any functional or structural DNA or RNA unit of interest. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, intergenic DNA, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), small nucleolar RNA, ribozymes, complementary DNA (cDNA), which is a DNA representation of mRNA, usually obtained by reverse transcription of messenger RNA (mRNA) or by amplification; DNA molecules produced synthetically or by amplification, genomic DNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. cDNA encoding for a gene or gene fragment referred herein may comprise at least one region encoding for exon sequences without an intervening intron sequence in the genomic equivalent sequence.

[0057] DKK1 Libraries

[0058] Provided herein are methods and compositions relating to dickkopf WNT signaling pathway inhibitor 1 (DKK1) variant immunoglobulins (e.g., antibody, VHH)comprising nucleic acids encoding for an immunoglobulin comprising a DKK1 binding domain. Immunoglobulins as described herein can stably support a DKK1 binding domain. Libraries as described herein may be further variegated to provide for variant libraries comprising nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence. Further described herein are protein libraries that may be generated when the nucleic acid libraries are translated. In some instances, nucleic acid libraries as described herein are transferred into cells to generate a cell library. Also provided herein are downstream applications for the libraries synthesized using methods described herein. Downstream applications include identification of variant nucleic acids or protein sequences with enhanced biologically relevant functions, e.g., improved stability, affinity, binding, functional activity, and for the treatment or prevention of a disease state associated with DKK1.

[0059] Provided herein are libraries comprising nucleic acids encoding for an immunoglobulin. In some instances, the immunoglobulin is an antibody. As used herein, the term antibody will be understood to include proteins having the characteristic two-armed, Y-shape of a typical antibody

molecule as well as one or more fragments of an antibody that retain the ability to specifically bind to an antigen. Exemplary antibodies include, but are not limited to, a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv) (including fragments in which the VL and VH are joined using recombinant methods by a synthetic or natural linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules, including single chain Fab and scFab), a single chain antibody, a Fab fragment (including monovalent fragments comprising the VL, VH, CL, and CH1 domains), a F(ab′)2 fragment (including bivalent fragments comprising two Fab fragments linked by a disulfide bridge at the hinge region), a Fd fragment (including fragments comprising the VH and CH1 fragment), a Fv fragment (including fragments comprising the VL and VH domains of a single arm of an antibody), a single-domain antibody (dAb or sdAb) (including fragments comprising a VH domain), an isolated complementarity determining region (CDR), a diabody (including fragments comprising bivalent dimers such as two VL and VH domains bound to each other and recognizing two different antigens), a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof. In some instances, the libraries disclosed herein comprise nucleic acids encoding for an immunoglobulin, wherein the immunoglobulin is a Fv antibody, including Fv antibodies comprised of the minimum antibody fragment which contains a complete antigen-recognition and antigen-binding site. In some embodiments, the Fv antibody consists of a dimer of one heavy chain and one light chain variable domain in tight, non-covalent association, and the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. In some embodiments, the six hypervariable regions confer antigen-binding specificity to the antibody. In some embodiments, a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen, including single domain antibodies isolated from camelid animals comprising one heavy chain variable domain such as VHH antibodies or nanobodies) has the ability to recognize and bind antigen. In some instances, the libraries disclosed herein comprise nucleic acids encoding for an immunoglobulin, wherein the immunoglobulin is a single-chain Fv or scFv, including antibody fragments comprising a VH, a VL, or both a VH and VL domain, wherein both domains are present in a single polypeptide chain. In some embodiments, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains allowing the scFv to form the desired structure for antigen binding. In some instances, a scFv is linked to the Fc fragment or a VHH is linked to the Fc fragment (including minibodies). In some instances, the antibody

comprises immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, e.g., molecules that contain an antigen binding site. Immunoglobulin molecules are of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG 1, IgG 2, IgG 3, IgG 4, IgA 1 and IgA 2), or subclass.

[0060] In some embodiments, libraries comprise immunoglobulins that are adapted to the species of an intended therapeutic target. Generally, these methods include "mammalization" and comprise methods for transferring donor antigen-binding information to a less immunogenic mammal antibody acceptor to generate useful therapeutic treatments. In some instances, the mammal is mouse, rat, equine, sheep, cow, primate (*e.g.,* chimpanzee, baboon, gorilla, orangutan, monkey), dog, cat, pig, donkey, rabbit, or human. In some instances, provided herein are libraries and methods for felinization and caninization of antibodies.

[0061] "Humanized" forms of non-human antibodies can be chimeric antibodies that contain minimal sequence derived from the non-human antibody. A humanized antibody is generally a human antibody (recipient antibody) in which residues from one or more CDRs are replaced by residues from one or more CDRs of a non-human antibody (donor antibody). The donor antibody can be any suitable non-human antibody, such as a mouse, rat, rabbit, chicken, or non-human primate antibody having a desired specificity, affinity, or biological effect. In some instances, selected framework region residues of the recipient antibody are replaced by the corresponding framework region residues from the donor antibody. Humanized antibodies may also comprise residues that are not found in either the recipient antibody or the donor antibody. In some instances, these modifications are made to further refine antibody performance.

[0062] "Caninization" can comprise a method for transferring non-canine antigen-binding information from a donor antibody to a less immunogenic canine antibody acceptor to generate treatments useful as therapeutics in dogs. In some instances, caninized forms of non-canine antibodies provided herein are chimeric antibodies that contain minimal sequence derived from non-canine antibodies. In some instances, caninized antibodies are canine antibody sequences ("acceptor" or "recipient" antibody) in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-canine species ("donor" antibody) such as mouse, rat, rabbit, cat, dogs, goat, chicken, bovine, horse, llama, camel, dromedaries, sharks, non-human primates, human, humanized, recombinant sequence, or an engineered sequence having the desired properties. In some instances, framework region (FR) residues of the canine antibody are replaced by corresponding non-canine FR residues. In some instances, caninized antibodies include residues that are not found in the recipient antibody or in the donor antibody. In some instances,

these modifications are made to further refine antibody performance. The caninized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc) of a canine antibody.

[0063] "Felinization" can comprise a method for transferring non-feline antigen-binding information from a donor antibody to a less immunogenic feline antibody acceptor to generate treatments useful as therapeutics in cats. In some instances, felinized forms of non-feline antibodies provided herein are chimeric antibodies that contain minimal sequence derived from non-feline antibodies. In some instances, felinized antibodies are feline antibody sequences ("acceptor" or "recipient" antibody) in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-feline species ("donor" antibody) such as mouse, rat, rabbit, cat, dogs, goat, chicken, bovine, horse, llama, camel, dromedaries, sharks, non-human primates, human, humanized, recombinant sequence, or an engineered sequence having the desired properties. In some instances, framework region (FR) residues of the feline antibody are replaced by corresponding non-feline FR residues. In some instances, felinized antibodies include residues that are not found in the recipient antibody or in the donor antibody. In some instances, these modifications are made to further refine antibody performance. The felinized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc) of a felinize antibody.

[0064] Provided herein are libraries comprising nucleic acids encoding for a non-immunoglobulin. For example, the non-immunoglobulin is an antibody mimetic. Exemplary antibody mimetics include, but are not limited to, anticalins, affilins, affibody molecules, affimers, affitins, alphabodies, avimers, atrimers, DARPins, fynomers, Kunitz domain-based proteins, monobodies, anticalins, knottins, armadillo repeat protein-based proteins, and bicyclic peptides.

[0065] Libraries described herein comprising nucleic acids encoding for an immunoglobulin comprising variations in at least one region of the immunoglobulin. Exemplary regions of the antibody for variation include, but are not limited to, a complementarity-determining region (CDR), a variable domain, or a constant domain. In some instances, the CDR is CDR1, CDR2, or CDR3. In some instances, the CDR is a heavy domain including, but not limited to, CDRH1, CDRH2, and CDRH3. In some instances, the CDR is a light domain including, but not limited to, CDRL1, CDRL2, and CDRL3. In some instances, the variable domain is variable domain, light chain (VL) or variable domain, heavy chain (VH). In some instances, the VL domain comprises kappa or lambda chains. In some instances, the constant domain is constant domain, light chain (CL) or constant domain, heavy chain (CH).

[0066] Methods described herein provide for synthesis of libraries comprising nucleic acids encoding for an immunoglobulin, wherein each nucleic acid encodes for a predetermined variant of at least one predetermined reference nucleic acid sequence. In some cases, the predetermined

reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the variant library comprises varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). An exemplary number of codons for variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[0067] In some instances, the at least one region of the immunoglobulin for variation is from heavy chain V-gene family, heavy chain D-gene family, heavy chain J-gene family, light chain V-gene family, or light chain J-gene family. In some instances, the light chain V-gene family comprises immunoglobulin kappa (IGK) gene or immunoglobulin lambda (IGL). Exemplary genes include, but are not limited to, IGHV1-18, IGHV1-69, IGHV1-8, IGHV3-21, IGHV3-23, IGHV3-30/33rn, IGHV3-28, IGHV1-69, IGHV3-74, IGHV4-39, IGHV4-59/61, IGKV1-39, IGKV1-9, IGKV2-28, IGKV3-11, IGKV3-15, IGKV3-20, IGKV4-1, IGLV1-51, IGLV2-14, IGLV1-40, and IGLV3-1. In some instances, the gene is IGHV1-69, IGHV3-30, IGHV3-23, IGHV3, IGHV1-46, IGHV3-7, IGHV1, or IGHV1-8. In some instances, the gene is IGHV1-69 and IGHV3-30. In some instances, the gene is IGHJ3, IGHJ6, IGHJ, IGHJ4, IGHJ5, IGHJ2, or IGH1. In some instances, the gene is IGHJ3, IGHJ6, IGHJ, or IGHJ4.

[0068] Provided herein are libraries comprising nucleic acids encoding for immunoglobulins, wherein the libraries are synthesized with various numbers of fragments. In some instances, the fragments comprise the CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, or VH domain. In some instances, the fragments comprise framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, the immunoglobulin libraries are synthesized with at least or about 2 fragments, 3 fragments, 4 fragments, 5 fragments, or more than 5 fragments. The length of each of the nucleic acid fragments or average length of the nucleic acids synthesized may be at least or about 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or more

than 600 base pairs. In some instances, the length is about 50 to 600, 75 to 575, 100 to 550, 125 to 525, 150 to 500, 175 to 475, 200 to 450, 225 to 425, 250 to 400, 275 to 375, or 300 to 350 base pairs.

[0069] Libraries comprising nucleic acids encoding for immunoglobulins as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 amino acids to about 75 amino acids. In some instances, the immunoglobulins comprise at least or about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, or more than 5000 amino acids.

[0070] A number of variant sequences for the at least one region of the immunoglobulin for variation are de novo synthesized using methods as described herein. In some instances, a number of variant sequences is de novo synthesized for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or combinations thereof. In some instances, a number of variant sequences is de novo synthesized for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). The number of variant sequences may be at least or about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, or more than 500 sequences. In some instances, the number of variant sequences is at least or about 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, or more than 8000 sequences. In some instances, the number of variant sequences is about 10 to 500, 25 to 475, 50 to 450, 75 to 425, 100 to 400, 125 to 375, 150 to 350, 175 to 325, 200 to 300, 225 to 375, 250 to 350, or 275 to 325 sequences.

[0071] Variant sequences for the at least one region of the immunoglobulin, in some instances, vary in length or sequence. In some instances, the at least one region that is de novo synthesized is for CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or combinations thereof. In some instances, the at least one region that is de novo synthesized is for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, or more than 50 variant nucleotides or amino acids as compared to wild-type. In some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, or 50 additional nucleotides or amino acids as compared to wild-type. In

some instances, the variant sequence comprises at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, or 50 less nucleotides or amino acids as compared to wild-type. In some instances, the libraries comprise at least or about 10^1, 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, or more than 10^{10} variants.

[0072] Following synthesis of libraries described herein, libraries may be used for screening and analysis. For example, libraries are assayed for library displayability and panning. In some instances, displayability is assayed using a selectable tag. Exemplary tags include, but are not limited to, a radioactive label, a fluorescent label, an enzyme, a chemiluminescent tag, a colorimetric tag, an affinity tag or other labels or tags that are known in the art. In some instances, the tag is histidine, polyhistidine, myc, hemagglutinin (HA), or FLAG. In some instances, libraries are assayed by sequencing using various methods including, but not limited to, single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (e.g., Sanger) sequencing, +S sequencing, or sequencing by synthesis.

[0073] In some instances, the libraries are assayed for functional activity, structural stability (e.g., thermal stable or pH stable), expression, specificity, or a combination thereof. In some instances, the libraries are assayed for immunoglobulin (e.g., an antibody) capable of folding. In some instances, a region of the antibody is assayed for functional activity, structural stability, expression, specificity, folding, or a combination thereof. For example, a VH region or VL region is assayed for functional activity, structural stability, expression, specificity, folding, or a combination thereof.

[0074] *DKK1 Libraries*

[0075] Provided herein are DKK1 variant immunoglobulins (e.g., antibody, VHH)comprising nucleic acids encoding for immunoglobulins (e.g., antibodies) that bind to DKK1. In some instances, the immunoglobulin sequences for DKK1 binding domains are determined by interactions between the DKK1 binding domains and the DKK1.

[0076] Sequences of DKK1 binding domains based on surface interactions of DKK1 are analyzed using various methods. For example, multispecies computational analysis is performed. In some instances, a structure analysis is performed. In some instances, a sequence analysis is performed. Sequence analysis can be performed using a database known in the art. Non-limiting examples of databases include, but are not limited to, NCBI BLAST (blast.ncbi.nlm.nih.gov/Blast.cgi), UCSC Genome Browser (genome.ucsc.edu/), UniProt (www.uniprot.org/), and IUPHAR/BPS Guide to PHARMACOLOGY (guidetopharmacology.org/).

[0077] Described herein are DKK1 binding domains designed based on sequence analysis among various organisms. For example, sequence analysis is performed to identify homologous sequences in different organisms. Exemplary organisms include, but are not limited to, mouse, rat, equine, sheep, cow, primate (*e.g.,* chimpanzee, baboon, gorilla, orangutan, monkey), dog, cat, pig, donkey, rabbit, fish, fly, and human.

[0078] Following identification of DKK1 binding domains, libraries comprising nucleic acids encoding for the DKK1 binding domains may be generated. In some instances, libraries of DKK1 binding domains comprise sequences of DKK1 binding domains designed based on conformational ligand interactions, peptide ligand interactions, small molecule ligand interactions, extracellular domains of DKK1, or antibodies that target DKK1. In some instances, libraries of DKK1 binding domains comprise sequences of DKK1 binding domains designed based on peptide ligand interactions. Libraries of DKK1 binding domains may be translated to generate protein libraries. In some instances, libraries of DKK1 binding domains are translated to generate peptide libraries, immunoglobulin libraries, derivatives thereof, or combinations thereof. In some instances, libraries of DKK1 binding domains are translated to generate protein libraries that are further modified to generate peptidomimetic libraries. In some instances, libraries of DKK1 binding domains are translated to generate protein libraries that are used to generate small molecules.

[0079] Methods described herein provide for synthesis of libraries of DKK1 binding domains comprising nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence. In some cases, the predetermined reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the libraries of DKK1 binding domains comprise varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon in a DKK1 binding domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons in a DKK1 binding domain. An exemplary number of codons for variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[0080] Methods described herein provide for synthesis of libraries comprising nucleic acids encoding for the DKK1 binding domains, wherein the libraries comprise sequences encoding for variation of length of the DKK1 binding domains. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45,

50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons less as compared to a predetermined reference sequence. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, or more than 300 codons more as compared to a predetermined reference sequence.

[0081] Provided herein are DKK1 variant immunoglobulins (e.g., antibody, VHH) comprising nucleic acids encoding for immunoglobulins comprising DKK1 binding domains comprising variation in domain type, domain length, or residue variation. In some instances, the domain is a region in the immunoglobulin comprising the DKK1 binding domains. For example, the region is the VH, CDRH1, CDRH2, CDRH3, VL, CDRL1, CDRL2, or CDRL3 domain. In some instances, the domain is the DKK1 binding domain.

[0082] Methods described herein provide for synthesis of a DKK1 binding library of nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence. In some cases, the predetermined reference sequence is a nucleic acid sequence encoding for a protein, and the variant library comprises sequences encoding for variation of at least a single codon such that a plurality of different variants of a single residue in the subsequent protein encoded by the synthesized nucleic acid are generated by standard translation processes. In some instances, the DKK1 binding library comprises varied nucleic acids collectively encoding variations at multiple positions. In some instances, the variant library comprises sequences encoding for variation of at least a single codon of a VH, CDRH1, CDRH2, CDRH3, VL, CDRL1, CDRL2, or CDRL3 domain. In some instances, the variant library comprises sequences encoding for variation of at least a single codon in a DKK1 binding domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons of a VH, CDRH1, CDRH2, CDRH3, VL, CDRL1, CDRL2, or CDRL3 domain. In some instances, the variant library comprises sequences encoding for variation of multiple codons in a DKK1 binding domain. An exemplary number of codons for variation include, but are not limited to, at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons.

[0083] Methods described herein provide for synthesis of a DKK1 binding library of nucleic acids each encoding for a predetermined variant of at least one predetermined reference nucleic acid sequence, wherein the DKK1 binding library comprises sequences encoding for variation of length of a domain. In some instances, the domain is VH, CDRH1, CDRH2, CDRH3, VL, CDRL1, CDRL2, or CDRL3 domain. In some instances, the domain is the DKK1 binding domain. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5,

10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 225, 250, 275, 300, or more than 300 codons less as compared to a predetermined reference sequence. In some instances, the library comprises sequences encoding for variation of length of at least or about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, or more than 300 codons more as compared to a predetermined reference sequence.

[0084] Provided herein are DKK1 variant immunoglobulins (e.g., antibody, VHH) comprising nucleic acids encoding for immunoglobulins comprising DKK1 binding domains, wherein the DKK1 binding libraries are synthesized with various numbers of fragments. In some instances, the fragments comprise the VH, CDRH1, CDRH2, CDRH3, VL, CDRL1, CDRL2, or CDRL3 domain. In some instances, the DKK1 variant immunoglobulins (e.g., antibody, VHH) are synthesized with at least or about 2 fragments, 3 fragments, 4 fragments, 5 fragments, or more than 5 fragments. The length of each of the nucleic acid fragments or average length of the nucleic acids synthesized may be at least or about 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or more than 600 base pairs. In some instances, the length is about 50 to 600, 75 to 575, 100 to 550, 125 to 525, 150 to 500, 175 to 475, 200 to 450, 225 to 425, 250 to 400, 275 to 375, or 300 to 350 base pairs.

[0085] DKK1 variant immunoglobulins (e.g., antibody, VHH) comprising nucleic acids encoding for immunoglobulins comprising DKK1 binding domains as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 to about 75 amino acids.

[0086] DKK1 variant immunoglobulins (e.g., antibody, VHH) comprising de novo synthesized variant sequences encoding for immunoglobulins comprising DKK1 binding domains comprise a number of variant sequences. In some instances, a number of variant sequences is de novo synthesized for a CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, CDRL3, VL, VH, or a combination thereof. In some instances, a number of variant sequences is de novo synthesized for framework element 1 (FW1), framework element 2 (FW2), framework element 3 (FW3), or framework element 4 (FW4). In some instances, a number of variant sequences is de novo synthesized for a GPCR binding domain. For example, the number of variant sequences is about 1 to about 10

sequences for the VH domain, about 10^8 sequences for the DKK1 binding domain, and about 1 to about 44 sequences for the VL domain. The number of variant sequences may be at least or about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, or more than 500 sequences. In some instances, the number of variant sequences is about 10 to 300, 25 to 275, 50 to 250, 75 to 225, 100 to 200, or 125 to 150 sequences.

[0087] Described herein are antibodies or antibody fragments thereof that binds DKK1. In some embodiments, the antibody or antibody fragment thereof comprises a sequence as set forth in **Tables 4-8**. In some embodiments, the antibody or antibody fragment thereof comprises a sequence that is at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence as set forth in **Tables 4-8**.

[0088] In some instances, an antibody or antibody fragment described herein comprises a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332.

[0089] In some instances, an antibody or antibody fragment described herein comprises a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746.

[0090] In some instances, an antibody or antibody fragment described herein comprises a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical

to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160.

[0091] In some instances, an antibody or antibody fragment described herein comprises a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464.

[0092] In some instances, an antibody or antibody fragment described herein comprises a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521.

[0093] In some instances, an antibody or antibody fragment described herein comprises a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 80% identical to a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 85% identical to a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 90% identical to a CDRL3 sequence of any

one of SEQ ID NOs: 2522-2727. In some instances, an antibody or antibody fragment described herein comprises a sequence that is at least 95% identical to a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727.

[0094] Described herein, in some embodiments, are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein the VH comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258, and wherein the VL comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 713-918. In some instances, the antibodies or antibody fragments comprise VH comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258. In some instances, the antibodies or antibody fragments comprise VL comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 713-918.

[0095] The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as EMBOSS MATCHER, EMBOSS WATER, EMBOSS STRETCHER, EMBOSS NEEDLE, EMBOSS LALIGN, BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[0096] In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y, where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that

program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

[0097] The term "homology" or "similarity" between two proteins is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one protein sequence to the second protein sequence. Similarity may be determined by procedures which are well-known in the art, for example, a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information).

[0098] The terms "complementarity determining region," and "CDR," which are synonymous with "hypervariable region" or "HVR," are known in the art to refer to non-contiguous sequences of amino acids within antibody variable regions, which confer antigen specificity and/or binding affinity. In general, there are three CDRs in each heavy chain variable region (CDRH1, CDRH2, CDRH3) and three CDRs in each light chain variable region (CDRL1, CDRL2, CDRL3). "Framework regions" and "FR" are known in the art to refer to the non-CDR portions of the variable regions of the heavy and light chains. In general, there are four FRs in each full-length heavy chain variable region (FR-H1, FR-H2, FR-H3, and FR-H4), and four FRs in each full-length light chain variable region (FR-L1, FR-L2, FR-L3, and FR-L4). The precise amino acid sequence boundaries of a given CDR or FR can be readily determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD ("Kabat" numbering scheme), Al-Lazikani et al., (1997) JMB 273,927-948 ("Chothia" numbering scheme); MacCallum et al., J. Mol. Biol. 262:732-745 (1996), "Antibody-antigen interactions: Contact analysis and binding site topography," J. Mol. Biol. 262, 732-745." ("Contact" numbering scheme); Lefranc MP et al., "IMGT unique numbering for immunoglobulin and T cell receptor variable domains and Ig superfamily V-like domains," Dev Comp Immunol, 2003 Jan;27(1):55-77 ("IMGT" numbering scheme); Honegger A and Plückthun A, "Yet another numbering scheme for immunoglobulin variable domains: an automatic modeling and analysis tool," J Mol Biol, 2001 Jun 8;309(3):657-70, ("Aho" numbering scheme); and Whitelegg NR and Rees AR, "WAM: an improved algorithm for modelling antibodies on the WEB," Protein Eng. 2000 Dec;13(12):819-24 ("AbM" numbering scheme. In certain embodiments the CDRs of the antibodies described herein can be defined by a method selected from Kabat, Chothia, IMGT, Aho, AbM, or combinations thereof.

[0099] The boundaries of a given CDR or FR may vary depending on the scheme used for identification. For example, the Kabat scheme is based on structural alignments, while the Chothia scheme is based on structural information. Numbering for both the Kabat and Chothia schemes is based upon the most common antibody region sequence lengths, with insertions accommodated by

insertion letters, for example, "30a," and deletions appearing in some antibodies. The two schemes place certain insertions and deletions ("indels") at different positions, resulting in differential numbering. The Contact scheme is based on analysis of complex crystal structures and is similar in many respects to the Chothia numbering scheme.

[00100] DKK1 variant immunoglobulins (e.g., antibody, VHH)comprising *de novo* synthesized variant sequences encoding for immunoglobulins comprising DKK1 binding domains comprise improved diversity. For example, variants are generated by placing DKK1binding domain variants in immunoglobulins comprising N-terminal CDRH3 variations and C-terminal CDRH3 variations. In some instances, variants include affinity maturation variants. Alternatively or in combination, variants include variants in other regions of the immunoglobulin including, but not limited to, CDRH1 and CDRH2. In some instances, the number of variants of the DKK1 variant immunoglobulins (e.g., antibody, VHH)is at least or about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, 10^{20}, or more than 10^{20} non-identical sequences.

[00101] In some instances, the at least one region of the antibody for variation is from heavy chain V-gene family, heavy chain D-gene family, heavy chain J-gene family, light chain V-gene family, or light chain J-gene family. In some instances, the light chain V-gene family comprises immunoglobulin kappa (IGK) gene or immunoglobulin lambda (IGL). Exemplary regions of the antibody for variation include, but are not limited to, IGHV1-18, IGHV1-69, IGHV1-8, IGHV3-21, IGHV3-23, IGHV3-30/33rn, IGHV3-28, IGHV1-69, IGHV3-74, IGHV4-39, IGHV4-59/61, IGKV1-39, IGKV1-9, IGKV2-28, IGKV3-11, IGKV3-15, IGKV3-20, IGKV4-1, IGLV1-51, IGLV2-14, IGLV1-40, and IGLV3-1. In some instances, the gene is IGHV1-69, IGHV3-30, IGHV3-23, IGHV3, IGHV1-46, IGHV3-7, IGHV1, or IGHV1-8. In some instances, the gene is IGHV1-69 and IGHV3-30. In some instances, the region of the antibody for variation is IGHJ3, IGHJ6, IGHJ, IGHJ4, IGHJ5, IGHJ2, or IGH1. In some instances, the region of the antibody for variation is IGHJ3, IGHJ6, IGHJ, or IGHJ4. In some instances, the at least one region of the antibody for variation is IGHV1-69, IGHV3-23, IGKV3-20, IGKV1-39, or combinations thereof. In some instances, the at least one region of the antibody for variation is IGHV1-69 and IGKV3-20, In some instances, the at least one region of the antibody for variation is IGHV1-69 and IGKV1-39. In some instances, the at least one region of the antibody for variation is IGHV3-23 and IGKV3-20. In some instances, the at least one region of the antibody for variation is IGHV3-23 and IGKV1-39.

[00102] Provided herein are libraries comprising nucleic acids encoding for a DKK1 antibody comprising variation in at least one region of the antibody, wherein the region is the CDR region. In some instances, the DKK1 antibody is a single domain antibody comprising one heavy chain variable domain such as a VHH antibody. In some instances, the VHH antibody comprises

variation in one or more CDR regions. In some instances, libraries described herein comprise at least or about 1, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2400, 2600, 2800, 3000, or more than 3000 sequences of a CDR1, CDR2, or CDR3. In some instances, libraries described herein comprise at least or about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, 10^{20}, or more than 10^{20} sequences of a CDR1, CDR2, or CDR3. For example, the libraries comprise at least 2000 sequences of a CDR1, at least 1200 sequences for CDR2, and at least 1600 sequences for CDR3. In some instances, each sequence is non-identical.

[00103] In some instances, the CDR1, CDR2, or CDR3 is of a variable domain, light chain (VL). CDR1, CDR2, or CDR3 of a variable domain, light chain (VL) can be referred to as CDRL1, CDRL2, or CDRL3, respectively. In some instances, libraries described herein comprise at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2400, 2600, 2800, 3000, or more than 3000 sequences of a CDR1, CDR2, or CDR3 of the VL. In some instances, libraries described herein comprise at least or about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, 10^{20}, or more than 10^{20} sequences of a CDR1, CDR2, or CDR3 of the VL. For example, the libraries comprise at least 20 sequences of a CDR1 of the VL, at least 4 sequences of a CDR2 of the VL, and at least 140 sequences of a CDR3 of the VL. In some instances, the libraries comprise at least 2 sequences of a CDR1 of the VL, at least 1 sequence of CDR2 of the VL, and at least 3000 sequences of a CDR3 of the VL. In some instances, the VL is IGKV1-39, IGKV1-9, IGKV2-28, IGKV3-11, IGKV3-15, IGKV3-20, IGKV4-1, IGLV1-51, IGLV2-14, IGLV1-40, or IGLV3-1. In some instances, the VL is IGKV2-28. In some instances, the VL is IGLV1-51.

[00104] In some instances, the CDR1, CDR2, or CDR3 is of a variable domain, heavy chain (VH). CDR1, CDR2, or CDR3 of a variable domain, heavy chain (VH) can be referred to as CDRH1, CDRH2, or CDRH3, respectively. In some instances, libraries described herein comprise at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2400, 2600, 2800, 3000, or more than 3000 sequences of a CDR1, CDR2, or CDR3 of the VH. In some instances, libraries described herein comprise at least or about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, 10^{20}, or more than 10^{20} sequences of a CDR1, CDR2, or CDR3 of the VH. For example, the libraries comprise at least 30 sequences of a CDR1 of the VH, at least 570 sequences of a CDR2 of the VH, and at least 10^8 sequences of a CDR3 of the VH. In some instances, the libraries comprise at least 30 sequences of a CDR1 of the VH, at least 860 sequences of a CDR2 of the VH, and at least 10^7 sequences of a CDR3 of the VH. In some instances, the VH is IGHV1-18,

IGHV1-69, IGHV1-8 IGHV3-21, IGHV3-23, IGHV3-30/33rn, IGHV3-28, IGHV3-74, IGHV4-39, or IGHV4-59/61. In some instances, the VH is IGHV1-69, IGHV3-30, IGHV3-23, IGHV3, IGHV1-46, IGHV3-7, IGHV1, or IGHV1-8. In some instances, the VH is IGHV1-69 or IGHV3-30. In some instances, the VH is IGHV3-23.

[00105] Libraries as described herein, in some embodiments, comprise varying lengths of a CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, or CDRH3. In some instances, the length of the CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, or CDRH3 comprises at least or about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 40, 50, 60, 70, 80, 90, or more than 90 amino acids in length. For example, the CDRH3 comprises at least or about 12, 15, 16, 17, 20, 21, or 23 amino acids in length. In some instances, the CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, or CDRH3 comprises a range of about 1 to about 10, about 5 to about 15, about 10 to about 20, or about 15 to about 30 amino acids in length.

[00106] Libraries comprising nucleic acids encoding for antibodies having variant CDR sequences as described herein comprise various lengths of amino acids when translated. In some instances, the length of each of the amino acid fragments or average length of the amino acid synthesized may be at least or about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, or more than 150 amino acids. In some instances, the length of the amino acid is about 15 to 150, 20 to 145, 25 to 140, 30 to 135, 35 to 130, 40 to 125, 45 to 120, 50 to 115, 55 to 110, 60 to 110, 65 to 105, 70 to 100, or 75 to 95 amino acids. In some instances, the length of the amino acid is about 22 amino acids to about 75 amino acids. In some instances, the antibodies comprise at least or about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, or more than 5000 amino acids.

[00107] Ratios of the lengths of a CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, or CDRH3 may vary in libraries described herein. In some instances, a CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, or CDRH3 comprising at least or about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 40, 50, 60, 70, 80, 90, or more than 90 amino acids in length comprises about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or more than 90% of the library. For example, a CDRH3 comprising about 23 amino acids in length is present in the library at 40%, a CDRH3 comprising about 21 amino acids in length is present in the library at 30%, a CDRH3 comprising about 17 amino acids in length is present in the library at 20%, and a CDRH3 comprising about 12 amino acids in length is present in the library at 10%. In some instances, a CDRH3 comprising about 20 amino acids in length is present in the library at 40%, a CDRH3 comprising about 16 amino acids in length is present in the library at 30%, a CDRH3

comprising about 15 amino acids in length is present in the library at 20%, and a CDRH3 comprising about 12 amino acids in length is present in the library at 10%.

[00108] Libraries as described herein encoding for a VHH antibody comprise variant CDR sequences that are shuffled to generate a library with a theoretical diversity of at least or about 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, 10^{20}, or more than 10^{20} sequences. In some instances, the library has a final library diversity of at least or about 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, 10^{20}, or more than 10^{20} sequences.

[00109] Provided herein are DKK1variant immunoglobulins (e.g., antibody, VHH)encoding for an immunoglobulin. In some instances, the DKK1 immunoglobulin is an antibody. In some instances, the DKK1 immunoglobulin is a VHH antibody. In some instances, the DKK1 immunoglobulin comprises a binding affinity (e.g., kD) to DKK1 of less than 1 nM, less than 1.2 nM, less than 2 nM, less than 5 nM, less than 10 nM, less than 11 nm, less than 13.5 nM, less than 15 nM, less than 20 nM, less than 25 nM, or less than 30 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 1 nM. In some instances, the DKK1immunoglobulin comprises a kD of less than 1.2 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 2 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 5 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 10 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 13.5 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 15 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 20 nM. In some instances, the DKK1immunoglobulin comprises a kD of less than 25 nM. In some instances, the DKK1 immunoglobulin comprises a kD of less than 30 nM.

[00110] Provided herein are DKK1 variant immunoglobulins (e.g., antibody, VHH)encoding for an immunoglobulin, wherein the immunoglobulin comprises a long half-life. In some instances, the half-life of the DKK1 immunoglobulin is at least or about 12 hours, 24 hours 36 hours, 48 hours, 60 hours, 72 hours, 84 hours, 96 hours, 108 hours, 120 hours, 140 hours, 160 hours, 180 hours, 200 hours, or more than 200 hours. In some instances, the half-life of the DKK1 immunoglobulin is in a range of about 12 hours to about 300 hours, about 20 hours to about 280 hours, about 40 hours to about 240 hours, or about 60 hours to about 200 hours.

[00111] DKK1 immunoglobulins as described herein may comprise improved properties. In some instances, the DKK1 immunoglobulins are monomeric. In some instances, the DKK1 immunoglobulins are not prone to aggregation. In some instances, at least or about 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the DKK1 immunoglobulins are monomeric. In some instances,

the DKK1 immunoglobulins are thermostable. In some instances, the DKK1 immunoglobulins result in reduced non-specific binding.

[00112] Following synthesis of DKK1 variant immunoglobulins (e.g., antibody, VHH)comprising nucleic acids encoding immunoglobulins comprising DKK1 binding domains, libraries may be used for screening and analysis. For example, libraries are assayed for library displayability and panning. In some instances, displayability is assayed using a selectable tag. Exemplary tags include, but are not limited to, a radioactive label, a fluorescent label, an enzyme, a chemiluminescent tag, a colorimetric tag, an affinity tag or other labels or tags that are known in the art. In some instances, the tag is histidine, polyhistidine, myc, hemagglutinin (HA), or FLAG. In some instances, the DKK1 variant immunoglobulins (e.g., antibody, VHH)comprises nucleic acids encoding immunoglobulins with multiple tags such as GFP, FLAG, and Lucy as well as a DNA barcode. In some instances, libraries are assayed by sequencing using various methods including, but not limited to, single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (e.g., Sanger) sequencing, +S sequencing, or sequencing by synthesis.

[00113] *Expression Systems*

[00114] Provided herein are libraries comprising nucleic acids encoding for immunoglobulins comprising DKK1 binding domains, wherein the libraries have improved specificity, stability, expression, folding, or downstream activity. In some instances, libraries described herein are used for screening and analysis.

[00115] Provided herein are libraries comprising nucleic acids encoding for immunoglobulins comprising DKK1 binding domains, wherein the nucleic acid libraries are used for screening and analysis. In some instances, screening and analysis comprise *in vitro*, in *vivo*, or *ex vivo* assays. Cells for screening include primary cells taken from living subjects or cell lines. Cells may be from prokaryotes (e.g., bacteria and fungi) or eukaryotes (e.g., animals and plants). Exemplary animal cells include, without limitation, those from a mouse, rabbit, primate, and insect. In some instances, cells for screening include a cell line including, but not limited to, Chinese Hamster Ovary (CHO) cell line, human embryonic kidney (HEK) cell line, or baby hamster kidney (BHK) cell line. In some instances, nucleic acid libraries described herein may also be delivered to a multicellular organism. Exemplary multicellular organisms include, without limitation, a plant, a mouse, rabbit, primate, and insect.

[00116] Nucleic acid libraries or protein libraries encoded thereof described herein may be screened for various pharmacological or pharmacokinetic properties. In some instances, the libraries are screened using *in vitro* assays, *in vivo* assays, or *ex vivo* assays. For example, *in vitro* pharmacological or pharmacokinetic properties that are screened include, but are not limited to, binding affinity, binding specificity, and binding avidity. Exemplary *in vivo* pharmacological or pharmacokinetic properties of libraries described herein that are screened include, but are not limited to, therapeutic efficacy, activity, preclinical toxicity properties, clinical efficacy properties, clinical toxicity properties, immunogenicity, potency, and clinical safety properties.

[00117] Pharmacological or pharmacokinetic properties that may be screened include, but are not limited to, cell binding affinity and cell activity. For example, cell binding affinity assays or cell activity assays are performed to determine agonistic, antagonistic, or allosteric effects of libraries described herein. In some instances, libraries as described herein are compared to cell binding or cell activity of ligands of DKK1.

[00118] Libraries as described herein may be screened in cell-based assays or in non-cell-based assays. Examples of non-cell-based assays include, but are not limited to, using viral particles, using *in vitro* translation proteins, and using proteoliposomes with DKK1.

[00119] Nucleic acid libraries as described herein may be screened by sequencing. In some instances, next generation sequence is used to determine sequence enrichment of DKK1 binding variants. In some instances, V gene distribution, J gene distribution, V gene family, CDR3 counts per length, or a combination thereof is determined. In some instances, clonal frequency, clonal accumulation, lineage accumulation, or a combination thereof is determined. In some instances, number of sequences, sequences with VH clones, clones, clones greater than 1, clonotypes, clonotypes greater than 1, lineages, simpsons, or a combination thereof is determined. In some instances, a percentage of non-identical CDR3s is determined. For example, the percentage of non-identical CDR3s is calculated as the number of non-identical CDR3s in a sample divided by the total number of sequences that had a CDR3 in the sample.

[00120] Provided herein are nucleic acid libraries, wherein the nucleic acid libraries may be expressed in a vector. Expression vectors for inserting nucleic acid libraries disclosed herein may comprise eukaryotic or prokaryotic expression vectors. Exemplary expression vectors include, without limitation, mammalian expression vectors: pSF-CMV-NEO-NH2-PPT-3XFLAG, pSF-CMV-NEO-COOH-3XFLAG, pSF-CMV-PURO-NH2-GST-TEV, pSF-OXB20-COOH-TEV-FLAG(R)-6His, pCEP4 pDEST27, pSF-CMV-Ub-KrYFP, pSF-CMV-FMDV-daGFP, pEF1a-mCherry-N1 Vector, pEF1a-tdTomato Vector, pSF-CMV-FMDV-Hygro, pSF-CMV-PGK-Puro, pMCP-tag(m), and pSF-CMV-PURO-NH2-CMYC; bacterial expression vectors: pSF-OXB20-

BetaGal,pSF-OXB20-Fluc, pSF-OXB20, and pSF-Tac; plant expression vectors: pRI 101-AN DNA and pCambia2301; and yeast expression vectors: pTYB21 and pKLAC2, and insect vectors: pAc5.1/V5-His A and pDEST8. In some instances, the vector is pcDNA3 or pcDNA3.1.

[00121] Described herein are nucleic acid libraries that are expressed in a vector to generate a construct comprising an immunoglobulin comprising sequences of DKK1 binding domains. In some instances, a size of the construct varies. In some instances, the construct comprises at least or about 500, 600, 700, 800, 900, 1000, 1100, 1300, 1400, 1500, 1600, 1700, 1800, 2000, 2400, 2600, 2800, 3000, 3200, 3400, 3600, 3800, 4000, 4200,4400, 4600, 4800, 5000, 6000, 7000, 8000, 9000, 10000, or more than 10000 bases. In some instances, a the construct comprises a range of about 300 to 1,000, 300 to 2,000, 300 to 3,000, 300 to 4,000, 300 to 5,000, 300 to 6,000, 300 to 7,000, 300 to 8,000, 300 to 9,000, 300 to 10,000, 1,000 to 2,000, 1,000 to 3,000, 1,000 to 4,000, 1,000 to 5,000, 1,000 to 6,000, 1,000 to 7,000, 1,000 to 8,000, 1,000 to 9,000, 1,000 to 10,000, 2,000 to 3,000, 2,000 to 4,000, 2,000 to 5,000, 2,000 to 6,000, 2,000 to 7,000, 2,000 to 8,000, 2,000 to 9,000, 2,000 to 10,000, 3,000 to 4,000, 3,000 to 5,000, 3,000 to 6,000, 3,000 to 7,000, 3,000 to 8,000, 3,000 to 9,000, 3,000 to 10,000, 4,000 to 5,000, 4,000 to 6,000, 4,000 to 7,000, 4,000 to 8,000, 4,000 to 9,000, 4,000 to 10,000, 5,000 to 6,000, 5,000 to 7,000, 5,000 to 8,000, 5,000 to 9,000, 5,000 to 10,000, 6,000 to 7,000, 6,000 to 8,000, 6,000 to 9,000, 6,000 to 10,000, 7,000 to 8,000, 7,000 to 9,000, 7,000 to 10,000, 8,000 to 9,000, 8,000 to 10,000, or 9,000 to 10,000 bases.

[00122] Provided herein are libraries comprising nucleic acids encoding for immunoglobulins, wherein the nucleic acid libraries are expressed in a cell. In some instances, the libraries are synthesized to express a reporter gene. Exemplary reporter genes include, but are not limited to, acetohydroxyacid synthase (AHAS), alkaline phosphatase (AP), beta galactosidase (LacZ), beta glucoronidase (GUS), chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), red fluorescent protein (RFP), yellow fluorescent protein (YFP), cyan fluorescent protein (CFP), cerulean fluorescent protein, citrine fluorescent protein, orange fluorescent protein , cherry fluorescent protein, turquoise fluorescent protein, blue fluorescent protein, horseradish peroxidase (HRP), luciferase (Luc), nopaline synthase (NOS), octopine synthase (OCS), luciferase, and derivatives thereof. Methods to determine modulation of a reporter gene are well known in the art, and include, but are not limited to, fluorometric methods (*e.g.* fluorescence spectroscopy, Fluorescence Activated Cell Sorting (FACS), fluorescence microscopy), and antibiotic resistance determination.

[00123] **Diseases and Disorders**

[00124] Provided herein are DKK1 variant immunoglobulins (e.g., antibody, VHH)comprising nucleic acids encoding for immunoglobulins (e.g., antibodies) comprising DKK1 binding domains

that may have therapeutic effects. In some instances, the DKK1 variant immunoglobulins (e.g., antibody, VHH)result in protein when translated that is used to treat a disease or disorder. In some instances, the protein is an immunoglobulin. In some instances, the protein is a peptidomimetic.

[00125] Exemplary diseases include, but are not limited to, cancer (e.g., gastro-esophageal cancer, endometrial cancer, ovarian cancer, prostate cancer, liver cancer, etc.), inflammatory diseases or disorders, a metabolic disease or disorder, a cardiovascular disease or disorder, a respiratory disease or disorder, pain, a digestive disease or disorder, a reproductive disease or disorder, an endocrine disease or disorder, or a neurological disease or disorder. In some instances, the cancer is a solid cancer or a hematologic cancer. In some instances, a modulator of DKK1 as described herein is used for treatment of weight gain (or for inducing weight loss), treatment of obesity, or treatment of Type II diabetes. In some instances, the DKK1 modulator is used for treating hypoglycemia. In some instances, the DKK1 modulator is used for treating post-bariatric hypoglycemia. In some instances, the DKK1 modulator is used for treating severe hypoglycemia. In some instances, the DKK1 modulator is used for treating hyperinsulinism. In some instances, the DKK1modulator is used for treating congenital hyperinsulinism.

[00126] DKK1 can be tumorigenic in cancer. DKK1 can also be immunosuppressive (e.g., via myeloid-derived suppressor cells (MDSCs) or natural killer (NK) cells). DKK1 can lead to immune suppression through T cell inactivation, MDSC accumulation, or NK cell clearance. DKK1 can inhibit Wnt binding to low-density lipoprotein (LDL) receptor related protein 5 (LRP5). DKK1 can inhibit Wnt binding to LDL receptor related protein 6 (LRP6). DKK1 can inhibit Wnt binding to an LRP5/6 complex. Mutations in Wnt activating genes can lead to increased DKK1 expression.

[00127] Antagonist mAb can activate an innate immune response with anti-angiogenic and direct antitumor effects, binding and removing DKK1 from the tumor microenvironment. Tumors with Wnt activating mutations can responded to DKK1 antagonism. For example, high tumoral DKK1 can be associated with longer progression-free survival in esophagogastic cancer patients.

[00128] In some instances, the subject is a mammal. In some instances, the subject is a mouse, rabbit, dog, or human. Subjects treated by methods described herein may be infants, adults, or children. Pharmaceutical compositions comprising antibodies or antibody fragments as described herein may be administered intravenously or subcutaneously.

[00129] Described herein are pharmaceutical compositions comprising antibodies or antibody fragment thereof that binds DKK1. In some embodiments, the antibody or antibody fragment thereof comprises a sequence as set forth in **Tables 4-8**. In some embodiments, the antibody or antibody fragment thereof comprises a sequence that is at least or about 70%, 80%, 85%, 90%,

91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence as set forth in **Tables 4-8**.

[00130] In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 80% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 85% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 90% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 95% identical to a CDRH1 sequence of any one of SEQ ID NOs: 1-98 or 919-1332.

[00131] In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 80% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 85% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 90% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 95% identical to a CDRH2 sequence of any one of SEQ ID NOs: 99-196 or 1333-1746.

[00132] In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 80% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 85% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-

2160. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 90% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 95% identical to a CDRH3 sequence of any one of SEQ ID NOs: 197-294 or 1747-2160.

[00133] In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 80% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 85% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 90% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 95% identical to a CDRL1 sequence of any one of SEQ ID NOs: 2259-2464.

[00134] In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 80% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 85% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 90% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 95% identical to a CDRL2 sequence of any one of SEQ ID NOs: 2465-2521.

[00135] In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 80% identical to a CDRL3 sequence of any

one of SEQ ID NOs: 2522-2727. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 85% identical to a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 90% identical to a C CDRL3 sequence of any one of SEQ ID NOs: 2522-2727. In some instances, a pharmaceutical composition comprises an antibody or antibody fragment described herein comprising a sequence that is at least 95% identical to a CDRL3 sequence of any one of SEQ ID NOs: 2522-2727.

[00136] In some embodiments, the antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-98 or 919-1332; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 99-196 or 1333-1746; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 197-294 or 1747-2160. In some embodiments, the antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRH1 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 1-98; (b) an amino acid sequence of CDRH2 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 99-196; and (c) an amino acid sequence of CDRH3 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 197-294.

[00137] In some embodiments, the antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 2259-2464; (b) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 2465-2521; and (c) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 2522-2727. In some embodiments, the antibody or antibody fragment comprising a variable domain, heavy chain region (VH) and a variable domain, light chain region (VL), wherein VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, wherein VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRL1 is at

least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 2259-2464; (b) an amino acid sequence of CDRL2 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 2465-2521; and (c) an amino acid sequence of CDRL3 is at least or about 80%, 85%, 90%, or 95% identical to any one of SEQ ID NOs: 2522-2727.

[00138] Described herein, in some embodiments, are antibodies or antibody fragments comprising a variable domain, heavy chain region (VH), wherein the VH comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258. In some instances, the antibodies or antibody fragments comprise VH comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258.

[00139] Described herein, in some embodiments, are antibodies or antibody fragments comprising a variable domain, light chain region (VL), wherein the VL comprises an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 713-918. In some instances, the antibodies or antibody fragments comprise VL comprising at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 713-918.

[00140] **Variant Libraries**

[00141] *Codon variation*

[00142] Variant nucleic acid libraries described herein may comprise a plurality of nucleic acids, wherein each nucleic acid encodes for a variant codon sequence compared to a reference nucleic acid sequence. In some instances, each nucleic acid of a first nucleic acid population contains a variant at a single variant site. In some instances, the first nucleic acid population contains a plurality of variants at a single variant site such that the first nucleic acid population contains more than one variant at the same variant site. The first nucleic acid population may comprise nucleic acids collectively encoding multiple codon variants at the same variant site. The first nucleic acid population may comprise nucleic acids collectively encoding up to 19 or more codons at the same position. The first nucleic acid population may comprise nucleic acids collectively encoding up to 60 variant triplets at the same position, or the first nucleic acid population may comprise nucleic acids collectively encoding up to 61 different triplets of codons at the same position. Each variant may encode for a codon that results in a different amino acid during translation.

[00143] A nucleic acid population may comprise varied nucleic acids collectively encoding up to 20 codon variations at multiple positions. In such cases, each nucleic acid in the population comprises variation for codons at more than one position in the same nucleic acid. In some instances, each nucleic acid in the population comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8,

9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more codons in a single nucleic acid. In some instances, each variant long nucleic acid comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more codons in a single long nucleic acid. In some instances, the variant nucleic acid population comprises variation for codons at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more codons in a single nucleic acid. In some instances, the variant nucleic acid population comprises variation for codons in at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more codons in a single long nucleic acid.

[00144] Highly Parallel Nucleic Acid Synthesis

[00145] Provided herein is a platform approach utilizing miniaturization, parallelization, and vertical integration of the end-to-end process from polynucleotide synthesis to gene assembly within nanowells on silicon to create a revolutionary synthesis platform. Devices described herein provide, with the same footprint as a 96-well plate, a silicon synthesis platform capable of increasing throughput by a factor of up to 1,000 or more compared to traditional synthesis methods, with production of up to approximately 1,000,000 or more polynucleotides, or 10,000 or more genes in a single highly-parallelized run.

[00146] With the advent of next-generation sequencing, high resolution genomic data has become an important factor for studies that delve into the biological roles of various genes in both normal biology and disease pathogenesis. At the core of this research is the central dogma of molecular biology and the concept of "residue-by-residue transfer of sequential information." Genomic information encoded in the DNA is transcribed into a message that is then translated into the protein that is the active product within a given biological pathway.

[00147] Another exciting area of study is on the discovery, development and manufacturing of therapeutic molecules focused on a highly-specific cellular target. High diversity DNA sequence libraries are at the core of development pipelines for targeted therapeutics. Gene mutants are used to express proteins in a design, build, and test protein engineering cycle that ideally culminates in an optimized gene for high expression of a protein with high affinity for its therapeutic target. As an example, consider the binding pocket of a receptor. The ability to test all sequence permutations of all residues within the binding pocket simultaneously will allow for a thorough exploration, increasing chances of success. Saturation mutagenesis, in which a researcher attempts to generate all possible mutations at a specific site within the receptor, represents one approach to this development challenge. Though costly and time- and labor-intensive, it enables each variant to be introduced into each position. In contrast, combinatorial mutagenesis, where a few selected

positions or short stretch of DNA may be modified extensively, generates an incomplete repertoire of variants with biased representation.

[00148] To accelerate the drug development pipeline, a library with the desired variants available at the intended frequency in the right position available for testing – in other words, a precision library – enables reduced costs as well as turnaround time for screening. Provided herein are methods for synthesizing nucleic acid synthetic variant libraries which provide for precise introduction of each intended variant at the desired frequency. To the end user, this translates to the ability to not only thoroughly sample sequence space but also be able to query these hypotheses in an efficient manner, reducing cost and screening time. Genome-wide editing can elucidate important pathways, libraries where each variant and sequence permutation can be tested for optimal functionality, and thousands of genes can be used to reconstruct entire pathways and genomes to re-engineer biological systems for drug discovery.

[00149] In a first example, a drug itself can be optimized using methods described herein. For example, to improve a specified function of an antibody, a variant polynucleotide library encoding for a portion of the antibody is designed and synthesized. A variant nucleic acid library for the antibody can then be generated by processes described herein (e.g., PCR mutagenesis followed by insertion into a vector). The antibody is then expressed in a production cell line and screened for enhanced activity. Example screens include examining modulation in binding affinity to an antigen, stability, or effector function (e.g., ADCC, complement, or apoptosis). Exemplary regions to optimize the antibody include, without limitation, the Fc region, Fab region, variable region of the Fab region, constant region of the Fab region, variable domain of the heavy chain or light chain (V_H or V_L), and specific complementarity-determining regions (CDRs) of V_H or V_L.

[00150] Nucleic acid libraries synthesized by methods described herein may be expressed in various cells associated with a disease state. Cells associated with a disease state include cell lines, tissue samples, primary cells from a subject, cultured cells expanded from a subject, or cells in a model system. Exemplary model systems include, without limitation, plant and animal models of a disease state.

[00151] To identify a variant molecule associated with prevention, reduction or treatment of a disease state, a variant nucleic acid library described herein is expressed in a cell associated with a disease state, or one in which a cell a disease state can be induced. In some instances, an agent is used to induce a disease state in cells. Exemplary tools for disease state induction include, without limitation, a Cre/Lox recombination system, LPS inflammation induction, and streptozotocin to induce hypoglycemia. The cells associated with a disease state may be cells from a model system or cultured cells, as well as cells from a subject having a particular disease condition. Exemplary

disease conditions include a bacterial, fungal, viral, autoimmune, or proliferative disorder (e.g., cancer). In some instances, the variant nucleic acid library is expressed in the model system, cell line, or primary cells derived from a subject, and screened for changes in at least one cellular activity. Exemplary cellular activities include, without limitation, proliferation, cycle progression, cell death, adhesion, migration, reproduction, cell signaling, energy production, oxygen utilization, metabolic activity, and aging, response to free radical damage, or any combination thereof.

[00152] Substrates

[00153] Devices used as a surface for polynucleotide synthesis may be in the form of substrates which include, without limitation, homogenous array surfaces, patterned array surfaces, channels, beads, gels, and the like. Provided herein are substrates comprising a plurality of clusters, wherein each cluster comprises a plurality of loci that support the attachment and synthesis of polynucleotides. In some instances, substrates comprise a homogenous array surface. For example, the homogenous array surface is a homogenous plate. The term "locus" as used herein refers to a discrete region on a structure which provides support for polynucleotides encoding for a single predetermined sequence to extend from the surface. In some instances, a locus is on a two-dimensional surface, *e.g.*, a substantially planar surface. In some instances, a locus is on a three-dimensional surface, *e.g.*, a well, microwell, channel, or post. In some instances, a surface of a locus comprises a material that is actively functionalized to attach to at least one nucleotide for polynucleotide synthesis, or preferably, a population of identical nucleotides for synthesis of a population of polynucleotides. In some instances, polynucleotide refers to a population of polynucleotides encoding for the same nucleic acid sequence. In some cases, a surface of a substrate is inclusive of one or a plurality of surfaces of a substrate. The average error rates for polynucleotides synthesized within a library described here using the systems and methods provided are often less than 1 in 1000, less than about 1 in 2000, less than about 1 in 3000 or less often without error correction.

[00154] Provided herein are surfaces that support the parallel synthesis of a plurality of polynucleotides having different predetermined sequences at addressable locations on a common support. In some instances, a substrate provides support for the synthesis of more than 50, 100, 200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2,000; 5,000; 10,000; 20,000; 50,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; 10,000,000 or more non-identical polynucleotides. In some cases, the surfaces provide support for the synthesis of more than 50, 100, 200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2,000; 5,000; 10,000; 20,000; 50,000; 100,000; 200,000; 300,000; 400,000;

500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; 10,000,000 or more polynucleotides encoding for distinct sequences. In some instances, at least a portion of the polynucleotides have an identical sequence or are configured to be synthesized with an identical sequence. In some instances, the substrate provides a surface environment for the growth of polynucleotides having at least 80, 90, 100, 120, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 bases or more.

[00155] Provided herein are methods for polynucleotide synthesis on distinct loci of a substrate, wherein each locus supports the synthesis of a population of polynucleotides. In some cases, each locus supports the synthesis of a population of polynucleotides having a different sequence than a population of polynucleotides grown on another locus. In some instances, each polynucleotide sequence is synthesized with 1, 2, 3, 4, 5, 6, 7, 8, 9 or more redundancy across different loci within the same cluster of loci on a surface for polynucleotide synthesis. In some instances, the loci of a substrate are located within a plurality of clusters. In some instances, a substrate comprises at least 10, 500, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 11000, 12000, 13000, 14000, 15000, 20000, 30000, 40000, 50000 or more clusters. In some instances, a substrate comprises more than 2,000; 5,000; 10,000; 100,000; 200,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,100,000; 1,200,000; 1,300,000; 1,400,000; 1,500,000; 1,600,000; 1,700,000; 1,800,000; 1,900,000; 2,000,000; 300,000; 400,000; 500,000; 600,000; 700,000; 800,000; 900,000; 1,000,000; 1,200,000; 1,400,000; 1,600,000; 1,800,000; 2,000,000; 2,500,000; 3,000,000; 3,500,000; 4,000,000; 4,500,000; 5,000,000; or 10,000,000 or more distinct loci. In some instances, a substrate comprises about 10,000 distinct loci. The amount of loci within a single cluster is varied in different instances. In some cases, each cluster includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 130, 150, 200, 300, 400, 500 or more loci. In some instances, each cluster includes about 50-500 loci. In some instances, each cluster includes about 100-200 loci. In some instances, each cluster includes about 100-150 loci. In some instances, each cluster includes about 109, 121, 130 or 137 loci. In some instances, each cluster includes about 19, 20, 61, 64 or more loci. Alternatively or in combination, polynucleotide synthesis occurs on a homogenous array surface.

[00156] In some instances, the number of distinct polynucleotides synthesized on a substrate is dependent on the number of distinct loci available in the substrate. In some instances, the density of loci within a cluster or surface of a substrate is at least or about 1, 10, 25, 50, 65, 75, 100, 130, 150, 175, 200, 300, 400, 500, 1,000 or more loci per mm^2. In some cases, a substrate comprises 10-500, 25-400, 50-500, 100-500, 150-500, 10-250, 50-250, 10-200, or 50-200 mm^2. In some instances, the

distance between the centers of two adjacent loci within a cluster or surface is from about 10-500, from about 10-200, or from about 10-100 um. In some instances, the distance between two centers of adjacent loci is greater than about 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 um. In some instances, the distance between the centers of two adjacent loci is less than about 200, 150, 100, 80, 70, 60, 50, 40, 30, 20 or 10 um. In some instances, each locus has a width of about 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 um. In some cases, each locus has a width of about 0.5-100, 0.5-50, 10-75, or 0.5-50 um.

[00157] In some instances, the density of clusters within a substrate is at least or about 1 cluster per 100 mm^2, 1 cluster per 10 mm^2, 1 cluster per 5 mm^2, 1 cluster per 4 mm^2, 1 cluster per 3 mm^2, 1 cluster per 2 mm^2, 1 cluster per 1 mm^2, 2 clusters per 1 mm^2, 3 clusters per 1 mm^2, 4 clusters per 1 mm^2, 5 clusters per 1 mm^2, 10 clusters per 1 mm^2, 50 clusters per 1 mm^2 or more. In some instances, a substrate comprises from about 1 cluster per 10 mm^2 to about 10 clusters per 1 mm^2. In some instances, the distance between the centers of two adjacent clusters is at least or about 50, 100, 200, 500, 1000, 2000, or 5000 um. In some cases, the distance between the centers of two adjacent clusters is between about 50-100, 50-200, 50-300, 50-500, and 100-2000 um. In some cases, the distance between the centers of two adjacent clusters is between about 0.05-50, 0.05-10, 0.05-5, 0.05-4, 0.05-3, 0.05-2, 0.1-10, 0.2-10, 0.3-10, 0.4-10, 0.5-10, 0.5-5, or 0.5-2 mm. In some cases, each cluster has a cross section of about 0.5 to about 2, about 0.5 to about 1, or about 1 to about 2 mm. In some cases, each cluster has a cross section of about 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 mm. In some cases, each cluster has an interior cross section of about 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.15, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9 or 2 mm.

[00158] In some instances, a substrate is about the size of a standard 96 well plate, for example between about 100 and about 200 mm by between about 50 and about 150 mm. In some instances, a substrate has a diameter less than or equal to about 1000, 500, 450, 400, 300, 250, 200, 150, 100 or 50 mm. In some instances, the diameter of a substrate is between about 25-1000, 25-800, 25-600, 25-500, 25-400, 25-300, or 25-200 mm. In some instances, a substrate has a planar surface area of at least about 100; 200; 500; 1,000; 2,000; 5,000; 10,000; 12,000; 15,000; 20,000; 30,000; 40,000; 50,000 mm^2 or more. In some instances, the thickness of a substrate is between about 50-2000, 50- 1000, 100-1000, 200-1000, or 250-1000 mm.

[00159] *Surface materials*

[00160] Substrates, devices, and reactors provided herein are fabricated from any variety of materials suitable for the methods, compositions, and systems described herein. In certain instances, substrate materials are fabricated to exhibit a low level of nucleotide binding. In some instances, substrate materials are modified to generate distinct surfaces that exhibit a high level of

nucleotide binding. In some instances, substrate materials are transparent to visible and/or UV light. In some instances, substrate materials are sufficiently conductive, *e.g.*, are able to form uniform electric fields across all or a portion of a substrate. In some instances, conductive materials are connected to an electric ground. In some instances, the substrate is heat conductive or insulated. In some instances, the materials are chemical resistant and heat resistant to support chemical or biochemical reactions, for example polynucleotide synthesis reaction processes. In some instances, a substrate comprises flexible materials. For flexible materials, materials can include, without limitation: nylon, both modified and unmodified, nitrocellulose, polypropylene, and the like. In some instances, a substrate comprises rigid materials. For rigid materials, materials can include, without limitation: glass; fuse silica; silicon, plastics (for example polytetraflouroethylene, polypropylene, polystyrene, polycarbonate, and blends thereof, and the like); and metals (for example, gold, platinum, and the like). The substrate, solid support or reactors can be fabricated from a material selected from the group consisting of silicon, polystyrene, agarose, dextran, cellulosic polymers, polyacrylamides, polydimethylsiloxane (PDMS), and glass. The substrates/solid supports or the microstructures/reactors therein may be manufactured with a combination of materials listed herein or any other suitable material known in the art.

[00161] Surface Architecture

[00162] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates have a surface architecture suitable for the methods, compositions, and systems described herein. In some instances, a substrate comprises raised and/or lowered features. One benefit of having such features is an increase in surface area to support polynucleotide synthesis. In some instances, a substrate having raised and/or lowered features is referred to as a three-dimensional substrate. In some cases, a three-dimensional substrate comprises one or more channels. In some cases, one or more loci comprise a channel. In some cases, the channels are accessible to reagent deposition via a deposition device such as a material deposition device. In some cases, reagents and/or fluids collect in a larger well in fluid communication one or more channels. For example, a substrate comprises a plurality of channels corresponding to a plurality of loci with a cluster, and the plurality of channels are in fluid communication with one well of the cluster. In some methods, a library of polynucleotides is synthesized in a plurality of loci of a cluster.

[00163] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates are configured for polynucleotide synthesis. In some instances, the structure is configured to allow for controlled flow and mass transfer paths for polynucleotide synthesis on a surface. In some instances, the configuration of a substrate allows for the controlled

and even distribution of mass transfer paths, chemical exposure times, and/or wash efficacy during polynucleotide synthesis. In some instances, the configuration of a substrate allows for increased sweep efficiency, for example by providing sufficient volume for a growing polynucleotide such that the excluded volume by the growing polynucleotide does not take up more than 50, 45, 40, 35, 30, 25, 20, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1%, or less of the initially available volume that is available or suitable for growing the polynucleotide. In some instances, a three-dimensional structure allows for managed flow of fluid to allow for the rapid exchange of chemical exposure.

[00164] Provided herein are substrates for the methods, compositions, and systems described herein, wherein the substrates comprise structures suitable for the methods, compositions, and systems described herein. In some instances, segregation is achieved by physical structure. In some instances, segregation is achieved by differential functionalization of the surface generating active and passive regions for polynucleotide synthesis. In some instances, differential functionalization is achieved by alternating the hydrophobicity across the substrate surface, thereby creating water contact angle effects that cause beading or wetting of the deposited reagents. Employing larger structures can decrease splashing and cross-contamination of distinct polynucleotide synthesis locations with reagents of the neighboring spots. In some cases, a device, such as a material deposition device, is used to deposit reagents to distinct polynucleotide synthesis locations. Substrates having three-dimensional features are configured in a manner that allows for the synthesis of a large number of polynucleotides (*e.g.*, more than about 10,000) with a low error rate (*e.g.*, less than about 1:500, 1:1000, 1:1500, 1:2,000, 1:3,000, 1:5,000, or 1:10,000). In some cases, a substrate comprises features with a density of about or greater than about 1, 5, 10, 20, 30, 40, 50, 60, 70, 80, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400 or 500 features per mm^2.

[00165] A well of a substrate may have the same or different width, height, and/or volume as another well of the substrate. A channel of a substrate may have the same or different width, height, and/or volume as another channel of the substrate. In some instances, the diameter of a cluster or the diameter of a well comprising a cluster, or both, is between about 0.05-50, 0.05-10, 0.05-5, 0.05-4, 0.05-3, 0.05-2, 0.05-1, 0.05-0.5, 0.05-0.1, 0.1-10, 0.2-10, 0.3-10, 0.4-10, 0.5-10, 0.5-5, or 0.5-2 mm. In some instances, the diameter of a cluster or well or both is less than or about 5, 4, 3, 2, 1, 0.5, 0.1, 0.09, 0.08, 0.07, 0.06, or 0.05 mm. In some instances, the diameter of a cluster or well or both is between about 1.0 and 1.3 mm. In some instances, the diameter of a cluster or well, or both is about 1.150 mm. In some instances, the diameter of a cluster or well, or both is about 0.08 mm. The diameter of a cluster refers to clusters within a two-dimensional or three-dimensional substrate.

[00166] In some instances, the height of a well is from about 20-1000, 50-1000, 100- 1000, 200-1000, 300-1000, 400-1000, or 500-1000 um. In some cases, the height of a well is less than about 1000, 900, 800, 700, or 600 um.

[00167] In some instances, a substrate comprises a plurality of channels corresponding to a plurality of loci within a cluster, wherein the height or depth of a channel is 5-500, 5-400, 5-300, 5-200, 5-100, 5-50, or 10-50 um. In some cases, the height of a channel is less than 100, 80, 60, 40, or 20 um.

[00168] In some instances, the diameter of a channel, locus (*e.g.*, in a substantially planar substrate) or both channel and locus (*e.g.*, in a three-dimensional substrate wherein a locus corresponds to a channel) is from about 1-1000, 1-500, 1-200, 1-100, 5-100, or 10-100 um, for example, to about 90, 80, 70, 60, 50, 40, 30, 20 or 10 um. In some instances, the diameter of a channel, locus, or both channel and locus is less than about 100, 90, 80, 70, 60, 50, 40, 30, 20 or 10 um. In some instances, the distance between the center of two adjacent channels, loci, or channels and loci is from about 1-500, 1-200, 1-100, 5-200, 5-100, 5-50, or 5-30, for example, to about 20 um.

[00169] Surface Modifications

[00170] Provided herein are methods for polynucleotide synthesis on a surface, wherein the surface comprises various surface modifications. In some instances, the surface modifications are employed for the chemical and/or physical alteration of a surface by an additive or subtractive process to change one or more chemical and/or physical properties of a substrate surface or a selected site or region of a substrate surface. For example, surface modifications include, without limitation, (1) changing the wetting properties of a surface, (2) functionalizing a surface, i.e., providing, modifying or substituting surface functional groups, (3) defunctionalizing a surface, i.e., removing surface functional groups, (4) otherwise altering the chemical composition of a surface, *e.g.*, through etching, (5) increasing or decreasing surface roughness, (6) providing a coating on a surface, *e.g.*, a coating that exhibits wetting properties that are different from the wetting properties of the surface, and/or (7) depositing particulates on a surface.

[00171] In some cases, the addition of a chemical layer on top of a surface (referred to as adhesion promoter) facilitates structured patterning of loci on a surface of a substrate. Exemplary surfaces for application of adhesion promotion include, without limitation, glass, silicon, silicon dioxide and silicon nitride. In some cases, the adhesion promoter is a chemical with a high surface energy. In some instances, a second chemical layer is deposited on a surface of a substrate. In some cases, the second chemical layer has a low surface energy. In some cases, surface energy of a chemical layer coated on a surface supports localization of droplets on the surface. Depending on

the patterning arrangement selected, the proximity of loci and/or area of fluid contact at the loci are alterable.

[00172] In some instances, a substrate surface, or resolved loci, onto which nucleic acids or other moieties are deposited, *e.g.*, for polynucleotide synthesis, are smooth or substantially planar (*e.g.*, two-dimensional) or have irregularities, such as raised or lowered features (*e.g.*, three-dimensional features). In some instances, a substrate surface is modified with one or more different layers of compounds. Such modification layers of interest include, without limitation, inorganic and organic layers such as metals, metal oxides, polymers, small organic molecules, and the like.

[00173] In some instances, resolved loci of a substrate are functionalized with one or more moieties that increase and/or decrease surface energy. In some cases, a moiety is chemically inert. In some cases, a moiety is configured to support a desired chemical reaction, for example, one or more processes in a polynucleotide synthesis reaction. The surface energy, or hydrophobicity, of a surface is a factor for determining the affinity of a nucleotide to attach onto the surface. In some instances, a method for substrate functionalization comprises: (a) providing a substrate having a surface that comprises silicon dioxide; and (b) silanizing the surface using a suitable silanizing agent described herein or otherwise known in the art, for example, an organofunctional alkoxysilane molecule. Methods and functionalizing agents are described in U.S. Patent No. 5474796, which is herein incorporated by reference in its entirety.

[00174] In some instances, a substrate surface is functionalized by contact with a derivatizing composition that contains a mixture of silanes, under reaction conditions effective to couple the silanes to the substrate surface, typically via reactive hydrophilic moieties present on the substrate surface. Silanization generally covers a surface through self-assembly with organofunctional alkoxysilane molecules. A variety of siloxane functionalizing reagents can further be used as currently known in the art, *e.g.*, for lowering or increasing surface energy. The organofunctional alkoxysilanes are classified according to their organic functions.

[00175] **Polynucleotide Synthesis**

[00176] Methods of the current disclosure for polynucleotide synthesis may include processes involving phosphoramidite chemistry. In some instances, polynucleotide synthesis comprises coupling a base with phosphoramidite. Polynucleotide synthesis may comprise coupling a base by deposition of phosphoramidite under coupling conditions, wherein the same base is optionally deposited with phosphoramidite more than once, i.e., double coupling. Polynucleotide synthesis may comprise capping of unreacted sites. In some instances, capping is optional. Polynucleotide synthesis may also comprise oxidation or an oxidation step or oxidation steps. Polynucleotide synthesis may comprise deblocking, detritylation, and sulfurization. In some instances,

polynucleotide synthesis comprises either oxidation or sulfurization. In some instances, between one or each step during a polynucleotide synthesis reaction, the device is washed, for example, using tetrazole or acetonitrile. Time frames for any one step in a phosphoramidite synthesis method may be less than about 2 min, 1 min, 50 sec, 40 sec, 30 sec, 20 sec and 10 sec.

[00177] Polynucleotide synthesis using a phosphoramidite method may comprise a subsequent addition of a phosphoramidite building block (*e.g.*, nucleoside phosphoramidite) to a growing polynucleotide chain for the formation of a phosphite triester linkage. Phosphoramidite polynucleotide synthesis proceeds in the 3' to 5' direction. Phosphoramidite polynucleotide synthesis allows for the controlled addition of one nucleotide to a growing nucleic acid chain per synthesis cycle. In some instances, each synthesis cycle comprises a coupling step. Phosphoramidite coupling involves the formation of a phosphite triester linkage between an activated nucleoside phosphoramidite and a nucleoside bound to the substrate, for example, via a linker. In some instances, the nucleoside phosphoramidite is provided to the device activated. In some instances, the nucleoside phosphoramidite is provided to the device with an activator. In some instances, nucleoside phosphoramidites are provided to the device in a 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100-fold excess or more over the substrate-bound nucleosides. In some instances, the addition of nucleoside phosphoramidite is performed in an anhydrous environment, for example, in anhydrous acetonitrile. Following addition of a nucleoside phosphoramidite, the device is optionally washed. In some instances, the coupling step is repeated one or more additional times, optionally with a wash step between nucleoside phosphoramidite additions to the substrate. In some instances, a polynucleotide synthesis method used herein comprises 1, 2, 3 or more sequential coupling steps. Prior to coupling, in many cases, the nucleoside bound to the device is de-protected by removal of a protecting group, where the protecting group functions to prevent polymerization. A common protecting group is 4,4′-dimethoxytrityl (DMT).

[00178] Following coupling, phosphoramidite polynucleotide synthesis methods optionally comprise a capping step. In a capping step, the growing polynucleotide is treated with a capping agent. A capping step is useful to block unreacted substrate-bound 5′-OH groups after coupling from further chain elongation, preventing the formation of polynucleotides with internal base deletions. Further, phosphoramidites activated with 1H-tetrazole may react, to a small extent, with the O6 position of guanosine. Without being bound by theory, upon oxidation with I_2 /water, this side product, possibly via O6-N7 migration, may undergo depurination. The apurinic sites may end up being cleaved in the course of the final deprotection of the polynucleotide thus reducing the yield of the full-length product. The O6 modifications may be removed by treatment with the

capping reagent prior to oxidation with I_2/water. In some instances, inclusion of a capping step during polynucleotide synthesis decreases the error rate as compared to synthesis without capping. As an example, the capping step comprises treating the substrate-bound polynucleotide with a mixture of acetic anhydride and 1-methylimidazole. Following a capping step, the device is optionally washed.

[00179] In some instances, following addition of a nucleoside phosphoramidite, and optionally after capping and one or more wash steps, the device bound growing nucleic acid is oxidized. The oxidation step comprises a phosphite triester which is oxidized into a tetracoordinated phosphate triester, a protected precursor of the naturally occurring phosphate diester internucleoside linkage. In some instances, oxidation of the growing polynucleotide is achieved by treatment with iodine and water, optionally in the presence of a weak base (*e.g.*, pyridine, lutidine, collidine). Oxidation may be carried out under anhydrous conditions using, *e.g.* tert-Butyl hydroperoxide or (1S)-(+)-(10-camphorsulfonyl)-oxaziridine (CSO). In some methods, a capping step is performed following oxidation. A second capping step allows for device drying, as residual water from oxidation that may persist can inhibit subsequent coupling. Following oxidation, the device and growing polynucleotide are optionally washed. In some instances, the step of oxidation is substituted with a sulfurization step to obtain polynucleotide phosphorothioates, wherein any capping steps can be performed after the sulfurization. Many reagents are capable of the efficient sulfur transfer, including but not limited to 3-(Dimethylaminomethylidene)amino)-3H-1,2,4-dithiazole-3-thione, DDTT, 3H-1,2-benzodithiol-3-one 1,1-dioxide, also known as Beaucage reagent, and N,N,N'N'-Tetraethylthiuram disulfide (TETD).

[00180] In order for a subsequent cycle of nucleoside incorporation to occur through coupling, the protected 5′ end of the device bound growing polynucleotide is removed so that the primary hydroxyl group is reactive with a next nucleoside phosphoramidite. In some instances, the protecting group is DMT and deblocking occurs with trichloroacetic acid in dichloromethane. Conducting detritylation for an extended time or with stronger than recommended solutions of acids may lead to increased depurination of solid support-bound polynucleotide and thus reduces the yield of the desired full-length product. Methods and compositions of the disclosure described herein provide for controlled deblocking conditions limiting undesired depurination reactions. In some instances, the device bound polynucleotide is washed after deblocking. In some instances, efficient washing after deblocking contributes to synthesized polynucleotides having a low error rate.

[00181] Methods for the synthesis of polynucleotides typically involve an iterating sequence of the following steps: application of a protected monomer to an actively functionalized surface (*e.g.*,

locus) to link with either the activated surface, a linker or with a previously deprotected monomer; deprotection of the applied monomer so that it is reactive with a subsequently applied protected monomer; and application of another protected monomer for linking. One or more intermediate steps include oxidation or sulfurization. In some instances, one or more wash steps precede or follow one or all of the steps.

[00182] Methods for phosphoramidite-based polynucleotide synthesis comprise a series of chemical steps. In some instances, one or more steps of a synthesis method involve reagent cycling, where one or more steps of the method comprise application to the device of a reagent useful for the step. For example, reagents are cycled by a series of liquid deposition and vacuum drying steps. For substrates comprising three-dimensional features such as wells, microwells, channels and the like, reagents are optionally passed through one or more regions of the device via the wells and/or channels.

[00183] Methods and systems described herein relate to polynucleotide synthesis devices for the synthesis of polynucleotides. The synthesis may be in parallel. For example, at least or about at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 1000, 10000, 50000, 75000, 100000 or more polynucleotides can be synthesized in parallel. The total number polynucleotides that may be synthesized in parallel may be from 2-100000, 3-50000, 4-10000, 5-1000, 6-900, 7-850, 8-800, 9-750, 10-700, 11-650, 12-600, 13-550, 14-500, 15-450, 16-400, 17-350, 18-300, 19-250, 20-200, 21-150,22-100, 23-50, 24-45, 25-40, 30-35. Those of skill in the art appreciate that the total number of polynucleotides synthesized in parallel may fall within any range bound by any of these values, for example 25-100. The total number of polynucleotides synthesized in parallel may fall within any range defined by any of the values serving as endpoints of the range. Total molar mass of polynucleotides synthesized within the device or the molar mass of each of the polynucleotides may be at least or at least about 10, 20, 30, 40, 50, 100, 250, 500, 750, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 25000, 50000, 75000, 100000 picomoles, or more. The length of each of the polynucleotides or average length of the polynucleotides within the device may be at least or about at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 400, 500 nucleotides, or more. The length of each of the polynucleotides or average length of the polynucleotides within the device may be at most or about at most 500, 400, 300, 200, 150, 100, 50, 45, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10 nucleotides, or less. The length of each of the polynucleotides or average length of the polynucleotides within the device may fall from 10-500, 9-400, 11-300, 12-200, 13-150, 14-100, 15-50, 16-45, 17-40, 18-35, 19-25. Those of skill in the art appreciate that the length of each of the polynucleotides or average

length of the polynucleotides within the device may fall within any range bound by any of these values, for example 100-300. The length of each of the polynucleotides or average length of the polynucleotides within the device may fall within any range defined by any of the values serving as endpoints of the range.

[00184] Methods for polynucleotide synthesis on a surface provided herein allow for synthesis at a fast rate. As an example, at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 125, 150, 175, 200 nucleotides per hour, or more are synthesized. Nucleotides include adenine, guanine, thymine, cytosine, uridine building blocks, or analogs/modified versions thereof. In some instances, libraries of polynucleotides are synthesized in parallel on substrate. For example, a device comprising about or at least about 100; 1,000; 10,000; 30,000; 75,000; 100,000; 1,000,000; 2,000,000; 3,000,000; 4,000,000; or 5,000,000 resolved loci is able to support the synthesis of at least the same number of distinct polynucleotides, wherein polynucleotide encoding a distinct sequence is synthesized on a resolved locus. In some instances, a library of polynucleotides is synthesized on a device with low error rates described herein in less than about three months, two months, one month, three weeks, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 days, 24 hours, or less. In some instances, larger nucleic acids assembled from a polynucleotide library synthesized with low error rate using the substrates and methods described herein are prepared in less than about three months, two months, one month, three weeks, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 days, 24 hours, or less.

[00185] In some instances, methods described herein provide for generation of a library of nucleic acids comprising variant nucleic acids differing at a plurality of codon sites. In some instances, a nucleic acid may have 1 site, 2 sites, 3 sites, 4 sites, 5 sites, 6 sites, 7 sites, 8 sites, 9 sites, 10 sites, 11 sites, 12 sites, 13 sites, 14 sites, 15 sites, 16 sites, 17 sites 18 sites, 19 sites, 20 sites, 30 sites, 40 sites, 50 sites, or more of variant codon sites.

[00186] In some instances, the one or more sites of variant codon sites may be adjacent. In some instances, the one or more sites of variant codon sites may not be adjacent but are separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more codons.

[00187] In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein all the variant codon sites are adjacent to one another, forming a stretch of variant codon sites. In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein none the variant codon sites are adjacent to one another. In some instances, a nucleic acid may comprise multiple sites of variant codon sites, wherein some the variant codon sites are adjacent to one another, forming a stretch of variant codon sites, and some of the variant codon sites are not adjacent to one another.

[00188] Referring to the Figures, **FIG. 3** illustrates an exemplary process workflow for synthesis of nucleic acids (e.g., genes) from shorter nucleic acids. The workflow is divided generally into phases: (1) de novo synthesis of a single stranded nucleic acid library, (2) joining nucleic acids to form larger fragments, (3) error correction, (4) quality control, and (5) shipment. Prior to de novo synthesis, an intended nucleic acid sequence or group of nucleic acid sequences is preselected. For example, a group of genes is preselected for generation.

[00189] Once large nucleic acids for generation are selected, a predetermined library of nucleic acids is designed for de novo synthesis. Various suitable methods are known for generating high density polynucleotide arrays. In the workflow example, a device surface layer is provided. In the example, chemistry of the surface is altered in order to improve the polynucleotide synthesis process. Areas of low surface energy are generated to repel liquid while areas of high surface energy are generated to attract liquids. The surface itself may be in the form of a planar surface or contain variations in shape, such as protrusions or microwells which increase surface area. In the workflow example, high surface energy molecules selected serve a dual function of supporting DNA chemistry, as disclosed in International Patent Application Publication WO/2015/021080, which is herein incorporated by reference in its entirety.

[00190] In situ preparation of polynucleotide arrays is generated on a solid support and utilizes single nucleotide extension process to extend multiple oligomers in parallel. A deposition device, such as a material deposition device, is designed to release reagents in a step-wise fashion such that multiple polynucleotides extend, in parallel, one residue at a time to generate oligomers with a predetermined nucleic acid sequence **302**. In some instances, polynucleotides are cleaved from the surface at this stage. Cleavage includes gas cleavage, *e.g.*, with ammonia or methylamine.

[00191] The generated polynucleotide libraries are placed in a reaction chamber. In this exemplary workflow, the reaction chamber (also referred to as "nanoreactor") is a silicon coated well, containing PCR reagents and lowered onto the polynucleotide library **303**. Prior to or after the sealing **304** of the polynucleotides, a reagent is added to release the polynucleotides from the substrate. In the exemplary workflow, the polynucleotides are released subsequent to sealing of the nanoreactor **305**. Once released, fragments of single stranded polynucleotides hybridize in order to span an entire long-range sequence of DNA. Partial hybridization **305** is possible because each synthesized polynucleotide is designed to have a small portion overlapping with at least one other polynucleotide in the pool.

[00192] After hybridization, a PCA reaction is commenced. During the polymerase cycles, the polynucleotides anneal to complementary fragments and gaps are filled in by a polymerase. Each cycle increases the length of various fragments randomly depending on which polynucleotides find

each other. Complementarity amongst the fragments allows for formation of a complete large span of double stranded DNA **306**.

[00193] After PCA is complete, the nanoreactor is separated from the device **307** and positioned for interaction with a device having primers for PCR **308**. After sealing, the nanoreactor is subject to PCR **309** and the larger nucleic acids are amplified. After PCR **310**, the nanochamber is opened **311**, error correction reagents are added **312**, the chamber is sealed **313** and an error correction reaction occurs to remove mismatched base pairs and/or strands with poor complementarity from the double stranded PCR amplification products **314**. The nanoreactor is opened and separated **315**. Error corrected product is next subject to additional processing steps, such as PCR and molecular bar coding, and then packaged **322** for shipment **323**.

[00194] In some instances, quality control measures are taken. After error correction, quality control steps include for example interaction with a wafer having sequencing primers for amplification of the error corrected product **316**, sealing the wafer to a chamber containing error corrected amplification product **317**, and performing an additional round of amplification **318**. The nanoreactor is opened **319** and the products are pooled **320** and sequenced **321**. After an acceptable quality control determination is made, the packaged product **322** is approved for shipment **323**.

[00195] In some instances, a nucleic acid generated by a workflow such as that in **FIG. 3** is subject to mutagenesis using overlapping primers disclosed herein. In some instances, a library of primers is generated by in situ preparation on a solid support and utilize single nucleotide extension process to extend multiple oligomers in parallel. A deposition device, such as a material deposition device, is designed to release reagents in a step wise fashion such that multiple polynucleotides extend, in parallel, one residue at a time to generate oligomers with a predetermined nucleic acid sequence **302**.

[00196] **Computer systems**

[00197] Any of the systems described herein, may be operably linked to a computer and may be automated through a computer either locally or remotely. In various instances, the methods and systems of the disclosure may further comprise software programs on computer systems and use thereof. Accordingly, computerized control for the synchronization of the dispense/vacuum/refill functions such as orchestrating and synchronizing the material deposition device movement, dispense action and vacuum actuation are within the bounds of the disclosure. The computer systems may be programmed to interface between the user specified base sequence and the position of a material deposition device to deliver the correct reagents to specified regions of the substrate.

[00198] The computer system **400** illustrated in **FIG. 4** may be understood as a logical apparatus that can read instructions from media **411** and/or a network port **405**, which can optionally be

connected to server **409** having fixed media **412**. The system, such as shown in **FIG. 4** can include a CPU **401**, disk drives **403**, optional input devices such as keyboard **415** and/or mouse **416** and optional monitor **407**. Data communication can be achieved through the indicated communication medium to a server at a local or a remote location. The communication medium can include any means of transmitting and/or receiving data. For example, the communication medium can be a network connection, a wireless connection or an internet connection. Such a connection can provide for communication over the World Wide Web. It is envisioned that data relating to the present disclosure can be transmitted over such networks or connections for reception and/or review by a party **422** as illustrated in **FIG. 4**.

[00199] **FIG. 5** is a block diagram illustrating a first example architecture of a computer system **500** that can be used in connection with example instances of the present disclosure. As depicted in **FIG. 5**, the example computer system can include a processor **502** for processing instructions. Non-limiting examples of processors include: Intel Xeon™ processor, AMD Opteron™ processor, Samsung 32-bit RISC ARM 1176JZ(F)-S v1.0™ processor, ARM Cortex-A8 Samsung S5PC100TM processor, ARM Cortex-A8 Apple A4™ processor, Marvell PXA 930™ processor, or a functionally-equivalent processor. Multiple threads of execution can be used for parallel processing. In some instances, multiple processors or processors with multiple cores can also be used, whether in a single computer system, in a cluster, or distributed across systems over a network comprising a plurality of computers, cell phones, and/or personal data assistant devices.

[00200] As illustrated in **FIG. 5**, a high-speed cache **504** can be connected to, or incorporated in, the processor **502** to provide a high speed memory for instructions or data that have been recently, or are frequently, used by the processor **502**. The processor **502** is connected to a north bridge **506** by a processor bus **508**. The north bridge **506** is connected to random access memory (RAM) **510** by a memory bus **512** and manages access to the RAM **510** by the processor **502**. The north bridge **506** is also connected to a south bridge **514** by a chipset bus **516**. The south bridge **514** is, in turn, connected to a peripheral bus **518**. The peripheral bus can be, for example, PCI, PCI-X, PCI Express, or other peripheral bus. The north bridge and south bridge are often referred to as a processor chipset and manage data transfer between the processor, RAM, and peripheral components on the peripheral bus **518**. In some alternative architectures, the functionality of the north bridge can be incorporated into the processor instead of using a separate north bridge chip. In some instances, system **500** can include an accelerator card **522** attached to the peripheral bus **518**. The accelerator can include field programmable gate arrays (FPGAs) or other hardware for accelerating certain processing. For example, an accelerator can be used for adaptive data restructuring or to evaluate algebraic expressions used in extended set processing.

[00201] Software and data are stored in external storage **524** and can be loaded into RAM **510** and/or cache **504** for use by the processor. The system **500** includes an operating system for managing system resources; non-limiting examples of operating systems include: Linux, Windows™, MACOSTM, BlackBerry OSTM, iOS™, and other functionally-equivalent operating systems, as well as application software running on top of the operating system for managing data storage and optimization in accordance with example instances of the present disclosure. In this example, system **500** also includes network interface cards (NICs) **520** and **521** connected to the peripheral bus for providing network interfaces to external storage, such as Network Attached Storage (NAS) and other computer systems that can be used for distributed parallel processing.

[00202] **FIG. 6** is a diagram showing a network **600** with a plurality of computer systems **602a**, and **602b**, a plurality of cell phones and personal data assistants **602c**, and Network Attached Storage (NAS) **604a**, and **604b**. In example instances, systems **602a**, **602b**, and **602c** can manage data storage and optimize data access for data stored in Network Attached Storage (NAS) **604a** and **604b**. A mathematical model can be used for the data and be evaluated using distributed parallel processing across computer systems **602a**, and **602b**, and cell phone and personal data assistant systems **602c**. Computer systems **602a**, and **602b**, and cell phone and personal data assistant systems **602c** can also provide parallel processing for adaptive data restructuring of the data stored in Network Attached Storage (NAS) **604a** and **604b**. **FIG. 6** illustrates an example only, and a wide variety of other computer architectures and systems can be used in conjunction with the various instances of the present disclosure. For example, a blade server can be used to provide parallel processing. Processor blades can be connected through a back plane to provide parallel processing. Storage can also be connected to the back plane or as Network Attached Storage (NAS) through a separate network interface. In some example instances, processors can maintain separate memory spaces and transmit data through network interfaces, back plane or other connectors for parallel processing by other processors. In other instances, some or all of the processors can use a shared virtual address memory space.

[00203] **FIG. 7** is a block diagram of a multiprocessor computer system **700** using a shared virtual address memory space in accordance with an example instance. The system includes a plurality of processors **702a-f** that can access a shared memory subsystem **704**. The system incorporates a plurality of programmable hardware memory algorithm processors (MAPs) **706a-f** in the memory subsystem **704**. Each MAP **706a-f** can comprise a memory **708a-f** and one or more field programmable gate arrays (FPGAs) **710a-f**. The MAP provides a configurable functional unit and particular algorithms or portions of algorithms can be provided to the FPGAs **710a-f** for processing in close coordination with a respective processor. For example, the MAPs can be used

to evaluate algebraic expressions regarding the data model and to perform adaptive data restructuring in example instances. In this example, each MAP is globally accessible by all of the processors for these purposes. In one configuration, each MAP can use Direct Memory Access (DMA) to access an associated memory **708a-f**, allowing it to execute tasks independently of, and asynchronously from the respective microprocessor **702a-f**. In this configuration, a MAP can feed results directly to another MAP for pipelining and parallel execution of algorithms.

[00204] The above computer architectures and systems are examples only, and a wide variety of other computer, cell phone, and personal data assistant architectures and systems can be used in connection with example instances, including systems using any combination of general processors, co-processors, FPGAs and other programmable logic devices, system on chips (SOCs), application specific integrated circuits (ASICs), and other processing and logic elements. In some instances, all or part of the computer system can be implemented in software or hardware. Any variety of data storage media can be used in connection with example instances, including random access memory, hard drives, flash memory, tape drives, disk arrays, Network Attached Storage (NAS) and other local or distributed data storage devices and systems.

[00205] In example instances, the computer system can be implemented using software modules executing on any of the above or other computer architectures and systems. In other instances, the functions of the system can be implemented partially or completely in firmware, programmable logic devices such as field programmable gate arrays (FPGAs) as referenced in **FIG. 5**, system on chips (SOCs), application specific integrated circuits (ASICs), or other processing and logic elements. For example, the Set Processor and Optimizer can be implemented with hardware acceleration through the use of a hardware accelerator card, such as accelerator card **522** illustrated in **FIG. 5**.

[00206] The following examples are set forth to illustrate more clearly the principle and practice of embodiments disclosed herein to those skilled in the art and are not to be construed as limiting the scope of any claimed embodiments. Unless otherwise stated, all parts and percentages are on a weight basis.

EXAMPLES

[00207] The following examples are given for the purpose of illustrating various embodiments of the disclosure and are not meant to limit the present disclosure in any fashion. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the disclosure.

Changes therein and other uses which are encompassed within the spirit of the disclosure as defined by the scope of the claims will occur to those skilled in the art.

[00208] Example 1: Functionalization of a device surface

[00209] A device was functionalized to support the attachment and synthesis of a library of polynucleotides. The device surface was first wet cleaned using a piranha solution comprising 90% H_2SO_4 and 10% H_2O_2 for 20 minutes. The device was rinsed in several beakers with DI water, held under a DI water gooseneck faucet for 5 min, and dried with N_2. The device was subsequently soaked in NH_4OH (1:100; 3 mL:300 mL) for 5 min, rinsed with DI water using a handgun, soaked in three successive beakers with DI water for 1 min each, and then rinsed again with DI water using the handgun. The device was then plasma cleaned by exposing the device surface to O_2. A SAMCO PC-300 instrument was used to plasma etch O_2 at 250 watts for 1 min in downstream mode.

[00210] The cleaned device surface was actively functionalized with a solution comprising N-(3-triethoxysilylpropyl)-4-hydroxybutyramide using a YES-1224P vapor deposition oven system with the following parameters: 0.5 to 1 torr, 60 min, 70 °C, 135 °C vaporizer. The device surface was resist coated using a Brewer Science 200X spin coater. SPR™ 3612 photoresist was spin coated on the device at 2500 rpm for 40 sec. The device was pre-baked for 30 min at 90 °C on a Brewer hot plate. The device was subjected to photolithography using a Karl Suss MA6 mask aligner instrument. The device was exposed for 2.2 sec and developed for 1 min in MSF 26A. Remaining developer was rinsed with the handgun and the device soaked in water for 5 min. The device was baked for 30 min at 100 °C in the oven, followed by visual inspection for lithography defects using a Nikon L200. A descum process was used to remove residual resist using the SAMCO PC-300 instrument to O_2 plasma etch at 250 watts for 1 min.

[00211] The device surface was passively functionalized with a 100 µL solution of perfluorooctyltrichlorosilane mixed with 10 µL light mineral oil. The device was placed in a chamber, pumped for 10 min, and then the valve was closed to the pump and left to stand for 10 min. The chamber was vented to air. The device was resist stripped by performing two soaks for 5 min in 500 mL NMP at 70 °C with ultrasonication at maximum power (9 on Crest system). The device was then soaked for 5 min in 500 mL isopropanol at room temperature with ultrasonication at maximum power. The device was dipped in 300 mL of 200 proof ethanol and blown dry with N_2. The functionalized surface was activated to serve as a support for polynucleotide synthesis.

[00212] Example 2: Synthesis of a 50-mer sequence on an oligonucleotide synthesis device

[00213] A two-dimensional oligonucleotide synthesis device was assembled into a flowcell, which was connected to a flowcell (Applied Biosystems (ABI394 DNA Synthesizer"). The two-dimensional oligonucleotide synthesis device was uniformly functionalized with N-(3-

TRIETHOXYSILYLPROPYL)-4-HYDROXYBUTYRAMIDE (Gelest) which was used to synthesize an exemplary polynucleotide of 50 bp ("50-mer polynucleotide") using polynucleotide synthesis methods described herein.

[00214] The sequence of the 50-mer was as described in SEQ ID NO: 393. 5'AGACAATCAACCATTTGGGGTGGACAGCCTTGACCTCTAGACTTCGGCAT##TTTTTTTTTT3' (SEQ ID NO.: 393), where # denotes Thymidine-succinyl hexamide CED phosphoramidite (CLP-2244 from ChemGenes), which is a cleavable linker enabling the release of oligos from the surface during deprotection.

[00215] The synthesis was done using standard DNA synthesis chemistry (coupling, capping, oxidation, and deblocking) according to the protocol in **Table 1** and an ABI synthesizer.

Table 1: Synthesis protocols

	Table 1	
General DNA Synthesis Process Name	**Process Step**	**Time (sec)**
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	23
	N2 System Flush	4
	Acetonitrile System Flush	4
DNA BASE ADDITION (Phosphoramidite + Activator Flow)	Activator Manifold Flush	2
	Activator to Flowcell	6
	Activator + Phosphoramidite to Flowcell	6
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Activator to Flowcell	0.5
	Activator + Phosphoramidite to Flowcell	5
	Incubate for 25sec	25
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
DNA BASE ADDITION (Phosphoramidite + Activator Flow)	Activator Manifold Flush	2
	Activator to Flowcell	5
	Activator +	18

Table 1		
General DNA Synthesis Process Name	**Process Step**	**Time (sec)**
	Phosphoramidite to Flowcell	
	Incubate for 25sec	25
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
CAPPING (CapA+B, 1:1, Flow)	CapA+B to Flowcell	15
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	Acetonitrile System Flush	4
OXIDATION (Oxidizer Flow)	Oxidizer to Flowcell	18
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	15
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	23
	N2 System Flush	4
	Acetonitrile System Flush	4
DEBLOCKING (Deblock Flow)	Deblock to Flowcell	36
WASH (Acetonitrile Wash Flow)	Acetonitrile System Flush	4
	N2 System Flush	4
	Acetonitrile System Flush	4
	Acetonitrile to Flowcell	18
	N2 System Flush	4.13
	Acetonitrile System Flush	4.13
	Acetonitrile to Flowcell	15

[00216] The phosphoramidite/activator combination was delivered similarly to the delivery of bulk reagents through the flowcell. No drying steps were performed as the environment stays "wet" with reagent the entire time.

[00217] The flow restrictor was removed from the ABI 394 synthesizer to enable faster flow. Without flow restrictor, flow rates for amidites (0.1M in ACN), Activator, (0.25M Benzoylthiotetrazole ("BTT"; 30-3070-xx from GlenResearch) in ACN), and Ox (0.02M I2 in 20% pyridine, 10% water, and 70% THF) were roughly ~100uL/sec, for acetonitrile ("ACN") and capping reagents (1:1 mix of CapA and CapB, wherein CapA is acetic anhydride in THF/Pyridine

and CapB is 16% 1-methylimidizole in THF), roughly ~200uL/sec, and for Deblock (3% dichloroacetic acid in toluene), roughly ~300uL/sec (compared to ~50uL/sec for all reagents with flow restrictor). The time to completely push out Oxidizer was observed, the timing for chemical flow times was adjusted accordingly and an extra ACN wash was introduced between different chemicals. After polynucleotide synthesis, the chip was deprotected in gaseous ammonia overnight at 75 psi. Five drops of water were applied to the surface to recover polynucleotides. The recovered polynucleotides were then analyzed on a BioAnalyzer small RNA chip.

[00218] Example 3: Synthesis of a 100-mer sequence on an oligonucleotide synthesis device

[00219] The same process as described in Example 2 for the synthesis of the 50-mer sequence was used for the synthesis of a 100-mer polynucleotide ("100-mer polynucleotide"; 5' CGGGATCCTTATCGTCATCGTCGTACAGATCCCGACCCATTTGCTGTCCACCAGTCATG CTAGCCATACCATGATGATGATGATGATGAGAACCCCGCAT##TTTTTTTTTT3', where # denotes Thymidine-succinyl hexamide CED phosphoramidite (CLP-2244 from ChemGenes); SEQ ID NO.: 2161) on two different silicon chips, the first one uniformly functionalized with N-(3-TRIETHOXYSILYLPROPYL)-4-HYDROXYBUTYRAMIDE and the second one functionalized with 5/95 mix of 11-acetoxyundecyltriethoxysilane and n-decyltriethoxysilane, and the polynucleotides extracted from the surface were analyzed on a BioAnalyzer instrument.

[00220] All ten samples from the two chips were further PCR amplified using a forward (5'ATGCGGGGTTCTCATCATC3'; SEQ ID NO.: 2162) and a reverse (5'CGGGATCCTTATCGTCATCG3'; SEQ ID NO.: 2163) primer in a 50uL PCR mix (25uL NEB Q5 mastermix, 2.5uL 10uM Forward primer, 2.5uL 10uM Reverse primer, 1uL polynucleotide extracted from the surface, and water up to 50uL) using the following thermalcycling program:

98 ℃, 30 sec

98 ℃, 10 sec; 63 ℃, 10 sec; 72 ℃, 10 sec; repeat 12 cycles

72 ℃, 2 min

[00221] The PCR products were also run on a BioAnalyzer, demonstrating sharp peaks at the 100-mer position. Next, the PCR amplified samples were cloned, and Sanger sequenced. **Table 2** summarizes the results from the Sanger sequencing for samples taken from spots 1-5 from chip 1 and for samples taken from spots 6-10 from chip 2.

Table 2: Sequencing results

Spot	Error rate	Cycle efficiency
1	1/763 bp	99.87%
2	1/824 bp	99.88%

Spot	Error rate	Cycle efficiency
3	1/780 bp	99.87%
4	1/429 bp	99.77%
5	1/1525 bp	99.93%
6	1/1615 bp	99.94%
7	1/531 bp	99.81%
8	1/1769 bp	99.94%
9	1/854 bp	99.88%
10	1/1451 bp	99.93%

[00222] Thus, the high quality and uniformity of the synthesized polynucleotides were repeated on two chips with different surface chemistries. Overall, 89% of the 100-mers that were sequenced were perfect sequences with no errors, corresponding to 233 out of 262.

[00223] **Table 3** summarizes error characteristics for the sequences obtained from the polynucleotide samples from spots 1-10.

Table 3: Error characteristics

Sample ID/Spot no.	OSA_0046/1	OSA_0047/2	OSA_0048/3	OSA_0049/4	OSA_0050/5	OSA_0051/6	OSA_0052/7	OSA_0053/8	OSA_0054/9	OSA_0055/10
Total Sequences	32	32	32	32	32	32	32	32	32	32
Sequencing Quality	25 of 28	27 of 27	26 of 30	21 of 23	25 of 26	29 of 30	27 of 31	29 of 31	28 of 29	25 of 28
Oligo Quality	23 of 25	25 of 27	22 of 26	18 of 21	24 of 25	25 of 29	22 of 27	28 of 29	26 of 28	20 of 25
ROI Match Count	2500	2698	2561	2122	2499	2666	2625	2899	2798	2348
ROI Mutation	2	2	1	3	1	0	2	1	2	1
ROI Multi Base Deletion	0	0	0	0	0	0	0	0	0	0
ROI Small Insertion	1	0	0	0	0	0	0	0	0	0
ROI Single Base Deletion	0	0	0	0	0	0	0	0	0	0
Large Deletion	0	0	1	0	0	1	1	0	0	0

Count										
Mutation: G>A	2	2	1	2	1	0	2	1	2	1
Mutation: T>C	0	0	0	1	0	0	0	0	0	0
ROI Error Count	3	2	2	3	1	1	3	1	2	1
ROI Error Rate	Err: ~1 in 834	Err: ~1 in 1350	Err: ~1 in 1282	Err: ~1 in 708	Err: ~1 in 2500	Err: ~1 in 2667	Err: ~1 in 876	Err: ~1 in 2900	Err: ~1 in 1400	Err: ~1 in 2349
ROI Minus Primer Error Rate	MP Err: ~1 in 763	MP Err: ~1 in 824	MP Err: ~1 in 780	MP Err: ~1 in 429	MP Err: ~1 in 1525	MP Err: ~1 in 1615	MP Err: ~1 in 531	MP Err: ~1 in 1769	MP Err: ~1 in 854	MP Err: ~1 in 1451

[00224] Example 4: Exemplary Sequences

Table 4. Variable Heavy Chain CDRs

DKK1 Variant	SEQ ID NO	CDR1 Sequence	SEQ ID NO	CDR2 Sequence	SEQ ID NO	CDR3 Sequence
DKK1-1	1	GRTFSRFAM	99	EGVASITSGGTTNY	197	AADDGARGSW
DKK1-2	2	GSAFSSTVM	100	EFVATINSLGGTSY	198	AAAYSGHFSGRVSDFLW
DKK1-3	3	GSTFSTYAM	101	EFVASINWGGGNTYY	199	AAKKVSFGDW
DKK1-4	4	GNIFRINAM	102	ELVAAISRSGGSTNY	200	AKDKNGPW
DKK1-5	5	GGLTFSTYAM	103	EFVAAVSWSGGNTYY	201	AAEIGYYSGGTYYSSEAW
DKK1-6	6	GIPFSTRTM	104	EFVAAISSGATTLY	202	AAGNGGRAYGYSRARYEW
DKK1-7	7	GISGSVFSRTPM	105	EFVAALSKDGARTYY	203	ARDLVGTDAFDIW
DKK1-8	8	GFTFSNYAM	106	EFVAAISWSDGSTYY	204	AAEGGYSGTYYYTGDFDW
DKK1-9	9	GRSFSMYAM	107	ELVAAISWSGGSTVY	205	AAEGGYSGTYYYTGDFDW
DKK1-10	10	GRTISNYAM	108	EFVAAISWRGGSTYY	206	AAAPRPKYVSVSYFSTSSNYDW
DKK1-11	11	GPTVDAYAM	109	EFVSAISWSGSATFY	207	AAAPRPKRVSVRYFSTSSNYDW
DKK1-12	12	GRTFNSRPM	110	EFVAAISSSASSTYY	208	AAGNGGRLYGHSRARYDW
DKK1-13	13	GFLMYDRAM	111	EIVAAISRTGSSIYY	209	AAGNGGRKYGHHRARYDW
DKK1-14	14	GSIFSRLAM	112	EFVAAISSSGISTIY	210	ARGQRGRWLEPLTGW
DKK1-15	15	GFTFGTTTM	113	ELVAAITSGGGTTYY	211	AKDLAAAGYYYYYGMDVW
DKK1-16	16	GNIFTRNVM	114	EFVGAINWSGGNTVY	212	ARHDHNNRGLDYW
DKK1-17	17	GGTFSRYAM	115	EFVAGISWTLGRTYY	213	ARDPFGKW
DKK1-18	18	GITFRFKAM	116	EFVAAINRSGRSTRY	214	AAESHGSTSPRNPLQYDW

DKK1-19	19	GRTYGM	117	EFVAGISWTLGRTYY	215	ASDESDAANW
DKK1-20	20	GPTFSIYDM	118	EFVTGSNTGGTTY	216	ATCTDFEYDW
DKK1-21	21	GIPSSIRAM	119	EWVSGISISDSSTYY	217	AAGKRYGYYDW
DKK1-22	22	GSTLSINAM	120	ELVAAISWSGGTAY	218	AAQSRYRSNYYDHDKYAW
DKK1-23	23	GYNFSTFCM	121	EWVAAISGGGSTMY	219	AASKWYGGFGDTDIEW
DKK1-24	24	GSSFSAYGM	122	EFVAGISWTLGRTYY	220	AADGVPEYSDYASGPVW
DKK1-25	25	GSTSRSYGM	123	EFVAGISWTLGRTYY	221	ARDPSGKW
DKK1-26	26	GFSLDYYGM	124	EVVASIRWNAKPYY	222	AAGKRYGYYDW
DKK1-27	27	GRTFSNYAM	125	EWVASISTSGKTTYY	223	AAGNGGRNYGHSRARYEW
DKK1-28	28	GLTTVYTM	126	EFVAAISWYVSTTFY	224	AAEGGYSGTYYYTGDFDW
DKK1-29	29	GSIGGLNAM	127	EFVAAINYSGRSTVY	225	AAGAGRDRGFSRAQYAW
DKK1-30	30	GRTFSKYAM	128	EFVAAISWSGESTYY	226	AAAPRPKRVSVSYFYTSSNYDW
DKK1-31	31	GRTLSRSAM	129	ELVAAISWSGGSTYY	227	AAGNGGRTYGHSRARYEW
DKK1-32	32	GRTFSNGPM	130	EFVAAISRGGKISHY	228	AAGNGGRYYGHSRARYDW
DKK1-33	33	GRSLNTYTM	131	ELVAVIISGGSTAY	229	AAGNGGRSYGHSRARYDW
DKK1-34	34	GFTFDDRAM	132	EFVAAISWSGGSTYY	230	AAAPRPKRVSVSYFYTSSNYDW
DKK1-35	35	GRTFTTYPM	133	EFVAAISSSGSSTVY	231	AAGNGGRQYGHSRARYDW
DKK1-36	36	GIPSTLRAM	134	EFVAAINWSGASTVY	232	AAGNGGRQYGHSRARYDW
DKK1-37	37	GRTFSSYSM	135	EFIAAINLSSGSTYY	233	AAGNGGRNYGHSRARYEW
DKK1-38	38	GTSFSIGAM	136	EWVSSISPGGLFPYY	234	AARDAIVGVTDTSGYRW
DKK1-39	39	GTVFSISDM	137	EWVSAISPGGGYTVY	235	ARSSWFDCGVQGRDLGNEYDW
DKK1-40	40	GRTISSFRM	138	EFVAAISRGGNVTPY	236	AANSDSGFDSYSVWAAYEW
DKK1-41	41	GRTLSRS	139	SWSGGS	237	GNGGRTYGHSRARYE
DKK1-42	42	GRTFSSL	140	TSGGR	238	GNGGRTYGHSRARYE
DKK1-43	43	GTSFSVG	141	SWSGGT	239	GNGGRQYGHSRARYD
DKK1-44	44	GRG	142	NRSGKS	240	GNGGRSYGHSRARYD
DKK1-45	45	GRTFSNF	143	SATGS	241	GNGGRQYGHSRARYD
DKK1-46	46	GRTLSSI	144	TRAGS	242	GNGGRYYGHSRARYD
DKK1-47	47	GRTFSSL	145	SSGGS	243	GNGGRTYGHSRARYD
DKK1-48	48	GRSFGNF	146	TSGGS	244	GNGGRSYGHSRARYD
DKK1-49	49	GFTFTNY	147	NWSGRR	245	APRPKRVSVQYFSTSSNYD
DKK1-50	50	GRTFSLY	148	NRSGKS	246	GNGGRQYGHSRARYD
DKK1-51	51	GRTFSTS	149	NRSGKT	247	GNGGRAYGYSRARYE
DKK1-52	52	GRTFSIS	150	SPSGN	248	GNGGRAYGYSRARYE

DKK1-53	53	GRTFSSY	151	SRSGT	249	GNGGRTYGHSRARYE
DKK1-54	54	GFTFDDR	152	STGGT	250	GNGGRTYGHSRARYE
DKK1-55	55	GFTFGDY	153	DWSGRR	251	APRPKRVSVSYFSTASNYD
DKK1-56	56	GRTFSSL	154	SSSGGT	252	GNGGRLYGHSRARYD
DKK1-57	57	GSTFSKA	155	TFSGAR	253	GNGGRTYGHSRARYD
DKK1-58	58	GRRFSAD	156	RSGGT	254	GNGGRQYGHSRARYD
DKK1-59	59	GFTVSNY	157	SWSGGS	255	APRPKRVSVRYFSTSSNYD
DKK1-60	60	GRAFSSS	158	NRGGKI	256	GNGGRLYGHSRARYD
DKK1-61	61	GRTFSSN	159	SRSGGS	257	GNGGRTYGHSRARYD
DKK1-62	62	GRTFSYN	160	NRSGKS	258	GNGGRHYGHSRARYD
DKK1-63	63	GFRMYDR	161	SRSGGR	259	GNGGRLYGHSRARYD
DKK1-64	64	GRTSSAY	162	SRSGAS	260	GNGGRSYGHSRARYD
DKK1-65	65	GRTFSRF	163	SARGM	261	GNGGRTYGHSRARYE
DKK1-66	66	GRTFSSY	164	NLSSGS	262	GNGGRNYGHSRARYE
DKK1-67	67	GRTFRSY	165	SMSGKE	263	GNGGRTYGHSRARYE
DKK1-68	68	GRTFSNY	166	STSGKT	264	GNGGRNYGHSRARYE
DKK1-69	69	GRTFSSY	167	SRSGGS	265	GNGGRHYGHSRARYD
DKK1-70	70	GTSFSIG	168	SRSGAS	266	GNGGRTYGHSRARYD
DKK1-71	71	GRTISNA	169	RSGGT	267	GNGGRQYGHSRARYD
DKK1-72	72	GGIYRVN	170	NWSGGS	268	GNGGRKYGHHRARYD
DKK1-73	73	GRTFSSK	171	NWSGGL	269	GNGGRAYGYSRARYE
DKK1-74	74	GIPFSSR	172	SRSGTG	270	GNGGRTYGHSRARYD
DKK1-75	75	GPTVDAY	173	SWSGSA	271	APRPKRVSVRYFSTSSNYD
DKK1-76	76	GIPFSTR	174	SSGAT	272	GNGGRAYGYSRARYE
DKK1-77	77	GRTFNSR	175	SSSASS	273	GNGGRLYGHSRARYD
DKK1-78	78	GFTFSSS	176	LRGGS	274	GNGGRHYGHSRARYD
DKK1-79	79	SIGIAFSSR	177	TRSGGK	275	GNGGRTYGHSRARYE
DKK1-80	80	GFLMYDR	178	SRTGSS	276	GNGGRKYGHHRARYD
DKK1-81	81	GIAFQGY	179	DTNGGH	277	EGGYRGTYYYTGDFD
DKK1-82	82	GRTFSNT	180	TSGGS	278	GNGGRHYGHNRPRYD
DKK1-83	83	GSTSSLR	181	SWSLSR	279	APRPKRVSVSYFSTASNYD
DKK1-84	84	GRTFTNY	182	NRGGST	280	GNRRRPYGYSHSRYD
DKK1-85	85	GITFKRY	183	TSRDGTT	281	GNGGRNYGHSRSRYE
DKK1-86	86	GRTFINY	184	IWTGVS	282	APRPNRVSVRYFSTNNNYD
DKK1-87	87	GRTFSGY	185	SWSGGS	283	GNGGRHYGHSRARYD
DKK1-88	88	GLTFSTY	186	ASNGN	284	GNGGRAYGYSRARYE
DKK1-89	89	GFTSDDY	187	SWSGGR	285	APRPKRVSVRYFSTSSNYD
DKK1-90	90	GRTFRSY	188	SWSPGR	286	APRPKRISVQYFTTSSNYD
DKK1-91	91	GFTVSSY	189	SWSGGR	287	APRPKRVSFSYFSTSSNYE
DKK1-92	92	GFGFGSY	190	SWTGGS	288	APRPKRVSVRYFNTSSNYD
DKK1-93	93	GRTFSRY	191	SWSGGS	289	GNGGRYYNHSRTRYE
DKK1-94	94	GRIFGGY	192	SWSGAS	290	GNGGSRYGHSRARYD
DKK1-95	95	GSIENIN	193	SSGGGI	291	GNGGRKYGHHRARYD
DKK1-96	96	GFTFSSFGNF	194	NWSSRS	292	GNGGRQYGHSRARYD
DKK1-97	97	GNIDRLY	195	SWSVSS	293	EGGYSGTYYYTGDFD

DKK1-98	98	GRTFSNF	196	LRGGS	294	APRPKRVSVSYFSTASNYD
DKK1-99	919	GRTFSNF	1333	LRGGS	1747	APRPKRVSVSYFSTASNYD
DKK1-100	920	GNIDRLY	1334	SWSVSS	1748	EGGYSGTYYYTGDFD
DKK1-101	921	GFTFSSFGNF	1335	NWSSRS	1749	GNGGRQYGHSRARYD
DKK1-102	922	GSIENIN	1336	SSGGGI	1750	GNGGRKYGHHRARYD
DKK1-103	923	GRIFGGY	1337	SWSGAS	1751	GNGGSRYGHSRARYD
DKK1-104	924	GRTFSRY	1338	SWSGGS	1752	GNGGRYYNHSRTRYE
DKK1-105	925	GFGFGSY	1339	SWTGGS	1753	APRPKRVSVRYFNTSSNYD
DKK1-106	926	GFTVSSY	1340	SWSGGR	1754	APRPKRVSFSYFSTSSNYE
DKK1-107	927	GRTFRSY	1341	SWSPGR	1755	APRPKRISVQYFTTSSNYD
DKK1-108	928	GFTSDDY	1342	SWSGGR	1756	APRPKRVSVRYFSTSSNYD
DKK1-109	929	GLTFSTY	1343	ASNGN	1757	GNGGRAYGYSRARYE
DKK1-110	930	GRTFSGY	1344	SWSGGS	1758	GNGGRHYGHSRARYD
DKK1-111	931	GRTFINY	1345	IWTGVS	1759	APRPNRVSVRYFSTNNNYD
DKK1-112	932	GITFKRY	1346	TSRDGTT	1760	GNGGRNYGHSRSRYE
DKK1-113	933	GRTFTNY	1347	NRGGST	1761	GNRRRPYGYSHSRYD
DKK1-114	934	GSTSSLR	1348	SWSLSR	1762	APRPKRVSVSYFSTASNYD
DKK1-115	935	GRTFSNT	1349	TSGGS	1763	GNGGRHYGHNRPRYD
DKK1-116	936	GIAFQGY	1350	DTNGGH	1764	EGGYRGTYYYTGDFD
DKK1-117	937	GFLMYDR	1351	SRTGSS	1765	GNGGRKYGHHRARYD
DKK1-118	938	SIGIAFSSR	1352	TRSGGK	1766	GNGGRTYGHSRARYE
DKK1-119	939	GFTFSSS	1353	LRGGS	1767	GNGGRHYGHSRARYD
DKK1-120	940	GRTFNSR	1354	SSSASS	1768	GNGGRLYGHSRARYD
DKK1-121	941	GIPFSTR	1355	SSGAT	1769	GNGGRAYGYSRARYE
DKK1-122	942	GPTVDAY	1356	SWSGSA	1770	APRPKRVSVRYFSTSSNYD
DKK1-123	943	GIPFSSR	1357	SRSGTG	1771	GNGGRTYGHSRARYD
DKK1-124	944	GRTFSSK	1358	NWSGGL	1772	GNGGRAYGYSRARYE
DKK1-125	945	GGIYRVN	1359	NWSGGS	1773	GNGGRKYGHHRARYD
DKK1-126	946	GRTISNA	1360	RSGGT	1774	GNGGRQYGHSRARYD
DKK1-127	947	GTSFSIG	1361	SRSGAS	1775	GNGGRTYGHSRARYD
DKK1-128	948	GRTFSSY	1362	SRSGGS	1776	GNGGRHYGHSRARYD
DKK1-129	949	GRTFSNY	1363	STSGKT	1777	GNGGRNYGHSRARYE
DKK1-130	950	GRTFRSY	1364	SMSGKE	1778	GNGGRTYGHSRARYE
DKK1-131	951	GRTFSSY	1365	NLSSGS	1779	GNGGRNYGHSRARYE
DKK1-132	952	GRTFSRF	1366	SARGM	1780	GNGGRTYGHSRARYE
DKK1-133	953	GRTSSAY	1367	SRSGAS	1781	GNGGRSYGHSRARYD
DKK1-134	954	GFRMYDR	1368	SRSGGR	1782	GNGGRLYGHSRARYD
DKK1-135	955	GRTFSYN	1369	NRSGKS	1783	GNGGRHYGHSRARYD
DKK1-136	956	GRTFSSN	1370	SRSGGS	1784	GNGGRTYGHSRARYD
DKK1-137	957	GRAFSSS	1371	NRGGKI	1785	GNGGRLYGHSRARYD
DKK1-138	958	GFTVSNY	1372	SWSGGS	1786	APRPKRVSVRYFSTSSNYD
DKK1-139	959	GRRFSAD	1373	RSGGT	1787	GNGGRQYGHSRARYD
DKK1-140	960	GSTFSKA	1374	TFSGAR	1788	GNGGRTYGHSRARYD
DKK1-141	961	GRTFSSL	1375	SSSGGT	1789	GNGGRLYGHSRARYD
DKK1-142	962	GFTFGDY	1376	DWSGRR	1790	APRPKRVSVSYFSTASNYD

DKK1-143	963	GFTFDDR	1377	STGGT	1791	GNGGRTYGHSRARYE
DKK1-144	964	GRTFSSY	1378	SRSGT	1792	GNGGRTYGHSRARYE
DKK1-145	965	GRTFSIS	1379	SPSGN	1793	GNGGRAYGYSRARYE
DKK1-146	966	GRTFSTS	1380	NRSGKT	1794	GNGGRAYGYSRARYE
DKK1-147	967	GRTFSLY	1381	NRSGKS	1795	GNGGRQYGHSRARYD
DKK1-148	968	GFTFTNY	1382	NWSGRR	1796	APRPKRVSVQYFSTSSNYD
DKK1-149	969	GRSFGNF	1383	TSGGS	1797	GNGGRSYGHSRARYD
DKK1-150	970	GRTFSSL	1384	SSGGS	1798	GNGGRTYGHSRARYD
DKK1-151	971	GRTLSSI	1385	TRAGS	1799	GNGGRYYGHSRARYD
DKK1-152	972	GRTFSNF	1386	SATGS	1800	GNGGRQYGHSRARYD
DKK1-153	973	GRG	1387	NRSGKS	1801	GNGGRSYGHSRARYD
DKK1-154	974	GTSFSVG	1388	SWSGGT	1802	GNGGRQYGHSRARYD
DKK1-155	975	GRTFSSL	1389	TSGGR	1803	GNGGRTYGHSRARYE
DKK1-156	976	GRTLSRS	1390	SWSGGS	1804	GNGGRTYGHSRARYE
DKK1-157	977	GRTISNY	1391	SWRGGS	1805	APRPKYVSVSYFSTSSNYD
DKK1-158	978	GHTFRGY	1392	SGRSGN	1806	GNGGRLYGHSRARYD
DKK1-159	979	GSIVRGN	1393	SSSGSS	1807	GNGGRTYGHSRARYE
DKK1-160	980	GRTFSSY	1394	SRSGGS	1808	GNGGRTYGHSRARYE
DKK1-161	981	GNIFGVN	1395	SGTGGS	1809	GNGGRTYGHSRARYE
DKK1-162	982	GHTFRGY	1396	NRSGSS	1810	GNGGRAYGYSRARYE
DKK1-163	983	GRTLRRY	1397	ISDGN	1811	GNGGRQYGHSRARYD
DKK1-164	984	GRALSSS	1398	WSGGR	1812	GNGGRYYGHSRARYD
DKK1-165	985	GRTFSNG	1399	TSTGS	1813	GNGGRLYGHSRARYD
DKK1-166	986	GLTFGSA	1400	TSGGR	1814	GNGGRQYGHSRARYD
DKK1-167	987	GFTFGST	1401	NWSGRR	1815	APRPKRVSVSYFYTSSNYD
DKK1-168	988	GRFTSSS	1402	TSGGR	1816	GNGGRAYGYSRARYE
DKK1-169	989	GRTFNSR	1403	TSDGS	1817	GNGGRQYGHSRARYD
DKK1-170	990	GRTLSS	1404	SQRG	1818	GNGGRQYGHSRARYD
DKK1-171	991	GGTFSRY	1405	NRSGKS	1819	GNGGRQYGHSRARYD
DKK1-172	992	GRTFNSR	1406	SSGST	1820	GNGGRSYGHSRARYD
DKK1-173	993	GSTFRGA	1407	TSAGGT	1821	GNGGRQYGHSRARYD
DKK1-174	994	GSTFSKA	1408	LSSGA	1822	GNGGRHYGHSRARYD
DKK1-175	995	GTTFRIN	1409	SRSGGS	1823	GNGGRSYGHSRARYD
DKK1-176	996	GFPVNRY	1410	SRSGGS	1824	GNGGRQYGHSRARYD
DKK1-177	997	GHTFNTY	1411	TSNGR	1825	GNGGRAYGYSRARYE
DKK1-178	998	GRTFGRR	1412	NWSGGS	1826	GNGGRHYGHSRARYD
DKK1-179	999	GFTFSSY	1413	SRSGGT	1827	GNGGRNYGHSRARYD
DKK1-180	1000	GRTFSNF	1414	SSGGR	1828	GNGGRHYGHSRARYD
DKK1-181	1001	GLTTVY	1415	SRTGGS	1829	GNGGRTYGHSRARYE
DKK1-182	1002	GTTFRIN	1416	NRSGKS	1830	GNGGRQYGHSRARYD
DKK1-183	1003	GRTFSTH	1417	TRLGV	1831	GNGGRAYGYSRARYE
DKK1-184	1004	GIPSTLR	1418	NWSGAS	1832	GNGGRQYGHSRARYD
DKK1-185	1005	GRTFSSY	1419	DWSGSR	1833	APRPKRVSVSYFYTSSNYD
DKK1-186	1006	GRTFSDI	1420	NWSGAR	1834	APRPKRVSVQYFSTSSNYD
DKK1-187	1007	GIPFSTR	1421	SWSGGS	1835	GNGGRQYGHSRARYD

DKK1-188	1008	GFTFDEY	1422	DWSGRR	1836	APRPKRISVSYFSTSSNYD
DKK1-189	1009	GFTFSNY	1423	SWSGGS	1837	APRPKRVSFSYFSTSSNYE
DKK1-190	1010	GITFKRY	1424	NWSGAS	1838	GNGGRQYGHSRARYD
DKK1-191	1011	GFTFGHY	1425	SWSLTR	1839	APRPKRVSVQYFSTSSNYD
DKK1-192	1012	GSITSIN	1426	SRSGAS	1840	GNGGRTYGHSRARYE
DKK1-193	1013	GGRIFSNY	1427	SWSGGS	1841	APRPKRVSVSYFSTASNYD
DKK1-194	1014	GRTF	1428	NWRSGGS	1842	GNGGRTYGHSRARYE
DKK1-195	1015	GGTFNGR	1429	SRSGGG	1843	GNGGRQYGHSRARYD
DKK1-196	1016	GFNFDDY	1430	SWSLSR	1844	APRPKRVSVSYFSTASNYD
DKK1-197	1017	SIGIAFSSR	1431	TRSGGK	1845	GNGGRSYGHSRARYD
DKK1-198	1018	GSTFRIN	1432	SASGS	1846	GNGGRTYGHSRARYE
DKK1-199	1019	GGIYRVN	1433	NWSGGS	1847	GNGGRQYGHSRARYD
DKK1-200	1020	GRSLNTY	1434	ISGGS	1848	GNGGRSYGHSRARYD
DKK1-201	1021	GRTFSNY	1435	STSGKT	1849	GNGGRQYGHSRARYD
DKK1-202	1022	GTTVRIR	1436	NGGGN	1850	GNGGRQYGHSRARYD
DKK1-203	1023	GRTFSTY	1437	NWSGSS	1851	GNGGRHYGHSRARYD
DKK1-204	1024	GIPFSTR	1438	SSGAT	1852	GNGGRHYGHSRARYD
DKK1-205	1025	GRTFSRY	1439	RIKDGS	1853	GNGGRQYGHSRARYD
DKK1-206	1026	GHTFNTY	1440	SRSGGK	1854	GNGGRNYGHSRARYE
DKK1-207	1027	GRSFSEY	1441	SRDGAA	1855	GNGGRKYGHHRARYD
DKK1-208	1028	GRTFTTY	1442	SSSGSS	1856	GNGGRQYGHSRARYD
DKK1-209	1029	GRTFSRY	1443	SWSGGS	1857	GNGGRQYGHSRARYD
DKK1-210	1030	GSIFTIN	1444	NWSGSS	1858	GNGGRKYGHHRARYD
DKK1-211	1031	GTSISNR	1445	SSGGNL	1859	GNGGRQYGHSRARYD
DKK1-212	1032	GFTFRRYV	1446	IEGAGSDT	1860	AKQIPGRKWTANGRKDY
DKK1-213	1033	GFTFNKYP	1447	ISPSGKKK	1861	AKYPKNFDY
DKK1-214	1034	GFTFSSAA	1448	ISGGGADT	1862	ARLPKRGPRFDY
DKK1-215	1035	GFTFNKYP	1449	IQQRGLKT	1863	AKGIRGWIGHDTQPFDY
DKK1-216	1036	GFTFDRYR	1450	ISPSGKKK	1864	AKYPKNFDY
DKK1-217	1037	GFTSNNFA	1451	ISGGGADT	1865	AKLQKRGPRFDY
DKK1-218	1038	GFTFGNYA	1452	ISSSGGET	1866	VKAPLRSGGVDY
DKK1-219	1039	GFTFDRYR	1453	ISPSGKKK	1867	AKFPSTHGKFDY
DKK1-220	1040	GLTFPNYG	1454	IDDRGRYT	1868	ARVIAAAGAFDY
DKK1-221	1041	GFTFNKYP	1455	ISNSGST	1869	AKRTRSKFDY
DKK1-222	1042	GFTFTHYS	1456	ITRSGST	1870	AKRTENRGVSFDY
DKK1-223	1043	GFTFEEKE	1457	ISSSGLWT	1871	AKGWRRFDY
DKK1-224	1044	GFTFDRYR	1458	ISPSGKKK	1872	AKYTWNGY
DKK1-225	1045	GFTFHKYG	1459	ISPSGKKK	1873	ASLSRGY
DKK1-226	1046	GFTFGNYA	1460	IWPRGQKT	1874	AKFRGRGFDY
DKK1-227	1047	GFTFAKYK	1461	ISPSGKKK	1875	AKAHNAFDY
DKK1-228	1048	GFTFSSYF	1462	ISGGGADT	1876	ARGNYFDY
DKK1-229	1049	GFTFDRYR	1463	ISGYGSTT	1877	AKFRGRGFDY
DKK1-230	1050	GFTFSRYA	1464	IGANGAPT	1878	AKDKRYRGSQHYFDY
DKK1-231	1051	GFTFRSYT	1465	ISNSGGST	1879	AKAGRKFDY
DKK1-232	1052	GFTFSDYD	1466	IGASGSAT	1880	AKQSGSEDHFDY

DKK1-233	1053	GFTFRRYV	1467	ISPSGKKK	1881	AKWRREGYTGSKFDY
DKK1-234	1054	GGFSLSRY	1468	INQAGLRT	1882	AKSRTGRYFDY
DKK1-235	1055	GFTFHKYG	1469	INPSRGYT	1883	AKGYRHFDY
DKK1-236	1056	GFTFNKYP	1470	ISSSGGET	1884	AKDLGQGFDY
DKK1-237	1057	GFTFNKYP	1471	ISSSGSST	1885	AKRTRSKFDY
DKK1-238	1058	GFTFRRYV	1472	ISGGGADT	1886	AGLPKRGPRFDY
DKK1-239	1059	GFTFSRYA	1473	IGPSGGKT	1887	ARLPKRGPWFDY
DKK1-240	1060	GFTFRRYV	1474	ISGGGADT	1888	AKPSRRFDY
DKK1-241	1061	GFTFSSYV	1475	IQQRGLKT	1889	ARSGPYYFDY
DKK1-242	1062	GFTFEDYQ	1476	ITGTGGET	1890	AKPGHRFDY
DKK1-243	1063	GFTFRRYV	1477	IYPSGGST	1891	AKDRYSQVHYALDY
DKK1-244	1064	GFTFKAYE	1478	ISPSGGIT	1892	ARHRAGSSGWYSDY
DKK1-245	1065	GFTFEVYT	1479	ISGRGDNT	1893	AKRTENRGVSFDY
DKK1-246	1066	GFTFGNYS	1480	IWPRGQKT	1894	AKVTGRGFDY
DKK1-247	1067	GFTFRRYV	1481	VNPNSGTS	1895	AKGPGTRGDY
DKK1-248	1068	GFTFSNYG	1482	ISPSGGWT	1896	ARYGAYFGLDY
DKK1-249	1069	GFTFAHEP	1483	INYAGNT	1897	AKKDYDYVWGSPYFDY
DKK1-250	1070	GFTFHEST	1484	ISSSGGET	1898	ARIRVGPSGGAFDY
DKK1-251	1071	GFTFNKYP	1485	ISPSGKKK	1899	AKFPSSQFRFDY
DKK1-252	1072	GFTFNKYP	1486	ISPSGKKK	1900	AKYPKNFNY
DKK1-253	1073	GFTFHKYG	1487	INYAGNT	1901	AKDKRYRGSQHYFDY
DKK1-254	1074	GLTFPNYG	1488	ISPSGKKK	1902	AREGLWAFDY
DKK1-255	1075	GFTFKAYE	1489	IIPNGGIT	1903	GRHRAGSIGWYSDY
DKK1-256	1076	GFTFRRYV	1490	IGASGSAT	1904	AKRTRSKFDY
DKK1-257	1077	GFTFRRYV	1491	ISGGGADT	1905	AKGRRRFDY
DKK1-258	1078	GFTSNNFA	1492	ISGGGADT	1906	AKLQKRGPRFDY
DKK1-259	1079	GFTFGNYA	1493	IWARGQKT	1907	AHLPGRGFEY
DKK1-260	1080	GFTFEDET	1494	IISSGGLT	1908	AKGFRIFDY
DKK1-261	1081	GFTFSNSY	1495	ITPKGDHT	1909	AKGARRFDY
DKK1-262	1082	GFTFSGYD	1496	IGRHGGRT	1910	AKSLGRFDY
DKK1-263	1083	GFTFRRYV	1497	IEGAGSDT	1911	ARLPKRGPRFDY
DKK1-264	1084	GFTFKSYG	1498	IWPRGQKT	1912	AKSGTRIKQGFDY
DKK1-265	1085	GFTFRRYV	1499	ISGGGADT	1913	ARLPKRGPRFDY
DKK1-266	1086	GFTFVAYN	1500	ISNSGGST	1914	AKNRAKFDY
DKK1-267	1087	GFTFRRYV	1501	ISSSGGET	1915	AKLPKRGPRFDY
DKK1-268	1088	GFTFRRYV	1502	IEGAGSDT	1916	AKFRGRGFDY
DKK1-269	1089	GFTFSRYG	1503	ISYGGSNK	1917	AKGVRKGFDY
DKK1-270	1090	GFTFGNYA	1504	IQQRGLKT	1918	ARGYRGYFDY
DKK1-271	1091	GYSISSGYH	1505	IDDRGRYT	1919	AKSNGRFDY
DKK1-272	1092	GFTFRRYV	1506	ISGSGGGT	1920	AKYFHGKFDY
DKK1-273	1093	GFTFHKYG	1507	ISPSGKKK	1921	AKGRWSIFDY
DKK1-274	1094	GFTFRRYV	1508	VNPNSGAS	1922	AKGPGTRGDY
DKK1-275	1095	GFTFNKYP	1509	IYPSGGST	1923	AKWSSRAFDY
DKK1-276	1096	GFTFRRYV	1510	IEGAGSDT	1924	ARLPKRGPRFDY
DKK1-277	1097	GFTFRRYV	1511	IEGAGSDT	1925	ARLPKRGPRFDY

DKK1-278	1098	GFTFSSYV	1512	ISPSGKKK	1926	AKYPKNFDY
DKK1-279	1099	GFTFRRYV	1513	ISGGGADT	1927	ARLPKRGPRFDY
DKK1-280	1100	GFTSNNFA	1514	INPSRGYT	1928	AKRTENRGVSFDY
DKK1-281	1101	GFTFNKYP	1515	ISPSGKKK	1929	AKFRGRGFDY
DKK1-282	1102	GFTFFPYA	1516	ISGGGADT	1930	ARLPKRGPRFDY
DKK1-283	1103	GFTFDQYD	1517	ITGSGGST	1931	ATAESDDTYDY
DKK1-284	1104	GFTFRRYV	1518	IEGAGSDT	1932	ARLPKRGPRFDY
DKK1-285	1105	GFTFRSYT	1519	ITGTGGET	1933	ARLPKRGPRFDY
DKK1-286	1106	GFTFRRYV	1520	IEARGGGT	1934	AKFRGRGFDY
DKK1-287	1107	GFTFGNYA	1521	IWPSGGQT	1935	AKDKRYRGSQHYFDY
DKK1-288	1108	GFTFNKYP	1522	SNSGST	1936	AKRTRSKFDY
DKK1-289	1109	GFTFHKYG	1523	IGRHGGRT	1937	AKAGSGFDY
DKK1-290	1110	GFTFSSYW	1524	IGPSGTST	1938	AESFRSRYFDY
DKK1-291	1111	GFTFGNYA	1525	IWPRGQKT	1939	ASLSRGY
DKK1-292	1112	GFTFRSYT	1526	ISGGGADT	1940	AKLPKRGPRFDY
DKK1-293	1113	GFTFSRYF	1527	ISGRGDNT	1941	AKRTENRGVSFDY
DKK1-294	1114	GFTFNKYP	1528	IQQRGLKT	1942	ARWTSGLDY
DKK1-295	1115	GFTFSRYF	1529	IDALGTDT	1943	AKGLRRFDY
DKK1-296	1116	GFTFDRYR	1530	ISSTGFKT	1944	AKFRGRGFDY
DKK1-297	1117	GFTFTHYS	1531	INGTGGET	1945	ARLPKRGPRFDY
DKK1-298	1118	GFTFSPYL	1532	IGPSGTST	1946	AKGRRIFDY
DKK1-299	1119	GFTFSNYF	1533	IDDRGRYT	1947	ARGGDYGSGDY
DKK1-300	1120	GFTFRRYV	1534	ISGGGADT	1948	ARPPKRGPRFDY
DKK1-301	1121	GFTFNKYP	1535	ISSSGGET	1949	AKRTRSKFDY
DKK1-302	1122	GFTFKSYG	1536	IGRHGGRT	1950	ARGGDYGSGDY
DKK1-303	1123	GFTFNKYP	1537	IGPSGGKT	1951	AKRTRSKFDY
DKK1-304	1124	GFTFRRYV	1538	ISGGGADT	1952	ARPPKRGPRFDY
DKK1-305	1125	GFTFEDET	1539	IISSGGLT	1953	AKGFRIFDY
DKK1-306	1126	GFTFNKYP	1540	ITRSGST	1954	AKWSSRAFDY
DKK1-307	1127	GFTFRRYV	1541	ISGGGADT	1955	AKHSKSSHRQSFDY
DKK1-308	1128	GFTFNKYP	1542	ISPSGKKK	1956	AKLTGRFDY
DKK1-309	1129	GFTFSRYF	1543	ISPSGKKK	1957	AKSGAYFDY
DKK1-310	1130	GFTFNKYP	1544	IEGRGTET	1958	AKRTRSKFDY
DKK1-311	1131	GFTFHKYG	1545	ISPSGKKK	1959	AKYPKNFDY
DKK1-312	1132	GFTFRRYV	1546	ISPSGKKK	1960	AKGVRKKFDY
DKK1-313	1133	GFTFRRYV	1547	ISGGGADT	1961	ARLPKRGPRFDY
DKK1-314	1134	GFTFGNYA	1548	ISPIGPRT	1962	AKRTENRGVSFDY
DKK1-315	1135	GFTLDYLA	1549	ISPSGKKK	1963	AKYTGRWEPFDY
DKK1-316	1136	GFTFTHYS	1550	ISGGGADT	1964	ARLPKRGPRFDY
DKK1-317	1137	GFTFRRYV	1551	ITGTGGET	1965	ARLPKRGPRFDY
DKK1-318	1138	GFTFRRYV	1552	ISPSGHGT	1966	ARRTGREYGGGWYFDY
DKK1-319	1139	GFTFPVYN	1553	ISESGTTT	1967	AKNRAKFDY
DKK1-320	1140	GFTFRRYV	1554	ISGGGADT	1968	ARLPKRGPRFDY
DKK1-321	1141	GFSFSAYA	1555	ISTSGGST	1969	ARGRAGADY
DKK1-322	1142	GFTFSRFA	1556	ISGSGAYT	1970	ARDIAAASFDY

DKK1-323	1143	GFTFTSYA	1557	VSGSGGTT	1971	AISYHFDYYFDY
DKK1-324	1144	GFTFSSYA	1558	ISGGGGAT	1972	ARECSGGSCSYYYGMDV
DKK1-325	1145	GSTFNNYA	1559	ISGSGSTT	1973	ARLAVSTSDYYYYGMDV
DKK1-326	1146	GFTFGRFA	1560	ITGSGTST	1974	ARDDRVRFSPVRRWFDP
DKK1-327	1147	GFTFSKYA	1561	ISATGGST	1975	ARVRSSSWYGDY
DKK1-328	1148	GFTFSRYA	1562	ISGSGVTT	1976	ARKTGGHYPFDY
DKK1-329	1149	GFTFSRSA	1563	ISASGANT	1977	ARDQARYYGMDV
DKK1-330	1150	GFTFRNYA	1564	ITSSGGST	1978	ASGLRARNGFDI
DKK1-331	1151	GFTFSNYA	1565	ISGSGGST	1979	ARGAILAY
DKK1-332	1152	GFTFSSYA	1566	VSGTGGTT	1980	ARDVGFGELHP
DKK1-333	1153	GFTFSSYA	1567	ISGSGYST	1981	ARGRTGTLYGMDV
DKK1-334	1154	GFSFNNYA	1568	ISGGGSNT	1982	ARVAASGSYYRAFDQ
DKK1-335	1155	GFTFRRYA	1569	ISSSGGNT	1983	ARDRGFGWFDP
DKK1-336	1156	GFTFRSYG	1570	ISGSGGRT	1984	AKVSYDSSGYYYDAFDI
DKK1-337	1157	GFTFANYA	1571	ISGSGGSA	1985	ARSGSFLSFDS
DKK1-338	1158	GFTFGRFA	1572	ISGSGGRT	1986	ARVDYKKKSYYNAMDA
DKK1-339	1159	GFTFRTSA	1573	ISSGGGGT	1987	ARGPRGRGAFDV
DKK1-340	1160	GFTFSSYA	1574	ISGSGGST	1988	ARDDRVRFSPVRRWFDP
DKK1-341	1161	GIHLSSYA	1575	ISGGGGGT	1989	ARGGHVGIRRPFDV
DKK1-342	1162	GFTFSKYA	1576	ISGSGGTT	1990	ARHAHGAGSYPFDY
DKK1-343	1163	GFPFSSYA	1577	ISGSGGRT	1991	GRAPRKYYGMDV
DKK1-344	1164	GFSFSAYA	1578	ISGRDTST	1992	ARVPLRGSGRLSFDY
DKK1-345	1165	GSPFSNYA	1579	ISGSGGST	1993	ARAPRSPILGVRRGLDP
DKK1-346	1166	GFSFSGYA	1580	ISGSSGRT	1994	VRGGTRGLGY
DKK1-347	1167	GFTFRTYG	1581	ISGSGETT	1995	ARLDHDSSGFYEAFDV
DKK1-348	1168	GLTFSRYA	1582	ISGRGGNT	1996	ARGGMRLGKSYYYYGMDV
DKK1-349	1169	GFAFSTSA	1583	ISASGGST	1997	ARLSVARGAYGMDV
DKK1-350	1170	GFTFGAYA	1584	ISGSGART	1998	ARRGRPPQYYFDS
DKK1-351	1171	GFTFRRYA	1585	VSGSGGTT	1999	ARGWEPGIAAN
DKK1-352	1172	GFTFSKHA	1586	ISGSGDTT	2000	ARHQYSGSGSFRY
DKK1-353	1173	GFTFRRSA	1587	IGGSGDNT	2001	AKHRGSFWFDP
DKK1-354	1174	GFSFRSYA	1588	ISGSGGNT	2002	TTMFGSGTFYTGFDF
DKK1-355	1175	GFTFSSSS	1589	ISGSGGTT	2003	ARAGARFVGFDY
DKK1-356	1176	GFTFSRFA	1590	ISGSGRNT	2004	ATFNPVGLFY
DKK1-357	1177	GFSFSTYA	1591	ISGSAVST	2005	ARSGSFLSFDS
DKK1-358	1178	GFTFSRYT	1592	VSGSGGRT	2006	ARSRNGRWFDP
DKK1-359	1179	GLTFRSYA	1593	ISGSGGST	2007	ARGASFDS
DKK1-360	1180	GFTFSNYA	1594	ISGSGART	2008	ARGRQRQRSTPLGRY
DKK1-361	1181	GFNFRDYA	1595	ISGRGSV	2009	ARGGDWVAFDY
DKK1-362	1182	GFTFSGYV	1596	ISGSGGRT	2010	ARRKGPTYGMDV
DKK1-363	1183	GFTFSTFA	1597	LSGSGGRT	2011	ARVTRYQGWLSHFDY
DKK1-364	1184	GFTLSTYA	1598	ISTSGGST	2012	ARVFVSSGWYDGMDV
DKK1-365	1185	GLTFNNYA	1599	ISGSGART	2013	ARGASLDV
DKK1-366	1186	GFTFGRYA	1600	ISGSGTTT	2014	ARAIGGRTAY
DKK1-367	1187	GFSFSAYA	1601	ISGRDTST	2015	ARVPLRGSGRLSFDY

DKK1-368	1188	GFTFGRYA	1602	ITASGGST	2016	ARVVTAMGYYYGMDV
DKK1-369	1189	GFTFSNYG	1603	ISAGGGNT	2017	ARDLGMRGPYYYYYGMDV
DKK1-370	1190	GFTFSYYG	1604	ISGGGAGT	2018	VASRNYLLDF
DKK1-371	1191	GFTFTKYA	1605	ISGRGGST	2019	ARGDLTVTRKYDS
DKK1-372	1192	GFTFRSYG	1606	ISRSGGNT	2020	ARTYSYGSFDY
DKK1-373	1193	GFNFRSYA	1607	ISGSGTTT	2021	ASWRAAPFDY
DKK1-374	1194	GFSFSAYA	1608	ISGRDTST	2022	ARVPLRGSGRLSFDY
DKK1-375	1195	GFTFGNYA	1609	ITGSGGST	2023	AKGKFHLDP
DKK1-376	1196	GFSFSSYA	1610	ISGRGGST	2024	TTDYGAIMDV
DKK1-377	1197	GFTFGRFA	1611	ISGSGTST	2025	ARDSRNYFGMGV
DKK1-378	1198	GFTFGNYA	1612	ISRSGGNT	2026	GRDGTRFGAFDI
DKK1-379	1199	GFTFNKFA	1613	ISGSGSRT	2027	ARGRSWYNH
DKK1-380	1200	GLTFSSYA	1614	ISGSGGNT	2028	ARFQPRPLRLFDY
DKK1-381	1201	GFTLRSYA	1615	ISGSGGYT	2029	ARASYGSGSYPLIH
DKK1-382	1202	GFTFSSFA	1616	VSGSGGST	2030	AGHRSNIGWDV
DKK1-383	1203	GSTFSSYA	1617	ISASGGRT	2031	ARDDRVRFSPVRRWFDP
DKK1-384	1204	GFTFRRSA	1618	ISGSGSGT	2032	ARSARGRWFDP
DKK1-385	1205	GFTFAGYA	1619	ISRSGDRT	2033	AKGQRAHQQLVRGAMDV
DKK1-386	1206	GFTFRTFA	1620	ISASGGTT	2034	AHRRRSKFWSGFGV
DKK1-387	1207	GFTFSRYA	1621	ISGSGVTT	2035	ARKTGGHYPFDY
DKK1-388	1208	GFTFDNYA	1622	ISGSGGSI	2036	VKGAPAGYLDS
DKK1-389	1209	GFRFSSYA	1623	ISGRGGST	2037	ARHNRERRAFDI
DKK1-390	1210	GFTFRSYA	1624	ISGGGGTT	2038	ARDSRVRGTHDYYYYGMDV
DKK1-391	1211	GFTFSKFA	1625	ISASGGRT	2039	ARGSLRFTP
DKK1-392	1212	GFTFSSSG	1626	ISPSGGST	2040	ARLSADRVFAFDI
DKK1-393	1213	GFSFSSFA	1627	ISGSGDVT	2041	AGHRSNIGWDV
DKK1-394	1214	GFTFGRFA	1628	ITGSGTST	2042	ARVPLRGSGRLSFDY
DKK1-395	1215	GFGFSSYA	1629	ITGSGGNT	2043	AKSRRPRYSYGFAFES
DKK1-396	1216	GVTFRNYA	1630	ISASGGSP	2044	ARDTSVGWFDP
DKK1-397	1217	GFTFRNYA	1631	ISGGGGRT	2045	VRDLTRRAAMDV
DKK1-398	1218	GFTFRSSA	1632	ISGSGRST	2046	ARNGAGSHYYAMDV
DKK1-399	1219	GFTFSRFA	1633	ISGSGGRT	2047	ASSKVTRSALDY
DKK1-400	1220	GFTFGNYA	1634	ISGSGSST	2048	GRESGRGSGT
DKK1-401	1221	GFTYSSYA	1635	ISGSGGST	2049	ARERELYYFYYGMDV
DKK1-402	1222	GFTFSTYG	1636	ITGSGGST	2050	ARHHNRRSSLDY
DKK1-403	1223	GFTFSSSG	1637	ISSTGGTT	2051	ARRGRRQLRYYYGMDV
DKK1-404	1224	GFSFSSSA	1638	ISGSGGTT	2052	ARARRRSFDW
DKK1-405	1225	GFTFSRYA	1639	ISGGRVST	2053	ARSLRGNAFDI
DKK1-406	1226	GFTFSGYA	1640	IRGSGGST	2054	AKDLQSRGY
DKK1-407	1227	GFTFNKFA	1641	ISVSGGNT	2055	ARHSRLAALLA
DKK1-408	1228	GFTFSSHV	1642	ISGSGAGT	2056	AVTGTTGWFDP
DKK1-409	1229	GFTFGRYA	1643	ISSSRGST	2057	ARVGIAGRGMDV
DKK1-410	1230	GFTFNTYG	1644	ISGRRT	2058	ARVSRGYPRRSDS
DKK1-411	1231	GFTVSSYA	1645	ISGGGGTT	2059	VRSSNWKFDQ
DKK1-412	1232	GFTFSRSA	1646	ISASGANT	2060	ARDQARYYGMDV

DKK1-413	1233	GFTFRSYD	1647	ISGSGVTT	2061	ARGRRLDY
DKK1-414	1234	GFAFTTYA	1648	ISGSGSTT	2062	ARSGSFLSFDS
DKK1-415	1235	GFTFSSYD	1649	ISGSGRNT	2063	ARGGGASNWFDP
DKK1-416	1236	GFSFSAYA	1650	ISGRDTST	2064	ARVPLRGSGRLSFDY
DKK1-417	1237	GFTFSRFA	1651	ISGTGSST	2065	ARVPGN
DKK1-418	1238	GIPFSSR	1652	SRSGTG	2066	GNGGRTYGHSRARYD
DKK1-419	1239	GGIYRVN	1653	NWSGGS	2067	GNGGRKYGHHRARYD
DKK1-420	1240	GFLMYDR	1654	SRTGSS	2068	GNGGRKYGHHRARYD
DKK1-421	1241	GRTFSRF	1655	SARGM	2069	GNGGRTYGHSRARYE
DKK1-422	1242	GTTFRIN	1656	NWNGGS	2070	GNGGRQYGHSRARYD
DKK1-423	1243	GRTFSNN	1657	LSGGS	2071	GNGGRNYGHSRARYD
DKK1-424	1244	GRTFSDI	1658	NWSGAR	2072	APRPKRVSVQYFSTSSNYD
DKK1-425	1245	GHTYNTY	1659	LRGGS	2073	GNGGRHYGHSRARYD
DKK1-426	1246	GRSLYDR	1660	SRTGSS	2074	GNGGRSYGHSRARYD
DKK1-427	1247	GRTFNNY	1661	SWSTGS	2075	EGGYSGTYYYTGDFD
DKK1-428	1248	GRTLYSY	1662	SWSAGS	2076	GNGGSKYGHSRARYD
DKK1-429	1249	GTFRDY	1663	YGTGGEL	2077	GNGGRQYGHSRARYD
DKK1-430	1250	GGGTFGSY	1664	TWNGTR	2078	APRPKRVSVSYFSTASNYD
DKK1-431	1251	GRTFSNY	1665	SWSGGS	2079	GNGGRTYGHSRARYD
DKK1-432	1252	GRTFTNY	1666	SRGGSA	2080	GNGGRHYGHSRARYD
DKK1-433	1253	GRTFSTH	1667	TRLGV	2081	GNGGRAYGYSRARYE
DKK1-434	1254	GRSFSMY	1668	SRDGAA	2082	GNGGRLYGHSRARYD
DKK1-435	1255	GLTFRNY	1669	SWSLSR	2083	APRPKRASVQYFSTSSNYD
DKK1-436	1256	GFTFDDR	1670	RWSGGI	2084	GNGGRSYGHSRARYD
DKK1-437	1257	GRTFSS	1671	NWSGAS	2085	GNGGRYYNHSRTRYE
DKK1-438	1258	GHTFNTY	1672	NSGGSY	2086	GNGGRNYGHSRARYE
DKK1-439	1259	GRIF	1673	SGSGVY	2087	GNGGRYYGHSRARYD
DKK1-440	1260	GRSFSEY	1674	SRDGAA	2088	GNGGRKYGHHRARYD
DKK1-441	1261	GFNSGSY	1675	SWSLSR	2089	APRPKRVSVSYFSTASNYD
DKK1-442	1262	GGTAY	1676	SWSLTR	2090	APRPKRVSVRYFSTSSNYD
DKK1-443	1263	GRTFTSY	1677	SGSGDD	2091	GNGGRQYGHSRARYD
DKK1-444	1264	GSTFRIN	1678	SASGS	2092	GNGGRTYGHSRARYE
DKK1-445	1265	GGTLNNNPM	1679	NWSGAR	2093	APRPKRISVQYFTTSSNYD
DKK1-446	1266	GRTFSTY	1680	GTRGA	2094	GNGGRQYGHSRARYD
DKK1-447	1267	GRTFNSY	1681	TRLGV	2095	GNGGRYYGHSRARYD
DKK1-448	1268	GIPFSSR	1682	GWYGS	2096	GNGGRQYGHSRARYD
DKK1-449	1269	GIDVNRN	1683	SWSGGR	2097	APRPKRVSVHYFSTSSNYD
DKK1-450	1270	GINFSRY	1684	DWSGSR	2098	APRPKRVSVSYFSTASNYD
DKK1-451	1271	GGTLRGY	1685	DWSGSR	2099	APRPKYVSVRYFSTSSNYD
DKK1-452	1272	GQTF	1686	NWNGDS	2100	GNGGRKYGHHRARYD
DKK1-453	1273	GYTFRAY	1687	TSGGS	2101	GNGGRTYGHSRARYE
DKK1-454	1274	GNIFTLN	1688	NSGGSY	2102	GNGGRKYGHHRARYD
DKK1-455	1275	GFRMYDR	1689	SGRSGN	2103	GNGGRNYGHSRARYD
DKK1-456	1276	GFTFSMW	1690	SRSGGS	2104	GNGGRYYNHSRTRYE
DKK1-457	1277	GFTFRSY	1691	HTGGG	2105	GNGGRNYGHSRARYD

DKK1-458	1278	GLPFSTK	1692	SSGGR	2106	GNGGRHYGHSRARYD
DKK1-459	1279	GNIFRIN	1693	NSGGSS	2107	GNGGRAYGYSRARYE
DKK1-460	1280	GGTFGHY	1694	SWSLTR	2108	APRPKRVSFSYFSTSSNYE
DKK1-461	1281	GRTFNSY	1695	TWGGST	2109	GNGGRSYGHSRARYD
DKK1-462	1282	GITFRRY	1696	NWGGGS	2110	GNGGRAYGYSRARYE
DKK1-463	1283	GRTFSYN	1697	SIGGR	2111	GNGGRSYGHSRARYD
DKK1-464	1284	GRTFSSL	1698	RSSGG	2112	GNGGRTYGHSRARYE
DKK1-465	1285	GPTFSTN	1699	YSGVRSGVS	2113	GNGGRHYGHSRARYD
DKK1-466	1286	GRTFSNY	1700	YGTGGEL	2114	GNGGRKYGHHRARYD
DKK1-467	1287	GRAIGSY	1701	TFSGAR	2115	APRPKRASVQYFSTSSNYD
DKK1-468	1288	GRTLSRN	1702	RSGA	2116	GNGGRHYGHSRARYD
DKK1-469	1289	GRTFIGY	1703	KFSGGT	2117	GNGGRYYGHSRARYD
DKK1-470	1290	GRTISNY	1704	SWRGGS	2118	APRPKYVSVSYFSTSSNYD
DKK1-471	1291	GRTISNY	1705	SWALSR	2119	APRPKRVSFSYFSTSSNYE
DKK1-472	1292	GTFTSY	1706	SWTGGS	2120	GNGGRYYNHSRTRYE
DKK1-473	1293	GRSFSMY	1707	SWSGGS	2121	EGGYSGTYYYTGDFD
DKK1-474	1294	GLTFRNY	1708	NWSGAR	2122	APRPKSISVRYFSTSSNYE
DKK1-475	1295	GFTFSSY	1709	SADGSD	2123	GKRYGYYD
DKK1-476	1296	GRTHSIY	1710	RWGTTD	2124	APRPTRVSVRYFSTRSNYN
DKK1-477	1297	GFSLDYV	1711	KPSGDT	2125	YLSFYSDYEVYD
DKK1-478	1298	GSIFRVN	1712	SMSGAN	2126	GNGGRQYGHSRARYD
DKK1-479	1299	GRTFSSL	1713	NWSGGN	2127	GNGGRKYGHHRARYD
DKK1-480	1300	GFLMYDR	1714	SRTGSS	2128	GNGGRAYGYSRARYE
DKK1-481	1301	GDISSY	1715	TWNGGTH	2129	GNGGRKYGHHRARYD
DKK1-482	1302	GRTHSIY	1716	NWNGDS	2130	GNGGRTYGHSRARYE
DKK1-483	1303	GIPFSSR	1717	SRSGTG	2131	GNGGRAYGYSRARYE
DKK1-484	1304	GRTFSNY	1718	VNGGS	2132	GNGGRAYGYSRARYE
DKK1-485	1305	GMTTIG	1719	SWDGGN	2133	GNGGRQYGHSRARYD
DKK1-486	1306	GRASGDY	1720	SWRGGN	2134	APRPKRVSFSYFSTSSNYE
DKK1-487	1307	GRTFSSY	1721	LSGGS	2135	GNGGRAYGYSRARYE
DKK1-488	1308	GRTFSEV	1722	HWSGGS	2136	GNGGRSYGHSRARYD
DKK1-489	1309	GSTFSIN	1723	TPRGL	2137	GNGGRAYGYSRARYE
DKK1-490	1310	GRTF	1724	IWRGGS	2138	GNGGRQYGHSRARYD
DKK1-491	1311	GGTFSSY	1725	SWSGSA	2139	GNGGRSYGHSRARYD
DKK1-492	1312	GRTFSNF	1726	LRGGS	2140	APRPKRVSVSYFSTASNYD
DKK1-493	1313	GGTFSRY	1727	SWSLTR	2141	APRPKRVSVQYFVTSSNYD
DKK1-494	1314	GRTLSRS	1728	RIKDGS	2142	GNGGRQYGHSRARYD
DKK1-495	1315	GRTFSSG	1729	SRSGTL	2143	APRPKRVSVQYFSTSSNYD
DKK1-496	1316	GRTFNSY	1730	NVGGG	2144	GNGGRTYGHSRARYD
DKK1-497	1317	GYTLKNYY	1731	SRSGGT	2145	APRPKRASVQYFSTSSNYD
DKK1-498	1318	GHTFNTY	1732	SYSG	2146	GNGGRAYGYSRARYE
DKK1-499	1319	GFTFDDR	1733	STSGTR	2147	GNGGRQYGHSRARYD
DKK1-500	1320	GRTLSSY	1734	GTSGP	2148	GNGGRTYGHSRARYE
DKK1-501	1321	GRIFTNT	1735	SWGGGL	2149	GNGGSRYGHSRARYD
DKK1-502	1322	GRIF	1736	SWTAGT	2150	GNGGRNYGHSRARYD

DKK1-503	1323	GNIFTRH	1737	NTGGGS	2151	GNGGRTYGHSRARYE
DKK1-504	1324	GRTFSNY	1738	SWSSGN	2152	GNGGRQYGHSRARYD
DKK1-505	1325	GRTFTSY	1739	GTHGT	2153	GNGGRQYGHSRARYD
DKK1-506	1326	GQT	1740	SRSG	2154	GNGGRAYGYSRARYE
DKK1-507	1327	GRSFSEY	1741	TWSGDM	2155	GNGGRHYGHSRARYD
DKK1-508	1328	GRSFSSY	1742	NTAGW	2156	GNGGRSYGHSRARYD
DKK1-509	1329	GLTFRNY	1743	SWSGGK	2157	APRPKRISVSYFSTTSNYD
DKK1-510	1330	GSTFSSY	1744	HTGG	2158	GNGGRQYGHSRARYD
DKK1-511	1331	GIDVNRN	1745	SWSGGT	2159	APRPKRVSVSYFSTASNYD
DKK1-512	1332	GGTFNVY	1746	NRSGKS	2160	APRPKRVSVRYFSTSSNYD

Table 5. Variable Heavy Chain Domain Sequences

DKK1 Variant	SEQ ID NO	VH Sequence
DKK1-1	295	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRFAMGWFRQAPGKEREGVASITSGGTTNYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADDGARGSWGQGTLVTVSS
DKK1-2	296	EVQLVESGGGLVQPGGSLRLSCAASGSAFSSTVMGWFRQAPGKEREFVATINSLGGTSYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAYSGHFSGRVSDFLWGQGTLVTVSS
DKK1-3	297	EVQLVESGGGLVQPGGSLRLSCAASGSTFSTYAMGWFRQAPGKEREFVASINWGGGNTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAKKVSFGDWGQGTLVTVSS
DKK1-4	298	EVQLVESGGGLVQPGGSLRLSCAASGNIFRINAMGWFRQAPGKERELVAAISRSGGSTNYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKDKNGPWGQGTLVTVSS
DKK1-5	299	EVQLVESGGGLVQPGGSLRLSCAASGGLTFSTYAMGWFRQAPGKEREFVAAVSWSGGNTYYA DSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEIGYYSGGTYYSSEAWGQGTLVTVSS
DKK1-6	300	EVQLVESGGGLVQPGGSLRLSCAASGIPFSTRTMGWFRQAPGKEREFVAAISSGATTLYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-7	301	EVQLVESGGGLVQPGGSLRLSCAASGISGSVFSRTPMGWFRQAPGKEREFVAALSKDGARTYY ADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDLVGTDAFDIWGQGTLVTVSS
DKK1-8	302	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMGWFRQAPGKEREFVAAISWSDGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-9	303	EVQLVESGGGLVQPGGSLRLSCAASGRSFSMYAMGWFRQAPGKERELVAAISWSGGSTVYAD SVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-10	304	EVQLVESGGGLVQPGGSLRLSCAASGRTISNYAMGWFRQAPGKEREFVAAISWRGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKYVSVSYFSTSSNYDWGQGTLVTV SS
DKK1-11	305	EVQLVESGGGLVQPGGSLRLSCAASGPTVDAYAMGWFRQAPGKEREFVSAISWSGSATFYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTV SS
DKK1-12	306	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSRPMGWFRQAPGKEREFVAAISSSASSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-13	307	EVQLVESGGGLVQPGGSLRLSCAASGFLMYDRAMGWFRQAPGKEREIVAAISRTGSSIYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-14	308	EVQLVESGGGLVQPGGSLRLSCAASGSIFSRLAMGWFRQAPGKEREFVAAISSSGISTIYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCARGQRGRWLEPLTGWGQGTLVTVSS
DKK1-15	309	EVQLVESGGGLVQPGGSLRLSCAASGFTFGTTTMGWFRQAPGKERELVAAITSGGGTTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKDLAAAGYYYYYGMDVWGQGTLVTVSS
DKK1-16	310	EVQLVESGGGLVQPGGSLRLSCAASGNIFTRNVMGWFRQAPGKEREFVGAINWSGGNTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARHDHNNRGLDYWGQGTLVTVSS
DKK1-17	311	EVQLVESGGGLVQPGGSLRLSCAASGGTFSRYAMGWFRQAPGKEREFVAGISWTLGRTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDPFGKWGQGTLVTVSS
DKK1-18	312	EVQLVESGGGLVQPGGSLRLSCAASGITFRFKAMGWFRQAPGKEREFVAAINRSGRSTRYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAESHGSTSPRNPLQYDWGQGTLVTVSS
DKK1-19	313	EVQLVESGGGLVQPGGSLRLSCAASGRTYGMGWFRQAPGKEREFVAGISWTLGRTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCASDESDAANWGQGTLVTVSS

DKK1-20	314	EVQLVESGGGLVQPGGSLRLSCAASGPTFSIYDMGWFRQAPGKEREFVTGSNTGGTTYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCATCTDFEYDWGQGTLVTVSS
DKK1-21	315	EVQLVESGGGLVQPGGSLRLSCAASGIPSSIRAMGWFRQAPGKEREWVSGISISDSSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGKRYGYYDWGQGTLVTVSS
DKK1-22	316	EVQLVESGGGLVQPGGSLRLSCAASGSTLSINAMGWFRQAPGKERELVAAISWSGGTAYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAQSRYRSNYYDHDKYAWGQGTLVTVSS
DKK1-23	317	EVQLVESGGGLVQPGGSLRLSCAASGYNFSTFCMGWFRQAPGKEREWVAAISGGGSTMYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAASKWYGGFGDTDIEWGQGTLVTVSS
DKK1-24	318	EVQLVESGGGLVQPGGSLRLSCAASGSSFSAYGMGWFRQAPGKEREFVAGISWTLGRTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAADGVPEYSDYASGPVWGQGTLVTVSS
DKK1-25	319	EVQLVESGGGLVQPGGSLRLSCAASGSTSRSYGMGWFRQAPGKEREFVAGISWTLGRTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARDPSGKWGQGTLVTVSS
DKK1-26	320	EVQLVESGGGLVQPGGSLRLSCAASGFSLDYYGMGWFRQAPGKEREVVASIRWNAKPYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGKRYGYYDWGQGTLVTVSS
DKK1-27	321	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYAMGWFRQAPGKEREWVASISTSGKTTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-28	322	EVQLVESGGGLVQPGGSLRLSCAASGLTTVYTMGWFRQAPGKEREFVAAISWYVSTTFYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-29	323	EVQLVESGGGLVQPGGSLRLSCAASGSIGGLNAMGWFRQAPGKEREFVAAINYSGRSTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGAGRDRGFSRAQYAWGQGTLVTVSS
DKK1-30	324	EVQLVESGGGLVQPGGSLRLSCAASGRTFSKYAMGWFRQAPGKEREFVAAISWSGESTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFYTSSNYDWGQGTLVT VSS
DKK1-31	325	EVQLVESGGGLVQPGGSLRLSCAASGRTLSRSAMGWFRQAPGKERELVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-32	326	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNGPMGWFRQAPGKEREFVAAISRGGKISHYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-33	327	EVQLVESGGGLVQPGGSLRLSCAASGRSLNTYTMGWFRQAPGKERELVAVIISGGSTAYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-34	328	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDRAMGWFRQAPGKEREFVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFYTSSNYDWGQGTLVT VSS
DKK1-35	329	EVQLVESGGGLVQPGGSLRLSCAASGRTFTTYPMGWFRQAPGKEREFVAAISSSGSSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-36	330	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVAAINWSGASTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-37	331	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYSMGWFRQAPGKEREFIAAINLSSGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-38	332	EVQLVESGGGLVQPGGSLRLSCAASGTSFSIGAMGWFRQAPGKEREWVSSISPGGLFPYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAARDAIVGVTDTSGYRWGQGTLVTVSS
DKK1-39	333	EVQLVESGGGLVQPGGSLRLSCAASGTVFSISDMGWFRQAPGKEREWVSAISPGGGYTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCARSSWFDCGVQGRDLGNEYDWGQGTLVT VSS
DKK1-40	334	EVQLVESGGGLVQPGGSLRLSCAASGRTISSFRMGWFRQAPGKEREFVAAISRGGNVTPYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAANSDSGFDSYSVWAAYEWGQGTLVTVSS
DKK1-41	335	EVQLVESGGGLVQPGGSLRLSCAASGRTLSRSAMGWFRQAPGKERELVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-42	336	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVAAITSGGRTYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-43	337	EVQLVESGGGLVQPGGSLRLSCAASGTSFSVGAMGWFRQAPGKEREFVGAVSWSGGTTVYAD SVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-44	338	EVQLVESGGGLVQPGGSLRLSCAASGRGAMGWFRQAPGKEREFVAAINRSGKSTYYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-45	339	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNFAMGWFRQAPGKEREFVAAISATGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-46	340	EVQLVESGGGLVQPGGSLRLSCAASGRTLSSITMGWFRQAPGKERELVATITRAGSTNYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-47	341	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVASISSGGSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS

DKK1-48	342	EVQLVESGGGLVQPGGSLRLSCAASGRSFGNFPMGWFRQAPGKERELVAAVTSGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-49	343	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMGWFRQAPGKEREVVAVVNWSGRRTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFSTSSNYDWGQGTLVTVSS
DKK1-50	344	EVQLVESGGGLVQPGGSLRLSCAASGRTFSLYTMGWFRQAPGKEREFVAAINRSGKSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-51	345	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTSAMGWFRQAPGKEREFVAVINRSGKTTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-52	346	EVQLVESGGGLVQPGGSLRLSCAASGRTFSISAMGWFRQAPGKEREFVAAISPSGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-53	347	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYPMGWFRQAPGKEREFVASISRSGTTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-54	348	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDRAMGWFRQAPGKEREFVAAISTGGTTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-55	349	EVQLVESGGGLVQPGGSLRLSCAASGFTFGDYAMGWFRQAPGKEREFVGAIDWSGRRITYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-56	350	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVARISSSGGTTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-57	351	EVQLVESGGGLVQPGGSLRLSCAASGSTFSKAVMGWFRQAPGKEREFVATITFSGARTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-58	352	EVQLVESGGGLVQPGGSLRLSCAASGRRFSADVMGWFRQAPGKEREFVAAIRSGGTTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-59	353	EVQLVESGGGLVQPGGSLRLSCAASGFTVSNYAMGWFRQAPGKEREFVAAISWSGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTVSS
DKK1-60	354	EVQLVESGGGLVQPGGSLRLSCAASGRAFSSSAMGWFRQAPGKEREFVAAINRGGKISHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-61	355	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSNVMGWFRQAPGKEREFVSAISRSGGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-62	356	EVQLVESGGGLVQPGGSLRLSCAASGRTFSYNPMGWFRQAPGKEREFVAAINRSGKSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-63	357	EVQLVESGGGLVQPGGSLRLSCAASGFRMYDRVMGWFRQAPGKEREFVATISRSGGRTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-64	358	EVQLVESGGGLVQPGGSLRLSCAASGRTSSAYAMGWFRQAPGKEREFVAAISRSGASAYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-65	359	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRFAMGWFRQAPGKERELVAAISARGMPAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-66	360	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYSMGWFRQAPGKEREFIAAINLSSGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-67	361	EVQLVESGGGLVQPGGSLRLSCAASGRTFRSYPMGWFRQAPGKEREFVAAISMSGKETWYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-68	362	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYAMGWFRQAPGKEREWVASISTSGKTTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-69	363	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYPMGWFRQAPGKEREFVAAISRSGGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-70	364	EVQLVESGGGLVQPGGSLRLSCAASGTSFSIGAMGWFRQAPGKERELLAAISRSGASAYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-71	365	EVQLVESGGGLVQPGGSLRLSCAASGRTISNAAMGWFRQAPGKERELVAVIRSGGTTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-72	366	EVQLVESGGGLVQPGGSLRLSCAASGGIYRVNTMGWFRQAPGKEREFVAAINWSGGSTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-73	367	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSKTMGWFRQAPGKEREFVAAINWSGGLTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-74	368	EVQLVESGGGLVQPGGSLRLSCAASGIPFSSRTMGWFRQAPGKEREFVAAISRSGTGTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-75	369	EVQLVESGGGLVQPGGSLRLSCAASGPTVDAYAMGWFRQAPGKEREFVSAISWSGSATFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTVSS

DKK1-76	370	EVQLVESGGGLVQPGGSLRLSCAASGIPFSTRTMGWFRQAPGKEREFVAAISSGATTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-77	371	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSRPMGWFRQAPGKEREFVAAISSSASSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-78	372	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSPMGWFRQAPGKERELVAVILRGGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-79	373	EVQLVESGGGLVQPGGSLRLSCAASSIGIAFSSRTMGWFRQAPGKEREFVAAVTRSGGKSYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-80	374	EVQLVESGGGLVQPGGSLRLSCAASGFLMYDRAMGWFRQAPGKEREIVAAISRTGSSIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-81	375	EVQLVESGGGLVQPGGSLRLSCAASGIAFQGYAMGWFRQAPGKERELVAAIDTNGGHTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYRGTYYYTGDFDWGQGTLVTVSS
DKK1-82	376	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNTLMGWFRQAPGKEREWVARITSGGSTHYADNVKGRFTIITDNSKNTAYLLMISLKPQNTAEYYWSAGNGGRHYGHNRPRYDWCHGGLVTVIT
DKK1-83	377	EVQLVESGGGLVQPGGSLRLSCAASGSTSSLRTMGWFRQAPGKEREFVAAISWSLSRTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-84	378	EVQLVESGGGLVQPGGSLRLSCAASGRTFTNYPMGWFRQAPGKEREFVAAINRGGSTTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNRRRPYGYSHSRYDWGQGTLVTVSS
DKK1-85	379	EVQLVESGGGLVQPGGSLRLSCAASGITFKRYVMGWFRQAPGKEREFVATITSRDGTTYYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYWAAGNGGRNYGHSRSRYEWGQGTLVTVSS
DKK1-86	380	EVQLVESGGGLVQPGGSLRLSCAASGRTFINYAMGWFRQAPGKEREFVAAIIWTGVSTYYADSVKGRFTIIADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPNRVSVRYFSTNNNYDWGQGTLVTVSS
DKK1-87	381	EVQLVESGGGLVQPGGSLRLSCAASGRTFSGYTMGWFRQAPGKEREFVAAISWSGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYHCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-88	382	EVQLVESGGGLVQPGGSLRLSCAASGLTFSTYPMGWFRQAPGKERELVALIASNGNTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-89	383	EVQLVESGGGLVQPGGSLRLSCAASGFTSDDYAMGWFRQAPGKEREFVAAISWSGGRTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTVSS
DKK1-90	384	EVQLVESGGGLVQPGGSLRLSCAASGRTFRSYAMGWFRQAPGKEREFVAAISWSPGRTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRISVQYFTTSSNYDWGQGTLVTVSS
DKK1-91	385	EVQLVESGGGLVQPGGSLRLSCAASGFTVSSYTMGWFRQAPGKEREFVAAISWSGGRTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSFSYFSTSSNYEWGQGTLVTVSS
DKK1-92	386	EVQLVESGGGLVQPGGSLRLSCAASGFGFGSYNMGWFRQAPGKEREFVAMISWTGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFNTSSNYDWGQGTLVTVSS
DKK1-93	387	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRYPMGWFRQAPGKEREFVAAISWSGGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYNHSRTRYEWGQGTLVTVSS
DKK1-94	388	EVQLVESGGGLVQPGGSLRLSCAASGRIFGGYAMGWFRQAPGKEREFVAAISWSGASAIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGSRYGHSRARYDWGQGTLVTVSS
DKK1-95	389	EVQLVESGGGLVQPGGSLRLSCAASGSIENINAMGWFRQAPGKEREFVAAISSGGGITIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-96	390	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGNFPMGWFRQAPGKEREFVAAINWSSRSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-97	391	EVQLVESGGGLVQPGGSLRLSCAASGNIDRLYAMGWFRQAPGKEREFVAAISWSVSSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-98	392	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNFAMGWFRQAPGKEREFVAVILRGGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS

Table 6. Additional Variable Heavy Chain Domain Sequences

DKK1 Variant	SEQ ID NO	VH Sequence

DKK1-99	394	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNFAMGWFRQAPGKEREFVAVILRGGSTNYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-100	395	EVQLVESGGGLVQPGGSLRLSCAASGNIDRLYAMGWFRQAPGKEREFVAAISWSVSSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-101	396	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSFGNFPMGWFRQAPGKEREFVAAINWSSRSTVYA DSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVS S
DKK1-102	397	EVQLVESGGGLVQPGGSLRLSCAASGSIENINAMGWFRQAPGKEREFVAAISSGGGITIYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-103	398	EVQLVESGGGLVQPGGSLRLSCAASGRIFGGYAMGWFRQAPGKEREFVAAISWSGASAIYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGSRYGHSRARYDWGQGTLVTVSS
DKK1-104	399	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRYPMGWFRQAPGKEREFVAAISWSGGSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYNHSRTRYEWGQGTLVTVSS
DKK1-105	400	EVQLVESGGGLVQPGGSLRLSCAASGFGFGSYNMGWFRQAPGKEREFVAMISWTGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFNTSSNYDWGQGTLVTV SS
DKK1-106	401	EVQLVESGGGLVQPGGSLRLSCAASGFTVSSYTMGWFRQAPGKEREFVAAISWSGGRTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSFSYFSTSSNYEWGQGTLVTVS S
DKK1-107	402	EVQLVESGGGLVQPGGSLRLSCAASGRTFRSYAMGWFRQAPGKEREFVAAISWSPGRTHYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRISVQYFTTSSNYDWGQGTLVTVS S
DKK1-108	403	EVQLVESGGGLVQPGGSLRLSCAASGFTSDDYAMGWFRQAPGKEREFVAAISWSGGRTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTV SS
DKK1-109	404	EVQLVESGGGLVQPGGSLRLSCAASGLTFSTYPMGWFRQAPGKERELVALIASNGNTHYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-110	405	EVQLVESGGGLVQPGGSLRLSCAASGRTFSGYTMGWFRQAPGKEREFVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYHCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-111	406	EVQLVESGGGLVQPGGSLRLSCAASGRTFINYAMGWFRQAPGKEREFVAAIIWTGVSTYYADSV KGRFTIIADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPNRVSVRYFSTNNNYDWGQGTLVTVS S
DKK1-112	407	EVQLVESGGGLVQPGGSLRLSCAASGITFKRYVMGWFRQAPGKEREFVATITSRDGTTYYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYWAAGNGGRNYGHSRSRYEWGQGTLVTVSS
DKK1-113	408	EVQLVESGGGLVQPGGSLRLSCAASGRTFTNYPMGWFRQAPGKEREFVAAINRGGSTTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNRRRPYGYSHSRYDWGQGTLVTVSS
DKK1-114	409	EVQLVESGGGLVQPGGSLRLSCAASGSTSSLRTMGWFRQAPGKEREFVAAISWSLSRTHYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-115	410	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNTLMGWFRQAPGKEREWVARITSGGSTHYADNV KGRFTIITDNSKNTAYLLMISLKPQNTAEYYWSAGNGGRHYGHNRPRYDWCHGGLVTVIT
DKK1-116	411	EVQLVESGGGLVQPGGSLRLSCAASGIAFQGYAMGWFRQAPGKERELVAAIDTNGGHTLYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYRGTYYYTGDFDWGQGTLVTVSS
DKK1-117	412	EVQLVESGGGLVQPGGSLRLSCAASGFLMYDRAMGWFRQAPGKEREIVAAISRTGSSIYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-118	413	EVQLVESGGGLVQPGGSLRLSCAASSIGIAFSSRTMGWFRQAPGKEREFVAAVTRSGGKSYYAD SVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-119	414	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSSPMGWFRQAPGKERELVAVILRGGSTNYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-120	415	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSRPMGWFRQAPGKEREFVAAISSSASSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-121	416	EVQLVESGGGLVQPGGSLRLSCAASGIPFSTRTMGWFRQAPGKEREFVAAISSGATTLYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-122	417	EVQLVESGGGLVQPGGSLRLSCAASGPTVDAYAMGWFRQAPGKEREFVSAISWSGSATFYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTV SS
DKK1-123	418	EVQLVESGGGLVQPGGSLRLSCAASGIPFSSRTMGWFRQAPGKEREFVAAISRSGTGTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-124	419	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSKTMGWFRQAPGKEREFVAAINWSGGLTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS

DKK1-125	420	EVQLVESGGGLVQPGGSLRLSCAASGGIYRVNTMGWFRQAPGKEREFVAAINWSGGSTIYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-126	421	EVQLVESGGGLVQPGGSLRLSCAASGRTISNAAMGWFRQAPGKERELVAVIRSGGTTLYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-127	422	EVQLVESGGGLVQPGGSLRLSCAASGTSFSIGAMGWFRQAPGKERELLAAISRSGASAYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-128	423	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYPMGWFRQAPGKEREFVAAISRSGGSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-129	424	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYAMGWFRQAPGKEREWVASISTSGKTTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-130	425	EVQLVESGGGLVQPGGSLRLSCAASGRTFRSYPMGWFRQAPGKEREFVAAISMSGKETWYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-131	426	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYSMGWFRQAPGKEREFIAAINLSSGSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-132	427	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRFAMGWFRQAPGKERELVAAISARGMPAYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-133	428	EVQLVESGGGLVQPGGSLRLSCAASGRTSSAYAMGWFRQAPGKEREFVAAISRSGASAYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-134	429	EVQLVESGGGLVQPGGSLRLSCAASGFRMYDRVMGWFRQAPGKEREFVATISRSGGRTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-135	430	EVQLVESGGGLVQPGGSLRLSCAASGRTFSYNPMGWFRQAPGKEREFVAAINRSGKSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-136	431	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSNVMGWFRQAPGKEREFVSAISRSGGSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-137	432	EVQLVESGGGLVQPGGSLRLSCAASGRAFSSSAMGWFRQAPGKEREFVAAINRGGKISHYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-138	433	EVQLVESGGGLVQPGGSLRLSCAASGFTVSNYAMGWFRQAPGKEREFVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTV SS
DKK1-139	434	EVQLVESGGGLVQPGGSLRLSCAASGRRFSADVMGWFRQAPGKEREFVAAIRSGGTTLYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-140	435	EVQLVESGGGLVQPGGSLRLSCAASGSTFSKAVMGWFRQAPGKEREFVATITFSGARTHYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-141	436	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVARISSSGGTTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-142	437	EVQLVESGGGLVQPGGSLRLSCAASGFTFGDYAMGWFRQAPGKEREFVGAIDWSGRRITYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTV SS
DKK1-143	438	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDRAMGWFRQAPGKEREFVAAISTGGTTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-144	439	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYPMGWFRQAPGKEREFVASISRSGTTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-145	440	EVQLVESGGGLVQPGGSLRLSCAASGRTFSISAMGWFRQAPGKEREFVAAISPSGNTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-146	441	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTSAMGWFRQAPGKEREFVAVINRSGKTTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-147	442	EVQLVESGGGLVQPGGSLRLSCAASGRTFSLYTMGWFRQAPGKEREFVAAINRSGKSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-148	443	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYAMGWFRQAPGKEREVVAVVNWSGRRTYYAD SVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFSTSSNYDWGQGTLVT VSS
DKK1-149	444	EVQLVESGGGLVQPGGSLRLSCAASGRSFGNFPMGWFRQAPGKERELVAAVTSGGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-150	445	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVASISSGGSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-151	446	EVQLVESGGGLVQPGGSLRLSCAASGRTLSSITMGWFRQAPGKERELVATITRAGSTNYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-152	447	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNFAMGWFRQAPGKEREFVAAISATGSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS

DKK1-153	448	EVQLVESGGGLVQPGGSLRLSCAASGRGAMGWFRQAPGKEREFVAAINRSGKSTYYADSVKGR FTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-154	449	EVQLVESGGGLVQPGGSLRLSCAASGTSFSVGAMGWFRQAPGKEREFVGAVSWSGGTTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-155	450	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVAAITSGGRTYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-156	451	EVQLVESGGGLVQPGGSLRLSCAASGRTLSRSAMGWFRQAPGKERELVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-157	452	EVQLVESGGGLVQPGGSLRLSCAASGRTISNYAMGWFRQAPGKEREFVAAISWRGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKYVSVSYFSTSSNYDWGQGTLVTV SS
DKK1-158	453	EVQLVESGGGLVQPGGSLRLSCAASGHTFRGYVMGWFRQAPGKEREFVAAISGRSGNTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-159	454	EVQLVESGGGLVQPGGSLRLSCAASGSIVRGNTMGWFRQAPGKEREFVAAISSSGSSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-160	455	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYPMGWFRQAPGKEREFVAAISRSGGSTLYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-161	456	EVQLVESGGGLVQPGGSLRLSCAASGNIFGVNPMGWFRQAPGKEREFVAFISGTGGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-162	457	EVQLVESGGGLVQPGGSLRLSCAASGHTFRGYAMGWFRQAPGKEREFVAAINRSGSSTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-163	458	EVQLVESGGGLVQPGGSLRLSCAASGRTLRRYVMGWFRQAPGKERELVARIISDGNTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-164	459	EVQLVESGGGLVQPGGSLRLSCAASGRALSSSVMGWFRQAPGKERELVALLWSGGRTLYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-165	460	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNGPMGWFRQAPGKEREWVASITSTGSTYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-166	461	EVQLVESGGGLVQPGGSLRLSCAASGLTFGSAPMGWFRQAPGKERELVAAITSGGRTYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-167	462	EVQLVESGGGLVQPGGSLRLSCAASGFTFGSTTMGWFRQAPGKEREFVAAVNWSGRRELYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFYTSSNYDWGQGTLVTV SS
DKK1-168	463	EVQLVESGGGLVQPGGSLRLSCAASGRFTSSSPMGWFRQAPGKERELVASITSGGRTSYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-169	464	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSRPMGWFRQAPGKERELVASITSDGSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-170	465	EVQLVESGGGLVQPGGSLRLSCAASGRTLSSVMGWFRQAPGKEREFVATISQRGRRYADSVKGR FTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-171	466	EVQLVESGGGLVQPGGSLRLSCAASGGTFSRYAMGWFRQAPGKEREFVAAINRSGKSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-172	467	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSRPMGWFRQAPGKERELVATISSGSTTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-173	468	EVQLVESGGGLVQPGGSLRLSCAASGSTFRGAAMGWFRQAPGKEREFVAAITSAGGTTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-174	469	EVQLVESGGGLVQPGGSLRLSCAASGSTFSKAVMGWFRQAPGKERELVAGILSSGATVYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-175	470	EVQLVESGGGLVQPGGSLRLSCAASGTTFRINVMGWFRQAPGKEREFVGAISRSGGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-176	471	EVQLVESGGGLVQPGGSLRLSCAASGFPVNRYSMGWFRQAPGKEREFVAAISRSGGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-177	472	EVQLVESGGGLVQPGGSLRLSCAASGHTFNTYPMGWFRQAPGKERELVAAITSNGRPSYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-178	473	EVQLVESGGGLVQPGGSLRLSCAASGRTFGRRAMGWFRQAPGKEREFVAAINWSGGSTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-179	474	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYPMGWFRQAPGKEREFVALISRSGGTTFYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYDWGQGTLVTVSS
DKK1-180	475	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNFAMGWFRQAPGKERELVAFSSSGGRTIYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-181	476	EVQLVESGGGLVQPGGSLRLSCAASGLTTVYTMGWFRQAPGKEREVVAAISRTGGSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS

DKK1-182	477	EVQLVESGGGLVQPGGSLRLSCAASGTTFRINVMGWFRQAPGKEREFVAAINRSGKSTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-183	478	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTHAMGWFRQAPGKEREFVAHITRLGVTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-184	479	EVQLVESGGGLVQPGGSLRLSCAASGIPSTLRAMGWFRQAPGKEREFVAAINWSGASTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-185	480	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYVMGWFRQAPGKEREFVAAIDWSGSRSYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFYTSSNYDWGQGTLVTV SS
DKK1-186	481	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDIAMGWFRQAPGKEREFVAAINWSGARTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFSTSSNYDWGQGTLVTV SS
DKK1-187	482	EVQLVESGGGLVQPGGSLRLSCAASGIPFSTRTMGWFRQAPGKEREFVAAISWSGGSTIYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-188	483	EVQLVESGGGLVQPGGSLRLSCAASGFTFDEYAMGWFRQAPGKEREFVGAIDWSGRRITYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRISVSYFSTSSNYDWGQGTLVTVSS
DKK1-189	484	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMGWFRQAPGKEREFVAAISWSGGSTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSFSYFSTSSNYEWGQGTLVTVS S
DKK1-190	485	EVQLVESGGGLVQPGGSLRLSCAASGITFKRYAMGWFRQAPGKEREFVAAINWSGASTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-191	486	EVQLVESGGGLVQPGGSLRLSCAASGFTFGHYAMGWFRQAPGKEREFVAAISWSLTRTHYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFSTSSNYDWGQGTLVTV SS
DKK1-192	487	EVQLVESGGGLVQPGGSLRLSCAASGSITSINPMGWFRQAPGKEREFVAAISRSGASAYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-193	488	EVQLVESGGGLVQPGGSLRLSCAASGGRIFSNYAMGWFRQAPGKEREFVAAISWSGGSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTV SS
DKK1-194	489	EVQLVESGGGLVQPGGSLRLSCAASGRTFTMGWFRQAPGKEREFVAAINWRSGGSTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-195	490	EVQLVESGGGLVQPGGSLRLSCAASGGTFNGRAMGWFRQAPGKEREFVAAISRSGGGIYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-196	491	EVQLVESGGGLVQPGGSLRLSCAASGFNFDDYAMGWFRQAPGKERELVAAISWSLSRTHYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTV SS
DKK1-197	492	EVQLVESGGGLVQPGGSLRLSCAASSIGIAFSSRTMGWFRQAPGKEREFVAAVTRSGGKSYYAD SVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-198	493	EVQLVESGGGLVQPGGSLRLSCAASGSTFRINVMGWFRQAPGKEREFVAAISASGSALYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-199	494	EVQLVESGGGLVQPGGSLRLSCAASGGIYRVNTMGWFRQAPGKEREFVAAINWSGGSTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-200	495	EVQLVESGGGLVQPGGSLRLSCAASGRSLNTYTMGWFRQAPGKERELVAVIISGGSTAYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-201	496	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYAMGWFRQAPGKEREWVASISTSGKTTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-202	497	EVQLVESGGGLVQPGGSLRLSCAASGTTVRIRTMGWFRQAPGKEREFVAAINGGGNTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-203	498	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTYSMGWFRQAPGKEREFVAAINWSGSSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-204	499	EVQLVESGGGLVQPGGSLRLSCAASGIPFSTRTMGWFRQAPGKEREFVAAISSGATTLYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-205	500	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRYAMGWFRQAPGKEREFVALIRIKDGSIYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-206	501	EVQLVESGGGLVQPGGSLRLSCAASGHTFNTYPMGWFRQAPGKERELVAAISRSGGKLYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-207	502	EVQLVESGGGLVQPGGSLRLSCAASGRSFSEYAMGWFRQAPGKEREFLAAISRDGAATYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-208	503	EVQLVESGGGLVQPGGSLRLSCAASGRTFTTYPMGWFRQAPGKEREFVAAISSSGSSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS

DKK1-209	504	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRYAMGWFRQAPGKEREFVAAISWSGGSTLYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-210	505	EVQLVESGGGLVQPGGSLRLSCAASGSIFTINAMGWFRQAPGKERELVAAINWSGSSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-211	506	EVQLVESGGGLVQPGGSLRLSCAASGTSISNRVMGWFRQAPGKERELVAGISSGGNLKAYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-212	507	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEGAGSDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKQIPGRKWTANGRKDYWGQGTLVTVSS
DKK1-213	508	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYPKNFDYWGQGTLVTVSS
DKK1-214	509	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSAAMSWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-215	510	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSAIQQRGLKTAYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGIRGWIGHDTQPFDYWGQGTLVTVSS
DKK1-216	511	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYRMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYPKNFDYWGQGTLVTVSS
DKK1-217	512	EVQLLESGGGLVQPGGSLRLSCAASGFTSNNFAMTWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLQKRGPRFDYWGQGTLVTVSS
DKK1-218	513	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSVISSSGGETSYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKAPLRSGGVDYWGQGTLVTVSS
DKK1-219	514	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYRMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFPSTHGKFDYWGQGTLVTVSS
DKK1-220	515	EVQLLESGGGLVQPGGSLRLSCAASGLTFPNYGMGWVRQAPGKGLEWVSSIDDRGRYTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVIAAAGAFDYWGQGTLVTVSS
DKK1-221	516	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVGYISNSGSTSYNDSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-222	517	EVQLLESGGGLVQPGGSLRLSCAASGFTFTHYSMGWVRQAPGKGLEWVSGITRSGSTNYRDSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTENRGVSFDYWGQGTLVTVSS
DKK1-223	518	EVQLLESGGGLVQPGGSLRLSCAASGFTFEEKEMIWVRQAPGKGLEWVSMISSSGLWTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGWRRFDYWGQGTLVTVSS
DKK1-224	519	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYRMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTWNGYWGQGTLVTVSS
DKK1-225	520	EVQLLESGGGLVQPGGSLRLSCAASGFTFHKYGMAWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASLSRGYWGQGTLVTVSS
DKK1-226	521	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSSIWPRGQKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRGRGFDYWGQGTLVTVSS
DKK1-227	522	EVQLLESGGGLVQPGGSLRLSCAASGFTFAKYKMWWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAHNAFDYWGQGTLVTVSS
DKK1-228	523	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYFMSWVRQAPGKGLEWVSAISGGGADTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGNYFDYWGQGTLVTVSS
DKK1-229	524	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYRMMWVRQAPGKGLEWVSSISGYGSTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRGRGFDYWGQGTLVTVSS
DKK1-230	525	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYAMNWVRQAPGKGLEWVSSIGANGAPTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDKRYRGSQHYFDYWGQGTLVTVSS
DKK1-231	526	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYTMGWVRQAPGKGLEWVSSISNSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAGRKFDYWGQGTLVTVSS
DKK1-232	527	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYDMSWVRQAPGKGLEWVSDIGASGSATSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKQSGSEDHFDYWGQGTLVTVSS
DKK1-233	528	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKWRREGYTGSKFDYWGQGTLVTVSS
DKK1-234	529	EVQLLESGGGLVQPGGSLRLSCAASGGFSLSRYMHWVRQAPGKGLEWVSTINQAGLRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSRTGRYFDYWGQGTLVTVSS
DKK1-235	530	EVQLLESGGGLVQPGGSLRLSCAASGFTFHKYGMAWVRQAPGKGLEWVGYINPSRGYTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGYRHFDYWGQGTLVTVSS
DKK1-236	531	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSVISSSGGETSYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGQGFDYWGQGTLVTVSS
DKK1-237	532	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSYISSSGSSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-238	533	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGLPKRGPRFDYWGQGTLVTVSS

DKK1-239	534	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYAMNWVRQAPGKGLEWVSYIGPSGGKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPWFDYWGQGTLVTVSS
DKK1-240	535	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPSRRFDYWGQGTLVTVSS
DKK1-241	536	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYVMIWVRQAPGKGLEWVSAIQQRGLKTAYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSGPYYFDYWGQGTLVTVSS
DKK1-242	537	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYQMGWVRQAPGKGLEWVSAITGTGGETYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKPGHRFDYWGQGTLVTVSS
DKK1-243	538	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSGIYPSGGSTVYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRYSQVHYALDYWGQGTLVTVSS
DKK1-244	539	EVQLLESGGGLVQPGGSLRLSCAASGFTFKAYEIGWVRQAPGKGLEWVSGISPSGGITTYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHRAGSSGWYSDYWGQGTLVTVSS
DKK1-245	540	EVQLLESGGGLVQPGGSLRLSCAASGFTFEVYTMAWVRQAPGKGLEWVSAISGRGDNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTENRGVSFDYWGQGTLVTVSS
DKK1-246	541	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMAWVRQAPGKGLEWVSNIWPRGQKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVTGRGFDYWGQGTLVTVSS
DKK1-247	542	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVADVNPNSGTSIYNDS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGPGTRGDYWGQGTLVTVSS
DKK1-248	543	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGVSWVRQAPGKGLEWVSSISPSGGWTEYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYGAYFGLDYWGQGTLVTVSS
DKK1-249	544	EVQLLESGGGLVQPGGSLRLSCAASGFTFAHEPMVWVRQAPGKGLEWVGKINYAGNTDYNDSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKKDYDYVWGSPYFDYWGQGTLVTVSS
DKK1-250	545	EVQLLESGGGLVQPGGSLRLSCAASGFTFHESTMTWVRQAPGKGLEWVSVISSSGGETSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARIRVGPSGGAFDYWGQGTLVTVSS
DKK1-251	546	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFPSSQFRFDYWGQGTLVTVSS
DKK1-252	547	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYPKNFNYWGQGTLVTVSS
DKK1-253	548	KVQLLESGGGLVQPGGSLRLSCAASGFTFHKYGMAWVRQAPGKGLEWVGKINYAGNTDYNDS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDKRYRGSQHYFDYWGQGTLVTVSS
DKK1-254	549	EVQLLESGGGLVQPGGSLRLSCAASGLTFPNYGMGWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGLWAFDYWGQGTLVTVSS
DKK1-255	550	EVQLLESGGGLVQPGGSLRLSCAASGFTFKAYEIGWVRQAPGKGVEWGSGIIPNGGITTYADSVK GRFTISRDNSXNTLYLLMNSLIAEDAAVYYCGRHRAGSIGWYSDYWGQGTLVTVSS
DKK1-256	551	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSDIGASGSATSYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-257	552	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGRRRFDYWGQGTLVTVSS
DKK1-258	553	EVQLLESGGGLVQPGGSLRLSCAASGFTSNNFAMTWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLQKRGPRFDYWGQGTLVTVSS
DKK1-259	554	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSTIWARGQKTYYAD SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHLPGRGFEYWGRGTRTPVSS
DKK1-260	555	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDETMSWVRQAPGKGLEWVSAIISSGGLTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGFRIFDYWGQGTLVTVSS
DKK1-261	556	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNSYISWVRQAPGKGLEWVSYITPKGDHTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGARRFDYWGQGTLVTVSS
DKK1-262	557	EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYDMQWVRQAPGKGLEWVSSIGRHGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSLGRFDYWGQGTLVTVSS
DKK1-263	558	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEGAGSDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-264	559	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYGMHWVRQAPGKGLEWVSSIWPRGQKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGTRIKQGFDYWGQGTLVTVSS
DKK1-265	560	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-266	561	EVQLLESGGGLVQPGGSLRLSCAASGFTFVAYNMGWVRQAPGKGLEWVSSISNSGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKNRAKFDYWGQGTLVTVSS
DKK1-267	562	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSVISSSGGETSYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPKRGPRFDYWGQGTLVTVSS
DKK1-268	563	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEGAGSDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRGRGFDYWGQGTLVTVSS

DKK1-269	564	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVAVISYGGSNKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGVRKGFDYWGQGTLVTVSS
DKK1-270	565	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSAIQQRGLKTAYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYRGYFDYWGQGTLVTVSS
DKK1-271	566	EVQLLESGGGLVQPGGSLRLSCAASGYSISSGYHWAWVRQAPGKGLEWVSSIDDRGRYTYYAD SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSNGRFDYWGQGTLVTVSS
DKK1-272	567	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAISGSGGGTSYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYFHGKFDYWGQGTLVTVSS
DKK1-273	568	EVQLLESGGGLVQPGGSLRLSCAASGFTFHKYGMAWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGRWSIFDYWGQGTLVTVSS
DKK1-274	569	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVADVNPNSGASIYNDS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGPGTRGDYWGQGTLVTVSS
DKK1-275	570	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSGIYPSGGSTVYDDS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKWSSRAFDYWGQGTLVTVSS
DKK1-276	571	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEGAGSDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-277	572	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEGAGSDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-278	573	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYVMIWVRQAPGKGLEWVSEISPSGKKKYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYPKNFDYWGQGTLVTVSS
DKK1-279	574	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-280	575	EVQLLESGGGLVQPGGSLRLSCAASGFTSNNFAMTWVRQAPGKGLEWVGYINPSRGYTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTENRGVSFDYWGQGTLVTVSS
DKK1-281	576	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRGRGFDYWGQGTLVTVSS
DKK1-282	577	EVQLLESGGGLVQPGGSLRLSCAASGFTFFPYAMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-283	578	EVQLLESGGGLVQPGGSLRLSCAASGFTFDQYDMSWVRQAPGKGLEWVSAITGSGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATAESDDTYDYWGQGTLVTVSS
DKK1-284	579	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEGAGSDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-285	580	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYTMVWVRQAPGKGLEWVSAITGTGGETYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-286	581	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAIEARGGGTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRGRGFDYWGQGTLVTVSS
DKK1-287	582	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSSIWPSGGQTWYAD SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDKRYRGSQHYFDYWGQGTLVTVSS
DKK1-288	583	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVGISNSGSTSYNDSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-289	584	EVQLLESGGGLVQPGGSLRLSCAASGFTFHKYGMAWVRQAPGKGLEWVSSIGRHGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAGSGFDYWGQGTLVTVSS
DKK1-290	585	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYWNHWVRQAPGKGLEWVSTIGPSGTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAESFRSRYFDYWGQGTLVTVSS
DKK1-291	586	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSSIWPRGQKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASLSRGYWGQGTLVTVSS
DKK1-292	587	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYTMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPKRGPRFDYWGQGTLVTVSS
DKK1-293	588	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYFMGWVRQAPGKGLEWVSAISGRGDNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTENRGVSFDYWGQGTLVTVSS
DKK1-294	589	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVGAIQQRGLKTAYAD SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWTSGLDYWGQGTLVTVSS
DKK1-295	590	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYFMGWVRQAPGKGLEWVSEIDALGTDTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGLRRFDYWGQGTLVTVSS
DKK1-296	591	EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYRMMWVRQAPGKGLEWVSSISSTGFKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKFRGRGFDYWGQGTLVTVSS
DKK1-297	592	EVQLLESGGGLVQPGGSLRLSCAASGFTFTHYSMGWVRQAPGKGLEWVSAINGTGGETYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-298	593	EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYLMSWVRQAPGKGLEWVSTIGPSGTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGRRIFDYWGQGTLVTVSS

DKK1-299	594	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYFMIWVRQAPGKGLEWVSSIDDRGRYTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGDYGSGDYWGQGTLVTVSS
DKK1-300	595	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPPKRGPRFDYWGQGTLVTVSS
DKK1-301	596	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSVISSSGGETSYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-302	597	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYGMHWVRQAPGKGLEWVSSIGRHGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGDYGSGDYWGQGTLVTVSS
DKK1-303	598	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSYIGPSGGKTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-304	599	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARPPKRGPRFDYWGQGTLVTVSS
DKK1-305	600	EVQLLESGGGLVQPGGSLRLSCAASGFTFEDETMSWVRQAPGKGLEWVSAIISSGGLTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGFRIFDYWGQGTLVTVSS
DKK1-306	601	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSGITRSGSTNYRDSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKWSSRAFDYWGQGTLVTVSS
DKK1-307	602	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHSKSSHRQSFDYWGQGTLVTVSS
DKK1-308	603	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLTGRFDYWGQGTLVTVSS
DKK1-309	604	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYFMGWVRQAPGKGLEWVSEISPSGKKKYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGAYFDYWGQGTLVTVSS
DKK1-310	605	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKYPMMWVRQAPGKGLEWVSWIEGRGTETYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS
DKK1-311	606	EVQLLESGGGLVQPGGSLRLSCAASGFTFHKYGMAWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYPKNFDYWGQGTLVTVSS
DKK1-312	607	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSEISPSGKKKYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGVRKKFDYWGQGTLVTVSS
DKK1-313	608	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-314	609	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMAWVRQAPGKGLEWVSYISPIGPRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRTENRGVSFDYWGQGTLVTVSS
DKK1-315	610	EVQLLESGGGLVQPGGSLRLSCAASGFTLDYLAIGWVRQAPGKGLEWVSEISPSGKKKYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPFDYWGQGTLVTVSS
DKK1-316	611	EVQLLESGGGLVQPGGSLRLSCAASGFTFTHYSMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-317	612	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSAITGTGGETYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-318	613	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVSTISPSGHGTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRTGREYGGGWYFDYWGQGTLVTVSS
DKK1-319	614	EVQLLESGGGLVQPGGSLRLSCAASGFTFPVYNMAWVRQAPGKGLEWVSSISESGTTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKNRAKFDYWGQGTLVTVSS
DKK1-320	615	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYVMGWVRQAPGKGLEWVAAISGGGADTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLPKRGPRFDYWGQGTLVTVSS
DKK1-321	616	EVQLLESGGGLVQPGGSLRLSCAASGFSFSAYAMNWVRQAPGKGLEWVSSISTSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRAGADYWGQGTLVTVSS
DKK1-322	617	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRFAMSWVRQAPGKGLEWVSAISGSGAYTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDIAAASFDYWGQGTLVTVSS
DKK1-323	618	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMTWVRQAPGKGLEWVSGVSGSGGTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAISYHFDYYFDYWGQGTLVTVSS
DKK1-324	619	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAISGGGGATYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARECSGGSCSYYYGMDVWGQGTLVTVSS
DKK1-325	620	EVQLLESGGGLVQPGGSLRLSCAASGSTFNNYAMSWVRQAPGKGLEWVSAISGSGSTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLAVSTSDYYYYGMDVWGQGTLVTVSS
DKK1-326	621	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRFAMSWVRQAPGKGLEWVSGITGSGTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDRVRFSPVRRWFDPWGQGTLVTVSS
DKK1-327	622	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYAMGWVRQAPGKGLEWVSAISATGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVRSSSWYGDYWGQGTLVTVSS
DKK1-328	623	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYAMTWVRQAPGKGLEWVSTISGSGVTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARKTGGHYPFDYWGQGTLVTVSS

DKK1-329	624	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRSAMSWVRQAPGKGLEWVSSISASGANTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQARYYGMDVRGQGTLVTVSS
DKK1-330	625	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKGLEWVSTITSSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASGLRARNGFDIWGQGTLVTVSS
DKK1-331	626	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMTWVRQAPGKGLEWVSGISGSGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGAILAYWGQGTLVTVSS
DKK1-332	627	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMIWVRQAPGKGLEWVSAVSGTGGTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDVGFGELHPWGQGTLVTVSS
DKK1-333	628	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSGISGSGYSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRTGTLYGMDVWGQGTLVTVSS
DKK1-334	629	EVQLLESGGGLVQPGGSLRLSCAASGFSFNNYAMSWVRQAPGKGLEWVSAISGGGSNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVAASGSYYRAFDQWGQGTLVTVSS
DKK1-335	630	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYAMSWVRQAPGKGLEWVSGISSSGGNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGFGWFDPWGQGTLVTVSS
DKK1-336	631	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYGMTWVRQAPGKGLEWVSTISGSGGRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVSYDSSGYYYDAFDIWGQGTLVTVSS
DKK1-337	632	EVQLLESGGGLVQPGGSLRLSCAASGFTFANYAMSWVRQAPGKGLEWVSAISGSGGSAYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDAAVYYCARSGSFLSFDSWGQGTLVTVSS
DKK1-338	633	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRFAISWVRQAPGKGLEWVSTISGSGGRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVDYKKKSYYNAMDAWGQGTLVTVSS
DKK1-339	634	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTSAMSWVRQAPGKGLEWVSAISSGGGGTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGPRGRGAFDVWGQGTLVTVSS
DKK1-340	635	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDRVRFSPVRRWFDPWGQGTLVTVSS
DKK1-341	636	EVQLLESGGGLVQPGGSLRLSCAASGIHLSSYAMSWVRQAPGKGLEWVSTISGGGGGTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGHVGIRRPFDVWGQGTLVTVSS
DKK1-342	637	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYAMSWVRQAPGKGLEWVSIISGSGGTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHAHGAGSYPFDYWGQGTLVTVSS
DKK1-343	638	EVQLLESGGGLVQPGGSLRLSCAASGFPFSSYAMGWVRQAPGKGLEWVSVISGSGGRTHYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGRAPRKYYGMDVWGQGTLVTVSS
DKK1-344	639	EVQLLESGGGLVQPGGSLRLSCAASGFSFSAYAMSWVRQAPGKGLEWVSAISGRDTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPLRGSGRLSFDYWGQGTLVTVSS
DKK1-345	640	EVQLLESGGGLVQPGGSLRLSCAASGSPFSNYAMSWVRQAPGKGLEWVSAISGSGGSTFYSDSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAPRSPILGVRRGLDPWGQGTLVTVSS
DKK1-346	641	EVQLLESGGGLVQPGGSLRLSCAASGFSFSGYAMNWVRQAPGKGLEWVSAISGSSGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRGGTRGLGYWGQGTLVTVSS
DKK1-347	642	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTYGMSWVRQAPGKGLEWVSAISGSGETTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLDHDSSGFYEAFDVWGQGTLVTVSS
DKK1-348	643	EVQLLESGGGLVQPGGSLRLSCAASGLTFSRYAMSWVRQAPGKGLEWVSSISGRGGNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGMRLGKSYYYYGMDVWGQGTLVTVSS
DKK1-349	644	EVQLLESGGGLVQPGGSLRLSCAASGFAFSTSAMSWVRQAPGKGLEWVSGISASGGSTHYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLSVARGAYGMDVWGQGTLVTVSS
DKK1-350	645	EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYAMSWVRQAPGKGLEWVSAISGSGARTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRGRPPQYYFDSWGQGTLVTVSS
DKK1-351	646	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRYAMSWVRQAPGKGLEWVSTVSGSGGTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGWEPGIAANWGQGTLVTVSS
DKK1-352	647	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKHAMSWVRQAPGKGLEWVSIISGSGDTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHQYSGSGSFRYWGQGTLVTVSS
DKK1-353	648	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRSAMSWVRQAPGKGLEWVSAIGGSGDNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHRGSFWFDPWGQGTLVTVSS
DKK1-354	649	EVQLLESGGGLVQPGGSLRLSCAASGFSFRSYAMNWVRQAPGKGLEWVSAISGSGGNTFYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTTMFGSGTFYTGFDFWGQGTLVTVSS
DKK1-355	650	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSSMSWIRQAPGKGLEWVSGISGSGGTTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAGARFVGFDYWGQGTLVTVSS
DKK1-356	651	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRFAMSWVRQAPGKGLEWVSAISGSGRNTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATFNPVGLFYWGQGTLVTVSS
DKK1-357	652	EVQLLESGGGLVQPGGSLRLSCAASGFSFSTYAMMWVRQAPGKGLEWVSAISGSAVSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDAAVYYCARSGSFLSFDSWGQGTLVTVSS
DKK1-358	653	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYTMNWVRQAPGKGLEWVSAVSGSGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSRNGRWFDPWGQGTLVTVSS

DKK1-359	654	EVQLLESGGGLVQPGGSLRLSCAASGLTFRSYAMSWVRQAPGKGLEWVSGISGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGASFDSWGQGTLVTVSS
DKK1-360	655	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMKWVRQAPGKGLEWVSGISGSGARTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRQRQRSTPLGRYWGQGTLVTVSS
DKK1-361	656	EVQLLESGGGLVQPGGSLRLSCAASGFNFRDYAMSWVRQAPGKGLEWVSAISGRGSVYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGDWVAFDYWGQGTLVTVSS
DKK1-362	657	EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYVMSWFRQAPGKGLEWVSGISGSGGRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRKGPTYGMDVWGQGTLVTVSS
DKK1-363	658	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTFAMAWVRQAPGKGLEWVSALSGSGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVTRYQGWLSHFDYWGQGTLVTVSS
DKK1-364	659	EVQLLESGGGLVQPGGSLRLSCAASGFTLSTYAMSWVRQAPGKGLEWVSTISTSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVFVSSGWYDGMDVWGQGTLVTVSS
DKK1-365	660	EVQLLESGGGLVQPGGSLRLSCAASGLTFNNYAMSWVRQAPGKGLEWVSGISGSGARTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGASLDVWGQGTLVTVSS
DKK1-366	661	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRYAMSWVRQAPGKGLEWVSTISGSGTTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAIGGRTAYWGQGTLVTVSS
DKK1-367	662	EVQLLESGGGLVQPGGSLRLSCAASGFSFSAYAMSWVRQAPGKGLEWVSAISGRDTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPLRGSGRLSFDYWGQGTLVTVSS
DKK1-368	663	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRYAMNWVRQAPGKGLEWVSTITASGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVVTAMGYYYGMDVWGQGTLVTVSS
DKK1-369	664	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGVSWVRQAPGKGLEWVSAISAGGGNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLGMRGPYYYYYGMDVWGQGTLVTVSS
DKK1-370	665	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYGMSWVRQAPGKGLEWVSAISGGGAGTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVASRNYLLDFWGQGTLVTVSS
DKK1-371	666	EVQLLESGGGLVQPGGSLRLSCAASGFTFTKYAMSWVRQAPGKGLEWVGAISGRGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGDLTVTRKYDSWGQGTLVTVSS
DKK1-372	667	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYGMTWVRQAPGKGLEWVSAISRSGGNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARTYSYGSFDYWGQGTLVTVSS
DKK1-373	668	EVQLLESGGGLVQPGGSLRLSCAASGFNFRSYAMNWVRQAPGKGLEWVSAISGSGTTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASWRAAPFDYWGQGTLVTVSS
DKK1-374	669	EVQLLESGGGLVQPGGSLRLSCAASGFSFSAYAMSWVRQAPGKGLEWVSAISGRDTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPLRGSGRLSFDYWGQGTLVTVSS
DKK1-375	670	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYAMTWVRQAPGKGLEWVSSITGSGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGKFHLDPWGQGTLVTVSS
DKK1-376	671	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMSWVRQAPGKGLEWVGAISGRGGSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTTDYGAIMDVWGQGTLVTVSS
DKK1-377	672	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRFAMSWVRQAPGKGLEWVSGISGSGTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDSRNYFGMGVWGQGTLVTVSS
DKK1-378	673	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYALSWVRQAPGKGLEWVSAISRSGGNTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGRDGTRFGAFDIWGQGTLVTVSS
DKK1-379	674	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKFAMTWVRQAPGKGLEWVSTISGSGSRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRSWYNHWGQGTLVTVSS
DKK1-380	675	EVQLLESGGGLVQHGGSLRLSCAASGLTFSSYALSWVRQAPGKGLEWVSDISGSGGNTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARFQPRPLRLFDYWGQGTLVTVSS
DKK1-381	676	EVQLLESGGGLVQPGGSLRLSCAASGFTLRSYAMTWVRQAPGKGLEWVSAISGSGGYTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARASYGSGSYPLIHWGQGTLVTVSS
DKK1-382	677	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFAMSWVRQAPGKGLEWVSTVSGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGHRSNIGWDVWGQGTLVTVSS
DKK1-383	678	EVQLLESGGGLVQPGGSLRLSCAASGSTFSSYAMSWVRQAPGKGLEWVSTISASGGRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDDRVRFSPVRRWFDPWGQGTLVTVSS
DKK1-384	679	EVQLLESGGGLVQPGGSLRLSCAASGFTFRRSAMSWVRQAPGKGLEWVSAISGSGSGTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSARGRWFDPWGQGTLVTVSS
DKK1-385	680	EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYAMSWVRQALGKGLEWVSAISRSGDRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGQRAHQQLVRGAMDVWGQGTLVTVSS
DKK1-386	681	EVQLLESGGGLVQPGGSLRLSCAASGFTFRTFAMSWVRQAPGKGLEWVSGISASGGTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAHRRRSKFWSGFGVWGQGTLVTVSS
DKK1-387	682	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYAMTWVRQAPGKGLEWVSTISGSGVTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARKTGGHYPFDYWGQGTLVTVSS
DKK1-388	683	EVQLLESGGGLVQPGGSLRLSCAASGFTFDNYAMTWVRQAPGKGLEWVSGISGSGGSIYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVKGAPAGYLDSWGQGTLVTVSS

DKK1-389	684	EVQLLESGGGLVQPGGSLRLSCAASGFRFSSYAMSWVRQAPGKGLEWVSTISGRGGSTDYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHNRERRAFDIWGQGTLVTVSS
DKK1-390	685	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYAMGWVRQAPGKGLEWVSGISGGGGTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDSRVRGTHDYYYYGMDVWGQGTLVTVS S
DKK1-391	686	EVQLLESGGGLVQPGGSLRLSCAASGFTFSKFAMNWVRQAPGKGLEWVSGISASGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGSLRFTPWGQGTLVTVSS
DKK1-392	687	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSGMSWVRQAPGKGLEWVSAISPSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLSADRVFAFDIWGQGTLVTVSS
DKK1-393	688	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSFAMAWVRQAPGKGLEWVSTISGSGDVTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGHRSNIGWDVWGQGTLVTVSS
DKK1-394	689	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRFAMSWVRQAPGKGLEWVSGITGSGTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPLRGSGRLSFDYWGQGTLVTVSS
DKK1-395	690	EVQLLESGGGLVQPGGSLRLSCAASGFGFSSYAMSWVRQAPGKGLEWVSGITGSGGNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSRRPRYSYGFAFESWGQGTLVTVSS
DKK1-396	691	EVQLLESGGGLVQPGGSLRLSCAASGVTFRNYAMSWVRQAPGKGLEWVSAISASGGSPYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDTSVGWFDPWGQGTLVTVSS
DKK1-397	692	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKGLEWVSSISGGGGRTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRDLTRRAAMDVWGQGTLVTVSS
DKK1-398	693	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSSAMSWVRQAPGKGLEWVSVISGSGRSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARNGAGSHYYAMDVWGQGTLVTVSS
DKK1-399	694	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRFAMGWVRQAPGKGLEWVSSISGSGGRTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASSKVTRSALDYWGQGTLVTVSS
DKK1-400	695	EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYALSWVRQAPGKGLEWVSAISGSGSSTFYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGRESGRGSGTWGQGTLVTVSS
DKK1-401	696	EVQLLESGGGLVQPGGSLRLSCAASGFTYSSYAMTWVRQAPGKGLEWVSVISGSGGSTYHADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARERELYYFYYGMDVWGQGTLVTVSS
DKK1-402	697	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYGMGWVRQAPGKGLEWVSTITGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHHNRRSSLDYWGQGTLVTVSS
DKK1-403	698	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSGMSWVRQAPGKGLEWVSGISSTGGTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRGRRQLRYYYGMDVWGQGTLVTVSS
DKK1-404	699	EVQLLESGGGLVQPGGSLRLSCAASGFSFSSSAMNWVRQAPGKGLEWVAAISGSGGTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARARRRSFDWWGQGTLVTVSS
DKK1-405	700	EVQLLESGGDLVQPGGSLRLSCAASGFTFSRYAMSWVRQAPGKGLEWVSAISGGRVSTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSLRGNAFDIWGQGTLVTVSS
DKK1-406	701	EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSSIRGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLQSRGYWGQGTLVTVSS
DKK1-407	702	EVQLLESGGGLVQPGGSLRLSCAASGFTFNKFAMSWVRQAPGKGLEWVSGISVSGGNTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARHSRLAALLAWGQGTLVTVSS
DKK1-408	703	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHVMGWVRQAPGKGMEWVSGISGSGAGTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVTGTTGWFDPWGQGTLVTVSS
DKK1-409	704	EVQLLESGGGLVQPGGSLRLSCAASGFTFGRYAMSWVRQAPGKGLEWVSGISSSRGSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVGIAGRGMDVWGQGTLVTVSS
DKK1-410	705	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYGMSWVRQAPGKGLEWVSAISGRRTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVSRGYPRRSDSWGQGTLVTVSS
DKK1-411	706	EVQLLESGGGLVQPGGSLRLSCAASGFTVSSYAMSWVRQAPGKGLEWVSGISGGGGTTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVRSSNWKFDQWGQGTLVTVSS
DKK1-412	707	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRSAMSWVRQAPGKGLEWVSSISASGANTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQARYYGMDVRGQGTLVTVSS
DKK1-413	708	EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYDMTWVRQAPGKGLEWVSSISGSGVTTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRRLDYWGQGTLVTVSS
DKK1-414	709	EVQLLESGGGLVQPGGSLRLSCAASGFAFTTYAMGWVRQAPGKGLEWVSAISGSGSTTYYADS VKSRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSGSFLSFDSWGQGTLVTVSS
DKK1-415	710	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMIWVRQAPRKGLEWVSAISGSGRNTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTTVYYCARGGGASNWFDPWGQGTLVTISS
DKK1-416	711	EVQLLESGGGLVQPGGSLRLSCAASGFSFSAYAMSWVRQAPGKGLEWVSAISGRDTSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPLRGSGRLSFDYWGQGTLVTVSS
DKK1-417	712	EVQLLESGGGLVQPGGSLRLSCAASGFTFSRFAMSWVRQAPGKGLEWVSSISGTGSSTYYADSV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARVPGNWGQGTLVTVSS

DKK1-418	2164	EVQLVESGGGLVQPGGSLRLSCAASGIPFSSRTMGWFRQAPGKEREFVAAISRSGTGTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-419	2165	EVQLVESGGGLVQPGGSLRLSCAASGGIYRVNTMGWFRQAPGKEREFVAAINWSGGSTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-420	2166	EVQLVESGGGLVQPGGSLRLSCAASGFLMYDRAMGWFRQAPGKEREIVAAISRTGSSIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-421	2167	EVQLVESGGGLVQPGGSLRLSCAASGRTFSRFAMGWFRQAPGKERELVAAISARGMPAYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-422	2168	EVQLVESGGGLVQPGGSLRLSCAASGTTFRINVMGWFRQAPGKEREFVAVVNWNGGSTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-423	2169	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNNVMGWFRQAPGKEREMVAAMLSGGSTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYDWGQGTLVTVSS
DKK1-424	2170	EVQLVESGGGLVQPGGSLRLSCAASGRTFSDIAMGWFRQAPGKEREFVAAINWSGARTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFSTSSNYDWGQGTLVTVSS
DKK1-425	2171	EVQLVESGGGLVQPGGSLRLSCAASGHTYNTYPMGWFRQAPGKERELVAVILRGGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-426	2172	EVQLVESGGGLVQPGGSLRLSCAASGRSLYDRAMGWFRQAPGKEREIVAAISRTGSSIYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-427	2173	EVQLVESGGGLVQPGGSLRLSCAASGRTFNNYAMGWFRQAPGKERELVAAISWSTGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-428	2174	EVQLVESGGGLVQPGGSLRLSCAASGRTLYSYPMGWFRQAPGKEREFVAAISWSAGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGSKYGHSRARYDWGQGTLVTVSS
DKK1-429	2175	EVQLVESGGGLVQPGGSLRLSCAASGTFRDYAMGWFRQAPGKERELVAAIYGTGGELVYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-430	2176	EVQLVESGGGLVQPGGSLRLSCAASGGGTFGSYAMGWFRQAPGKEREFVSAITWNGTRTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-431	2177	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYPMGWFRQAPGKEREFVAATSWSGGSKYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-432	2178	EVQLVESGGGLVQPGGSLRLSCAASGRTFTNYAMGWFRQAPGKEREFVATISRGGSATYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-433	2179	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTHAMGWFRQAPGKEREFVAHITRLGVTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-434	2180	EVQLVESGGGLVQPGGSLRLSCAASGRSFSMYAMGWFRQAPGKEREFVAAISRDGAATYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRLYGHSRARYDWGQGTLVTVSS
DKK1-435	2181	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREFVAAVSWSLSRTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRASVQYFSTSSNYDWGQGTLVTVSS
DKK1-436	2182	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDRAMGWFRQAPGKERELVAAIRWSGGITWYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-437	2183	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSVMGWFRQAPGKEREFVAAINWSGASTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYNHSRTRYEWGQGTLVTVSS
DKK1-438	2184	EVQLVESGGGLVQPGGSLRLSCAASGHTFNTYPMGWFRQAPGKEREFVAAINSGGSYTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYEWGQGTLVTVSS
DKK1-439	2185	EVQLVESGGGLVQPGGSLRLSCAASGRIFTMGWFRQAPGKEREFVAAISGSGVYTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-440	2186	EVQLVESGGGLVQPGGSLRLSCAASGRSFSEYAMGWFRQAPGKEREFLAAISRDGAATYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-441	2187	EVQLVESGGGLVQPGGSLRLSCAASGFNSGSYTMGWFRQAPGKEREFVAAISWSLSRTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-442	2188	EVQLVESGGGLVQPGGSLRLSCAASGGTAYAMGWFRQAPGKEREFVAAISWSLTRTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTVSS
DKK1-443	2189	EVQLVESGGGLVQPGGSLRLSCAASGRTFTSYPMGWFRQAPGKEREFVAAISGSGDDTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-444	2190	EVQLVESGGGLVQPGGSLRLSCAASGSTFRINVMGWFRQAPGKEREFVAAISASGSALYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-445	2191	EVQLVESGGGLVQPGGSLRLSCAASGGTLNNNPMAMGWFRQAPGKEREFVASINWSGARAYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRISVQYFTTSSNYDWGQGTLVTVSS

DKK1-446	2192	EVQLVESGGGLVQPGGSLRLSCAASGRTFSTYPMGWFRQAPGKEREFVAGIGTRGAPVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-447	2193	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSYPMGWFRQAPGKEREFVAHITRLGVTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-448	2194	EVQLVESGGGLVQPGGSLRLSCAASGIPFSSRTMGWFRQAPGKEREFVAAVGWYGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-449	2195	EVQLVESGGGLVQPGGSLRLSCAASGIDVNRNAMGWFRQAPGKERELVAAISWSGGRTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVHYFSTSSNYDWGQGTLVTVSS
DKK1-450	2196	EVQLVESGGGLVQPGGSLRLSCAASGINFSRYGMGWFRQAPGKEREFVAAIDWSGSRSYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-451	2197	EVQLVESGGGLVQPGGSLRLSCAASGGTLRGYGMGWFRQAPGKEREFVAAIDWSGSRSYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKYVSVRYFSTSSNYDWGQGTLVTVSS
DKK1-452	2198	EVQLVESGGGLVQPGGSLRLSCAASGQTFNMGWFRQAPGKEREFVAAVNWNGDSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-453	2199	EVQLVESGGGLVQPGGSLRLSCAASGYTFRAYVMGWFRQAPGKEREWVARITSGGSTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-454	2200	EVQLVESGGGLVQPGGSLRLSCAASGNIFTLNVMGWFRQAPGKEREFVAAINSGGSYTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-455	2201	EVQLVESGGGLVQPGGSLRLSCAASGFRMYDRAMGWFRQAPGKEREFVAAISGRSGNTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYDWGQGTLVTVSS
DKK1-456	2202	EVQLVESGGGLVQPGGSLRLSCAASGFTFSMWPMGWFRQAPGKEREFVAAISRSGGSTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYNHSRTRYEWGQGTLVTVSS
DKK1-457	2203	EVQLVESGGGLVQPGGSLRLSCAASGFTFRSYPMGWFRQAPGKEREFVALIHTGGGTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYDWGQGTLVTVSS
DKK1-458	2204	EVQLVESGGGLVQPGGSLRLSCAASGLPFSTKSMGWFRQAPGKERELVAFSSSGGRTIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-459	2205	EVQLVESGGGLVQPGGSLRLSCAASGNIFRINAMGWFRQAPGKEREWVARINSGGSSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-460	2206	EVQLVESGGGLVQPGGSLRLSCAASGGTFGHYAMGWFRQAPGKEREFVAVISWSLTRTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSFSYFSTSSNYEWGQGTLVTVSS
DKK1-461	2207	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSYPMGWFRQAPGKEREFVAAITWGGSTTLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGNLVTVSS
DKK1-462	2208	EVQLVESGGGLVQPGGSLRLSCAASGITFRRYPMGWFRQAPGKEREFVAGVNWGGGSTKYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-463	2209	EVQLVESGGGLVQPGGSLRLSCAASGRTFSYNPMGWFRQAPGKEREMVATISIGGRTSYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-464	2210	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKEREFVAAIRSSGGLFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-465	2211	EVQLVESGGGLVQPGGSLRLSCAASGPTFSTNTMGWFRQAPGKEREFVAAIYSGVRSGVSAIYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-466	2212	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYPMGWFRQAPGKEREFVAAIYGTGGELVYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-467	2213	EVQLVESGGGLVQPGGSLRLSCAASGRAIGSYAMGWFRQAPGKEREFVATITFSGARTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRASVQYFSTSSNYDWGQGTLVTVSS
DKK1-468	2214	EVQLVESGGGLVQPGGSLRLSCAASGRTLSRNTMGWFRQAPGKEREFVATIRSGAPVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-469	2215	EVQLVESGGGLVQPGGSLRLSCAASGRTFIGYHMGWFRQAPGKERELVAIKFSGGTTNYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYGHSRARYDWGQGTLVTVSS
DKK1-470	2216	EVQLVESGGGLVQPGGSLRLSCAASGRTISNYAMGWFRQAPGKEREFVAAISWRGGSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKYVSVSYFSTSSNYDWGQGTLVTVSS
DKK1-471	2217	EVQLVESGGGLVQPGGSLRLSCAASGRTISNYAMGWFRQAPGKEREFVAAISWALSRTHYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSFSYFSTSSNYEWGQGTLVTVSS
DKK1-472	2218	EVQLVESGGGLVQPGGSLRLSCAASGTFTSYPMGWFRQAPGKEREFVAAISWTGGSTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRYYNHSRTRYEWGQGTLVTVSS

DKK1-473	2219	EVQLVESGGGLVQPGGSLRLSCAASGRSFSMYAMGWFRQAPGKERELVAAISWSGGSTVYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAEGGYSGTYYYTGDFDWGQGTLVTVSS
DKK1-474	2220	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREFVAAINWSGARTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKSISVRYFSTSSNYEWGQGTLVTVS S
DKK1-475	2221	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMGWFRQAPGKEREWVSAISADGSDKRYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGKRYGYYDWGQGTLVTVSS
DKK1-476	2222	EVQLVESGGGLVQPGGSLRLSCAASGRTHSIYPMGWFRQAPGKEREFVATIRWGTTDTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPTRVSVRYFSTRSNYNWGQGTLVTVSS
DKK1-477	2223	EVQLVESGGGLVQPGGSLRLSCAASGFSLDYVGMGWFRQAPGKEREGVSTIKPSGDTTNYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAKYLSFYSDYEVYDWGQGTLVTVSS
DKK1-478	2224	EVQLVESGGGLVQPGGSLRLSCAASGSIFRVNVMGWFRQAPGKEREFVGAISMSGANTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-479	2225	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSLPMGWFRQAPGKERELVAALNWSGGNTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQGTLVTVSS
DKK1-480	2226	EVQLVESGGGLVQPGGSLRLSCAASGFLMYDRAMGWFRQAPGKEREIVAAISRTGSSIYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-481	2227	EVQLVESGGGLVQPGGSLRLSCAASGDISSYVMGWFRQAPGKEREFVARITWNGGTHTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRKYGHHRARYDWGQSTLVTVSS
DKK1-482	2228	EVQLVESGGGLVQPGGSLRLSCAASGRTHSIYPMGWFRQAPGKERELVAAVNWNGDSTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-483	2229	EVQLVESGGGLVQPGGSLRLSCAASGIPFSSRTMGWFRQAPGKEREFVAAISRSGTGTYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-484	2230	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYPMGWFRQAPGKERELVAIIVNGGSTYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-485	2231	EVQLVESGGGLVQPGGSLRLSCAASGMTTIGPMGWFRQAPGKEREFVAAISWDGGNTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-486	2232	EVQLVESGGGLVQPGGSLRLSCAASGRASGDYAMGWFRQAPGKEREFVAAISWRGGNTYYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSFSYFSTSSNYEWGQGTLVTVS S
DKK1-487	2233	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYPMGWFRQAPGKEREWVAHLLSGGSTVYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-488	2234	EVQLVESGGGLVQPGGSLRLSCAASGRTFSEVVMGWFRQAPGKERELVAVAHWSGGSTFYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-489	2235	EVQLVESGGGLVQPGGSLRLSCAASGSTFSINRMGWFRQAPGKEREFVARITPRGLTEYADSVKG RFTISADNSKNTTYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-490	2236	EVQLVESGGGLVQPGGSLRLSCAASGRTFSFGWFRQAPGKEREFVAAVIWRGGSTYYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-491	2237	EVQLVESGGGLVQPGGSLRLSCAASGGTFSSYPMGWFRQAPGKEREFVAAISWSGSATFYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-492	2238	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNFAMGWFRQAPGKEREFVAVILRGGSTYADSVKG RFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-493	2239	EVQLVESGGGLVQPGGSLRLSCAASGGTFSRYAMGWFRQAPGKEREFVAAISWSLTRTHYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFVTSSNYDWGQGTLVTV SS
DKK1-494	2240	EVQLVESGGGLVQPGGSLRLSCAASGRTLSRSNMGWFRQAPGKEREHVALIRIKDGSIYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-495	2241	EVQLVESGGGLVQPGGSLRLSCAASGRTFSSGTMGWFRQAPGKERELVAAISRSGTLKAYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVQYFSTSSNYDWGQGTLVTVSS
DKK1-496	2242	EVQLVESGGGLVQPGGSLRLSCAASGRTFNSYPMGWFRQAPGKEREFVAAINVGGGTYYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYDWGQGTLVTVSS
DKK1-497	2243	EVQLVESGGGLVQPGGSLRLSCAASGYTLKNYYAMGWFRRAPGKEREFVAAISRSGGTTFYADS VKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRASVQYFSTSSNYDWGQGTLVTV SS
DKK1-498	2244	EVQLVESGGGLVQPGGSLRLSCAASGHTFNTYPMGWFRQAPGKEREFVAAVSYSGSYYADSVK GRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-499	2245	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDRAMGWFRQAPGKEREFVASISTSGTRTLYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-500	2246	EVQLVESGGGLVQPGGSLRLSCAASGRTLSSYAMGWFRQAPGKEREWVATIGTSGPPRYADSV KGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS

DKK1-501	2247	EVQLVESGGGLVQPGGSLRLSCAASGRIFTNTAMGWFRQAPGKEREFVAAISWGGGLTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGSRYGHSRARYDWGQGTLVTVSS
DKK1-502	2248	EVQLVESGGGLVQPGGSLRLSCAASGRIFTMGWFRQAPGKEREFVAAISWTAGTTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRNYGHSRARYDWGQGTLVTVSS
DKK1-503	2249	EVQLVESGGGLVQPGGSLRLSCAASGNIFTRHIMGWFRQAPGKEREWVARINTGGGSTFYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRTYGHSRARYEWGQGTLVTVSS
DKK1-504	2250	EVQLVESGGGLVQPGGSLRLSCAASGRTFSNYPMGWFRQAPGKEREFVAAISWSSGNAYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAVGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-505	2251	EVQLVESGGGLVQPGGSLRLSCAASGRTFTSYPMGWFRQAPGKEREWVATIGTHGTPLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-506	2252	EVQLVESGGGLVQPGGSLRLSCAASGQTFNGWFRQAPGKEREFVATISRSGVLYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRAYGYSRARYEWGQGTLVTVSS
DKK1-507	2253	EVQLVESGGGLVQPGGSLRLSCAASGRSFSEYPMGWFRQAPGKEREFVAAITWSGDMSVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRHYGHSRARYDWGQGTLVTVSS
DKK1-508	2254	EVQLVESGGGLVQPGGSLRLSCAASGRSFSSYPMGWFRQAPGKEREFVATINTAGWTTYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRSYGHSRARYDWGQGTLVTVSS
DKK1-509	2255	EVQLVESGGGLVQPGGSLRLSCAASGLTFRNYAMGWFRQAPGKEREFVAAISWSGGKLYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRISVSYFSTTSNYDWGQGTLVTVSS
DKK1-510	2256	EVQLVESGGGLVQPGGSLRLSCAASGSTFSSYPMGWFRQAPGKERELVALIHTGGTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAGNGGRQYGHSRARYDWGQGTLVTVSS
DKK1-511	2257	EVQLVESGGGLVQPGGSLRLSCAASGIDVNRNAMGWFRQAPGKEREFVGAVSWSGGTTVYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVSYFSTASNYDWGQGTLVTVSS
DKK1-512	2258	EVQLVESGGGLVQPGGSLRLSCAASGGTFNVYAMGWFRQAPGKEREFVAAINRSGKSTYYADSVKGRFTISADNSKNTAYLQMNSLKPEDTAVYYCAAAPRPKRVSVRYFSTSSNYDWGQGTLVTVSS

Table 7. Variable Light Chain Domain Sequences

DKK1 Variant	SEQ ID NO	VH Sequence
DKK1-212	713	DIQMTQSPSSLSASVGDRVTITCSGDKLRNKYASWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQSYDDHDRIVFGQGTKVEIK
DKK1-213	714	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYSASVLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-214	715	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLVIYGRNKRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSPLTFGQGTKVEIK
DKK1-215	716	DIQMTQSPSSLSASVGDRVTITCRTSQDISNYLNWYQQKPGKAPKLLIYAASDLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYNLPWTFGQGTKVEIK
DKK1-216	717	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYAASGLPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCASRDRSGHGVFGQGTKVEIK
DKK1-217	718	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYGASSRATGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPLTFGQGTKVEIK
DKK1-218	719	DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYGRNKRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSYRSGRAFGQGTKVEIK
DKK1-219	720	DIQMTQSPSSLSASVGDRVTITCRASQDVSSGVAWYQQKPGKAPKLLIYDASSLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCKQSYTLRTFGQGTKVEIK
DKK1-220	721	DIQMTQSPSSLSASVGDRVTITCRPSQRISRYLNWYQQKPGKAPKLLIYGKKNRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSPPLTFGQGTKVEIK
DKK1-221	722	DIQMTQSPSSLSASVGDRVTITCRASQTIGDYLNWYQQKPGKAPKLLIYHTSRLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCGQDYTSPRTFGQGTKVEIK
DKK1-222	723	DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYQDFKRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSRTFGQGTKVEIK
DKK1-223	724	DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYGKKNRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPSFGQGTKVEIK
DKK1-224	725	DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYGNNNRPSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSSWAGSRSGTVFGQGTKVEIK

DKK1-225	726	DIQMTQSPSSLSASVGDRVTITCRASQNIRSYLNWYQQKPGKAPKLLIYATSNLASGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCNSRDTSINHPVIFGQGTKVEIK
DKK1-226	727	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDNTNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-227	728	DIQMTQSPSSLSASVGDRVTITCSGDRLGEKYVSWYQQKPGKAPKLLIYDNTNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCLAWDTRTSGAVFGQGTKVEIK
DKK1-228	729	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLLIYAKNNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQSYGSHSNFVVFGQGTKVEIK
DKK1-229	730	DIQMTQSPSSLSASVGDRVTITCRASQTIGDYLNWYQQKPGKAPKLLIYAASSLYSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQSYDLRYSHVFGQGTKLEIK
DKK1-230	731	DIQMTQSPSSLSASVGDRVTITCRASQDIKNYLNWYQQKPGKAPKLLIYGTSYRYSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCASRSSKGNPHVLFGQGTKVEIK
DKK1-231	732	DIQMTQSPSSLSASVGDRVTITCRASQNIRSYLNWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQRARHPHTFGQGTKVEIK
DKK1-232	733	DIQMTQSPSSLSASVGDRVTITCSGDNLRSYYVHWYQQKPGKAPKLLIYQDFKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQSYDDHDRIVFGQGTKVEIK
DKK1-233	734	DIQMTQSPSSLSASVGDRVTITCTGDKLAEKYVSWYQQKPGKAPKLLIYDNNIRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCLAWDTRTSGAVFGQGTKVEIK
DKK1-234	735	DIQMTQSPSSLSASVGDRVTITCRASSSVSYMHWYQQKPGKAPKLLIYAASTLQRGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGKTLPLTFGQGTKVEIK
DKK1-235	736	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLLIYAVTSLASGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSTILPLTFGQGTKVEIK
DKK1-236	737	DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYGRNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQRARHPHTFGQGTKVEIK
DKK1-237	738	DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYDDIDRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGSSLPLTFGQGTKVEIK
DKK1-238	739	DIQMTQSPSSLSASVGDRVTITCSGGSGSYGWYQQKPGKAPKLLIYGNNNRPSGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCNSRDTSGNHRVFGQGTKVEIK
DKK1-239	740	DIQMTQSPSSLSASVGDRVTITCRTSQDISNYLNWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCNSRDTSGNHLVFGQGTKVEIK
DKK1-240	741	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTYSTRTFGQGTKVEIK
DKK1-241	742	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLLIYGRNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQAWGSSTVIFGQGTKVEIK
DKK1-242	743	DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYRKSNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQRARHPHTFGQGTKVEIK
DKK1-243	744	DIQMTQSPSSLSASVGDRVTITCTSSQSLFNVRSQKNYLAWYQQKPGKAPKLLIYDTSKVASGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCSSRDNSDNHLVVFGQGTKVEIK
DKK1-244	745	DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSAPLTFGQGTKVEIK
DKK1-245	746	DIQMTQSPSSLSASVGDRVTITCTGDKLAEKYVSWYQQKPGKAPKLLIYHTSRLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQVWDTGTVVFGQGTKVEIK
DKK1-246	747	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDNNNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-247	748	DIQMTQSPSSLSASVGDRVTITCRASQPIAYFLSWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCASRSSKGNPHVLFGQGTKVEIK
DKK1-248	749	DIQMTQSPSSLSASVGDRVTITCKASDHIGKFLTWYQQKPGKAPKLLIYAASTLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYETPLTFGQGTKVEIK
DKK1-249	750	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLLIYAVTSLASGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSTIMPLTFGQGTKVEIK
DKK1-250	751	DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYQQKPGKAPKLLIYRKSNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-251	752	DIQMTQSPSSLSASVGDRVTITCQASQSISSYLAWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQRDTTPWTFGQGTKVEIK
DKK1-252	753	DIQMTQSPSSLSASVGDRVTITCRASQDIKNYYKWYQQKPGKAPKLLIYENNNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQARDRNTYVAFGQGTKVEIK
DKK1-253	754	DIQMTQSPSSLSASVGDRVTITCRASQYIGTALNWYQQKPGKAPKLLIYDNNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCNSRDTSGLHYVFGQGTKVEIK
DKK1-254	755	DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYGQHNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYDAYPPTFGQGTKVEIK

DKK1-255	756	DIQMTQSPSSLSASVGDRVTITCRASQSIGRYMNWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSAPLTFGQGTKVEIK
DKK1-256	757	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYEDTKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCLQYASSPFTFGQGTKVEIK
DKK1-257	758	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKALKLLIYAVTSLASGVPSRFSGSGF GTDFTLTISSLQPEDFATYYCQQSFSVPAFGQGTKVEIK
DKK1-258	759	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYGASSRATGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNTPLTFGQGTKVEIK
DKK1-259	760	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAHKLMIYDNNNRPSGVPSRFSGS GCGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-260	761	DIQMTQSPSSLSASVGDRVTITCRASQRISSFLNWYQQKPGKAPKLLIYRKSNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCSQSTRVPPTFGQGTKVEIK
DKK1-261	762	DIQMTQSPSSLSASVGDRVTITCRPNQNIATYINWYQQKPGKAPKLLIYHTSRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCSSWAGSRSGTVFGQGTKVEIK
DKK1-262	763	DIQMTQSPSSLSASVGDRVTITCSGDLRNKYASWYQQKPGKAPKLLIYGQHNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCSSGSRSGTVFGQGTKVEIK
DKK1-263	764	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYANTNGPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSAPYTFGQGTKVEIK
DKK1-264	765	DIQMTQSPSSLSASVGDRVTITCQASQSIYSFLSWYQQKPGKAPKLLIYRKSNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTATWPFTFGQGTKVEIK
DKK1-265	766	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDNTNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-266	767	DIQMTQSPSSLSASVGDRVTITCKASDHIGKFLTWYQQKPGKAPKLLIYHTSRLHSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYKYPLTFGQGTKVEIK
DKK1-267	768	DIQMTQSPSSLSASVGDRVTITCRASHNINSYLNWYQQKPGKAPKLLIYQDFKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPLTFGQGTKVEIK
DKK1-268	769	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDNTNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-269	770	DIQMTQSPSSLSASVGDRVTITCRTSQDISNYLNWYQQKPGKAPKLLIYGTSYRYSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGYTLPWTFGQGTKVEIK
DKK1-270	771	DIQMTQSPSSLSASVGDRVTITCRANQNIGNFLNWYQQKPGKAPKLLIYHTSRLHSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSAPLTFGQGTKVEIK
DKK1-271	772	DIQMTQSPSSLSASVGDRVTITCSASSSVTYMHWYQQKPGKAPKLLIYHDNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYDNPLTFGQGTKVEIK
DKK1-272	773	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCLQFDHTPFTFGQGTKVEIK
DKK1-273	774	DIQMTQSPSSLSASVGDRVTITCRTSQDIGNYLNWYQQKPGKAPKLLIYHTSRLHSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGYRFPLTFGQGTKVEIK
DKK1-274	775	DIQMTQSPSSLSASVGDRVTITCRASQPIAYFLSWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCASRSSKGNPHVLFGQGTKVEIK
DKK1-275	776	DIQMTQSPSSLSASVGDRVTITCSGDNLRGYYASWYQQKPGKAPKLLIYQDFKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSPLTFGQGTKVEIK
DKK1-276	777	DIQMTQSPSSLSASVGDRVTITCRSSQLVHSTGNTYLHWYQQKPGKAPKLLIYGASSRATGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCSQSTHVPTFGQGTKVEIK
DKK1-277	778	DIQMTQSPSSLSASVGDRVTITCQGASLRNYYASWYQQKPGKAPKLLIYENNNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCSTRSRKGNPHVLFGQGTKVEIK
DKK1-278	779	DIQMTQSPSSLSASVGDRVTITCRASQDIKNYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSPPLTFGQGTKVEIK
DKK1-279	780	DIQMTQSPSSLSASVGDRVTITCRASQDVSSGVAWYQQKPGKAPKLLIYDDIDRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCHQRSSYPWTFGQGTKVEIK
DKK1-280	781	DIQMTQSPSSLSASVGDRVTITCRASQGVRTSLAWYQQKPGKAPKLLIYSASVLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQAWDNSAVIFGQGTKVEIK
DKK1-281	782	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDNTNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-282	783	DIQMTQSPSSLSASVGDRVTITCTGDKLAEKNVSWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTYSTPLTFGQGTKVEIK
DKK1-283	784	DIQMTQSPSSLSASVGDRVTITCRASQTIGDYLNWYQQKPGKAPKLLIYAASGLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSNSWPYTFGQGTKVEIK
DKK1-284	785	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLLIYLSSDLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCAQTGTHPTTFGQGTKVEIK

DKK1-285	786	DIQMTQSPSSLSASVGDRVTITCRTSQSLSSYLHWYQQKPGKAPKLLIYEDTKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCHTWHHNPHTGETNHFGQGTKVEIK
DKK1-286	787	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDNTNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-287	788	DIQMTQSPSSLSASVGDRVTITCRASQDVSSGVAWYQQKPGKAPKLLIYGASRLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCNSRDTSGLHYVFGQGTKVEIK
DKK1-288	789	DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYENNNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSPPLTFGQGTKVEIK
DKK1-289	790	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYGASSRATGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSSPLTFGQGTKVEIK
DKK1-290	791	DIQMTQSPSSLSASVGDRVTITCRATQSIRSFLNWYQQKPGKAPKLLIYGQHNRPSGVPSRFSGSGS GIDFTLTISSLQPEDFATYYCQQYYDWPLTFGQGTKVEIK
DKK1-291	792	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYYSGWTFGQGTKVEIK
DKK1-292	793	DIQMTQSPSSLSASVGDRVTITCRTSQSLSSYLHWYQQKPGKAPKLLIYGRNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQNVLSTPYTFGQGTKVEIK
DKK1-293	794	DIQMTQSPSSLSASVGDRVTITCSGDLRNKYASWYQQKPGKAPKLLIYGTSNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQAWVSSTVVFGQGTKVEIK
DKK1-294	795	DIQMTQSPSSLSASVGDRVTITCRASQSVDRYFNWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCSQSTHVPLTFGQGTKVEIK
DKK1-295	796	DIQMTQSPSSLSASVGDRVTITCRASQFIGRYFNWYQQKPGKAPKLLIYGRNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-296	797	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYGKKNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPRTFGQGTKVEIK
DKK1-297	798	DIQMTQSPSSLSASVGDRVTITCRASQTIGDYLNWYQQKPGKAPKLLIYGASRLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCSQSTHVPTFGQGTKVEIK
DKK1-298	799	DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYGQHNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYHSYPPTFGQGTKVEIK
DKK1-299	800	DIQMTQSPSSLSASVGDRVTITCRASQSIRRFLNWYQQKPGKAPKLLIYGASSRATGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSFSVPAFGQGTKVEIK
DKK1-300	801	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYGNNNRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSAPLTFGQGTKVEIK
DKK1-301	802	DIQMTQSPSSLSASVGDRVTITCRPNQNIATYINWYQQKPGKAPKLLIYHDNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCLQDYNYPLTFGQGTKVEIK
DKK1-302	803	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYGRNKRPSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTYNVPPTFGQGTKVEIK
DKK1-303	804	DIQMTQSPSSLSASVGDRVTITCRANQNIGNFLNWYQQKPGKAPKLLIYNAKTLPEGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCASRDRSGHGVFGQGTKVEIK
DKK1-304	805	DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCSSRDRSGNHRVFGQGTKVEIK
DKK1-305	806	DIQMTQSPSSLSASVGDRVTITCRASQRISSFLNWYQQKPGKAPKLLIYQNDKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-306	807	DIQMTQSPSSLSASVGDRVTITCRASQSISSYVNWYQQKPGKAPKLLIYHDNKRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCAQNLEIPRTFGQGTKVEIK
DKK1-307	808	DIQMTQSPSSLSASVGDRVTITCSGDKLGDKYAYWYQQKPGKAPKLLIYHDNKRPSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQPSFYFPYTFGQGTKVEIK
DKK1-308	809	DIQMTQSPSSLSASVGDRVTITCRASQDIYQNLDWYQQKPGKAPKLLIYGKNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYYSGWTFGQGTKVEIK
DKK1-309	810	DIQMTQSPSSLSASVGDRVTITCQASQSISSYLAWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYWAFPVTFGQGTKVEIK
DKK1-310	811	DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYAKNNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPRTFGQGTKVEIK
DKK1-311	812	DIQMTQSPSSLSASVGDRVTITCSASQDINKYLNWYQQKPGKAPKLLIYDTSKVASGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPNTFGQGTKVEIK
DKK1-312	813	DIQMTQSPSSLSASVGDRVTITCRASQNIRSYLNWYQQKPGKAPKLLIYDNNIRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCLQDYNLWTFGQGTKVEIK
DKK1-313	814	DIQMTQSPSSLSASVGDRVTITCRASQSIREYLHWYQQKPGKAPKLLIYATSNLASGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQAWDTSTAVFGQGTKVEIK
DKK1-314	815	DIQMTQSPSSLSASVGDRVTITCSGDLGEKYVSWYQQKPGKAPKLLIYATSTLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQAWASSTVVFGQGTKVEIK

DKK1-315	816	DIQMTQSPSSLSASVGDRVTITCRPNQNIATYINWYQQKPGKAPKLLIYGNNNRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCSTRSSKGNPHVLFGQGTKVEIK
DKK1-316	817	DIQMTQSPSSLSASVGDRVTITCRASKVSTSGYVYMHWYQQKPGKAPKLLIYENNNRPSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQYWAFPVTFGQGTKVEIK
DKK1-317	818	DIQMTQSPSSLSASVGDRVTITCRASSSVSYMHWYQQKPGKAPKLLIYGENSRPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKVEIK
DKK1-318	819	DIQMTQSPSSLSASVGDRVTITCRASQDVSSGVAWYQQKPGKAPKLLIYGSSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQYHSYPPTFGQGTKVEIK
DKK1-319	820	DIRMTQSPSSLSASVGDRVTITCRASQSVDRYFNWYQQKPGKAPKLLIYHTSRLHSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQAWDNRAVVFGQGTKVEIK
DKK1-320	821	DIQMTQSPSSLSASVGDRVTITCQSSQSVYSNNELSWYQQKPGKAPKLLIYGNNNRPSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSTPTFGQGTKVEIK
DKK1-321	822	DIQMTQSPSSLSASVGDRVTITCRSSQSISTYLNWYQQKPGKAPKLLIYAASRSQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYIIPWTFGGGTKVEIK
DKK1-322	823	DIQMTQSPSSLSASVGDRVTITCRASHSISSYLNWYQQKPGKAPKLLIYTASRLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYNTPFTFGGGTKVEIK
DKK1-323	824	DIQMTQSPSSLSASVGDRVTITCRASQSIHSYLNWYQQKPGKAPKLLIYTASALQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSFSSPLTFGQGTKVEIK
DKK1-324	825	DIQMTQSPSSLSASVGDRVTITCRAGQSVSRFLNWYQQKPGKAPKLLIYAAATLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYDTPFTFGGGTKVEIK
DKK1-325	826	DIQMTQSPSSLSASVGDRVTITCRTSQSIGTYLNWYQQKPGKSPKLLIYDASILQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYNTPLTFGGGTKVEIK
DKK1-326	827	DIQMTQSPSSLSASVGDRVTITCRASQSIGIHLNWYQQKPGKAPKLLIYGATSLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNTPPYTFGGGTKVEIK
DKK1-327	828	DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQKPGKAPKLLIYATSRLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGYTSPLTFGGGTKVEIK
DKK1-328	829	DIQMAQSPSSLSASVGDRVTITCRASQGIATYLNWYQQKPGKAPKLLIYGASTLRTGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTFTNTPLTFGGGTKVEIK
DKK1-329	830	DIQMTQSPSSLSASVGDRVTITCRASQSIGSYLNWYQQKPGKAPKLLIYAASSLKSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSHNIPRTFGGGTKVEIK
DKK1-330	831	DIQMTQSPSSLSASVGDRVTITCRASQSISRNLNWYQQKPGKAPKLLIYGASRLHSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGYITPQTFGGGTKVEIK
DKK1-331	832	DIQMTQSPSSLSASVGDRVTITCRASQSVRTYLNWYQQKPGKAPKLLIYRASRLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSFTTPLTFGGGTKVEIK
DKK1-332	833	DIQMTQSPSSLSASVGDRVTITCRASQSIGSHLSWYQQKPGKAPKLLIYRASRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSPPITFGGGTKVEIK
DKK1-333	834	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYGASKLQRGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSSSVPWTFGGGTKVEIK
DKK1-334	835	DIQMTQSPSSLSASVGDRVTITCRASQNIGNYLNWYQQKPGKAPKLLIYAASTLASGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQNYNTPLTFGGGTKVEIK
DKK1-335	836	DIQMTQSPSSLSASVGDRVTITCRSSQSISTYLNWYQQKPGKAPKLLIYAASRLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYTPPITFGGGTKVEIK
DKK1-336	837	DIQMTQSPSSLSASVGDRVTITCRASQNIGSYLNWYQQKPGKAPKLLIYAASKLHSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYNTPVTFGGGTKVEIK
DKK1-337	838	DIQMTQSPSSLSASVGDRVTITCRASQSISRFLNWYQQKPGKAPKLLIYGASALQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYIPPLTFGGGTKVEIK
DKK1-338	839	DIQMTQSPSSLSASVGDRVTITCRASESITTYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYITPLTFGGGTKVEIK
DKK1-339	840	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLHWYQQKPGKAPKLLIYAASTLHSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNSITFGGGTKVEIK
DKK1-340	841	DIQMTQSPSSLSASVGDRVTITCRSSQSIGSNLNWYQQKPGKAPKLLIYATSNLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYRIPRTFGGGTKVEIK
DKK1-341	842	DIQMTQSPSSLPASVGDRVTITCRASQSISRYLSWYQQKPGKAPKLLIYAASRLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPTTFGGGTKVEIK
DKK1-342	843	DIQMTQSPSSLSASVGDRVTITCRASQYIGTYLNWYQQKPGKAPKLLIYAASNLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSDLTFGGGTKVEIK
DKK1-343	844	DIQMTQSPSSLSASVGDRVTITCRASESISRNLNWYQQKPGKAPKLLIYAASSLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSGPPYTFGGGTKVEIK
DKK1-344	845	DIQMTQSPSSLSASVGDRVTITCRSSQSISTYLNWYQQKPGKAPKLLIYAASRSQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYIIPWTFGGGTKVEIK

DKK1-345	846	DIQMTQSPSSLSASVGDRVTITCRASQSVSNFLNWYQQKPGKAPKLLIYGASNLHSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSFPFSFGGGTKVEIK
DKK1-346	847	DIQMTQSPSSLSASVGDRVTITCRASRNIRTYLNWYQQKPGKAPKLLIYRASTLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYKTPVTFGGGTKVEIK
DKK1-347	848	DIQMTQSPSSLSASVGDRVTITCRASQSIGNFLNWYQQKPGKAPKLLIYRASRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNTPITFGGGTKVEIK
DKK1-348	849	DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQKPGKAPKLLIYGATNLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTLPFTFGGGTKVEIK
DKK1-349	850	DIQMTQSPSSLSASVGDRVTITCRASQSIRTYLNWYQQKPGKAPKLLIYGAVNLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQRDTFGGGTKVEIK
DKK1-350	851	DIQMTQSPSSLSASVGDRVTITCRASQNIYTYLNWYQQKPGKAPKPLIYLASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTRFTFGGGTKVEIK
DKK1-351	852	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLSWYQQKPGKAPKLLIYGSSNLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPTFGGGTKVEIK
DKK1-352	853	DIQMTQSPSSLSASVGDRVTITCRASQNIGRYLNWYQQKPGKAPKLLIYSASKLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTYSPPLTFGGGTKVEIK
DKK1-353	854	DIQMTQSPSSLSASVGDRVTITCRASQTISAYLNWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSGLTFGGGTKVEIK
DKK1-354	855	DIQMTQSPSSLSASVGDRVTITCRASQSIRGYLNWYQQKPGKAPKLLIYSTSSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYNTPLTFGGGTKVEIK
DKK1-355	856	DIQMTQYPSSLSASVGDRVTITCRASQSVSYYLNWYQQKPGKAPKLLIYGSSNLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTYSSPVTFGGGTKVEIK
DKK1-356	857	DIQMTQSPSSLSASVGDRVTITCRASQPISSYLNWYQQKPGKAPKLLIYSASSLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGYSAPLTFGGGTKVEIK
DKK1-357	858	DIQMTQSPSSLSASVGDRVTITCQTSQSIGKYLNWYQQKPGKAPKLLIYGASRVQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTYSTPLTFGGGTKVEIK
DKK1-358	859	DIQMTQSPSSLSASVGDRVTITCRASQSIGAYLNWYQQKPGKAPKLLIYGTSSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYGTLITFGGGTKVEIK
DKK1-359	860	DIQMTQSPSSLSASVGDRVTITCRASQTISTFLNWYQQKPGKAPKLLIYGASRLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIK
DKK1-360	861	DIQMTQSPSSLSASVGDRVTITCRASQSIGRYLNWYQQKPGKAPKLLIYAVSNLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPSFGGGTKVEIK
DKK1-361	862	DIQMTQSPSSLSASVGDRVTITCRSSQSISNYLNWYQQKPGKAPKLLIYGASRLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSLPLTFGGGTKVEIK
DKK1-362	863	DIQMTQSPSSLSASVGDRVTITCRASQTISRSLNWYQQKPGKAPKLLIYGASRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSFTTPYTFGGGTKVEIK
DKK1-363	864	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLDWYQQKPGKAPKLLIYAASRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYRSPLTFGGGTKVEIK
DKK1-364	865	DIQMTQSPSSLSASVGDRVTITCRASRSIGTYLNWYQQKPGKAPKLLIYAASKLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYITPLTFGGGTKVEIK
DKK1-365	866	DIQMTQSPSSLSASVGDRVTITCRASQNINRYLNWYQQKPGKAPKLLIYASSRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSSPITFGGGTKVEIK
DKK1-366	867	DIQMTQSPSSLSASVGDRVTITCRASQSVSSYLSWYQQKPGKAPKLLIYATSNLQRGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCHQTYSTPRTFGGGTKVEIK
DKK1-367	868	DIQMTQSPSSLSASVGDRVTITCRASQSIGIHLNWYQQKPGKAPKLLIYGATSLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNTPPYTFGGGTKVEIK
DKK1-368	869	DIQMTQSPSSLSASVGDRVTITCRASRSISTYLNWYQQKPGKAPKLLIYEVSSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYITPLTFGGGTKVEIK
DKK1-369	870	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLSWYQQKPGKAPKLLIYAASRLQRGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQGYSSPLTFGGGTKVEIK
DKK1-370	871	DIQMTQSPSSLSASVGDRVTITCRASQSISNFLSWYQQKPGKAPKLLIYGTSSLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSIPFTFGGGTKVEIK
DKK1-371	872	DIQMTQSPSSLSASVGDRVTITCRASQGISFYLNWYQQKPGKAPKLLIYAASRLQRGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPQITFGGGTKVEIK
DKK1-372	873	DIQMTQSPSSLSASVGDRVTITCRASQNIKTYLNWYQQKPGKAPKLLIYGASSLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCLQTYSVPLTFGGGTKVEIK
DKK1-373	874	DIQMTQSPSSLSASVGDRVTITCRASQYISNYLNWYQQKPGKAPKLLIYGASSIQNGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSLPLTFGGGTKVEIK
DKK1-374	875	DIQMTQSPSSLSASVGDRVTITCRASQTISTFLNWYQQKPGKAPKLLIYGASRLQGGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIK

DKK1-375	876	DIQMTQSPSSLSASVGDRVTITCRASQSISRFLNWYQQKPGKAPKLLIYGASRLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYKTPRTFGGGTKVEIK
DKK1-376	877	DIQMTQSPSSLSASVGDRVTITCRASESIDNYLNWYQQKPGKAPKLLIYGATSLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYNIPFTFGGGTKVEIK
DKK1-377	878	DIQMTQSPSSLSASVGDRVTITCRTSQSISNFLNWYQQKPGKAPKLLIYTASKLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYRVPRTFGGGTKVEIK
DKK1-378	879	DIQMTQSPSSLSASVGDRVTITCRASQSIGTNLNWYQQKPGKAPKLLIYAASALQGGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSIPLTFGGGTKVEIK
DKK1-379	880	DIQMTQSPSSLSASVGDRVTITCRASQTITRYLNWYQQKPGKAPKLLIYAATSLHSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPETFGGGTKVEIK
DKK1-380	881	DIQMTQSPSSLSASVGDRVTITCRASQSIGNFLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSIPPTFGGGTKVEIK
DKK1-381	882	DIQMTQSPSSLSASVGDRVTITCRASHSISRYLNWYQQKPGKAPKLLIYGASNLPSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTHTFGGGTKVEIK
DKK1-382	883	DIQMTQSPSSLSASVGDRVTITCRASQGISFYLNWYQQKPGKAPKLLIYGASILQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSPPLTFGGGTKVEIK
DKK1-383	884	DIQMTQSPSSLSASVGDRVTITCRASQSVSNYLNWYQQKPGKAPKLLIYGASTLQAGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYVTPPTFGGGTKVEIK
DKK1-384	885	DIQMTQSPSSLSASVGDRVTITCRASQSIGSFLNWYQQKPGKAPKLLIYAAFRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSPPFTFGGGTKVEIK
DKK1-385	886	DIQMTQSPSSLSASVGDRVTITCRASQSITRHLNWYQQKPGKAPKLLIYAASRLQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPGTFGGGTKVEIK
DKK1-386	887	DIQMTQSPSSLSASVGDRVTITCRASQRISRYLNWYQQKPGKAPKLLIYGASNLQGGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYRTPITFGGGTKVEIK
DKK1-387	888	DIQMTQSPSSLSASVGDRVTITCRASQYIGNYLNWYQQKPGKAPKLLIYAVSRLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSFSAPYTFGGGTKVEIK
DKK1-388	889	DIQMTQSPSSLSASVGDRVTITCRASQYISTFLNWYQQKPGKAPKLLIYSASRLQNGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSPLTFGGGTKVEIK
DKK1-389	890	DIQMTQSPSSLSASVGDRVTITCRASRSISRYLNWYQQKPGKAPKLLIYGASILQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYTPPRTFGGGTKVETK
DKK1-390	891	DIQMTQSPSSLSASVGDRVTITCRASQSISRSLNWYQQKPGKAPKLLIYGASSLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSFTIPWTFGGGTKVEIK
DKK1-391	892	DIQMTQSPSSLSASAGDRVTITCRASQSITSYLNWYQQKPGKAPKLLIYAASRLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNTPVTFGGGTKVEIK
DKK1-392	893	DIQMTQSPSSLSASVGDRVTITCRASQNIAGYLNWYQQKPGKAPKLLIYAASRLHSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSSSTPITFGGGTKVEIK
DKK1-393	894	DIQMTQSPSSLSASVGDRVTITCRASQTIRTYLNWYQQKPGKAPKLLIYATSSLQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYRPPLTFGGGTKVEIK
DKK1-394	895	DIQMTQSPSSLSASVGDRVTITCRASQSIGIHLNWYQQKPGKAPKLLIYGATSLESGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYNTPPYTFGGGTKVEIK
DKK1-395	896	DIQMTQSPSSLSASVGDRVTITCRSSQSISTYLHWYQQKPGKAPKLLIYGASKLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSAPRTFGGGTKVEIK
DKK1-396	897	DIQMTQSPSSLSASVGDRVTITCRASQSIGRYLNWYQQKPGKAPKLLIYGASRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYRTPLTFGGGTKVEIK
DKK1-397	898	DIQMTQSPSSLSASVGDRVTITCRASHTISRYLNWYQQKPGKAPRLLIYAASDLQTGVPSRFSGGG SGTDFTLTISSLQPEDFATYYCQQSFTAPDTFGGGTKVEIK
DKK1-398	899	DIQMTQSPSSLSASVGDRVTITCRTSQSISRYLNWYQQKPGKAPKLLIYTTSDLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSDLTFGGGTKVEIK
DKK1-399	900	DIQMTQSPSSLSASVGDRVTITCRASQRINTYLNWYQQKPGKAPKLLIYGAFRLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYRVPRTFGGGTKVEIK
DKK1-400	901	DIQMTQSPSSLSASVGDRVTITCRASQSINHYLNWYQQKPGKAPKLLIYGASRLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSLPRTFGGGTKVEIK
DKK1-401	902	DIQMTQSPSSLSASVGDRVTITCRASQTIGRYLNWYQQKPGKAPKLLIYATSSLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYSTPYTFGGGTKVEIK
DKK1-402	903	DIQMTQSPSSLSASVGDRVTITCRASQSIGEYLNWYQQKPGKAPKLLIYAASRLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQNYRSPLTFGGGTKVEIK
DKK1-403	904	DIQMTQSPSSLSASVGDRVTITCRASQSIYRYLNWYQQKPGKAPKLLIYAATTLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSPPLTFGGGTKVEIK
DKK1-404	905	DIQMTQSPSSLSASVGDRVTITCRASQNIGRYLNWYQQKPGKAPKLLIYEVSSLRSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYRTPGTFGGGTKVEIK

DKK1-405	906	DIQMTQSPSSLSASVGDRVTITCRAGQSIRNYLNWYQQKPGKAPKLLIYAATTLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSFLTPWTFGGGTKVEIK
DKK1-406	907	DIQMTQSPSSLSASVGDRVTITCRASQSISRHLNWYQQKPGKAPKLLIYGATRLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSKPYTFGGGTKVEIK
DKK1-407	908	DIQMTQSPSSLSASVGDRVTITCRASQSISRYLHWYQQKPGKAPKLLIYAATSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPLSFGGGTKVEIK
DKK1-408	909	DIQMTQSPSSLSASVGDRVTITCRTSQSIGTYLNWYQQKPGKAPKLLIYDTSNLQGGVPSRFSGSGS GTDFTLAISSLQPEDFATYYCQQSFTSPLTFGGGTKVEIK
DKK1-409	910	DIQMTQSPSSLSASVGDRVTITCRASQGIATYLNWYQQKPGKAPKLLIYAASSLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTHSTPLTFGGGTKVEIK
DKK1-410	911	DIQMTQSPSSLSASVGDRVTITCRASQNIGGYLNWYQQKPGKAPKLLIYRASRLQSGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPLLTFGGGTKVEIK
DKK1-411	912	DIQMTQSPSSLSASVGDRVTITCRASQYIGNYLNWYQQKPGKAPKLLIYASSTLQRGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTSSTPLTFGGGTKVEIK
DKK1-412	913	DIQMTQSPSSLSASVGDRVTITCRTSQSIGTYLNWYQQKPGKSPKLLIYDASILQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQNYNTPLTFGGGTKVEIK
DKK1-413	914	DIQMTQSPSSLSASVGDRVTITCQASQNIGRYLNWYQQKPGKAPKLLIYAASALQGGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYTPPRTFGGGTKVEIK
DKK1-414	915	DIQMTQSPSSLSASVGDRVTITCRASQSISRHLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQTYRTPLTFGGGTKVEIK
DKK1-415	916	DIQMTQSPSSLSASVGDRVTITCRASQSIHNYLNWYQQKPGKAPKLLIYAASSLHDGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQSYSTPYTFGGGTKVEIK
DKK1-416	917	DIQMAQSPSSLSASVGDRVTITCRASQGIATYLNWYQQKPGKAPKFLIYGASTLRTGVPSRFSGSG SGTDFTLTISSLQPEDFATYYCQQTFTNTPLTFGGGTKVEIK
DKK1-417	918	DIQMTQSPSSLSASVGDRVTITCRASQTITKYLNWYQQKPGKAPKLLIYATSNLQTGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSAPVTFGGGTKVEIK

Table 8. Variable Light Chain CDRs

DKK1 Variant	SEQ ID NO	CDR1 Sequence	SEQ ID NO	CDR2 Sequence	SEQ ID NO	CDR3 Sequence
DKK1-212	2259	KLRNKY	2465	GAS	2522	QSYDDHDRIV
DKK1-213	2260	QPIGPD	2466	SAS	2523	QQSYSTPT
DKK1-214	2261	QSISSY	2467	GRN	2524	QQSYSSPLT
DKK1-215	2262	QDISNY	2468	AAS	2525	QQYYNLPWT
DKK1-216	2263	QDIYQN	2469	AAS	2526	ASRDRSGHGV
DKK1-217	2264	QPIGPD	2470	GAS	2527	QQSYNTPLT
DKK1-218	2265	QSIRRY	2471	GRN	2528	QHSYRSGRA
DKK1-219	2266	QDVSSG	2472	DAS	2529	KQSYTLRT
DKK1-220	2267	QRISRY	2473	GKK	2530	QQSYSPPLT
DKK1-221	2268	QTIGDY	2474	HTS	2531	GQDYTSPRT
DKK1-222	2269	QTIERR	2475	QDF	2532	QQSRT
DKK1-223	2270	QSIRRY	2476	GKK	2533	QQSYSTPS
DKK1-224	2271	QTIERR	2477	GNN	2534	SSWAGSRSGTV
DKK1-225	2272	QNIRSY	2478	ATS	2535	NSRDTSINHPVI
DKK1-226	2273	QDINKY	2479	DNT	2536	QQSYSTPT
DKK1-227	2274	DRLGEKY	2480	DNT	2537	LAWDTRTSGAV
DKK1-228	2275	QSISSY	2481	AKN	2538	QSYGSHSNFVV
DKK1-229	2276	QTIGDY	2482	AAS	2539	QSYDLRYSHV
DKK1-230	2277	QDIKNY	2483	GTS	2540	ASRSSKGNPHVL
DKK1-231	2278	QNIRSY	2484	GKN	2541	QQRARHPHT
DKK1-232	2279	DNLRSYY	2485	QDF	2542	QSYDDHDRIV

DKK1-233	2280	KLAEKY	2486	DNN	2543	LAWDTRTSGAV
DKK1-234	2281	SSVSY	2487	AAS	2544	QQGKTLPLT
DKK1-235	2282	QSISSY	2488	AVT	2545	QQSTILPLT
DKK1-236	2283	QSIRRY	2489	GRN	2546	QQRARHPHT
DKK1-237	2284	QTIERR	2490	DDI	2547	QQGSSLPLT
DKK1-238	2285	SGS	2491	GNN	2548	NSRDTSGNHRV
DKK1-239	2286	QDISNY	2492	QND	2549	NSRDTSGNHLV
DKK1-240	2287	QDIYQN	2493	QND	2550	QQTYSTRT
DKK1-241	2288	QSISSY	2494	GRN	2551	QAWGSSTVI
DKK1-242	2289	QSIRRY	2495	RKS	2552	QQRARHPHT
DKK1-243	2290	QSLFNVRSQKNY	2496	DTS	2553	SSRDNSDNHLVV
DKK1-244	2291	QSIRRY	2497	GKN	2554	QQSYSAPLT
DKK1-245	2292	KLAEKY	2498	HTS	2555	QVWDTGTVV
DKK1-246	2293	QDINKY	2499	DNN	2556	QQSYSTPT
DKK1-247	2294	QPIAYF	2500	GKN	2557	ASRSSKGNPHVL
DKK1-248	2295	DHIGKF	2501	AAS	2558	QQSYETPLT
DKK1-249	2296	QSISSY	2502	AVT	2559	QQSTIMPLT
DKK1-250	2297	QSIRRY	2503	RKS	2560	QQSYSTPT
DKK1-251	2298	QSISSY	2504	QND	2561	QQRDTTPWT
DKK1-252	2299	QDIKNY	2505	ENN	2562	QARDRNTYVA
DKK1-253	2300	QYIGTA	2506	DNN	2563	NSRDTSGLHYV
DKK1-254	2301	QSISGY	2507	GQH	2564	QQYDAYPPT
DKK1-255	2302	QSIGRY	2508	GK	2565	QQSYSAPLT
DKK1-256	2303	QDIYQN	2509	EDT	2566	LQYASSPFT
DKK1-257	2304	QPIGPD	2510	AVT	2567	QQSFSVPA
DKK1-258	2305	QPIGPD	2511	GAS	2568	QQSYNTPLT
DKK1-259	2306	QDINKY	2512	DNN	2569	QQSYSTPT
DKK1-260	2307	QRISSF	2513	RKS	2570	SQSTRVPPT
DKK1-261	2308	QNIATY	2514	HTS	2571	SSWAGSRSGTV
DKK1-262	2309	GDLRNKY	2515	GQH	2572	SSGSRSGTV
DKK1-263	2310	QPIGPD	2516	ANT	2573	QQSYSAPYT
DKK1-264	2311	QSIYSF	2517	RKS	2574	QQTATWPFT
DKK1-265	2312	QDINKY	2518	DNT	2575	QQSYSTPT
DKK1-266	2313	DHIGKF	2519	HTS	2576	QQSYKYPLT
DKK1-267	2314	HNINSY	2520	QDF	2577	QQSYSSPLT
DKK1-268	2315	QDINKY	2521	DNT	2578	QQSYSTPT
DKK1-269	2316	QDISNY	2522	GTS	2579	QQGYTLPWT
DKK1-270	2317	QNIGNF	2523	HTS	2580	QQSYSAPLT
DKK1-271	2318	SSVTY	2524	HDN	2581	QQSYDNPLT
DKK1-272	2319	QDIYQN	2525	QND	2582	LQFDHTPFT
DKK1-273	2320	QDIGNY	2526	HTS	2583	QQGYRFPLT
DKK1-274	2321	QPIAYF	2527	GKN	2584	ASRSSKGNPHVL
DKK1-275	2322	DNLRGYY	2528	QDF	2585	QQSYSPLT
DKK1-276	2323	QLVHSTGNTY	2529	GAS	2586	SQSTHVPT
DKK1-277	2324	SLRNYY	2530	ENN	2587	STRSRKGNPHVL

DKK1-278	2325	QDIKNY	2531	QAS	2588	QQSYSPPLT
DKK1-279	2326	QDVSSG	2532	DDI	2589	HQRSSYPWT
DKK1-280	2327	QGVRTS	2533	SAS	2590	QAWDNSAVI
DKK1-281	2328	QDINKY	2534	DNT	2591	QQSYSTPT
DKK1-282	2329	KLAEKN	2535	QND	2592	QQTYSTPLT
DKK1-283	2330	QTIGDY	2536	AAS	2593	QQSNSWPYT
DKK1-284	2331	QSISSY	2537	LSS	2594	AQTGTHPTT
DKK1-285	2332	QSLSSY	2538	EDT	2595	HTWHHNPHTGETNH
DKK1-286	2333	QDINKY	2539	DNT	2596	QQSYSTPT
DKK1-287	2334	QDVSSG	2540	GAS	2597	NSRDTSGLHYV
DKK1-288	2335	QTIERR	2541	ENN	2598	QQTYSPPLT
DKK1-289	2336	QDINKY	2542	GAS	2599	QQSYSSPLT
DKK1-290	2337	QSIRSF	2543	GQH	2600	QQYYDWPLT
DKK1-291	2338	QDIYQN	2544	GKN	2601	QQYYSGWT
DKK1-292	2339	QSLSSY	2545	GRN	2602	QNVLSTPYT
DKK1-293	2340	GDLRNKY	2546	GTS	2603	QAWVSSTVV
DKK1-294	2341	QSVDRY	2547	SAS	2604	SQSTHVPLT
DKK1-295	2342	QFIGRY	2548	GRN	2605	QQSYSTPT
DKK1-296	2343	QPIGPD	2549	GKK	2606	QQSYSTPRT
DKK1-297	2344	QTIGDY	2550	GAS	2607	SQSTHVPT
DKK1-298	2345	QTIERR	2551	GQH	2608	QQYHSYPPT
DKK1-299	2346	QSIRRF	2552	GAS	2609	QQSFSVPA
DKK1-300	2347	QDIYQN	2553	GNN	2610	QQSYSAPLT
DKK1-301	2348	QNIATY	2554	HDN	2611	LQDYNYPLT
DKK1-302	2349	QDINKY	2555	GRN	2612	QQTYNVPPT
DKK1-303	2350	QNIGNF	2556	NAK	2613	ASRDRSGHGV
DKK1-304	2351	QTIERR	2557	QND	2614	SSRDRSGNHRV
DKK1-305	2352	QRISSF	2558	QND	2615	QQSYSTPT
DKK1-306	2353	QSISSY	2559	HDN	2616	AQNLEIPRT
DKK1-307	2354	DKLGDKY	2560	HDN	2617	QPSFYFPYT
DKK1-308	2355	QDIYQN	2561	GKN	2618	QQYYSGWT
DKK1-309	2356	QSISSY	2562	GAS	2619	QQYWAFPVT
DKK1-310	2357	QSISGY	2563	AKN	2620	QQSYSSPRT
DKK1-311	2358	QDINKY	2564	DTS	2621	QQSYSTPNT
DKK1-312	2359	QNIRSY	2565	DNN	2622	LQDYNLWT
DKK1-313	2360	QSIREY	2566	ATS	2623	QAWDTSTAV
DKK1-314	2361	GDLGEKY	2567	ATS	2624	QAWASSTVV
DKK1-315	2362	QNIATY	2568	GNN	2625	STRSSKGNPHVL
DKK1-316	2363	KVSTSGYVY	2569	ENN	2626	QQYWAFPVT
DKK1-317	2364	SSVSY	2570	GEN	2627	QQSYSTPWT
DKK1-318	2365	QDVSSG	2571	GS	2628	QQYHSYPPT
DKK1-319	2366	QSVDRY	2572	HTS	2629	QAWDNRAVV
DKK1-320	2367	QSVYSNNE	2573	GNN	2630	QQSYSTPT
DKK1-321	2368	QSISTY	2574	AAS	2631	QQNYIIPWT
DKK1-322	2369	HSISSY	2575	TAS	2632	QQNYNTPFT

DKK1-323	2370	QSIHSY	2576	TAS	2633	QQSFSSPLT
DKK1-324	2371	QSVSRF	2577	AAA	2634	QQSYDTPFT
DKK1-325	2372	QSIGTY	2578	DAS	2635	QQNYNTPLT
DKK1-326	2373	QSIGIH	2579	GAT	2636	QQSYNTPPYT
DKK1-327	2374	QSIRSY	2580	ATS	2637	QQGYTSPLT
DKK1-328	2375	QGIATY	2581	GAS	2638	QQTFTNTPLT
DKK1-329	2376	QSIGSY	2582	AAS	2639	QQSHNIPRT
DKK1-330	2377	QSISRN	2583	GAS	2640	QQGYITPQT
DKK1-331	2378	QSVRTY	2584	RAS	2641	QQSFTTPLT
DKK1-332	2379	QSIGSH	2585	RAS	2642	QQSYSPPIT
DKK1-333	2380	QSISRY	2586	GAS	2643	QQSSSVPWT
DKK1-334	2381	QNIGNY	2587	AAS	2644	QQNYNTPLT
DKK1-335	2382	QSISTY	2588	AAS	2645	QQSYTPPIT
DKK1-336	2383	QNIGSY	2589	AAS	2646	QQSYNTPVT
DKK1-337	2384	QSISRF	2590	GAS	2647	QQSYIPPLT
DKK1-338	2385	ESITTY	2591	TAS	2648	QQNYITPLT
DKK1-339	2386	QSISTY	2592	AAS	2649	QQSYNSIT
DKK1-340	2387	QSIGSN	2593	ATS	2650	QQSYRIPRT
DKK1-341	2388	QSISRY	2594	AAS	2651	QQSYSTPTT
DKK1-342	2389	QYIGTY	2595	AAS	2652	QQSYSDLT
DKK1-343	2390	ESISRN	2596	AAS	2653	QQSYSGPPYT
DKK1-344	2391	QSISTY	2597	AAS	2654	QQNYIIPWT
DKK1-345	2392	QSVSNF	2598	GAS	2655	QQSYSFPFS
DKK1-346	2393	RNIRTY	2599	RAS	2656	QQSYKTPVT
DKK1-347	2394	QSIGNF	2600	RAS	2657	QQSYNTPIT
DKK1-348	2395	QSIRSY	2601	GAT	2658	QQSYSTLPFT
DKK1-349	2396	QSIRTY	2602	GAV	2659	QQRDT
DKK1-350	2397	QNIYTY	2603	LAS	2660	QQSYSTRFT
DKK1-351	2398	QSISRY	2604	GSS	2661	QQSYSSPT
DKK1-352	2399	QNIGRY	2605	SAS	2662	QQTYSPPLT
DKK1-353	2400	QTISAY	2606	GAS	2663	QQSYSGLT
DKK1-354	2401	QSIRGY	2607	STS	2664	QQNYNTPLT
DKK1-355	2402	QSVSYY	2608	GSS	2665	QQTYSSPVT
DKK1-356	2403	QPISSY	2609	SAS	2666	QQGYSAPLT
DKK1-357	2404	QSIGKY	2610	GAS	2667	QQTYSTPLT
DKK1-358	2405	QSIGAY	2611	GTS	2668	QQSYGTLIT
DKK1-359	2406	QTISTF	2612	GAS	2669	QQSYSTPLT
DKK1-360	2407	QSIGRY	2613	AVS	2670	QQSYSTPS
DKK1-361	2408	QSISNY	2465	GAS	2671	QQSYSLPLT
DKK1-362	2409	QTISRS	2466	GAS	2672	QQSFTTPYT
DKK1-363	2410	QSISSY	2467	AAS	2673	QQNYRSPLT
DKK1-364	2411	RSIGTY	2468	AAS	2674	QQNYITPLT
DKK1-365	2412	QNINRY	2469	ASS	2675	QQSYSSPIT
DKK1-366	2413	QSVSSY	2470	ATS	2676	HQTYSTPRT
DKK1-367	2414	QSIGIH	2471	GAT	2677	QQSYNTPPYT

DKK1-368	2415	RSISTY	2472	EVS	2678	QQNYITPLT
DKK1-369	2416	QSISRY	2473	AAS	2679	QQGYSSPLT
DKK1-370	2417	QSISNF	2474	GTS	2680	QQSYSIPFT
DKK1-371	2418	QGISFY	2475	AAS	2681	QQSYSTPQIT
DKK1-372	2419	QNIKTY	2476	GAS	2682	LQTYSVPLT
DKK1-373	2420	QYISNY	2477	GAS	2683	QQTYSLPLT
DKK1-374	2421	QTISTF	2478	GAS	2684	QQSYSTPLT
DKK1-375	2422	QSISRF	2479	GAS	2685	QQSYKTPRT
DKK1-376	2423	ESIDNY	2480	GAT	2686	QQNYNIPFT
DKK1-377	2424	QSISNF	2481	TAS	2687	QQSYRVPRT
DKK1-378	2425	QSIGTN	2482	AAS	2688	QQSYSIPLT
DKK1-379	2426	QTITRY	2483	AAT	2689	QQSYSTPET
DKK1-380	2427	QSIGNF	2484	DAS	2690	QQSYSIPPT
DKK1-381	2428	HSISRY	2485	GAS	2691	QQSYSTHT
DKK1-382	2429	QGISFY	2486	GAS	2692	QQSYSPPLT
DKK1-383	2430	QSVSNY	2487	GAS	2693	QQSYVTPPT
DKK1-384	2431	QSIGSF	2488	AAF	2694	QQTYSPPFT
DKK1-385	2432	QSITRH	2489	AAS	2695	QQSYSTPGT
DKK1-386	2433	QRISRY	2490	GAS	2696	QQSYRTPIT
DKK1-387	2434	QYIGNY	2491	AVS	2697	QQSFSAPYT
DKK1-388	2435	QYISTF	2492	SAS	2698	QQSYSPLT
DKK1-389	2436	RSISRY	2493	GAS	2699	QQSYTPPRT
DKK1-390	2437	QSISRS	2494	GAS	2700	QQSFTIPWT
DKK1-391	2438	QSITSY	2495	AAS	2701	QQSYNTPVT
DKK1-392	2439	QNIAGY	2496	AAS	2702	QQSSSTPIT
DKK1-393	2440	QTIRTY	2497	ATS	2703	QQSYRPPLT
DKK1-394	2441	QSIGIH	2498	GAT	2704	QQSYNTPPYT
DKK1-395	2442	QSISTY	2499	GAS	2705	QQTYSAPRT
DKK1-396	2443	QSIGRY	2500	GAS	2706	QQSYRTPLT
DKK1-397	2444	HTISRY	2501	AAS	2707	QQSFTAPDT
DKK1-398	2445	QSISRY	2502	TTS	2708	QQSYSDLT
DKK1-399	2446	QRINTY	2503	GAF	2709	QQSYRVPRT
DKK1-400	2447	QSINHY	2504	GAS	2710	QQSYSLPRT
DKK1-401	2448	QTIGRY	2505	ATS	2711	QQTYSTPYT
DKK1-402	2449	QSIGEY	2506	AAS	2712	QQNYRSPLT
DKK1-403	2450	QSIYRY	2507	AAT	2713	QQSYSPPLT
DKK1-404	2451	QNIGRY	2508	EVS	2714	QQSYRTPGT
DKK1-405	2452	QSIRNY	2509	AAT	2715	QQSFLTPWT
DKK1-406	2453	QSISRH	2510	GAT	2716	QQSYSKPYT
DKK1-407	2454	QSISRY	2511	AAT	2717	QQSYSTPLS
DKK1-408	2455	QSIGTY	2512	DTS	2718	QQSFTSPLT
DKK1-409	2456	QGIATY	2513	AAS	2719	QQTHSTPLT
DKK1-410	2457	QNIGGY	2514	RAS	2720	QQSYSTPLLT
DKK1-411	2458	QYIGNY	2515	ASS	2721	QQTSSTPLT
DKK1-412	2459	QSIGTY	2516	DAS	2722	QQNYNTPLT

DKK1-413	2460	QNIGRY	2517	AAS	2723	QQSYTPPRT
DKK1-414	2461	QSISRH	2518	GAS	2724	QQTYRTPLT
DKK1-415	2462	QSIHNY	2519	AAS	2725	QQSYSTPYT
DKK1-416	2463	QGIATY	2520	GAS	2726	QQTFTNTPLT
DKK1-417	2464	QTITKY	2521	ATS	2727	QQSYSAPVT

[00225] Example 5: DKK1 Variants

[00226] In this experiment, the antibodies were tested for their yield, SPR affinity, and enrichment from eluted phage (**Tables 9-10**).

[00227] Variable heavy chain and light chain domains of anti-DKK1 antibodies were reformatted to IgG2, or VHH-Fc based on IgG2 Fc for nanobody leads. Reformatted leads were then DNA back-translated, synthesized, and cloned into mammalian expression vector pTwist CMV BG WPRE Neo. Light chain variable domains were reformatted into kappa and lambda frameworks accordingly. Clonal genes were delivered as purified plasmid DNA ready for transient transfection in HEK Expi293 cells (Thermo Fisher Scientific). Cultures in a volume of 1.2 mL were grown to four days, harvested, and purified using Protein A resin (PhyNexus) on the Hamilton Microlab STAR platform into 43 mM Citrate 148 mM HEPES, pH 6. 1.2 ml. Yield was calculated by measuring absorbance at 280 nm on Lunatic instrumentation (UNCLE). Results are depicted in **FIG. 10A**.

[00228] SPR experiments were performed on a Carterra LSA SPR biosensor equipped with a HC30M chip at 25°C in HBS-TE. Antibodies were diluted to 10 µg/mL and amine-coupled to the sensor chip by EDC/NHS activation, followed by ethanolamine HCl quenching. Increasing concentrations of analyte were flowed over the sensor chip in HBS-TE with 0.5 mg/mL BSA with 5-minute association and 15-minute dissociation. Following each injection cycle the surface was regenerated with 2x 30-second injections of IgG elution buffer (Thermo). Data were analyzed in Carterra's Kinetics Tool software with 1:1 binding model. Results are depicted in **FIGs. 10B-C** and 11A-B.

[00229] Long-read NGS sequencing was performed by submitting PCR amplicons of DNA corresponding to the scFv or VHH of each clone to Loop Genomics for processing. Returned contiguous FASTQ files were processed by the AIRR Python API to extract and annotate antibody sequences. "NGS enrichment" refers to the number of instances that specific antibody appeared in round 4 sequencing. "Cluster enrichment" refers to the number of instances that the exact antibody appeared in round 4 or a variant within a Levenshtein distance of 3 appeared in round 4 sequencing. "Cluster rank" lists the antibody rank order of the antibody belonging to the largest size cluster enrichment to the lowest. Results can be seen in **FIGs. 9A-C**

Table 9. Antibody Yield, SPR Affinity, and Enrichment of Antibodies

DKK1 Variant	1.2 ml yield (ug)	ka (M-1 s-1)	kd (s-1)	KD (M)	Rmax (RU)	NGS Enrichment	Cluster Enrichment	Cluster Rank
DKK1-1	73.0	-	-	-	-	-	-	-
DKK1-2	166.0	-	-	-	-	-	-	-
DKK1-3	56.0	-	-	-	-	-	-	-
DKK1-4	98.0	-	-	-	-	-	-	-
DKK1-5	147.0	-	-	-	-	-	-	-
DKK1-6	96.0	2.24E+05	8.60E-04	3.84E-09	90.1	48	53	5
DKK1-7	131.0	-	-	-	-	-	-	-
DKK1-8	232.0	-	-	-	-	3	-	-
DKK1-9	n/a	n/a	n/a	n/a	n/a	3	-	-
DKK1-10	105.0	4.51E+05	4.02E-04	8.92E-10	32.5	16	17	41
DKK1-11	56.0	-	-	-	-	46	49	6
DKK1-12	82.0	-	-	-	-	44	53	4
DKK1-13	267.0	-	-	-	-	53	62	1
DKK1-14	119.0	-	-	-	-	2	-	-
DKK1-15	117.0	-	-	-	-	2	-	-
DKK1-16	243.0	-	-	-	-	2	-	-
DKK1-17	51.0	-	-	-	-	2	-	-
DKK1-18	131.0	3.76E+04	1.29E-04	3.42E-09	18.5	-	-	-
DKK1-19	96.0	-	-	-	-	5	-	-
DKK1-20	5.0	-	-	-	-	-	-	-
DKK1-21	307.0	-	-	-	-	1	-	-
DKK1-22	211.0	-	-	-	-	1	-	-
DKK1-23	89.0	-	-	-	-	-	-	-
DKK1-24	40.0	4.21E+05	3.00E-04	7.13E-10	126.5	1	-	-
DKK1-25	129.0	-	-	-	-	-	-	-
DKK1-26	77.0	8.82E+05	1.00E-06	1.13E-12	18.8	-	-	-
DKK1-27	192.0	-	-	-	-	33	40	13
DKK1-28	84.0	6.27E+05	1.00E-05	1.59E-11	68.7	2	-	-
DKK1-29	47.0	-	-	-	-	-	-	-
DKK1-30	37.0	4.15E+05	3.03E-04	7.29E-10	95.1	3	-	-
DKK1-31	42.0	-	-	-	-	9	17	40
DKK1-32	157.0	-	-	-	-	8	-	-
DKK1-33	68.0	-	-	-	-	12	13	84
DKK1-34	180.0	3.46E+05	6.04E-04	1.75E-09	163.7	3	-	-
DKK1-35	89.0	-	-	-	-	4	12	92
DKK1-36	370.0	-	-	-	-	7	13	68
DKK1-37	260.0	9.13E+04	9.16E-05	1.00E-09	42.5	24	30	15
DKK1-38	61.0	-	-	-	-	-	-	-
DKK1-39	28.0	-	-	-	-	-	-	-
DKK1-40	7.0	1.10E+05	6.43E-04	5.86E-09	47.3	-	-	-
DKK1-41	140.4	1.02E+05	8.28E-04	8.13E-09	224.6	9	17	40
DKK1-42	124.0	8.91E+04	2.59E-03	2.91E-08	81.1	3	17	39
DKK1-43	147.4	2.01E+05	3.93E-03	1.96E-08	230.7	10	17	38
DKK1-44	110.0	1.78E+05	1.24E-04	6.93E-10	173.7	13	17	37
DKK1-45	142.7	6.63E+04	1.72E-03	2.60E-08	218.5	12	18	36
DKK1-46	124.0	1.27E+05	2.90E-03	2.27E-08	186.7	13	18	35
DKK1-47	88.9	2.73E+05	6.68E-03	2.45E-08	161.5	11	19	34
DKK1-48	72.5	9.94E+04	3.06E-03	3.08E-08	202.1	6	19	33
DKK1-49	28.1	4.11E+04	3.18E-03	7.75E-08	88.4	16	19	32
DKK1-50	138.1	9.14E+04	1.74E-03	1.90E-08	80.7	12	19	31
DKK1-51	107.6	4.91E+04	4.25E-03	8.66E-08	161.0	18	19	30
DKK1-52	152.1	8.29E+04	2.99E-03	3.60E-08	120.4	15	20	29
DKK1-53	154.4	8.72E+04	3.54E-03	4.05E-08	187.4	15	20	28
DKK1-54	152.1	1.06E+05	3.72E-04	3.51E-09	486.9	19	20	27
DKK1-55	131.0	2.29E+05	8.89E-04	3.89E-09	535.3	16	21	26

DKK1-56	163.8	4.34E+04	2.05E-03	4.72E-08	114.9	15	22	25
DKK1-57	128.7	9.24E+04	3.06E-03	3.31E-08	232.1	11	22	24
DKK1-58	79.6	9.61E+04	3.31E-03	3.44E-08	249.1	18	22	23
DKK1-59	67.9	1.29E+05	1.40E-02	1.08E-07	230.6	9	23	22
DKK1-60	42.1	1.02E+05	1.79E-03	1.75E-08	213.3	22	25	21
DKK1-61	32.8	7.00E+04	4.39E-03	6.26E-08	170.1	13	25	20
DKK1-62	65.5	1.26E+05	2.19E-03	1.74E-08	93.5	20	26	19
DKK1-63	28.1	n.b.	n.b.	n.b.	n.b.	24	27	18
DKK1-64	49.1	n.b.	n.b.	n.b.	n.b.	22	28	17
DKK1-65	124.0	3.61E+04	2.26E-03	6.27E-08	133.1	23	28	16
DKK1-66	49.1	1.23E+05	4.92E-03	3.99E-08	4450.4	24	30	15
DKK1-67	81.9	2.17E+05	1.47E-03	6.77E-09	180.3	29	34	14
DKK1-68	58.5	5.61E+04	2.42E-03	4.31E-08	77.9	33	40	13
DKK1-69	51.5	1.08E+05	7.22E-04	6.68E-09	237.0	19	40	12
DKK1-70	37.4	2.05E+05	2.14E-03	1.04E-08	333.0	29	42	11
DKK1-71	42.1	1.13E+05	3.45E-03	3.06E-08	292.4	29	42	10
DKK1-72	100.6	2.06E+05	3.62E-03	1.76E-08	133.7	35	42	9
DKK1-73	51.5	1.03E+05	1.77E-03	1.71E-08	45.7	41	44	8
DKK1-74	63.2	1.65E+05	4.31E-03	2.61E-08	205.2	34	46	7
DKK1-75	74.9	1.05E+06	8.32E-03	7.90E-09	118.5	46	49	6
DKK1-76	51.5	1.23E+05	2.03E-03	1.66E-08	240.7	48	53	5
DKK1-77	28.1	1.26E+05	1.26E-03	1.00E-08	197.8	44	53	4
DKK1-78	39.8	2.09E+05	3.52E-03	1.68E-08	290.0	43	54	3
DKK1-79	53.8	1.58E+05	1.19E-03	7.55E-09	148.7	50	55	2
DKK1-80	81.9	4.40E+05	7.60E-05	1.73E-10	190.9	53	62	1
DKK1-81	79.6					-	-	-
DKK1-82	7.0					-	-	-
DKK1-83	98.3					-	-	-
DKK1-84	67.9					-	-	-
DKK1-85	4.7					-	-	-
DKK1-86	16.4					-	-	-
DKK1-87	149.8					-	-	-
DKK1-88	238.7	5.94E+04	1.81E-03	3.06E-08	637.9	5	-	-
DKK1-89	126.4	5.09E+04	4.35E-03	8.55E-08	405.5	-	-	-
DKK1-90	322.9	3.73E+04	3.07E-03	8.23E-08	359.2	-	-	-
DKK1-91	114.7	8.07E+04	1.03E-02	1.27E-07	439.7	-	-	-
DKK1-92	152.1	9.36E+04	3.62E-03	3.87E-08	142.0	-	-	-
DKK1-93	117.0	6.25E+04	4.13E-04	6.62E-09	422.2	-	-	-
DKK1-94	98.3	7.24E+04	2.01E-03	2.78E-08	418.1	-	-	-
DKK1-95	133.4	9.41E+04	2.69E-03	2.85E-08	491.0	-	-	-
DKK1-96	163.8	6.03E+04	1.54E-03	2.54E-08	661.4	-	-	-
DKK1-97	156.8	6.57E+04	1.00E-05	1.52E-10	411.3	-	-	-
DKK1-98	154.4	1.34E+05	2.02E-01	1.50E-06	83.7	-	-	-

Table 10. Antibody Yield, SPR Affinity, and Enrichment of Antibodies

TSLP Variant	yield	kon (M-1 s-1)	koff (s-1)	KD (M)	Rmax (RU)	100nM FACS (MFI Ratio)	EC50 FACS (nM)
DKK1-99	154.44	1.34E+05	2.02E-01	1.50E-06	83.7	1.70	
DKK1-100	156.78	6.57E+04	1.00E-05	1.52E-10	411.3	5.30	
DKK1-101	163.8	6.03E+04	1.54E-03	2.54E-08	661.4	16.90	
DKK1-102	133.38	9.41E+04	2.69E-03	2.85E-08	491.0	8.00	
DKK1-103	98.28	7.24E+04	2.01E-03	2.78E-08	418.1	9.10	

DKK1-104	117	6.25E+04	4.13E-04	6.62E-09	422.2	6.90	
DKK1-105	152.1	9.36E+04	3.62E-03	3.87E-08	142.0	2.10	
DKK1-106	114.66	8.07E+04	1.03E-02	1.27E-07	439.7	4.20	
DKK1-107	322.92	3.73E+04	3.07E-03	8.23E-08	359.2	1.30	
DKK1-108	126.36	5.09E+04	4.35E-03	8.55E-08	405.5	1.10	
DKK1-109	238.68	5.94E+04	1.81E-03	3.06E-08	637.9	15.50	
DKK1-110	149.76					6.50	
DKK1-111	16.38						
DKK1-112	4.68						
DKK1-113	67.86					2.20	
DKK1-114	98.28					4.40	
DKK1-115	7.02						
DKK1-116	79.56					3.50	
DKK1-117	81.9	4.40E+05	7.60E-05	1.73E-10	190.9	45.10	
DKK1-118	53.82	1.58E+05	1.19E-03	7.55E-09	148.7		
DKK1-119	39.78	2.09E+05	3.52E-03	1.68E-08	290.0		
DKK1-120	28.08	1.26E+05	1.26E-03	1.00E-08	197.8		
DKK1-121	51.48	1.23E+05	2.03E-03	1.66E-08	240.7		
DKK1-122	74.88	1.05E+06	8.32E-03	7.90E-09	118.5		
DKK1-123	63.18	1.65E+05	4.31E-03	2.61E-08	205.2		
DKK1-124	51.48	1.03E+05	1.77E-03	1.71E-08	45.7		
DKK1-125	100.62	2.06E+05	3.62E-03	1.76E-08	133.7		
DKK1-126	42.12	1.13E+05	3.45E-03	3.06E-08	292.4		
DKK1-127	37.44	2.05E+05	2.14E-03	1.04E-08	333.0		
DKK1-128	51.48	1.08E+05	7.22E-04	6.68E-09	237.0		
DKK1-129	58.5	5.61E+04	2.42E-03	4.31E-08	77.9		
DKK1-130	81.9	2.17E+05	1.47E-03	6.77E-09	180.3	30.00	
DKK1-131	49.14	1.23E+05	4.92E-03	3.99E-08	4450.4		
DKK1-132	124.02	3.61E+04	2.26E-03	6.27E-08	133.1		
DKK1-133	49.14	n.b.	n.b.	n.b.	n.b.		
DKK1-134	28.08	n.b.	n.b.	n.b.	n.b.		
DKK1-135	65.52	1.26E+05	2.19E-03	1.74E-08	93.5		
DKK1-136	32.76	7.00E+04	4.39E-03	6.26E-08	170.1		
DKK1-137	42.12	1.02E+05	1.79E-03	1.75E-08	213.3		
DKK1-138	67.86	1.29E+05	1.40E-02	1.08E-07	230.6		
DKK1-139	79.56	9.61E+04	3.31E-03	3.44E-08	249.1		
DKK1-140	128.7	9.24E+04	3.06E-03	3.31E-08	232.1		
DKK1-141	163.8	4.34E+04	2.05E-03	4.72E-08	114.9		
DKK1-142	131.04	2.29E+05	8.89E-04	3.89E-09	535.3	4.20	
DKK1-143	152.1	1.06E+05	3.72E-04	3.51E-09	486.9	22.40	

DKK1-144	154.44	8.72E+04	3.54E-03	4.05E-08	187.4		
DKK1-145	152.1	8.29E+04	2.99E-03	3.60E-08	120.4		
DKK1-146	107.64	4.91E+04	4.25E-03	8.66E-08	161.0		
DKK1-147	138.06	9.14E+04	1.74E-03	1.90E-08	80.7		
DKK1-148	28.08	4.11E+04	3.18E-03	7.75E-08	88.4		
DKK1-149	72.54	9.94E+04	3.06E-03	3.08E-08	202.1		
DKK1-150	88.92	2.73E+05	6.68E-03	2.45E-08	161.5		
DKK1-151	124.02	1.27E+05	2.90E-03	2.27E-08	186.7		
DKK1-152	142.74	6.63E+04	1.72E-03	2.60E-08	218.5		
DKK1-153	109.98	1.78E+05	1.24E-04	6.93E-10	173.7	7.20	
DKK1-154	147.42	2.01E+05	3.93E-03	1.96E-08	230.7		
DKK1-155	124.02	8.91E+04	2.59E-03	2.91E-08	81.1		
DKK1-156	140.4	1.02E+05	8.28E-04	8.13E-09	224.6		
DKK1-157	180.18	1.23E+04	3.73E-03	3.03E-07	196.2		
DKK1-158	58.5	4.77E+05	1.01E-02	2.12E-08	175.5		
DKK1-159	72.54	8.09E+04	1.93E-03	2.39E-08	266.8		
DKK1-160	93.6	1.02E+05	3.08E-04	3.03E-09	295.9		
DKK1-161	58.5	2.61E+05	4.68E-03	1.79E-08	231.9		
DKK1-162	105.3	6.41E+04	2.95E-03	4.60E-08	224.6		
DKK1-163	44.46	1.38E+02	1.77E-02	1.28E-04	16396.4		
DKK1-164	168.48	2.00E+04	2.14E-03	1.07E-07	293.9		
DKK1-165	163.8	1.55E+05	2.83E-03	1.83E-08	70.4		
DKK1-166	152.1	9.84E+04	2.58E-03	2.62E-08	321.8		
DKK1-167	39.78	1.65E+04	2.83E-02	1.71E-06	950.7		
DKK1-168	74.88	1.88E+05	7.97E-03	4.23E-08	165.5		
DKK1-169	140.4	7.50E+04	4.68E-03	6.23E-08	261.2		
DKK1-170	128.7	n.b.	n.b.	n.b.	n.b.		
DKK1-171	18.72	5.83E+04	2.06E-03	3.54E-08	67.4		
DKK1-172	86.58	2.29E+04	3.05E-03	1.33E-07	264.4		
DKK1-173	147.42	1.59E+05	2.62E-03	1.65E-08	217.9		
DKK1-174	42.12	9.10E+04	3.53E-03	3.88E-08	250.0		
DKK1-175	65.52	1.74E+05	3.45E-03	1.98E-08	129.8		
DKK1-176	51.48	6.53E+04	4.68E-03	7.17E-08	154.3		
DKK1-177	100.62	5.92E+04	1.70E-02	2.87E-07	178.9		
DKK1-178	156.78	1.93E+05	1.27E-03	6.61E-09	277.4	7.00	
DKK1-179	77.22	6.18E+04	5.17E-03	8.36E-08	213.3		
DKK1-180	42.12	6.27E+04	3.49E-03	5.56E-08	164.6		
DKK1-181	35.1	1.66E+05	7.46E-03	4.48E-08	181.8		
DKK1-182	65.52	3.44E+05	3.24E-03	9.40E-09	231.3		
DKK1-183	35.1	7.32E+04	2.53E-03	3.46E-08	41.7		

DKK1-184	65.52	1.12E+05	2.35E-04	2.11E-09	386.0	13.80	
DKK1-185	49.14	1.56E+05	5.80E-03	3.73E-08	245.3		
DKK1-186	67.86	9.26E+04	4.76E-03	5.14E-08	194.5		
DKK1-187	86.58	2.06E+05	3.44E-03	1.67E-08	168.1		
DKK1-188	49.14	1.37E+05	1.49E-03	1.08E-08	435.0		
DKK1-189	49.14	2.64E+05	9.14E-03	3.47E-08	231.2		
DKK1-190	65.52	8.99E+04	8.75E-04	9.74E-09	149.6		
DKK1-191	70.2	1.10E+05	5.76E-05	5.26E-10	378.2	4.40	
DKK1-192	91.26	4.78E+04	1.76E-03	3.68E-08	167.7		
DKK1-193	74.88	2.03E+05	7.54E-03	3.71E-08	183.7		
DKK1-194	79.56	n.b.	n.b.	n.b.	n.b.		
DKK1-195	70.2	4.34E+04	3.05E-03	7.04E-08	271.6		
DKK1-196	149.76	9.80E+04	2.01E-03	2.05E-08	438.6		
DKK1-197	124.02	2.81E+05	2.41E-03	8.58E-09	112.5		
DKK1-198	86.58	1.15E+05	3.42E-03	2.97E-08	228.1		
DKK1-199	63.18	7.56E+04	5.46E-03	7.23E-08	200.8		
DKK1-200	133.38	4.66E+04	1.63E-03	3.49E-08	112.0		
DKK1-201	58.5	1.45E+05	9.81E-03	6.74E-08	141.5		
DKK1-202	58.5	1.57E+05	1.09E-02	6.92E-08	248.8		
DKK1-203	112.32	6.07E+04	6.57E-04	1.08E-08	317.8		
DKK1-204	114.66	8.36E+04	1.95E-03	2.33E-08	280.2		
DKK1-205	105.3	n.b.	n.b.	n.b.	n.b.		
DKK1-206	147.42	n.b.	n.b.	n.b.	n.b.		
DKK1-207	147.42	3.42E+05	2.46E-03	7.19E-09	158.5		
DKK1-208	154.44	9.36E+04	2.24E-04	2.39E-09	310.2		
DKK1-209	159.12	1.82E+05	1.03E-03	5.64E-09	260.8	18.00	
DKK1-210	128.7	n.b.	n.b.	n.b.	n.b.		
DKK1-211	91.26	n.b.	n.b.	n.b.	n.b.		
DKK1-212	9.36						
DKK1-213	0					0.70	
DKK1-214	7.02					0.20	
DKK1-215	28.08					0.20	
DKK1-216	7.02					0.10	
DKK1-217	44.46					0.20	
DKK1-218	7.02						
DKK1-219	7.02					0.60	
DKK1-220	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-221	18.72	n.b.	n.b.	n.b.	n.b.	1.00	
DKK1-222	18.72	n.b.	n.b.	n.b.	n.b.	1.60	
DKK1-223	14.04	n.b.	n.b.	n.b.	n.b.	2.20	

DKK1-224	21.06						
DKK1-225	16.38					1.20	
DKK1-226	14.04	1.25E+05	8.99E-02	7.17E-07	42.1	2.60	
DKK1-227	25.74					0.40	
DKK1-228	11.7	4.50E+05	1.06E-02	2.35E-08	94.0	1.10	
DKK1-229	25.74	n.b.	n.b.	n.b.	n.b.	1.50	
DKK1-230	18.72					0.20	
DKK1-231	4.68						
DKK1-232	56.16					36.50	
DKK1-233	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-234	25.74					1.30	
DKK1-235	35.1					6.50	
DKK1-236	9.36					0.10	
DKK1-237	21.06	n.b.	n.b.	n.b.	n.b.	4.10	
DKK1-238	14.04	n.b.	n.b.	n.b.	n.b.	0.30	
DKK1-239	11.7					0.70	
DKK1-240	4.68						
DKK1-241	102.96					0.70	
DKK1-242	4.68						
DKK1-243	35.1					10.30	
DKK1-244	7.02					2.90	
DKK1-245	11.7	n.b.	n.b.	n.b.	n.b.	319.70	
DKK1-246	4.68					0.30	
DKK1-247	4.68	1.83E+04	8.02E-03	4.39E-07	58.1	0.20	
DKK1-248	112.32	3.73E+05	4.63E-03	1.24E-08	541.0	26.00	
DKK1-249	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-250	9.36					0.70	
DKK1-251	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-252	4.68						
DKK1-253	18.72	n.b.	n.b.	n.b.	n.b.	0.20	
DKK1-254	53.82	1.39E+05	2.36E-02	1.70E-07	256.8	2.50	
DKK1-255	2.34						
DKK1-256	49.14	n.b.	n.b.	n.b.	n.b.	0.10	
DKK1-257	11.7	n.b.	n.b.	n.b.	n.b.	0.10	
DKK1-258							
DKK1-259	0						
DKK1-260	16.38	n.b.	n.b.	n.b.	n.b.		
DKK1-261	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-262	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-263	18.72	n.b.	n.b.	n.b.	n.b.		

DKK1-264	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-265	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-266	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-267	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-268	42.12	n.b.	n.b.	n.b.	n.b.		
DKK1-269	14.04	n.b.	n.b.	n.b.	n.b.		
DKK1-270	25.74	n.b.	n.b.	n.b.	n.b.		
DKK1-271	21.06	n.b.	n.b.	n.b.	n.b.		
DKK1-272	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-273	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-274	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-275	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-276	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-277	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-278	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-279	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-280	21.06	n.b.	n.b.	n.b.	n.b.		
DKK1-281	16.38	n.b.	n.b.	n.b.	n.b.		
DKK1-282	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-283	25.74	1.30E+05	3.35E-03	2.58E-08	355.6		
DKK1-284	51.48	n.b.	n.b.	n.b.	n.b.		
DKK1-285	49.14	n.b.	n.b.	n.b.	n.b.		
DKK1-286	16.38	n.b.	n.b.	n.b.	n.b.		
DKK1-287	14.04	n.b.	n.b.	n.b.	n.b.		
DKK1-288	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-289	70.2	n.b.	n.b.	n.b.	n.b.		
DKK1-290	35.1	9.25E+04	2.42E-03	2.61E-08	123.8		
DKK1-291	25.74	n.b.	n.b.	n.b.	n.b.		
DKK1-292	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-293	28.08	n.b.	n.b.	n.b.	n.b.		
DKK1-294	23.4	2.23E+04	4.74E-03	2.12E-07	135.9		
DKK1-295	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-296	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-297		n.b.	n.b.	n.b.	n.b.		
DKK1-298		n.b.	n.b.	n.b.	n.b.		
DKK1-299		n.b.	n.b.	n.b.	n.b.		
DKK1-300		n.b.	n.b.	n.b.	n.b.		
DKK1-301		n.b.	n.b.	n.b.	n.b.		
DKK1-302	21.06	n.b.	n.b.	n.b.	n.b.		
DKK1-303	7.02	n.b.	n.b.	n.b.	n.b.		

DKK1-304	14.04	n.b.	n.b.	n.b.	n.b.		
DKK1-305	53.82	n.b.	n.b.	n.b.	n.b.		
DKK1-306		n.b.	n.b.	n.b.	n.b.		
DKK1-307		n.b.	n.b.	n.b.	n.b.		
DKK1-308		n.b.	n.b.	n.b.	n.b.		
DKK1-309		n.b.	n.b.	n.b.	n.b.		
DKK1-310		n.b.	n.b.	n.b.	n.b.		
DKK1-311		n.b.	n.b.	n.b.	n.b.		
DKK1-312	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-313		n.b.	n.b.	n.b.	n.b.		
DKK1-314	32.76	n.b.	n.b.	n.b.	n.b.		
DKK1-315	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-316	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-317	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-318	32.76	n.b.	n.b.	n.b.	n.b.		
DKK1-319	23.4	n.b.	n.b.	n.b.	n.b.		
DKK1-320	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-321	63.18	3.72E+05	3.04E-03	8.17E-09	154.1	92.00	
DKK1-322	74.88	4.82E+05	8.51E-03	1.77E-08	387.2	38.70	
DKK1-323	56.16	n.b.	n.b.	n.b.	n.b.	3.40	
DKK1-324	79.56	n.b.	n.b.	n.b.	n.b.	0.80	
DKK1-325	21.06	5.04E+05	4.22E-03	8.39E-09	93.7	17.90	
DKK1-326	58.5	3.34E+05	2.98E-03	8.92E-09	58.8		
DKK1-327	32.76	4.66E+05	4.80E-03	1.03E-08	75.1		
DKK1-328	21.06	n.b.	n.b.	n.b.	n.b.		
DKK1-329	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-330	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-331	16.38	n.b.	n.b.	n.b.	n.b.		
DKK1-332	28.08	1.55E+05	6.92E-04	4.48E-09	619.7	13.30	
DKK1-333	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-334	16.38	1.31E+05	7.03E-03	5.36E-08	144.8		
DKK1-335	70.2	1.01E+05	1.37E-03	1.36E-08	48.7		
DKK1-336	44.46	5.67E+04	1.75E-01	3.10E-06	76.9		
DKK1-337	30.42	4.83E+05	1.74E-03	3.61E-09	314.7	3.30	
DKK1-338	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-339	35.1	4.23E+05	4.81E-03	1.14E-08	60.1		
DKK1-340	42.12	n.b.	n.b.	n.b.	n.b.		
DKK1-341	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-342	9.36	4.85E+05	1.98E-03	4.09E-09	72.2	1.90	
DKK1-343	11.7	n.b.	n.b.	n.b.	n.b.		

DKK1-344	23.4	n.b.	n.b.	n.b.	n.b.		
DKK1-345	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-346	4.68	3.28E+06	4.85E-02	1.48E-08	51.5		
DKK1-347	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-348	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-349	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-350	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-351	16.38	n.b.	n.b.	n.b.	n.b.		
DKK1-352	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-353	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-354	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-355	11.7	2.26E+05	1.31E-02	5.79E-08	127.4		
DKK1-356	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-357	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-358	30.42	4.66E+04	2.22E-03	4.77E-08	94.2		
DKK1-359	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-360	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-361	7.02	3.93E+05	5.20E-03	1.32E-08	53.5		
DKK1-362	16.38	n.b.	n.b.	n.b.	n.b.		
DKK1-363	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-364	7.02	2.36E+05	3.16E-03	1.34E-08	47.4		
DKK1-365	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-366	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-367	14.04	n.b.	n.b.	n.b.	n.b.		
DKK1-368	7.02	4.23E+03	2.53E-02	5.97E-06	2264.0		
DKK1-369	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-370	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-371	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-372	7.02	5.47E+04	3.29E-03	6.01E-08	71.5		
DKK1-373	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-374	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-375	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-376	9.36	3.77E+05	3.05E-03	8.08E-09	286.0	4.00	
DKK1-377	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-378	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-379	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-380	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-381	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-382	46.8	4.16E+05	1.10E-03	2.65E-09	301.7	7.10	
DKK1-383	63.18	n.b.	n.b.	n.b.	n.b.		

DKK1-384	14.04	n.b.	n.b.	n.b.	n.b.		
DKK1-385	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-386	25.74	n.b.	n.b.	n.b.	n.b.		
DKK1-387	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-388	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-389	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-390	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-391	4.68	1.25E+06	4.17E-02	3.34E-08	86.0		
DKK1-392	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-393	16.38	3.34E+05	1.97E-03	5.92E-09	190.4	15.90	
DKK1-394	7.02	n.b.	n.b.	n.b.	n.b.		
DKK1-395	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-396	37.44	6.22E+05	9.97E-03	1.60E-08	121.9		
DKK1-397	63.18	n.b.	n.b.	n.b.	n.b.		
DKK1-398	39.78	n.b.	n.b.	n.b.	n.b.		
DKK1-399	18.72	n.b.	n.b.	n.b.	n.b.		
DKK1-400	51.48	n.b.	n.b.	n.b.	n.b.		
DKK1-401	39.78	n.b.	n.b.	n.b.	n.b.		
DKK1-402	39.78	n.b.	n.b.	n.b.	n.b.		
DKK1-403	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-404	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-405	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-406	9.36	n.b.	n.b.	n.b.	n.b.		
DKK1-407	35.1	n.b.	n.b.	n.b.	n.b.		
DKK1-408	32.76	2.04E+05	3.91E-03	1.91E-08	405.1		
DKK1-409	25.74	n.b.	n.b.	n.b.	n.b.		
DKK1-410	4.68	n.b.	n.b.	n.b.	n.b.		
DKK1-411	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-412	32.76	n.b.	n.b.	n.b.	n.b.		
DKK1-413	2.34	n.b.	n.b.	n.b.	n.b.		
DKK1-414	18.72	9.75E+04	1.82E-03	1.87E-08	126.3		
DKK1-415	14.04	n.b.	n.b.	n.b.	n.b.		
DKK1-416	11.7	n.b.	n.b.	n.b.	n.b.		
DKK1-417	28.08	n.b.	n.b.	n.b.	n.b.		

[00230] Example 5: Panning and screening for identification of antibodies for DKK1

[00231] This example describes identification of antibodies for DKK1. Phage displayed libraries were panned for biding to DKK1. Panning was performed as shown in **FIG. 21**.

[00232] Carterra kinetics results showed that VHH-Fc hits bind with high affinity to DKK1 (**FIGs. 12A-12D**).

[00233] **FIG. 13** shows the results of a TCF/LEF reporter (Wnt signaling) assay. Wnt signaling activation was plotted with SPR binding affinity.

[00234] **FIGs. 14A-14B** show the results of an immune cell activation assay.

[00235] A tumor cell killing assay was performed as depicted in **FIG. 15A**. Results showed that high affinity binders that were also Wnt signaling activators were not always the same as strong immune cell activators and tumor killers (**FIGs. 15B-15G**).

[00236] **FIG. 16** depicts antibody yield results from 1mL Expi293 cell culture. It took 31 days to create 113 anti DKK1 VHH-Fc from DNA synthesis to antibody production.

[00237] **Example 6: Testing DKK1 antibodies**

[00238] This example describes assays used to determine the efficacy of anti-DKK1 leads identified in Example 5.

[00239] As seen in **FIG. 17A**, two epitope bins were apparent among top anti-DKK1 leads. These leads bound to two distinct cysteine-rich domains (CRDs) in hDKK1 (CRD1 or CRD2), resulting in different activation pathways (**FIGs. 17B-17C**).

[00240] Anti-DKK1 VHH leads were found to block DKK1 binding to the receptor (**FIGs. 18A-18C**) DKK1 binding to LRP5/6 blocks Wnt TCF/LEF signaling; however anti-DKK1 leads blocked DKK1 binding to the receptor, which resulted in TCF/LEF signal activation.

[00241] Dual functional activity of DKK1-100 and DKK1-99 was tested in signaling assays, immune cell activation, and tumor cell killing (**FIGs. 19A-19C**). **FIGs. 22A-22C** showed that antagonism of DKK1 inhibition of WNT in TCF/LEF assays is biphasic. Transient and cell line TCF/LEF reporter rankings were found to match in functional assays (**FIGs. 23A-23B**).

[00242] DKK1 antibodies were tested for binding to LRP6 (**FIG. 24** and **FIGs. 25A-25C**) and for activation of immune cells (**FIGs. 26A-26B** and **FIGs. 27A-27C**). Signaling titration assays were used to identify antagonists (**FIGs. 28A-28D**). Additional immune assays were also performed (**FIGs. 28A-28B**).

[00243] **Example 7: *In vivo* efficacy of DKK1 antibodies**

[00244] Preclinical studies in tumor regression are described in **FIG. 20A**, using a mouse model. Results of *in vivo* efficacy in PC3 tumor regression in SCID mice is shown in **FIG. 20B-20D**.

[00245] Lung tumor organoid killing by immune cells with DKK1 inhibition is shown in **FIG. 30**.

[00246] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED IS:

1. An antibody or antibody fragment comprising a variable domain, heavy chain region (VH), wherein the VH comprises complementarity determining regions CDRH1, CDRH2, and CDRH3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-98 or 919-1332; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 99-196 or 1333-1746; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 197-294 or 1747-2160.

2. The antibody or antibody fragment of claim 1, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.

3. The antibody or antibody fragment of claim 1, wherein the antibody is a single domain antibody.

4. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment.

5. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM.

6. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM.

7. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM.

8. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM.

9. The antibody or antibody fragment of claim 1, wherein the antibody or antibody fragment binds to DKK1.

10. An antibody or antibody fragment comprising a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258.

11. The antibody or antibody fragment of claim 10, wherein the antibody or antibody fragment binds to a spike glycoprotein.

12. The antibody or antibody fragment of claim 10, wherein the antibody or antibody fragment binds to a receptor binding domain of the spike glycoprotein.

13. The antibody or antibody fragment of claim 10, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM.

14. The antibody or antibody fragment of claim 10, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM.

15. The antibody or antibody fragment of claim 10, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM.

16. The antibody or antibody fragment of claim 10, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM.

17. The antibody or antibody fragment of claim 10, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.

18. The antibody or antibody fragment of claim 10, wherein the antibody is a single domain antibody.

19. A nucleic acid composition comprising: a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising complementarity determining regions CDRH1, CDRH2, and CDRH3, and wherein (a) an amino acid sequence of CDRH1 is as set forth in any one of SEQ ID NOs: 1-98 or 919-1332; (b) an amino acid sequence of CDRH2 is as set forth in any one of SEQ ID NOs: 99-196 or 1333-1746; and (c) an amino acid sequence of CDRH3 is as set forth in any one of SEQ ID NOs: 197-294 or 1747-2160; and an excipient.

20. A nucleic acid composition comprising: a) a first nucleic acid encoding a variable domain, heavy chain region (VH) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 295-392, 394-712, or 2164-2258; and an excipient.

21. An antibody or antibody fragment comprising a variable domain, light chain region (VL), wherein the VL comprises complementarity determining regions CDRL1, CDRL2, and CDRL3,

and wherein (a) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 2259-2464; (b) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 2465-2521; and (c) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 2522-2727.

22. The antibody or antibody fragment of claim 21, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab′)2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.

23. The antibody or antibody fragment of claim 21, wherein the antibody is a single domain antibody.

24. The antibody or antibody fragment of claim 21, wherein the antibody or antibody fragment.

25. The antibody or antibody fragment of claim 21, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM.

26. The antibody or antibody fragment of claim 21, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM.

27. The antibody or antibody fragment of claim 21, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM.

28. The antibody or antibody fragment of claim 21, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM.

29. The antibody or antibody fragment of claim 21, wherein the antibody or antibody fragment binds to DKK1.

30. An antibody or antibody fragment comprising a variable domain, light chain region (VL) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 713-918.

31. The antibody or antibody fragment of claim 30, wherein the antibody or antibody fragment binds to a spike glycoprotein.

32. The antibody or antibody fragment of claim 30, wherein the antibody or antibody fragment binds to a receptor binding domain of the spike glycoprotein.

33. The antibody or antibody fragment of claim 30, wherein the antibody or antibody fragment comprises a K_D of less than 50 nM.

34. The antibody or antibody fragment of claim 30, wherein the antibody or antibody fragment comprises a K_D of less than 25 nM.

35. The antibody or antibody fragment of claim 30, wherein the antibody or antibody fragment comprises a K_D of less than 10 nM.

36. The antibody or antibody fragment of claim 30, wherein the antibody or antibody fragment comprises a K_D of less than 5 nM.

37. The antibody or antibody fragment of claim 30, wherein the antibody is a monoclonal antibody, a polyclonal antibody, a bi-specific antibody, a multispecific antibody, a grafted antibody, a human antibody, a humanized antibody, a synthetic antibody, a chimeric antibody, a camelized antibody, a single-chain Fvs (scFv), a single chain antibody, a Fab fragment, a F(ab')2 fragment, a Fd fragment, a Fv fragment, a single-domain antibody, an isolated complementarity determining region (CDR), a diabody, a fragment comprised of only a single monomeric variable domain, disulfide-linked Fvs (sdFv), an intrabody, an anti-idiotypic (anti-Id) antibody, or ab antigen-binding fragments thereof.

38. The antibody or antibody fragment of claim 30, wherein the antibody is a single domain antibody.

39. A nucleic acid composition comprising: a first nucleic acid encoding a variable domain, light chain region (VL) comprising complementarity determining regions CDRL1, CDRL2, and CDRL3, and wherein (a) an amino acid sequence of CDRL1 is as set forth in any one of SEQ ID NOs: 2259-2464; (b) an amino acid sequence of CDRL2 is as set forth in any one of SEQ ID NOs: 2465-2521; and (c) an amino acid sequence of CDRL3 is as set forth in any one of SEQ ID NOs: 2522-2727; and an excipient.

40. A nucleic acid composition comprising: a) a first nucleic acid encoding a variable domain, light chain region (VL) comprising an amino acid sequence at least about 90% identical to a sequence as set forth in any one of SEQ ID NOs: 713-918; and an excipient.

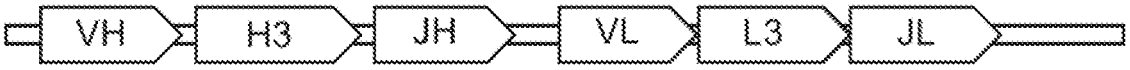


FIG. 1A



FIG. 1B

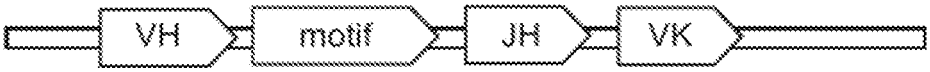




FIG. 2

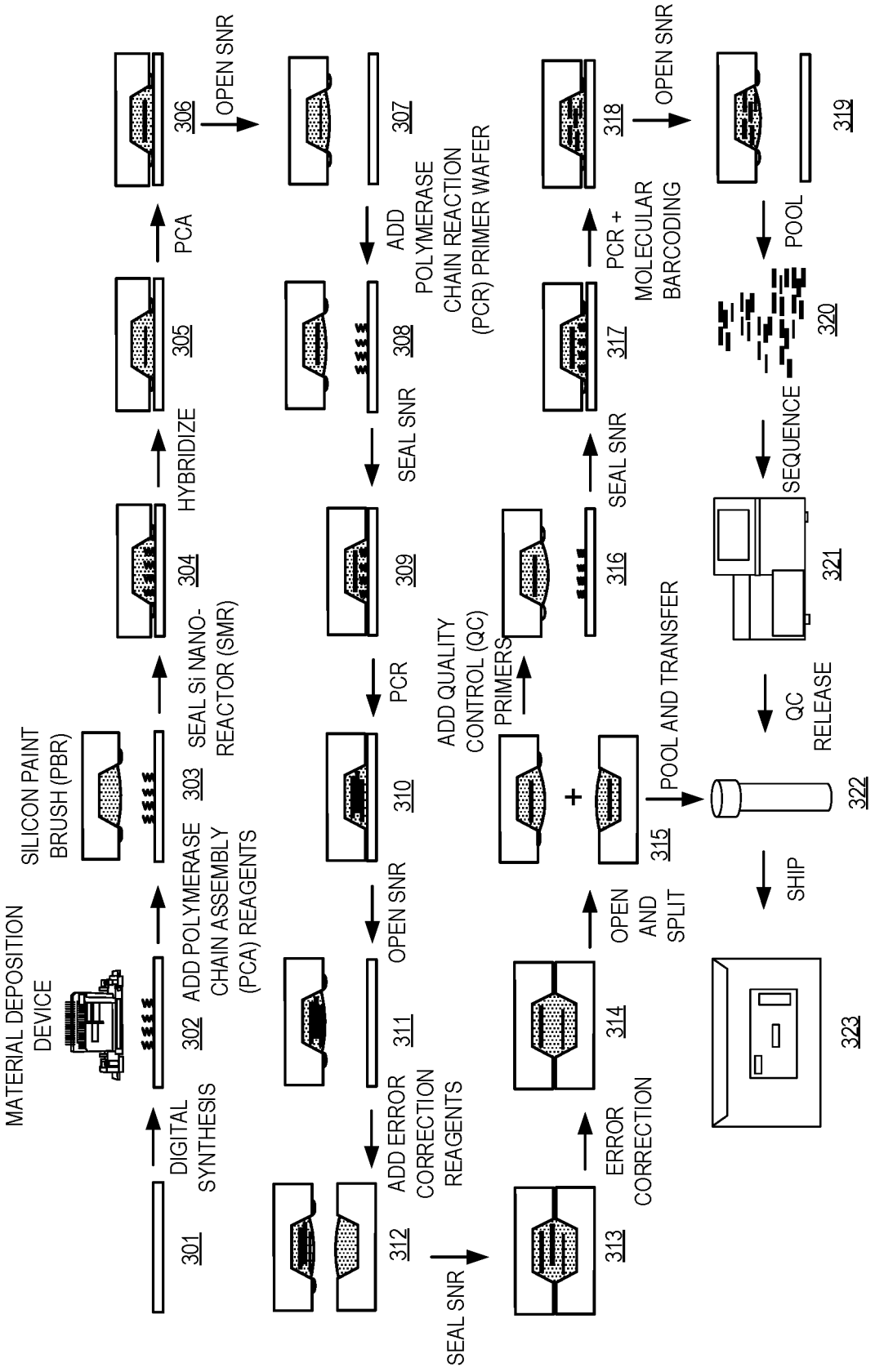

MATERIAL DEPOSITION DEVICE
SILICON PAINT BRUSH (PBR)
301
DIGITAL SYNTHESIS
302
ADD POLYMERASE CHAIN ASSEMBLY (PCA) REAGENTS
303
SEAL Si NANO-REACTOR (SMR)
304
HYBRIDIZE
305
PCA
306
OPEN SNR
307
ADD POLYMERASE CHAIN REACTION (PCR) PRIMER WAFER
308
SEAL SNR
309
PCR
310
OPEN SNR
311
ADD ERROR CORRECTION REAGENTS
312
SEAL SNR
313
ERROR CORRECTION
314
OPEN AND SPLIT
315
POOL AND TRANSFER
316
SEAL SNR
317
PCR + MOLECULAR BARCODING
318
OPEN SNR
319
POOL
320
SEQUENCE
321
QC RELEASE
322
SHIP
323
ADD QUALITY CONTROL (QC) PRIMERS

FIG. 3

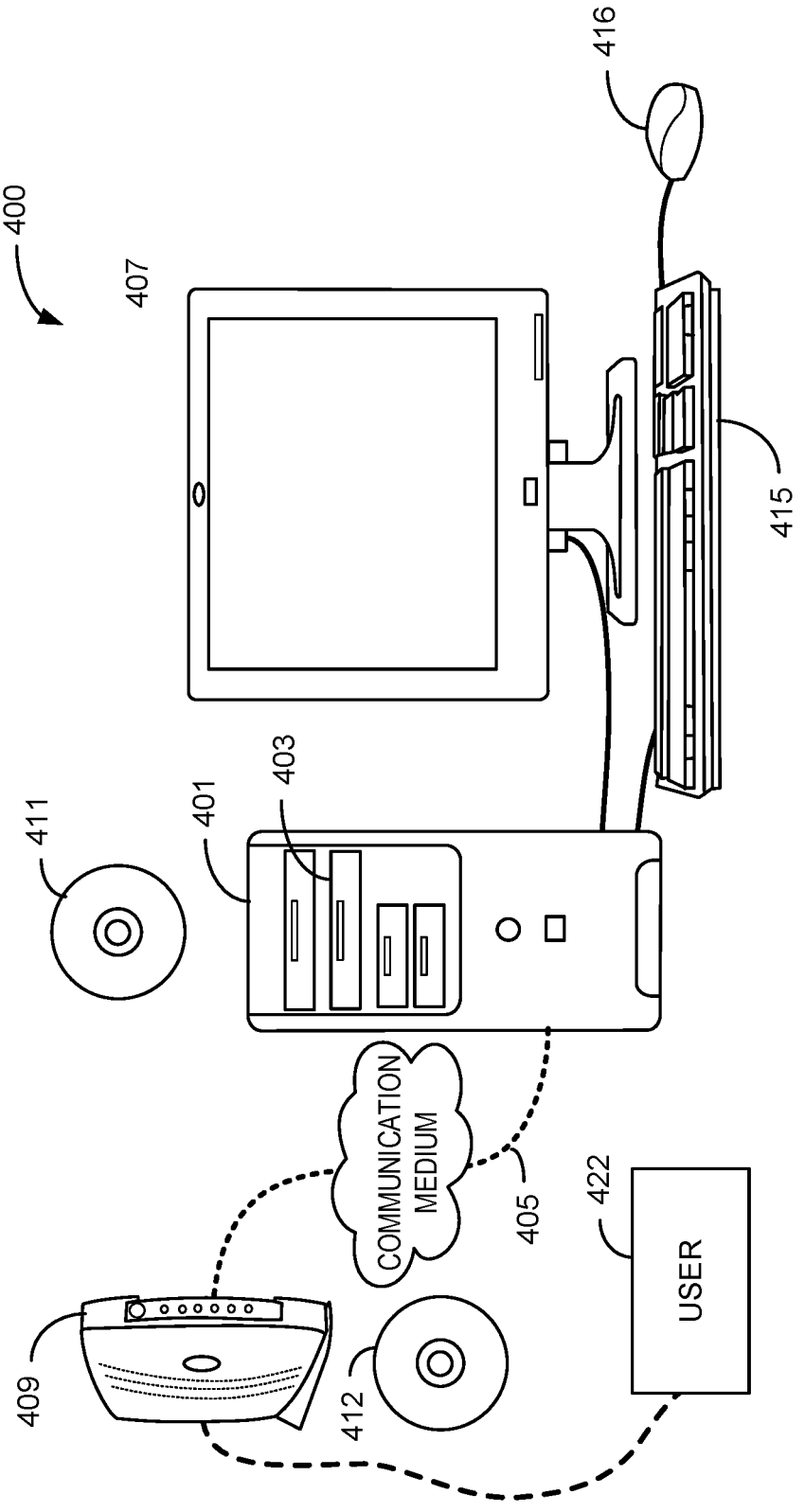

400
407
416
415
403
401
411
COMMUNICATION MEDIUM
405
422
USER
409
412

FIG. 4

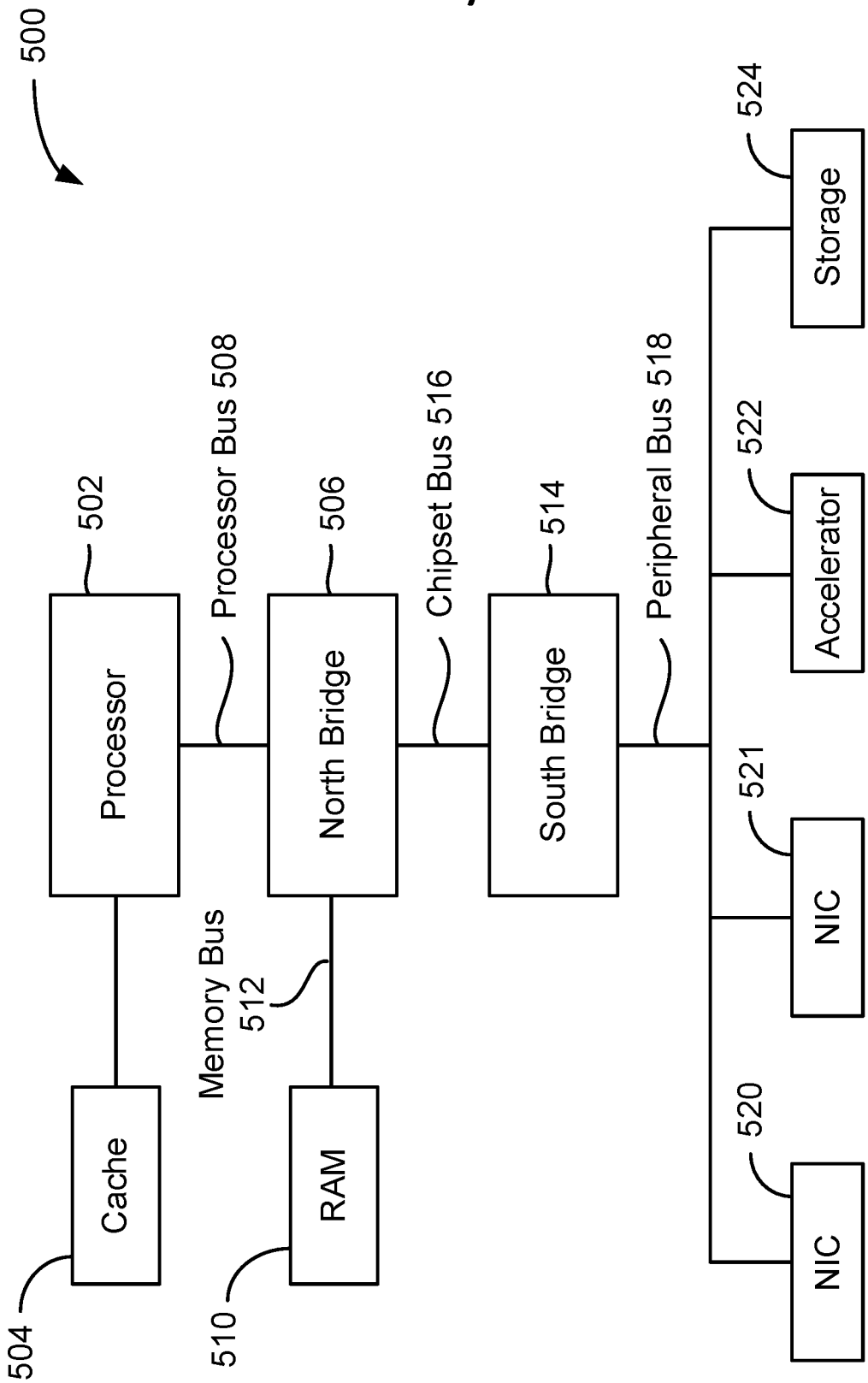

500
Processor
502
Processor Bus 508
North Bridge
506
Chipset Bus 516
South Bridge
514
Peripheral Bus 518
Storage
524
Accelerator
522
NIC
521
NIC
520
Cache
504
Memory Bus
512
RAM
510

FIG. 5

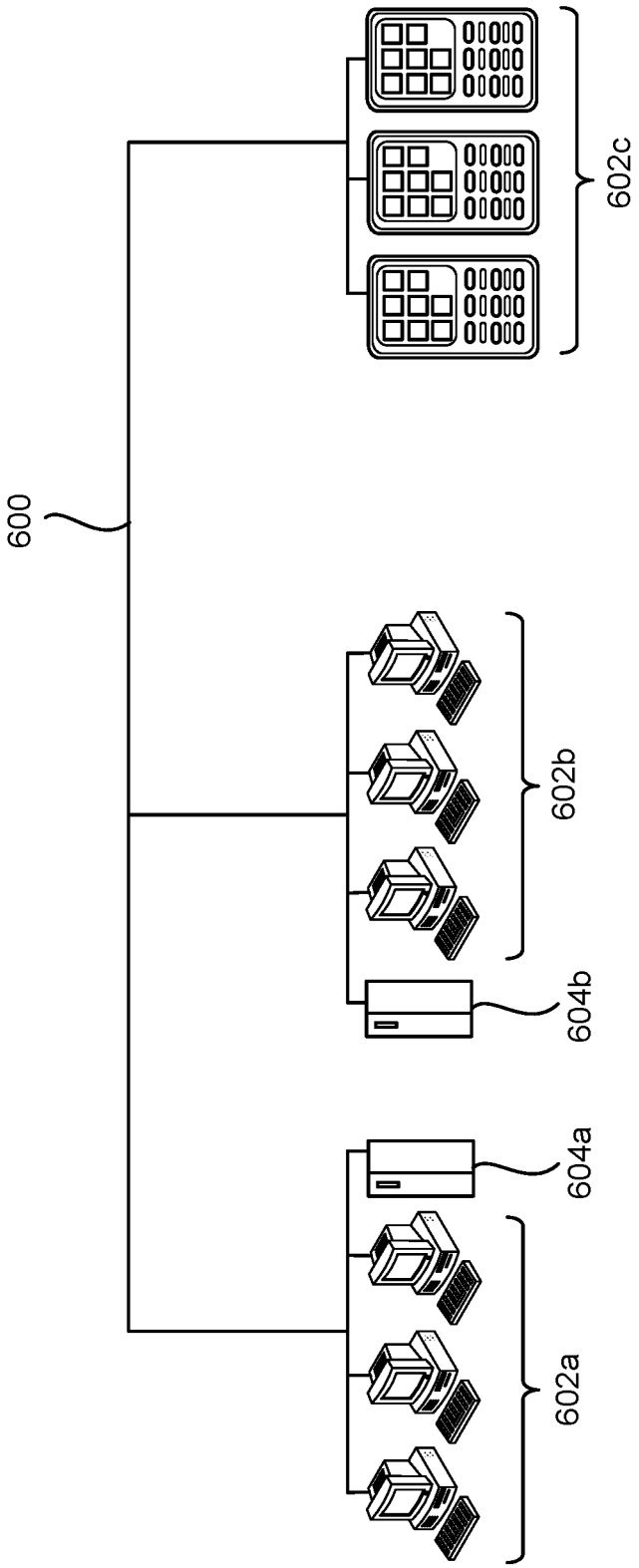


FIG. 6

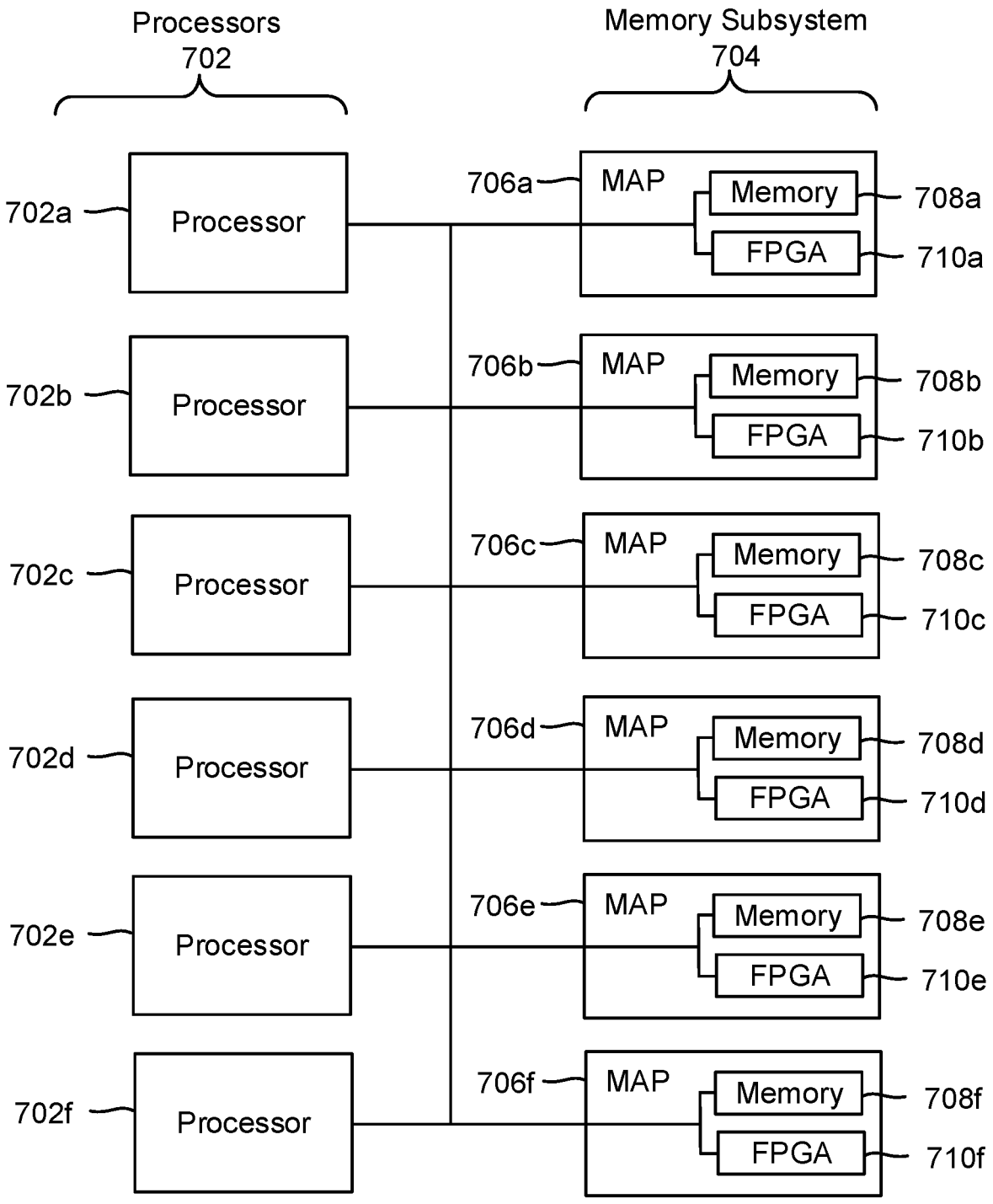

Processors
702
Memory Subsystem
704
702a
Processor
706a
MAP
Memory
708a
FPGA
710a
702b
Processor
706b
MAP
Memory
708b
FPGA
710b
702c
Processor
706c
MAP
Memory
708c
FPGA
710c
702d
Processor
706d
MAP
Memory
708d
FPGA
710d
702e
Processor
706e
MAP
Memory
708e
FPGA
710e
702f
Processor
706f
MAP
Memory
708f
FPGA
710f

FIG. 7

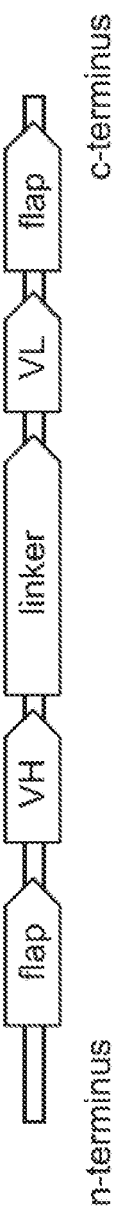


FIG. 8A



FIG. 8B



FIG. 8C

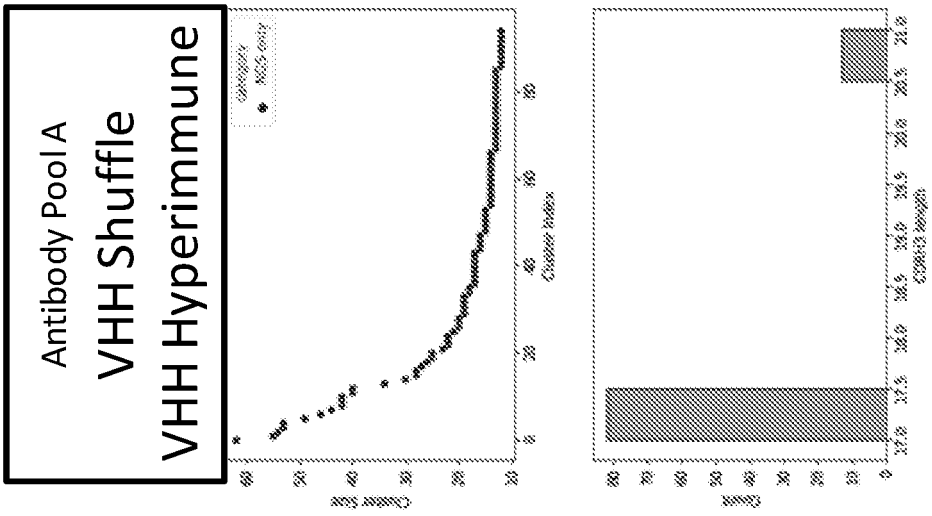


FIG. 9A

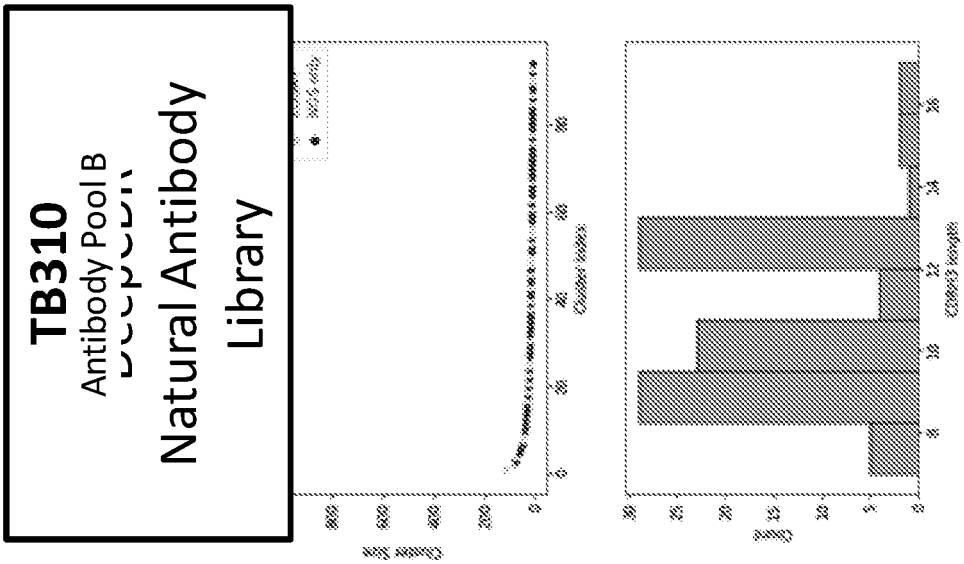


FIG. 9B

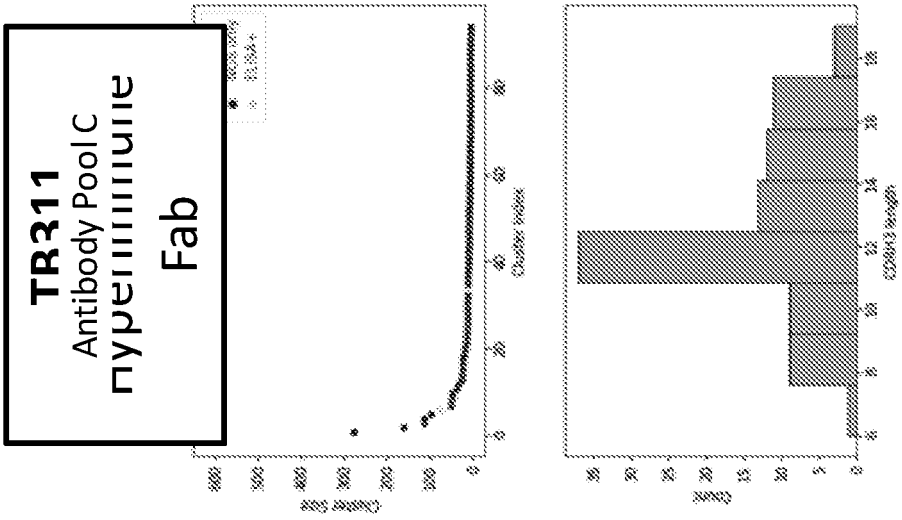


FIG. 9C

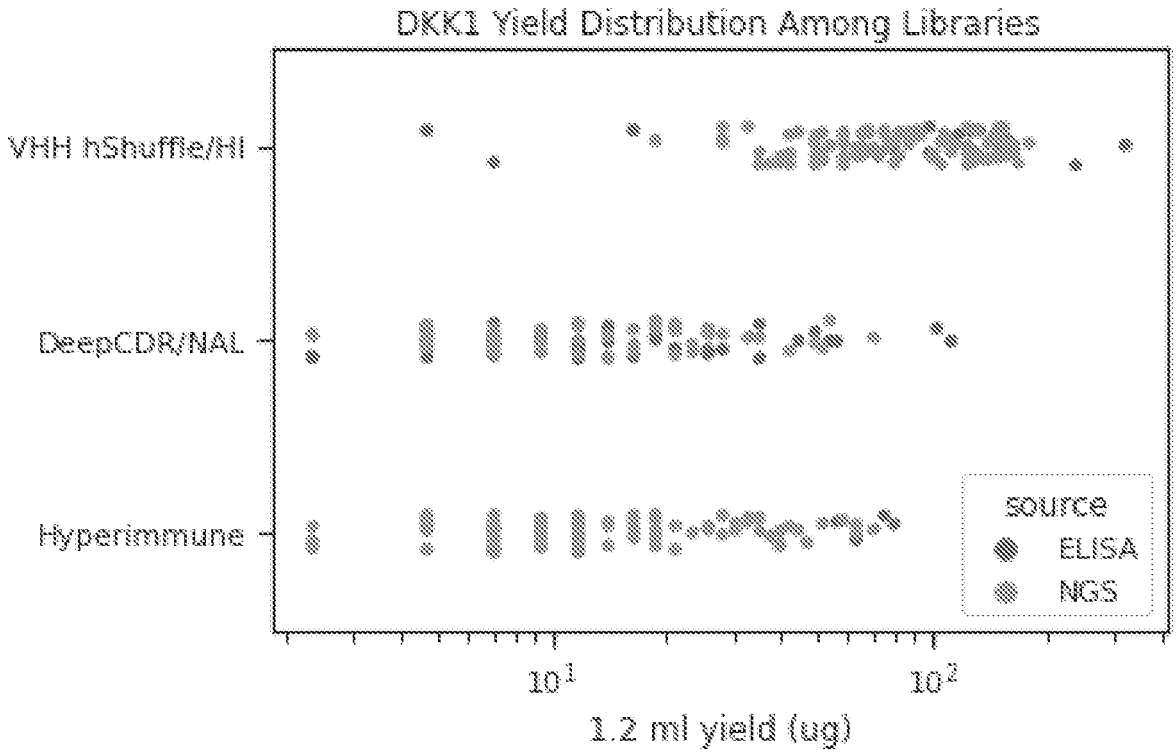


FIG. 10A

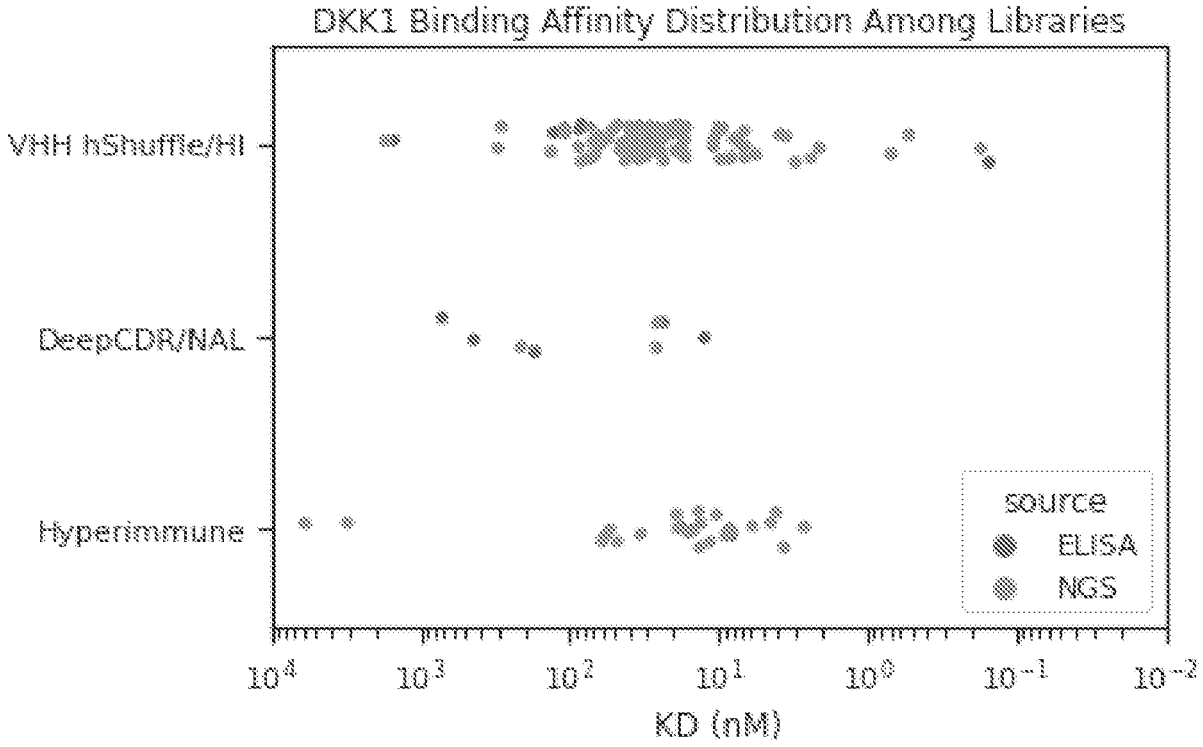


FIG. 10B

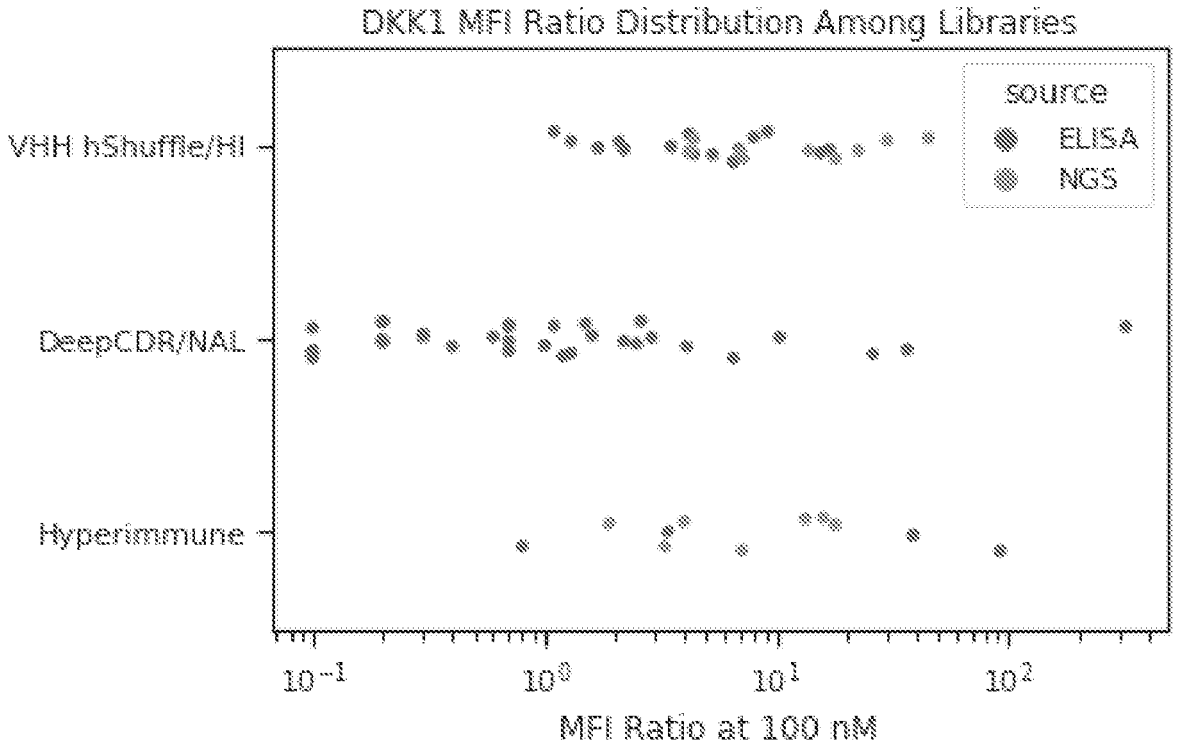

DKK1 MFI Ratio Distribution Among Libraries
source
ELISA
NGS
VHH hShuffle/HI
DeepCDR/NAL
Hyperimmune
10^{-1}
10^{0}
10^{1}
10^{2}
MFI Ratio at 100 nM

FIG. 10C

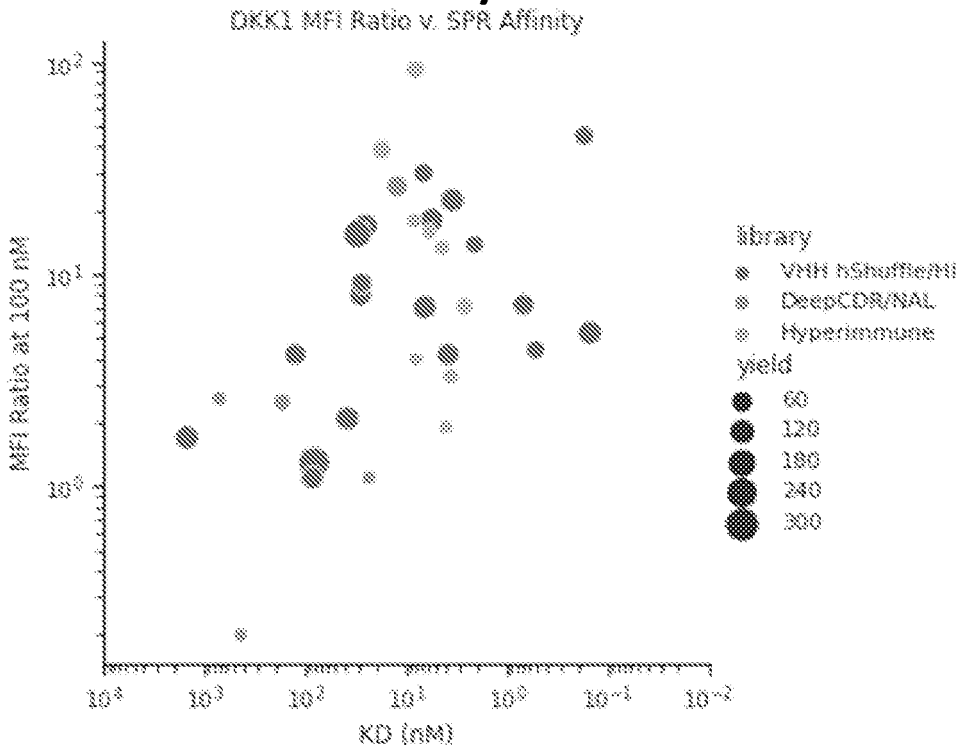


FIG. 11A

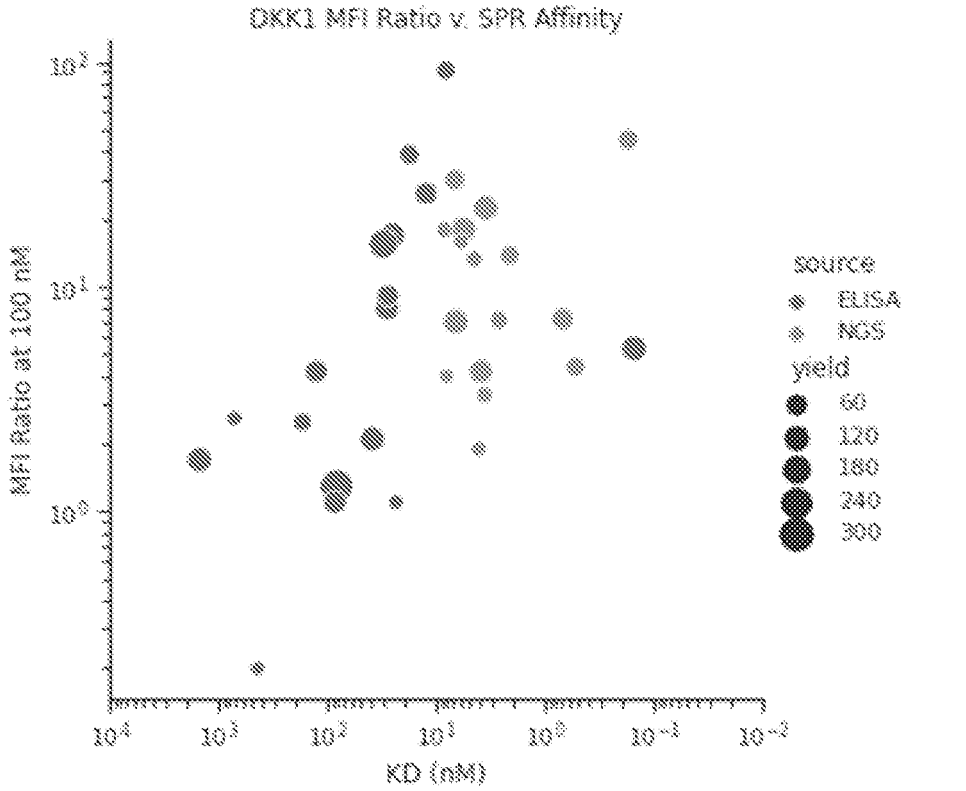


FIG. 11B

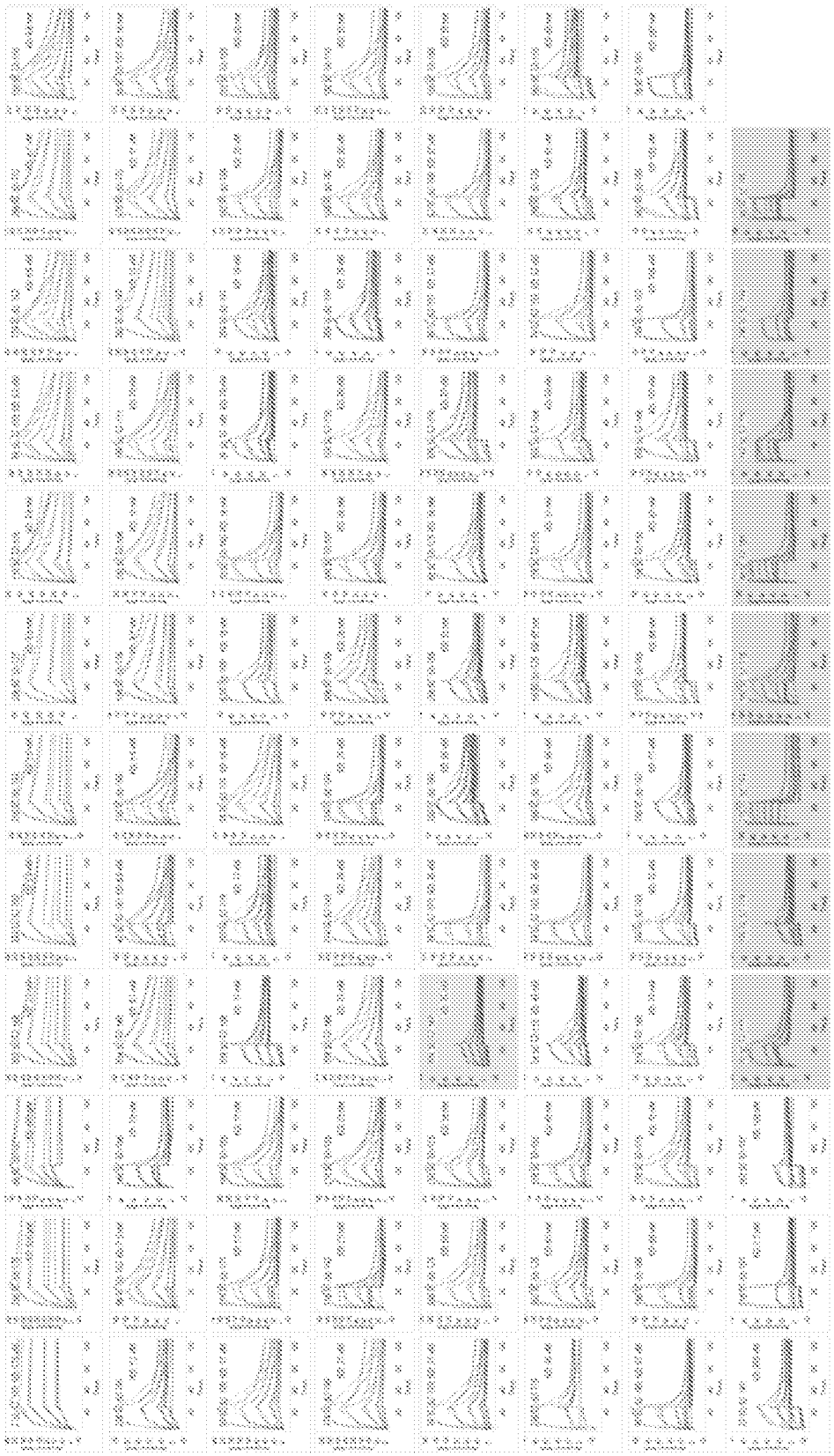


FIG. 12A

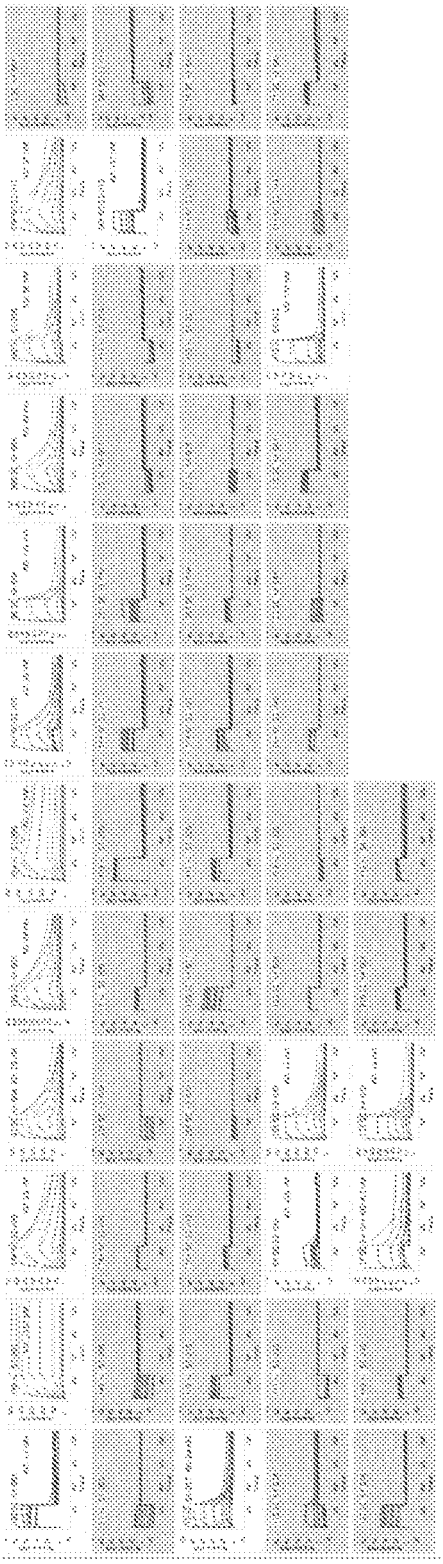


FIG. 12B

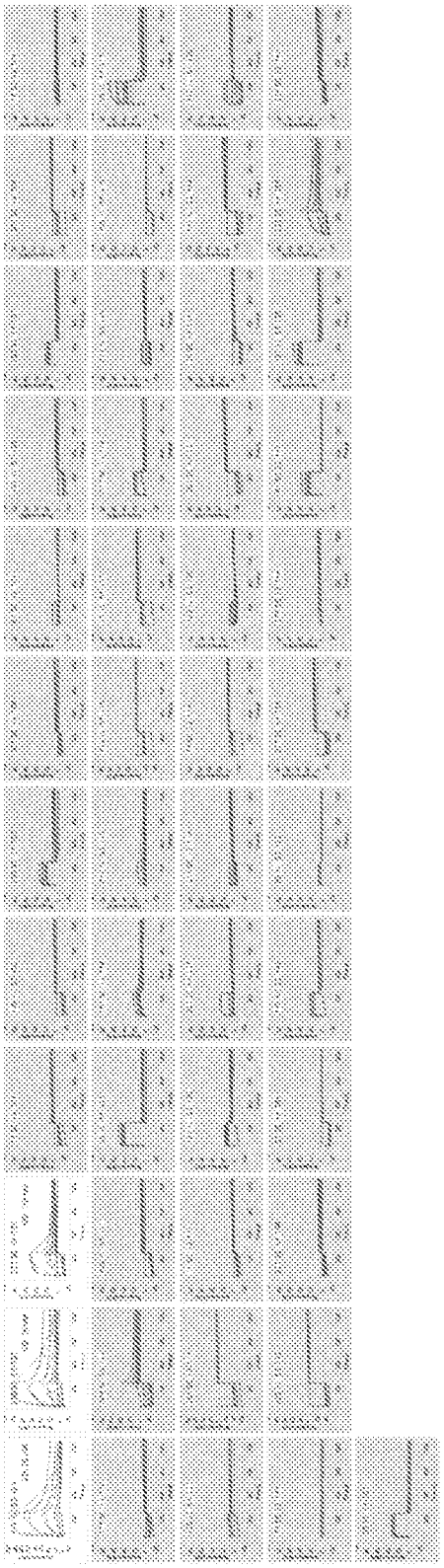


FIG. 12C

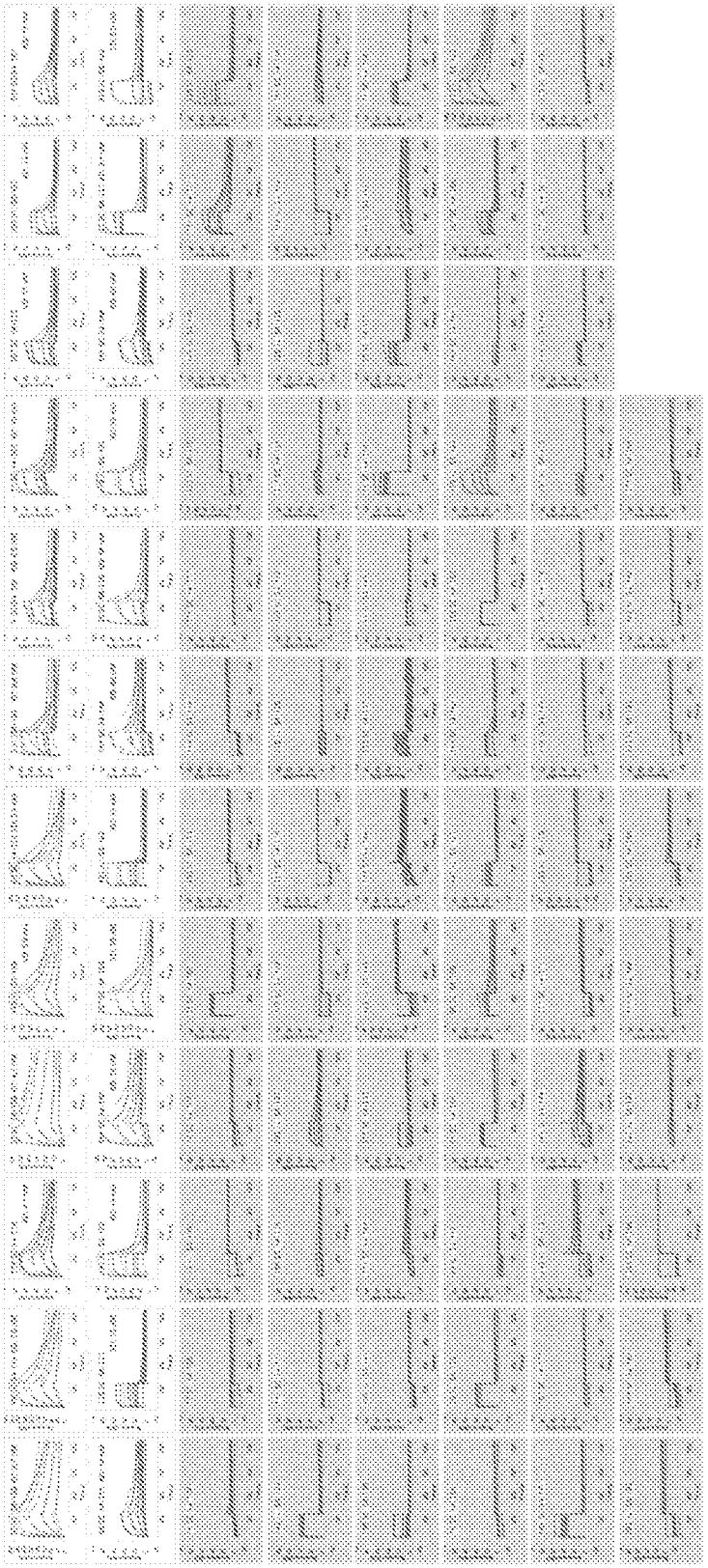


FIG. 12D

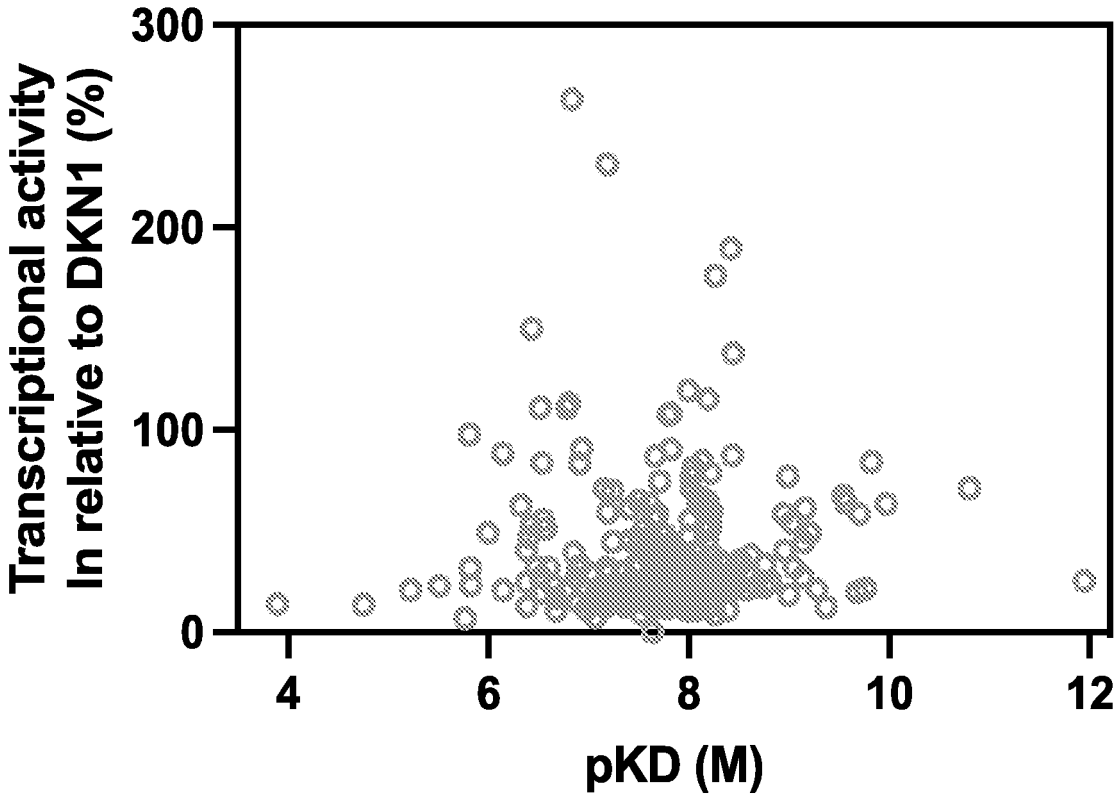

Transcriptional activity
In relative to DKN1 (%)
300
200
100
0
4
6
8
10
12
pKD (M)

FIG. 13

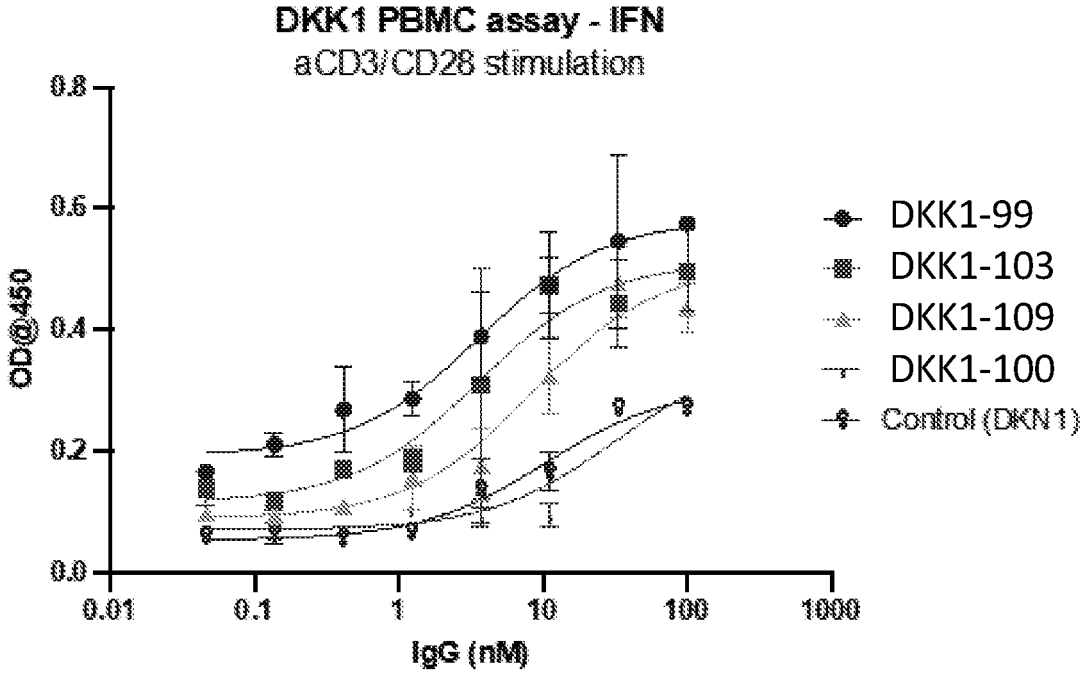


FIG. 14A

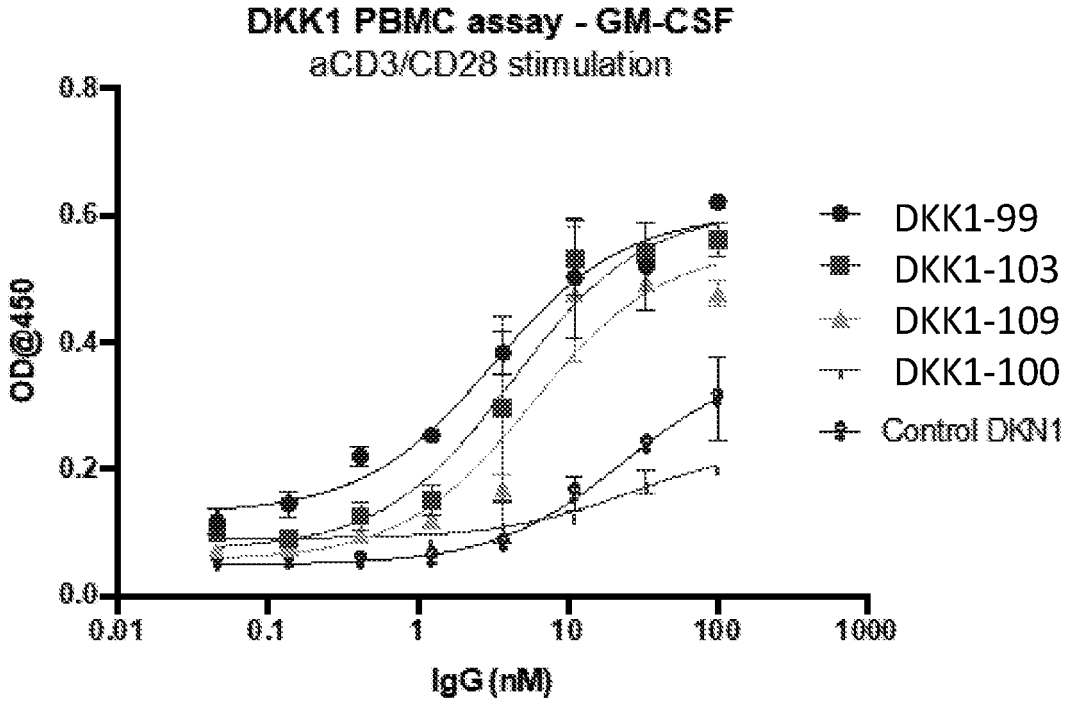


FIG. 14B

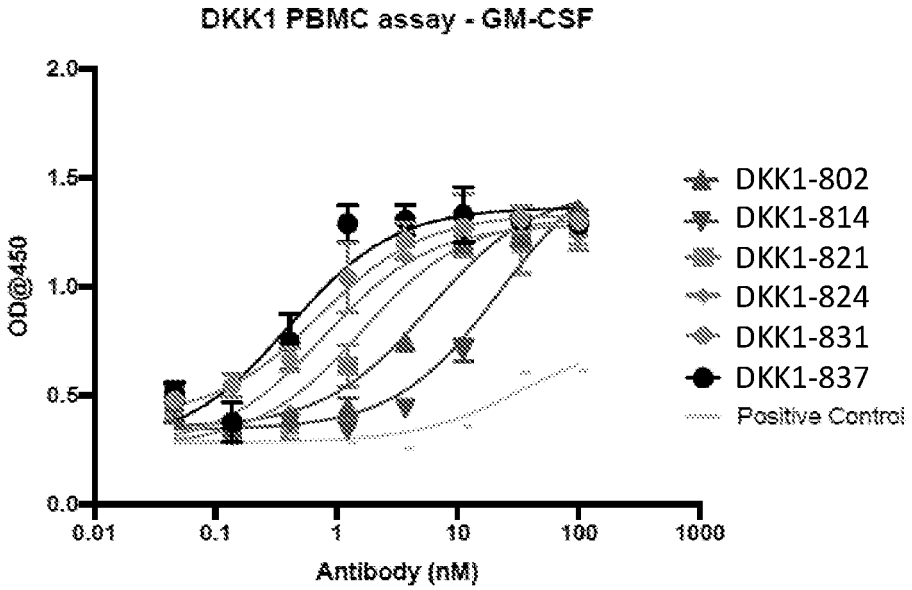


FIG. 14C

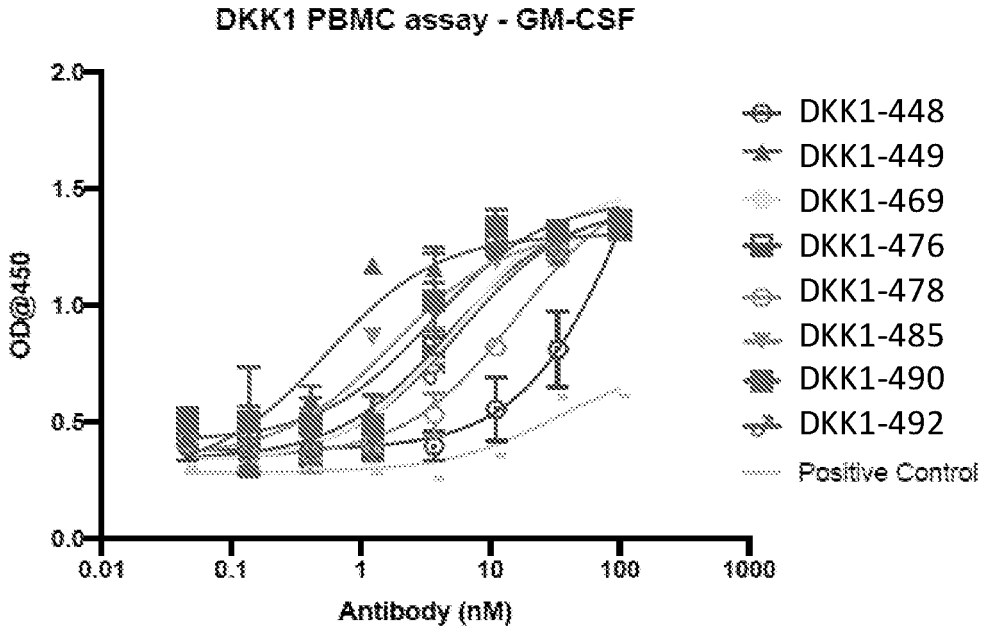


FIG. 14D

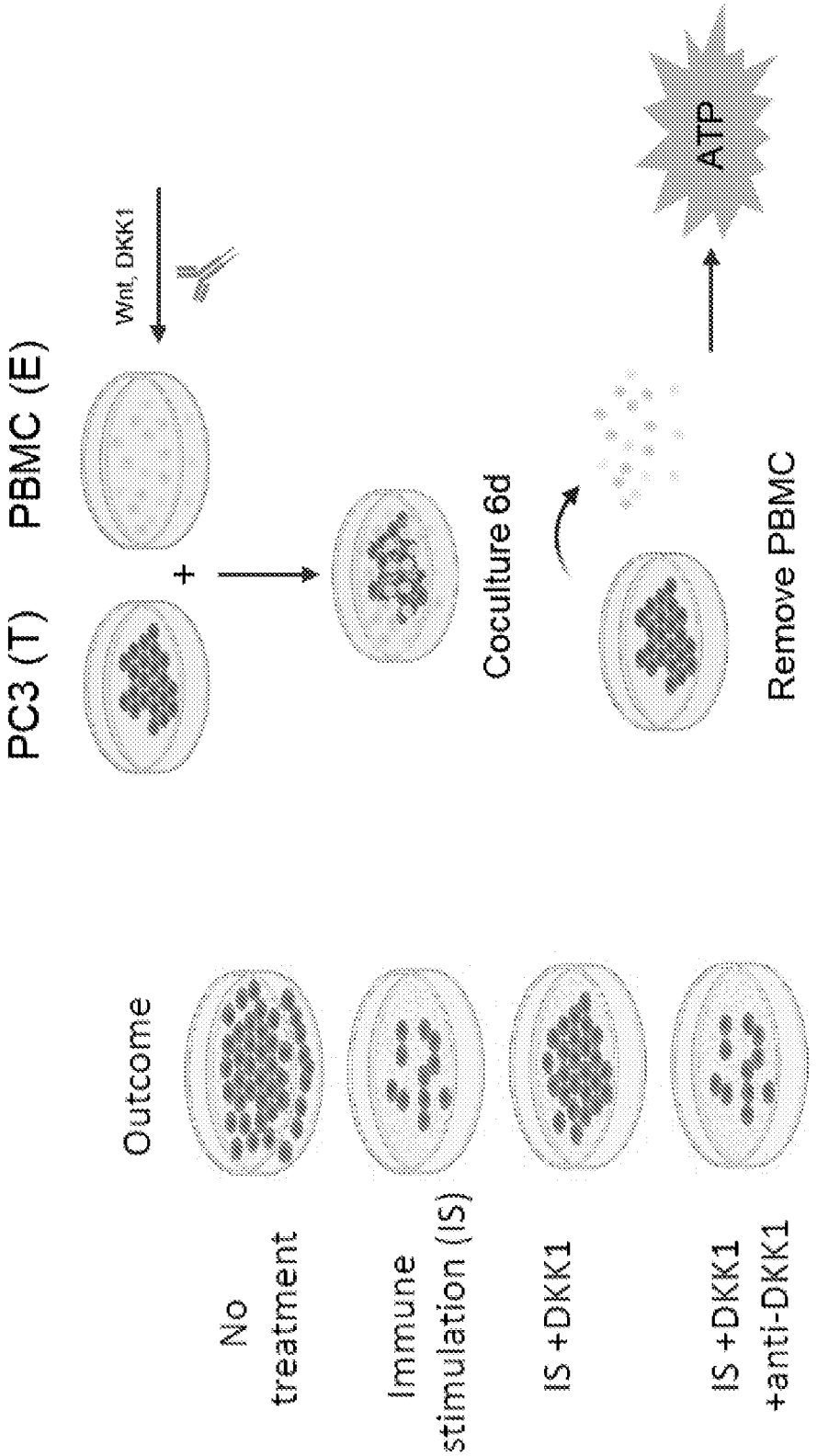

PC3 (T)
PBMC (E)
Wnt, DKK1
+
Coculture 6d
ATP
Remove PBMC
Outcome
No treatment
Immune stimulation (IS)
IS +DKK1
IS +DKK1 +anti-DKK1
Readout: PC3 ATP

FIG. 15A

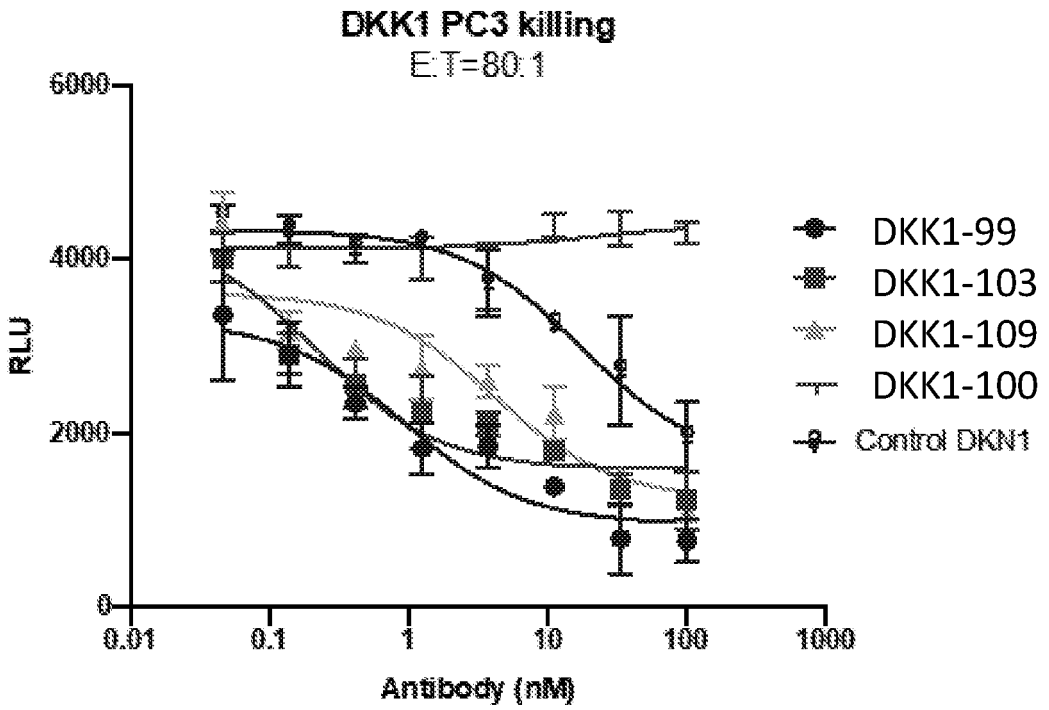


FIG. 15B

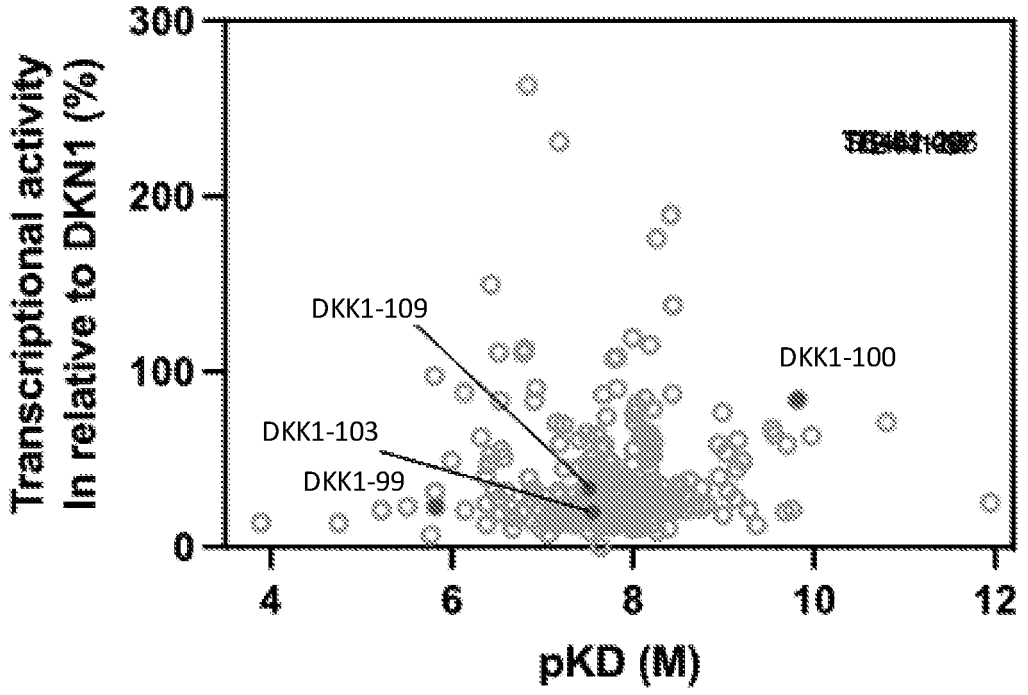


FIG. 15C

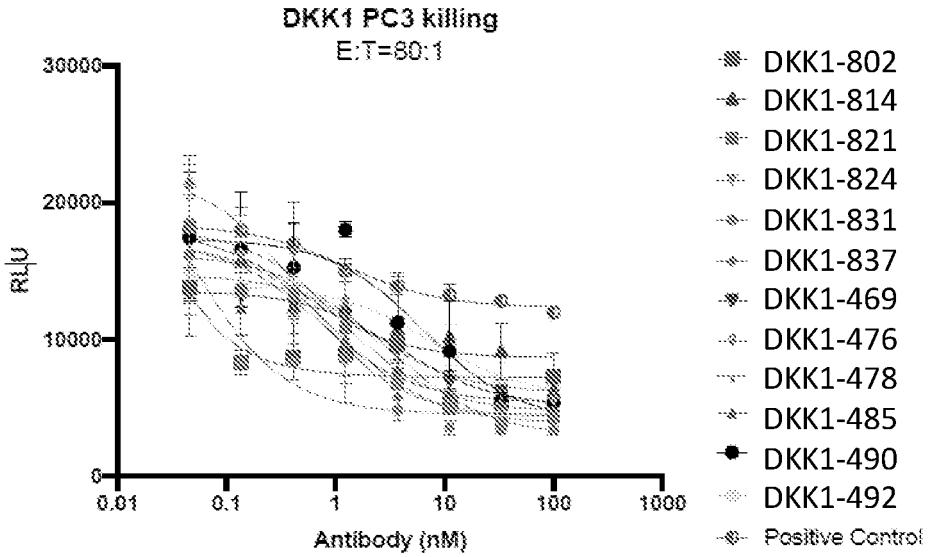


FIG. 15D

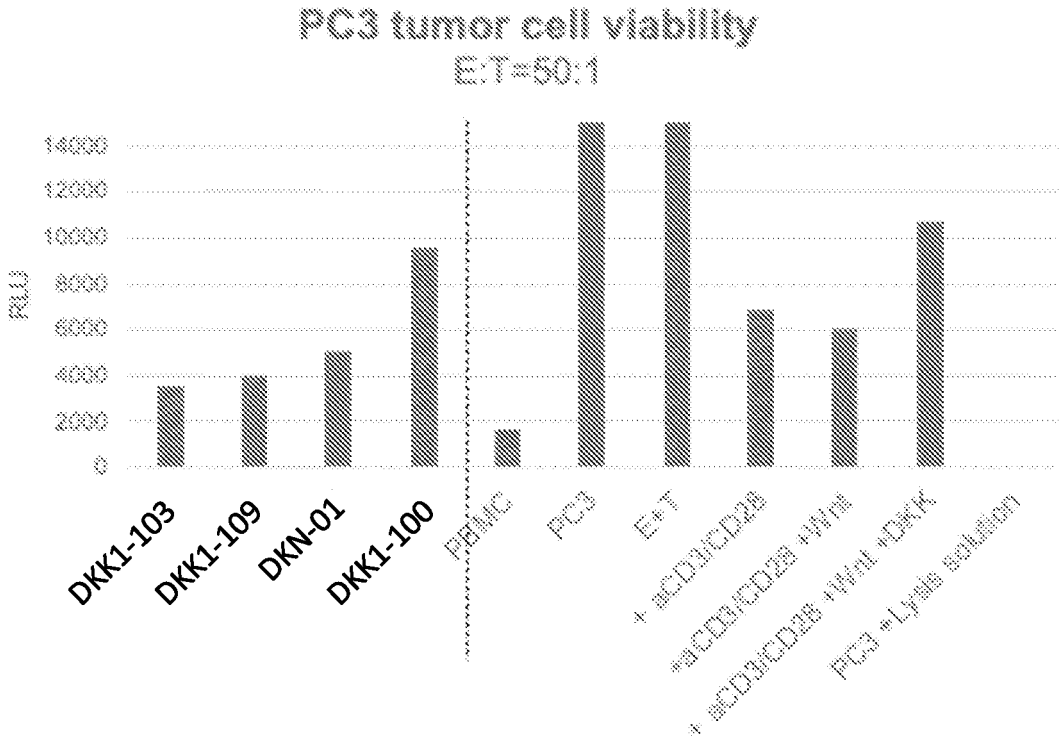


FIG. 15E

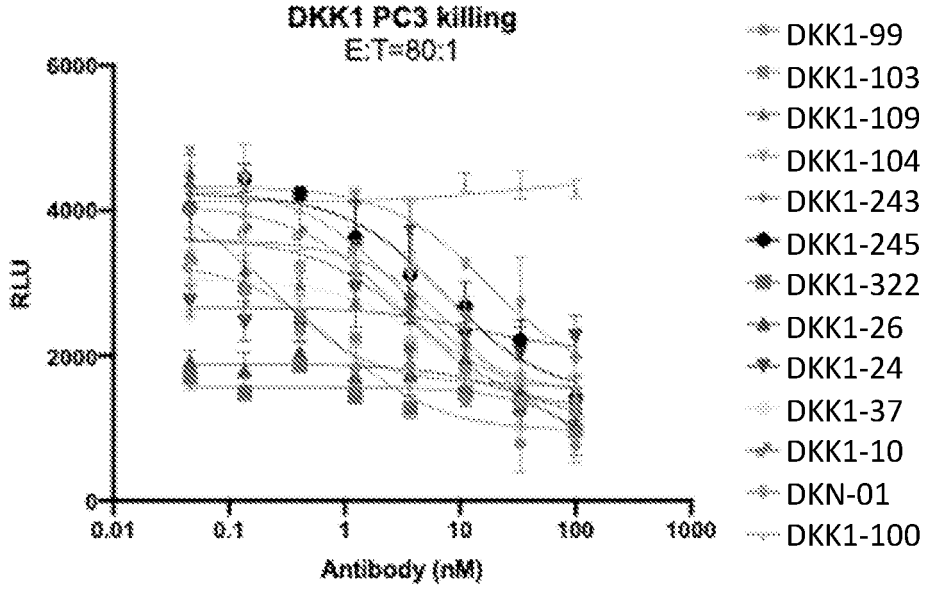


FIG. 15F

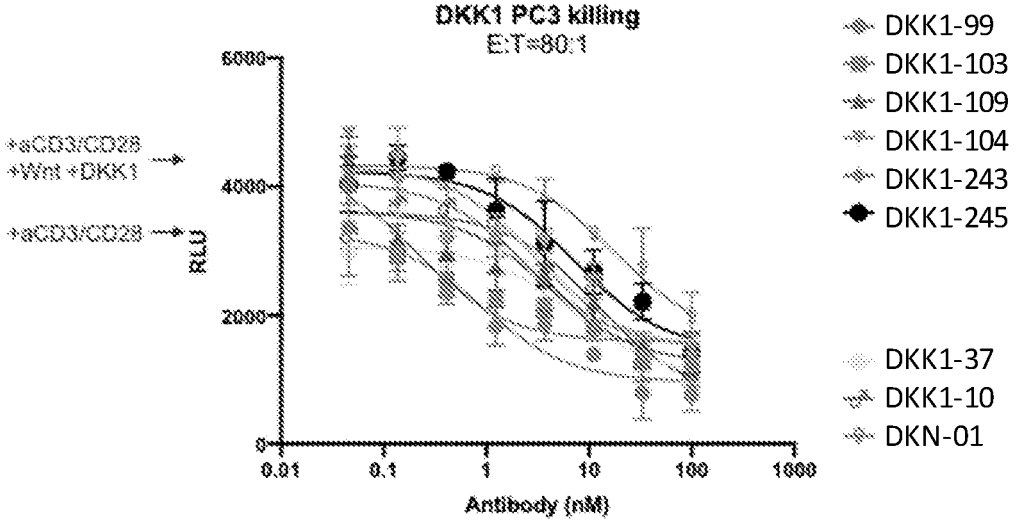


FIG. 15G

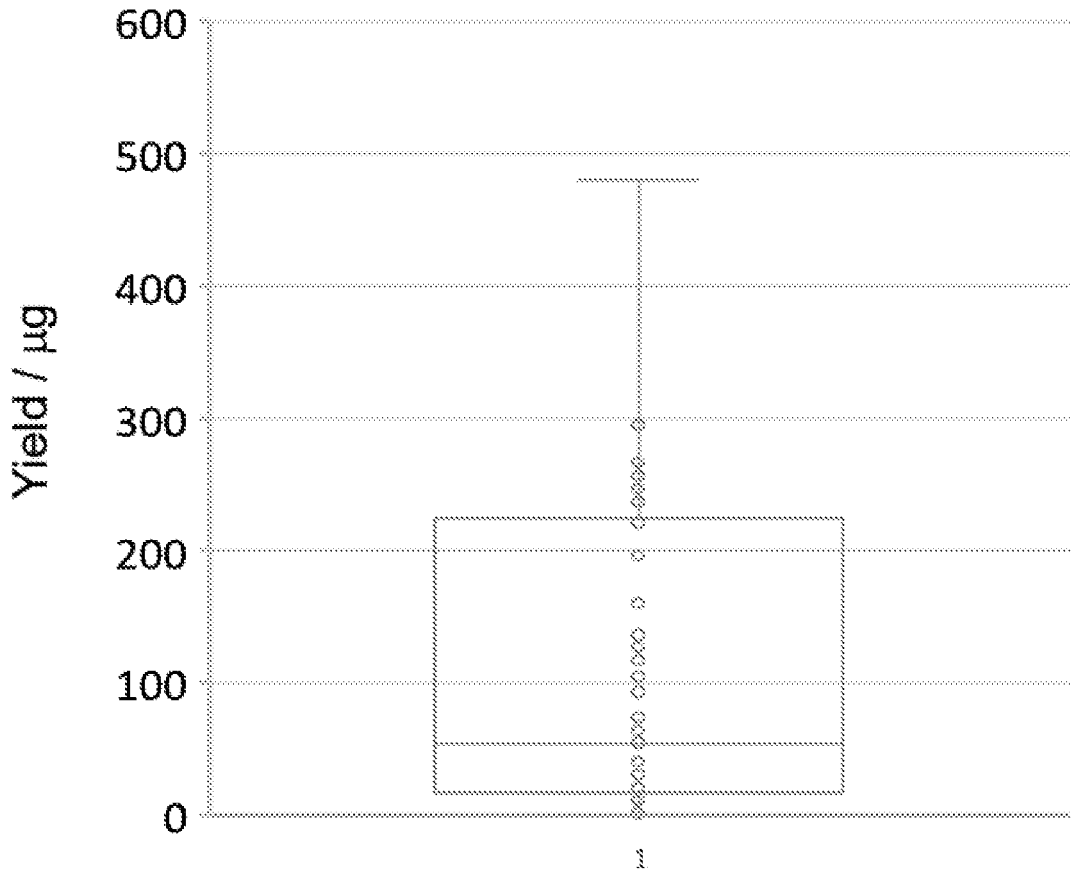


FIG. 16

Bins	ID	1 DKK1-24	1 DKK1-825	1 DKK1-28	1 DKN-01	2 DKK1-37	2 DKK1-109	2 DKK1-93	2 DKK1-100	2 DKK1-245	2 DKK1-99	2 DKK1-103	2 DKK1-10	2 DKK1-243
1	DKK1-24													
1	DKK1-825													
1	DKK1-28													
1	DKN-01													
2	DKK1-37													
2	DKK1-109													
2	DKK1-93													
2	DKK1-100													
2	DKK1-245													
2	DKK1-99													
2	DKK1-103													
2	DKK1-10													
2	DKK1-243													

FIG. 17A

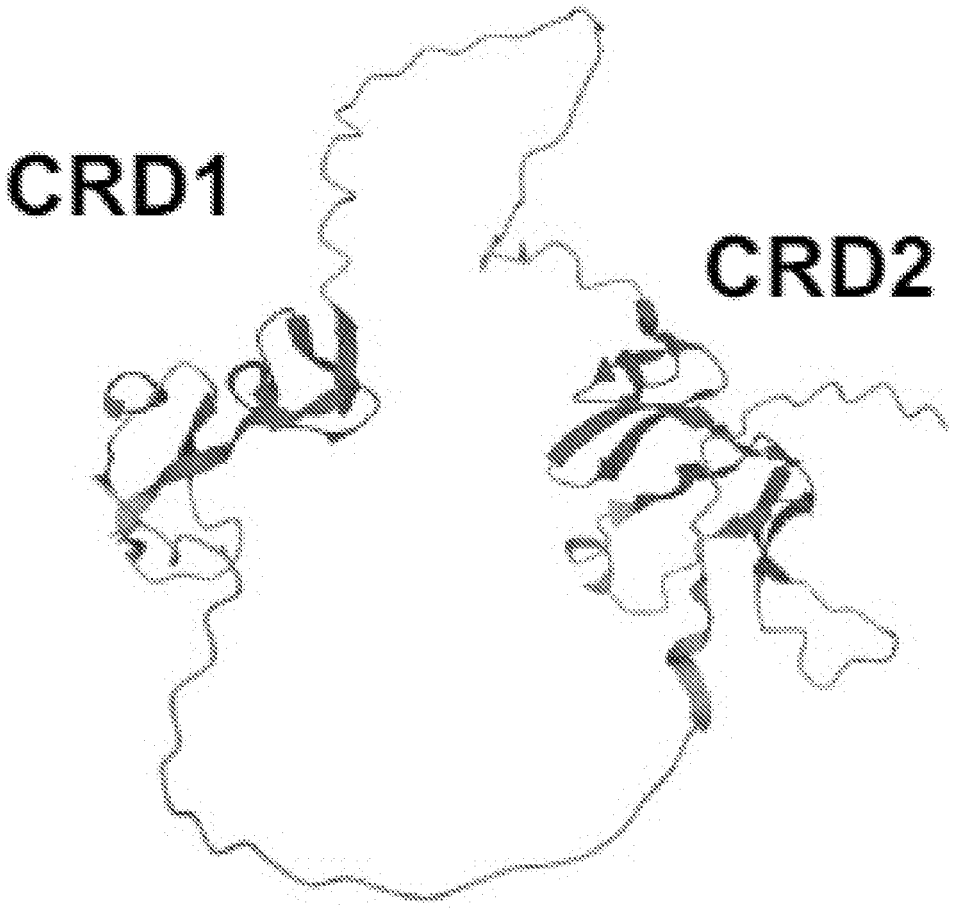


FIG. 17B

Name	DKK1 CRD1	DKK1 CRD2	R&D DKK1
	K_D (M)	K_D (M)	K_D (M)
DKK1-99 IgG2	5.22E-06	N/A	2.49E-07
DKK1-103 IgG2	3.71E-09	N/A	7.35E-08
DKK1-109 IgG2	9.29E-09	N/A	4.46E-08
DKK1-100 IgG2	N/A	2.08E-10	7.73E-10
Positive Control	N/A	7.91E-10	9.77E-10
DKK1-805	N/A	3.25E-09	5.22E-08
DKK1-820	N/A	7.54E-09	8.74E-09
DKK1-821	N/A	N/A	3.65E-08
DKK1-824	5.59E-09	1.45E-05	5.58E-08
DKK1-825	N/A	6.90E-10	6.36E-11
DKK1-830	N/A	1.69E-10	3.22E-11
DKK1-831	2.49E-08	N/A	1.09E-07
DKK1-837	2.26E-08	N/A	4.21E-08
DKK1-839	N/A	1.68E-11	4.94E-12
DKK1-739	N/A	4.43E-11	1.57E-09
DKK1-744	N/A	1.49E-09	3.14E-11
DKK1-448	N/A	2.57E-09	8.23E-08
DKK1-449	9.22E-08	N/A	1.41E-07
DKK1-473	N/A	1.09E-09	1.61E-09
DKK1-477	N/A	2.77E-10	1.73E-09
DKK1-478	N/A	7.08E-09	2.75E-09
DKK1-481	N/A	N/A	1.12E-08
DKK1-485	2.79E-09	N/A	1.56E-08

FIG. 17C

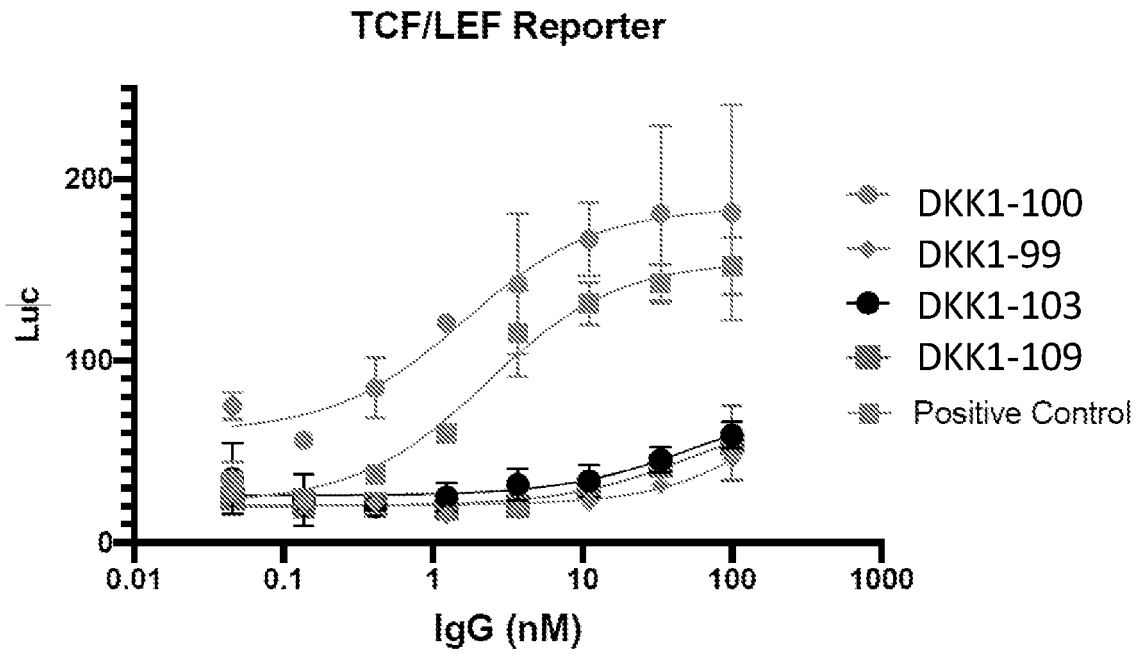


FIG. 18A

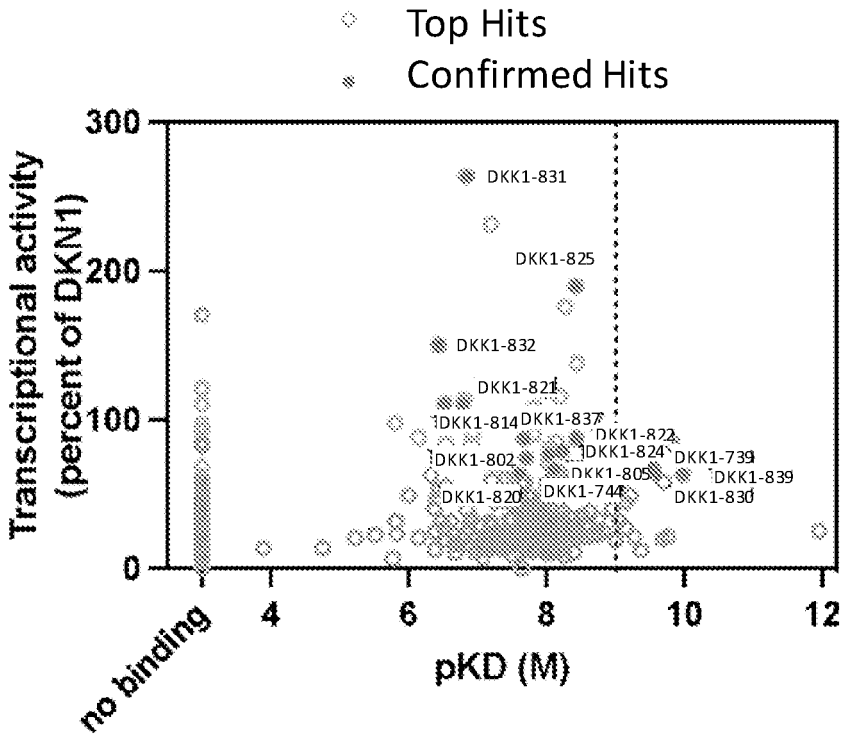


FIG. 18B

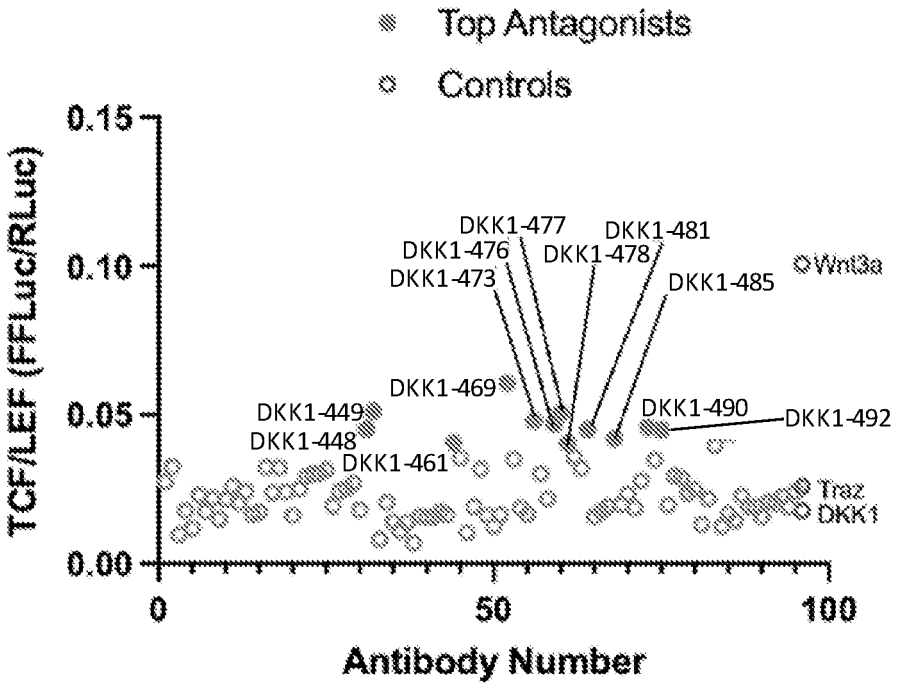


FIG. 18C

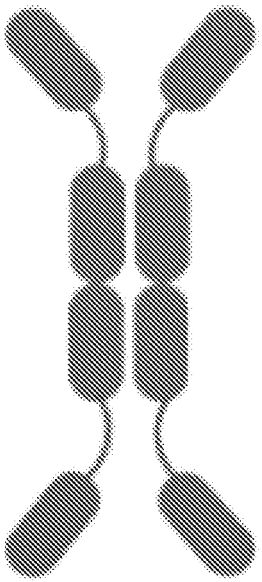


FIG. 19A

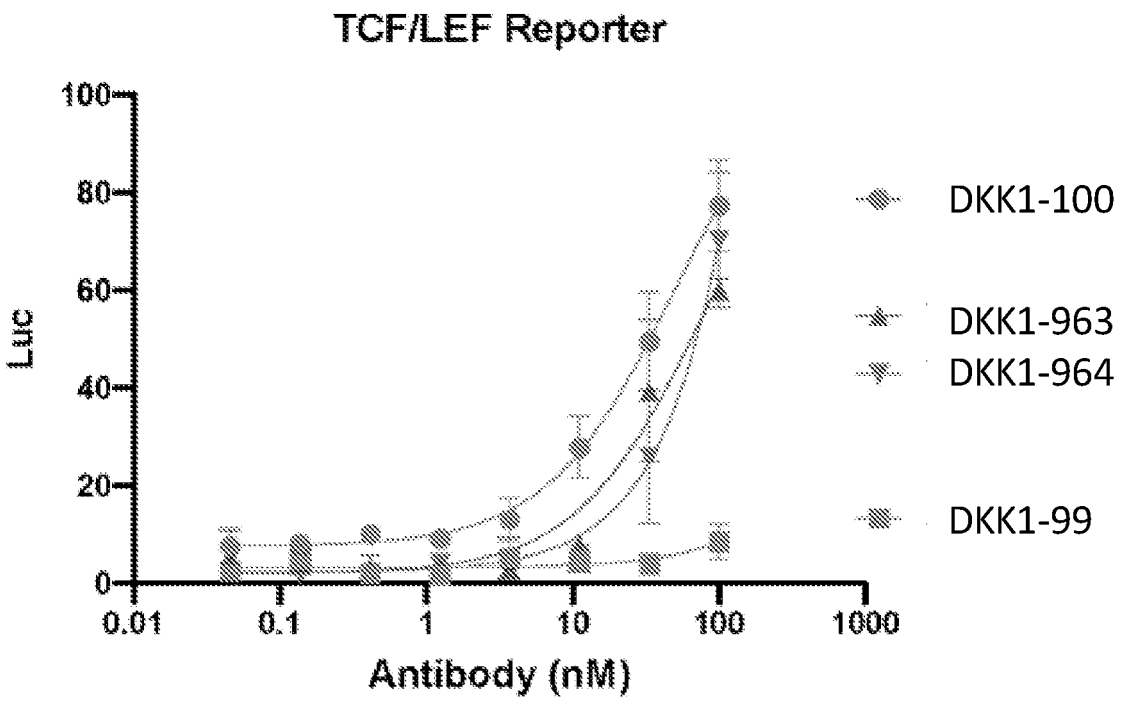


FIG. 19B

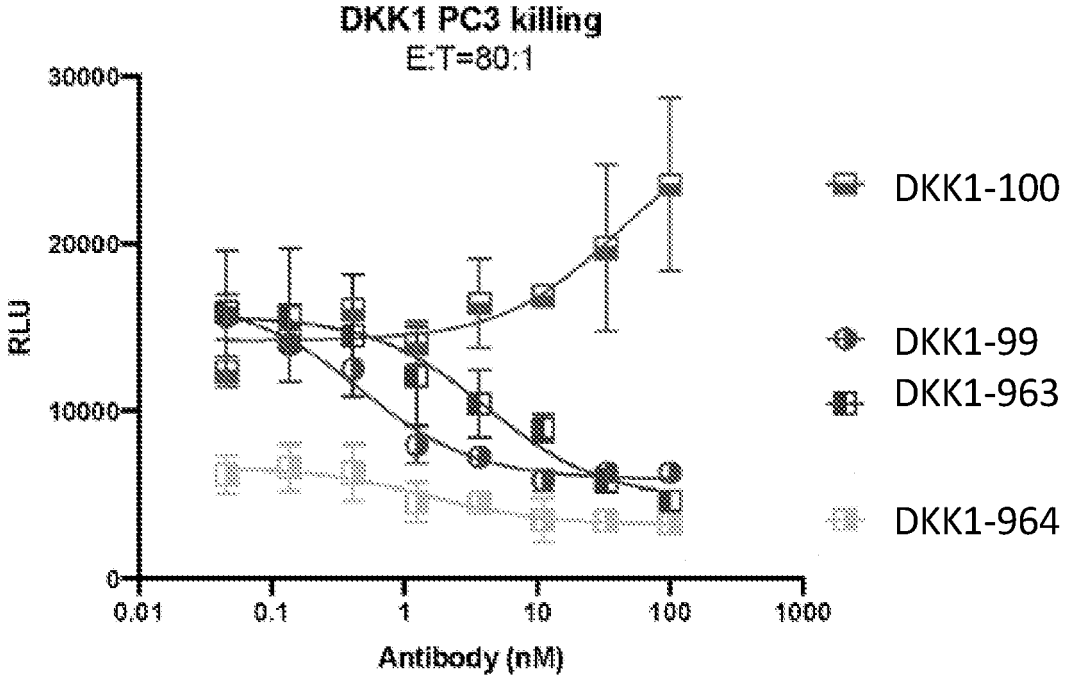


FIG. 19C

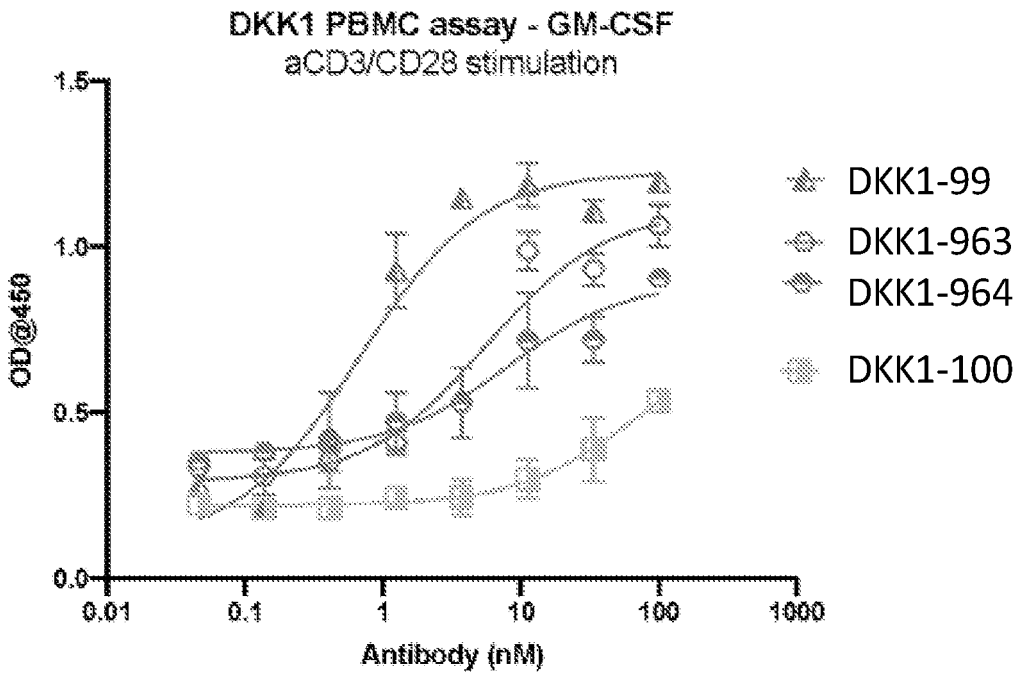

DKK1 PBMC assay - GM-CSF
aCD3/CD28 stimulation
OD@450
1.5
1.0
0.5
0.0
0.01
0.1
1
10
100
1000
Antibody (nM)
DKK1-99
DKK1-963
DKK1-964
DKK1-100

FIG. 19D

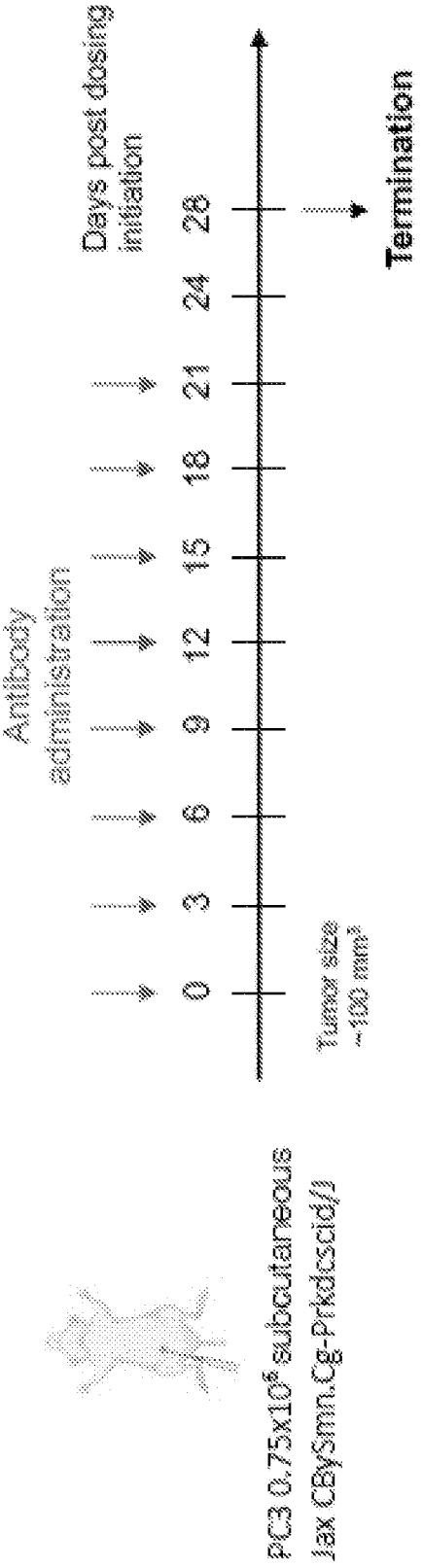

Days post dosing initiation
0
3
6
9
12
15
18
21
24
28
Antibody administration
Termination
Tumor size ~100 mm³
PC3 0.75x10⁶ subcutaneous
Jax CBySmn.Cg-Prkdcscid/J

FIG. 20A

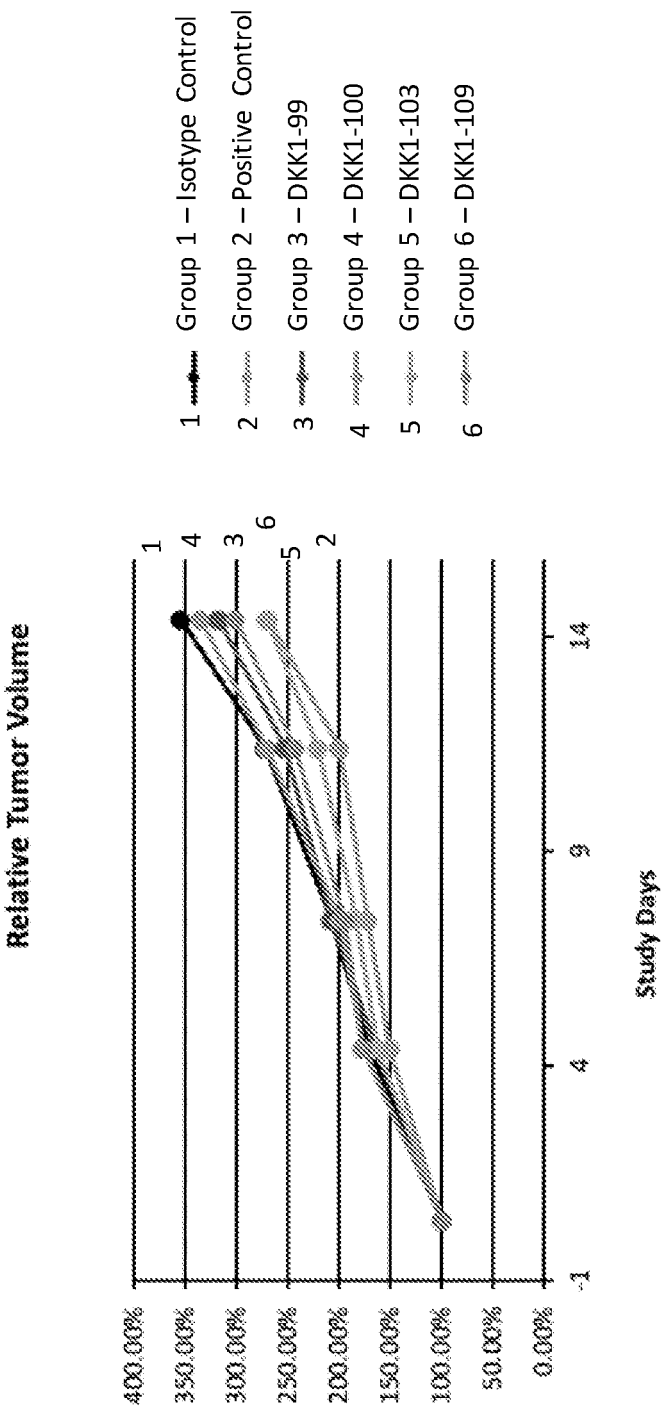

Relative Tumor Volume
400.00%
350.00%
300.00%
250.00%
200.00%
150.00%
100.00%
50.00%
0.00%
-1
4
9
14
Study Days
1
2
3
4
5
6
1 Group 1 – Isotype Control
2 Group 2 – Positive Control
3 Group 3 – DKK1-99
4 Group 4 – DKK1-100
5 Group 5 – DKK1-103
6 Group 6 – DKK1-109

FIG. 20B

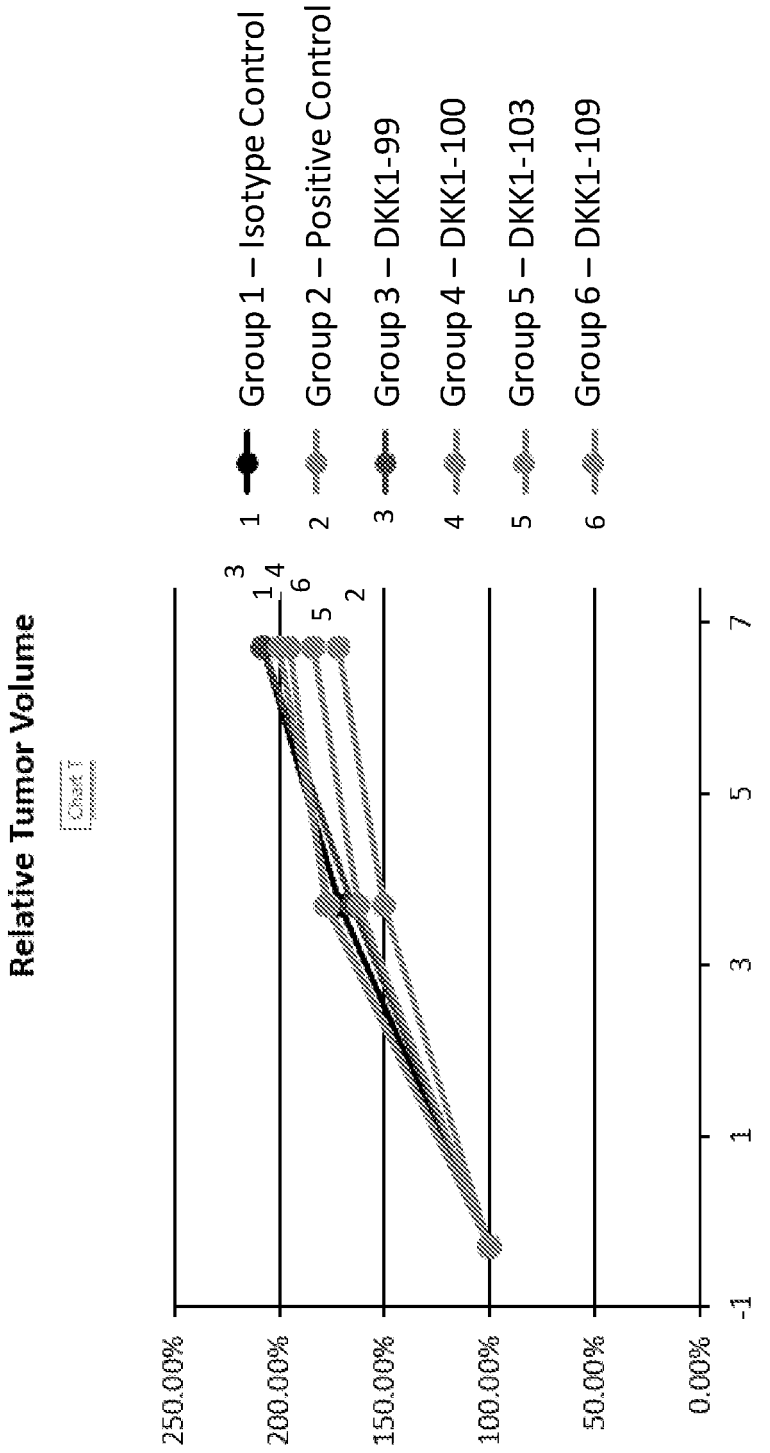

Relative Tumor Volume
Chart 1
250.00%
200.00%
150.00%
100.00%
50.00%
0.00%
-1
1
3
5
7
Study Days
1 Group 1 – Isotype Control
2 Group 2 – Positive Control
3 Group 3 – DKK1-99
4 Group 4 – DKK1-100
5 Group 5 – DKK1-103
6 Group 6 – DKK1-109

FIG. 20C

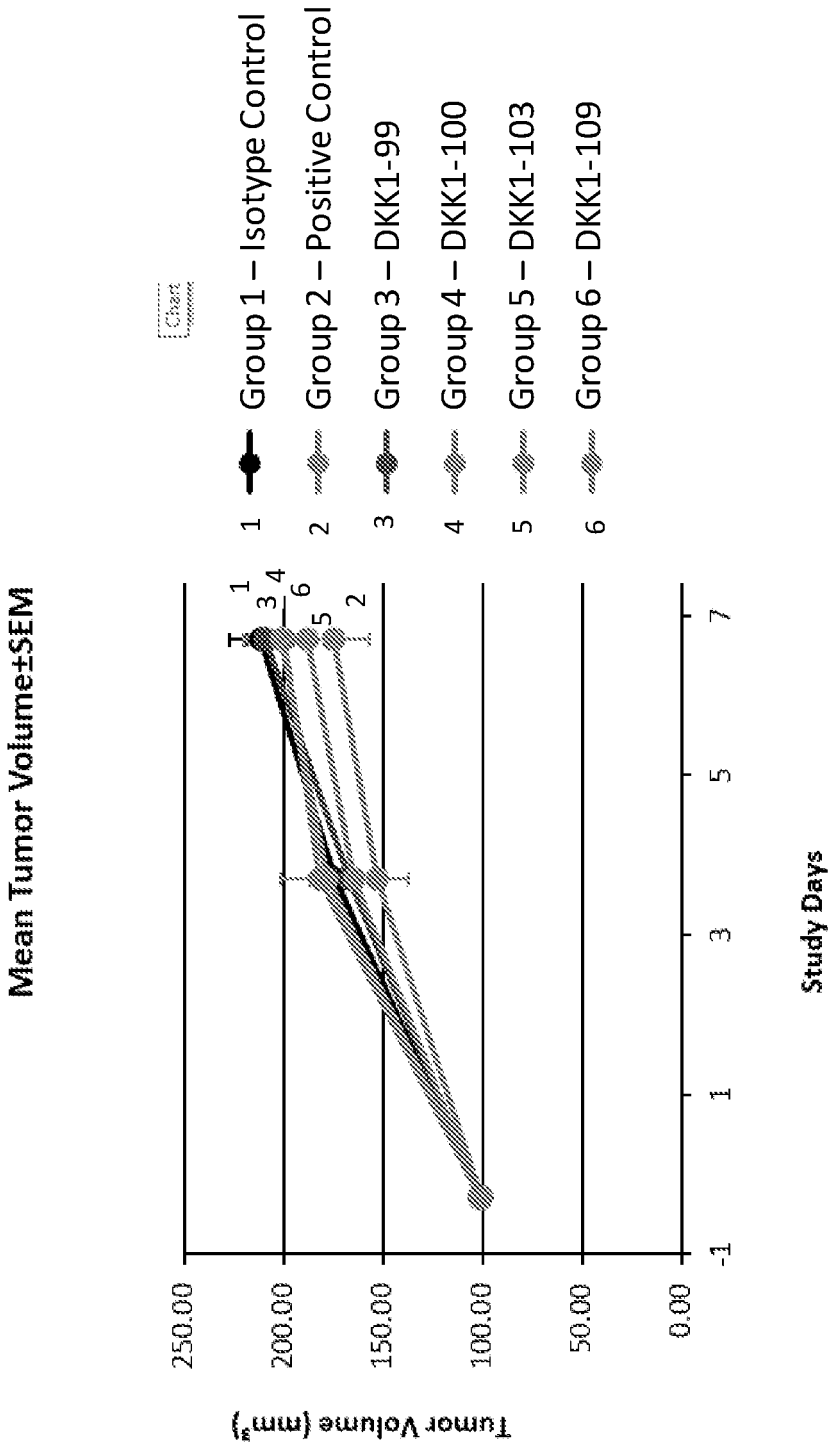

Mean Tumor Volume±SEM
Chart
1 Group 1 – Isotype Control
2 Group 2 – Positive Control
3 Group 3 – DKK1-99
4 Group 4 – DKK1-100
5 Group 5 – DKK1-103
6 Group 6 – DKK1-109
Tumor Volume (mm³)
250.00
200.00
150.00
100.00
50.00
0.00
-1
1
3
5
7
Study Days

FIG. 20D

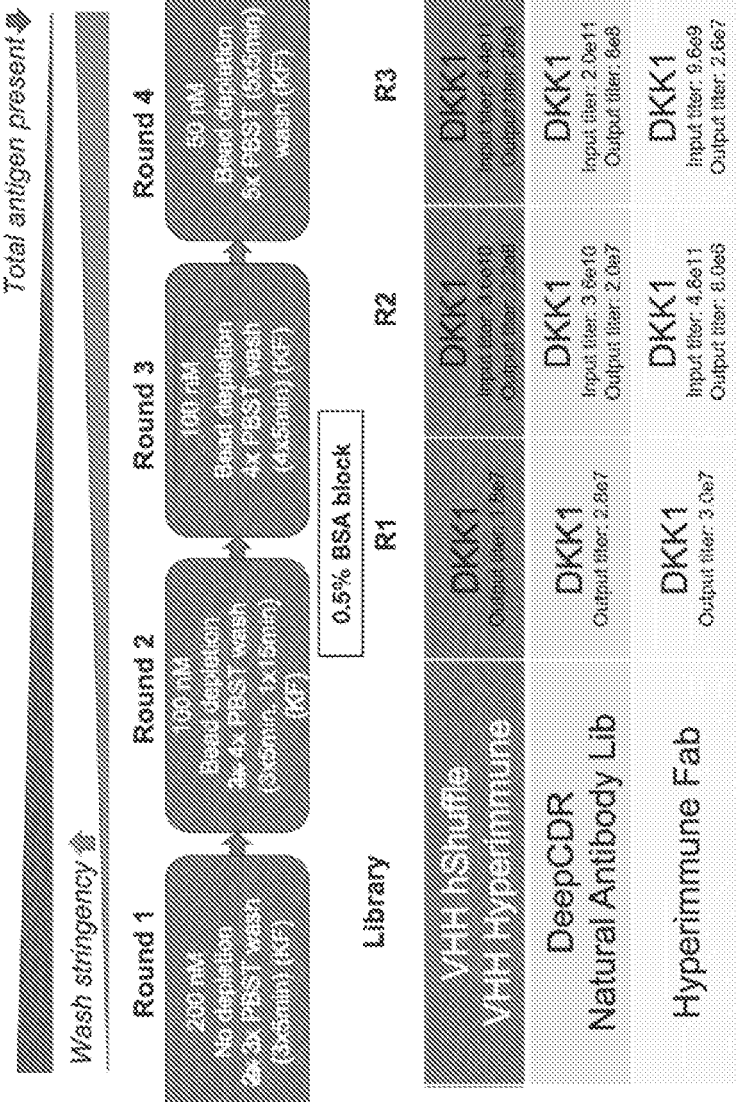

Total antigen present
Wash stringency
Round 1
Round 2
Round 3
Round 4
200 nM
No depletion
4-5x PBST wash
(plasma, 1 hr/rm)
(IgG)
100 nM
Bead depletion
4-5x PBST wash
(plasma, 1 hr/rm)
(IgG)
10 nM
Bead depletion
4-5x PBST wash
(plasma, 1 hr/rm)
(IgG)
50 nM
Bead depletion
4-5x PBST wash
(plasma, 1 hr/rm)
wash (IgG)
0.5% BSA block
Library
R1
R2
R3
R4
VHH hShuffle
VHH Hyperimmune
DKK1
DeepCDR
Natural Antibody Lib
DKK1
Output titer: 2.8e7
DKK1
Input titer: 3.6e10
Output titer: 2.0e7
DKK1
Input titer: 2.0e11
Output titer: 8e8
DKK1
Input titer: 4e10
Output titer: 4.6e6
Hyperimmune Fab
DKK1
Output titer: 3.0e7
DKK1
Input titer: 4.8e11
Output titer: 8.0e8
DKK1
Input titer: 9.6e9
Output titer: 2.6e7
DKK1
Input titer: 2e10
Output titer: 3e8

FIG. 21

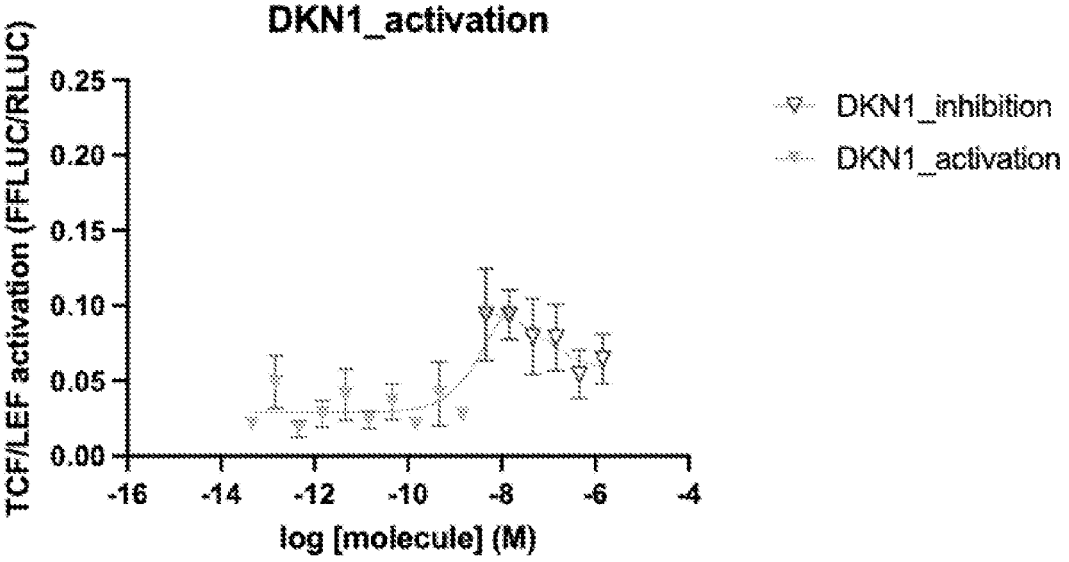


FIG. 22A

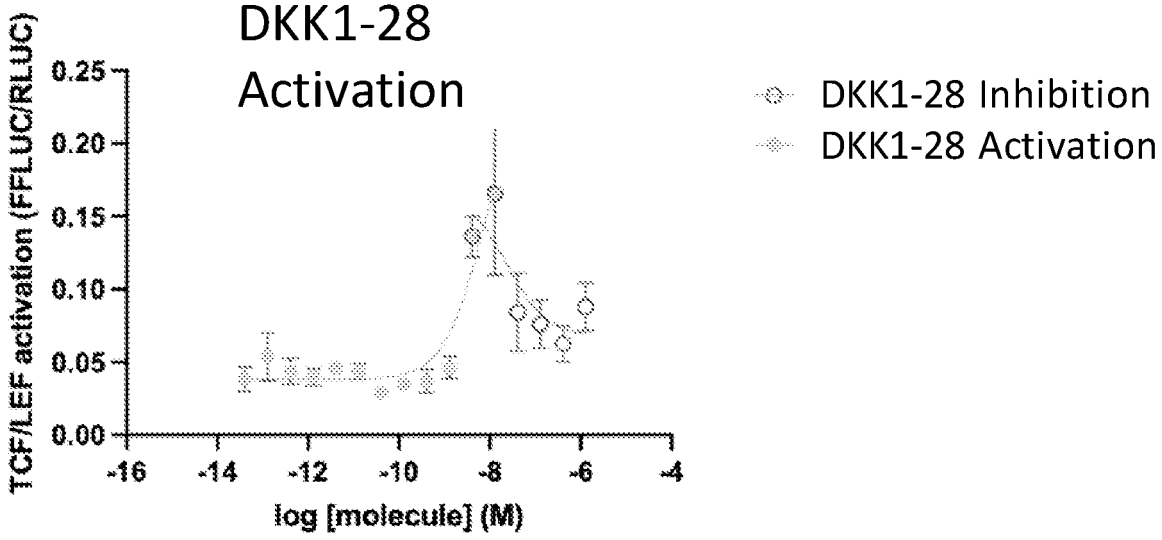


FIG. 22B

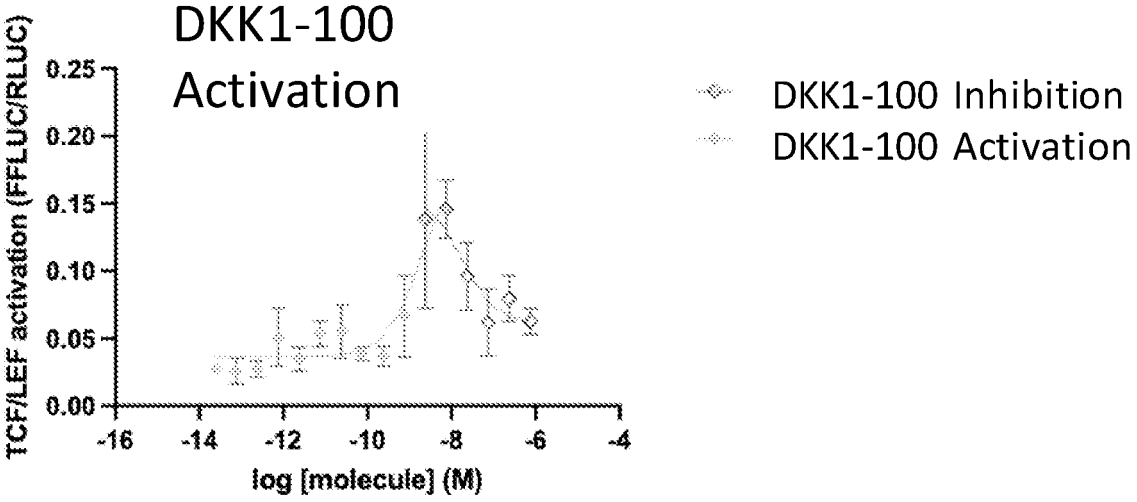


FIG. 22C

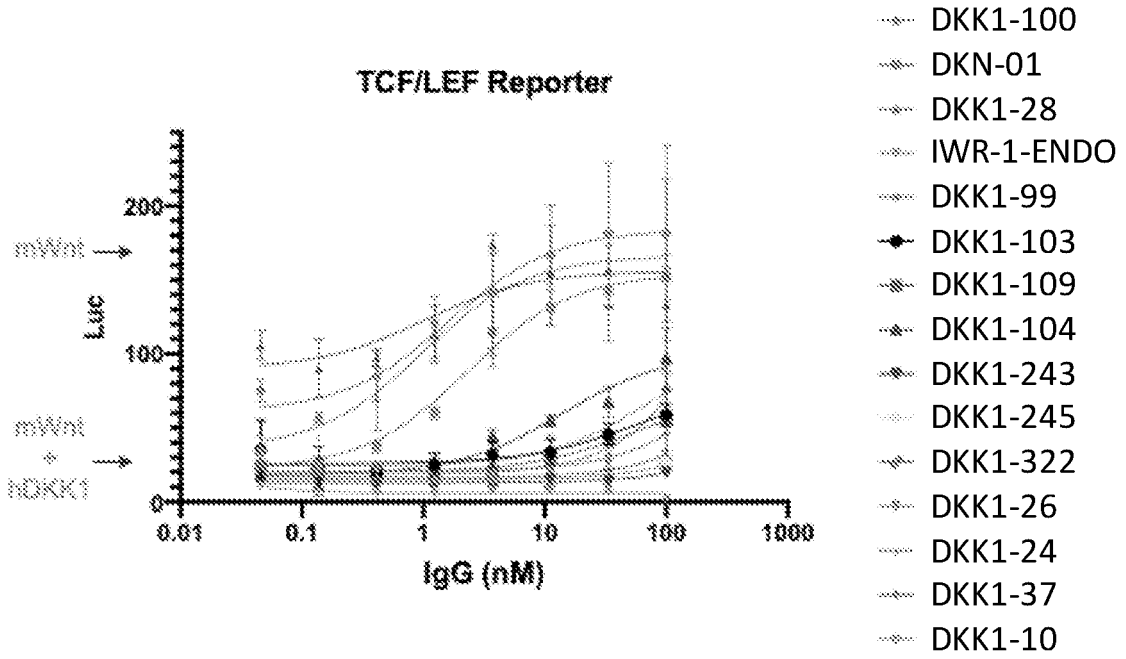


FIG. 23A

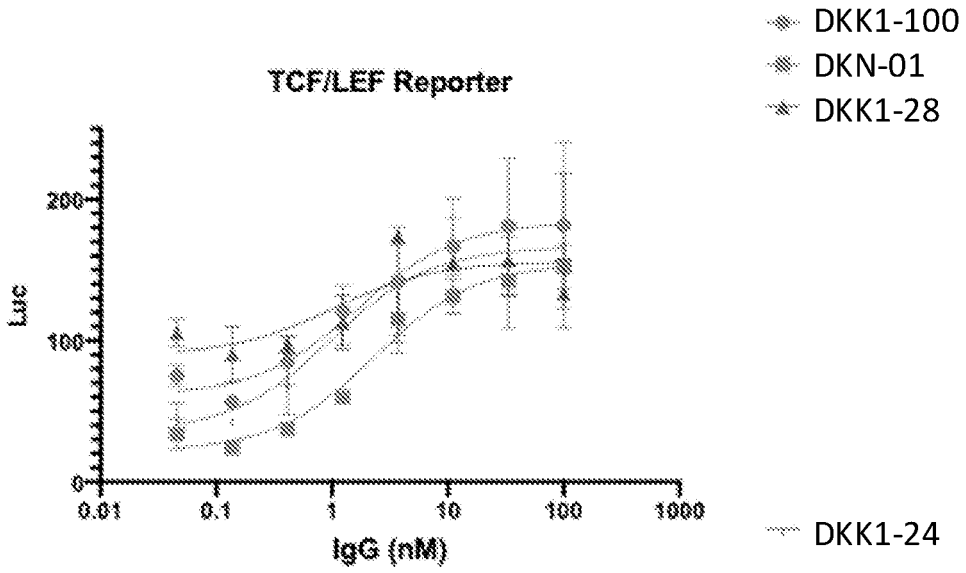


FIG. 23B

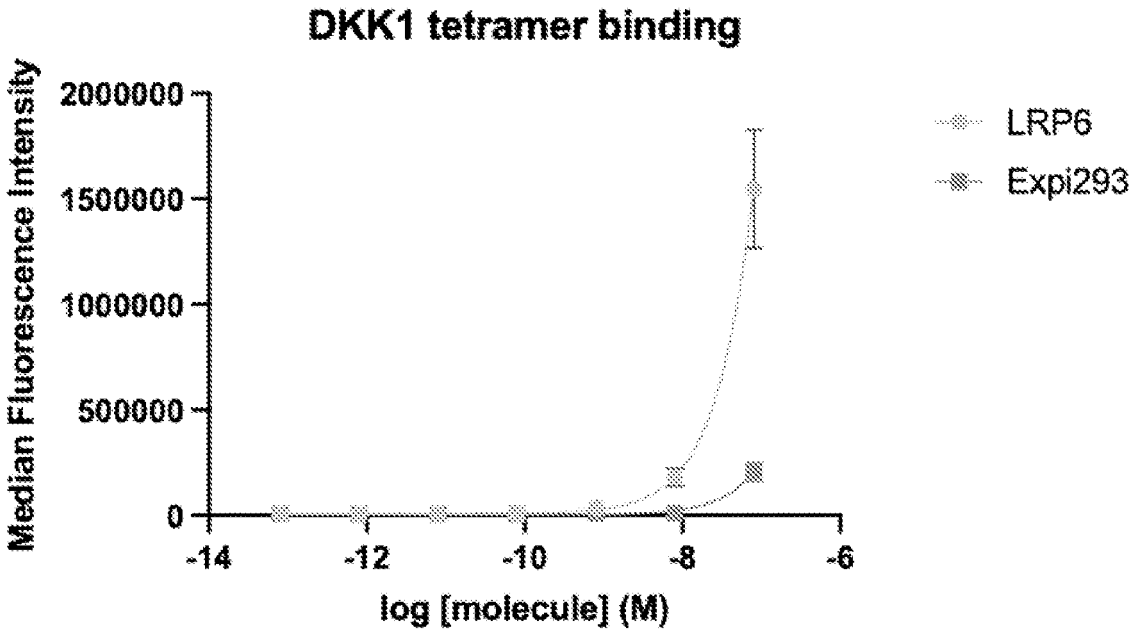


FIG. 24

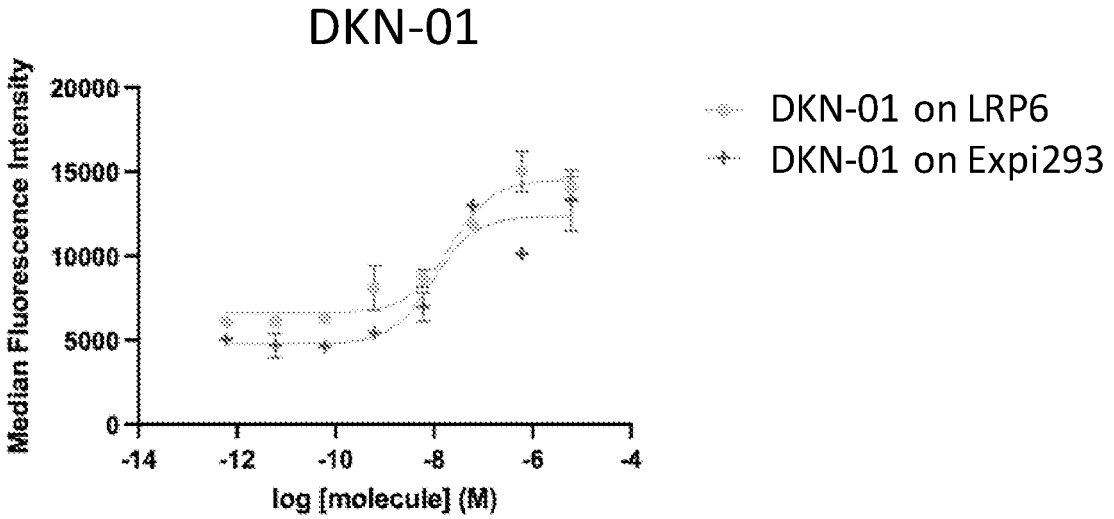


FIG. 25A

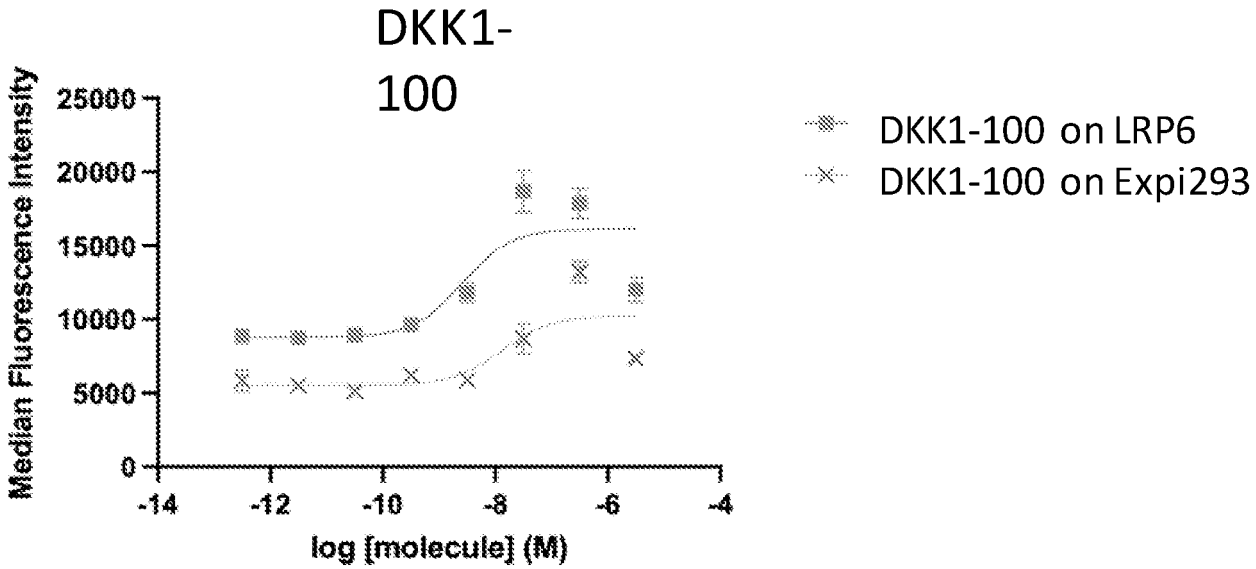


FIG. 25B

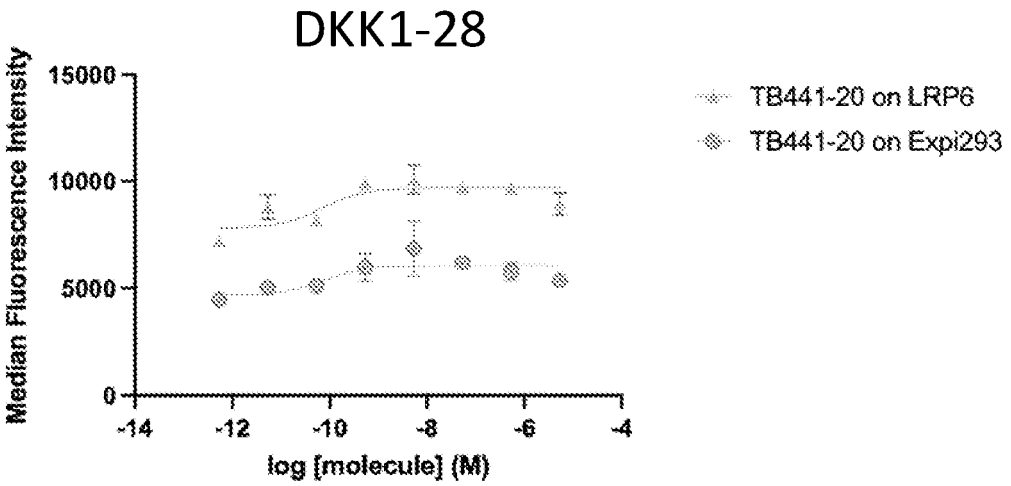


FIG. 25C

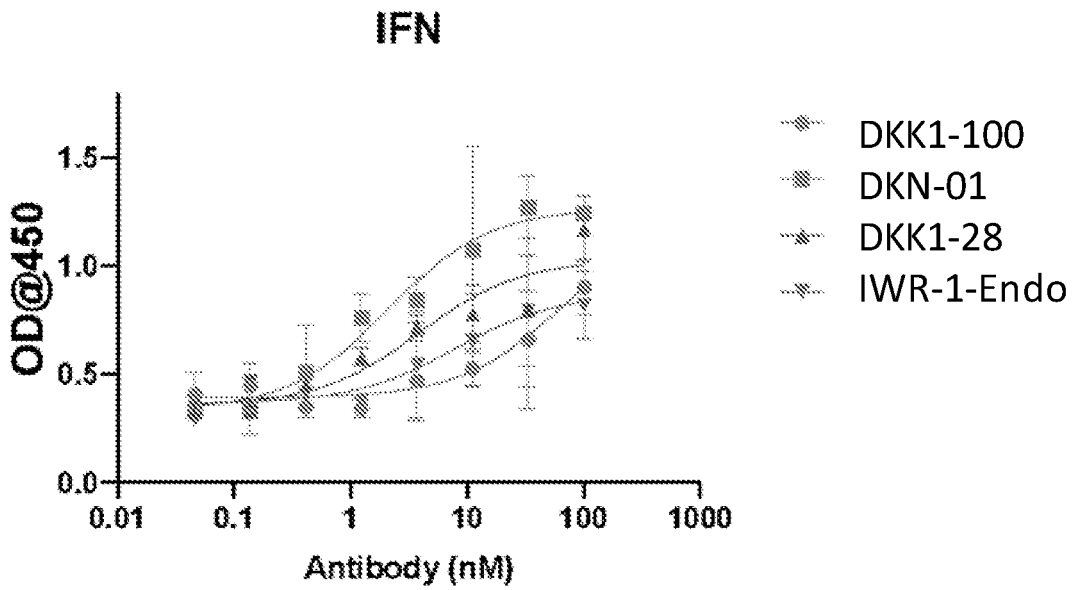


FIG. 26A

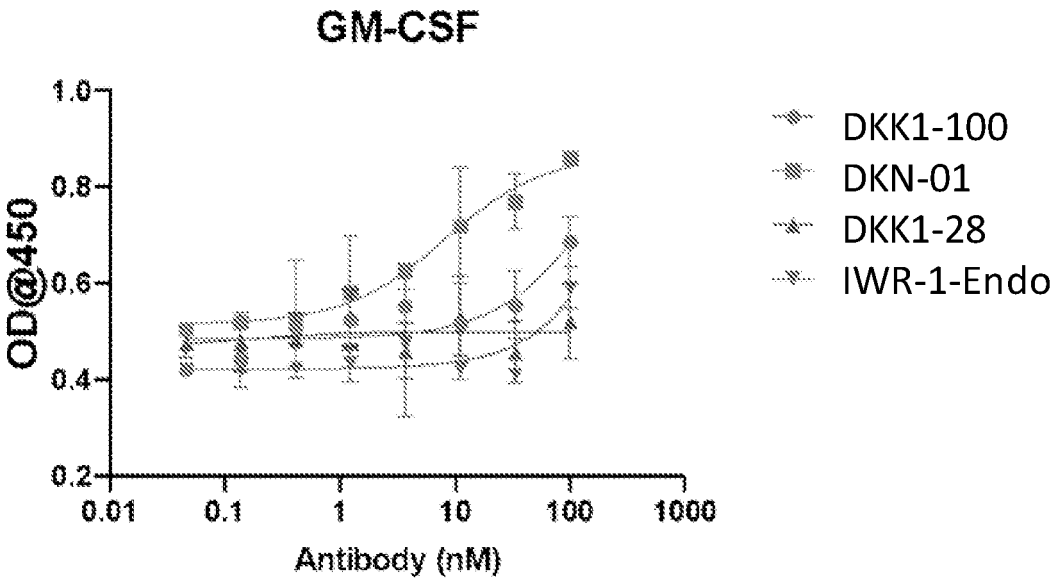


FIG. 26B

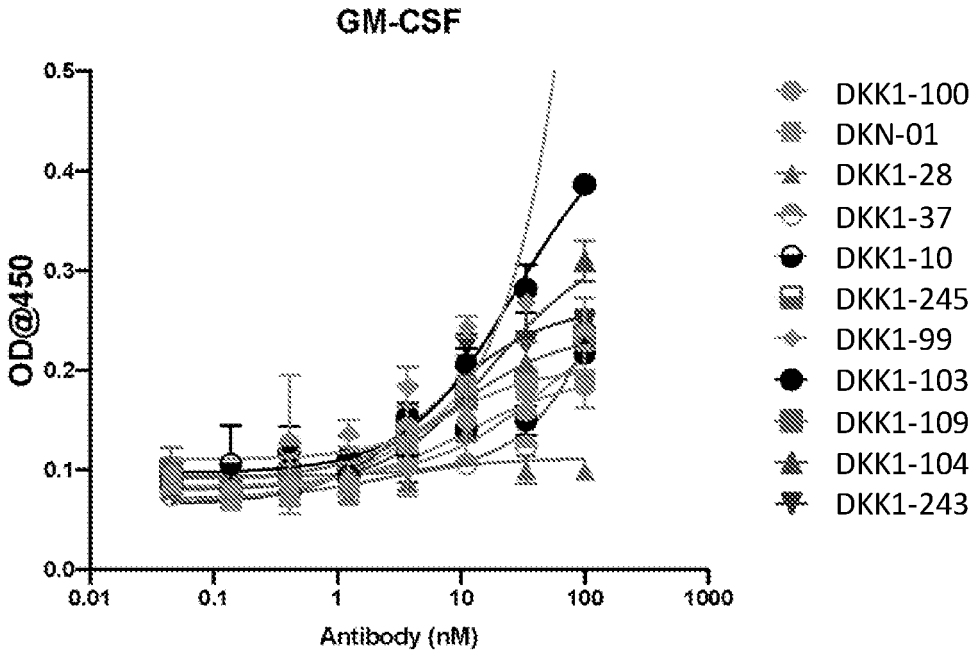


FIG. 27A

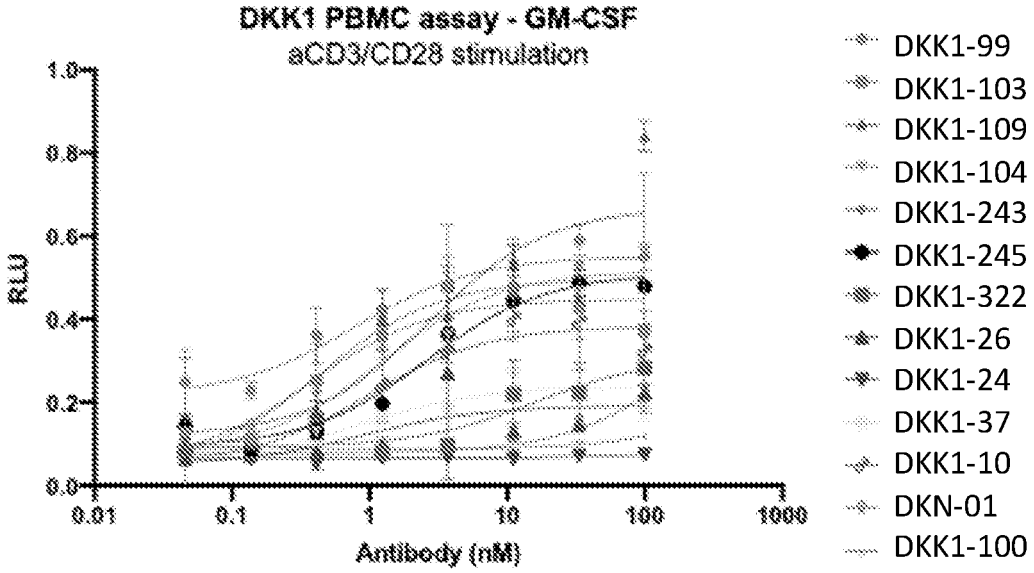


FIG. 27B

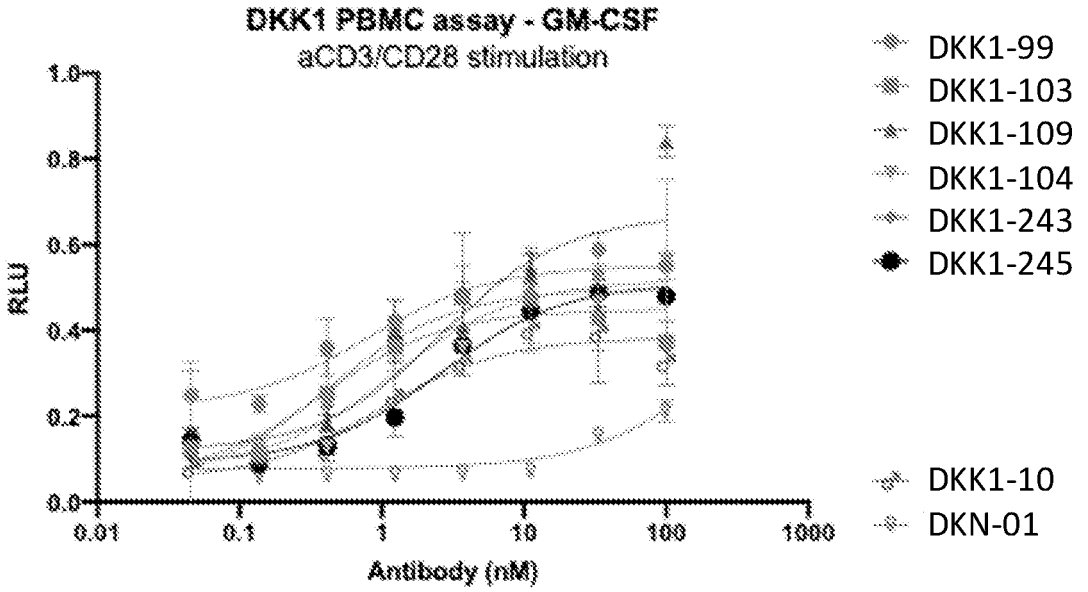


FIG. 27C

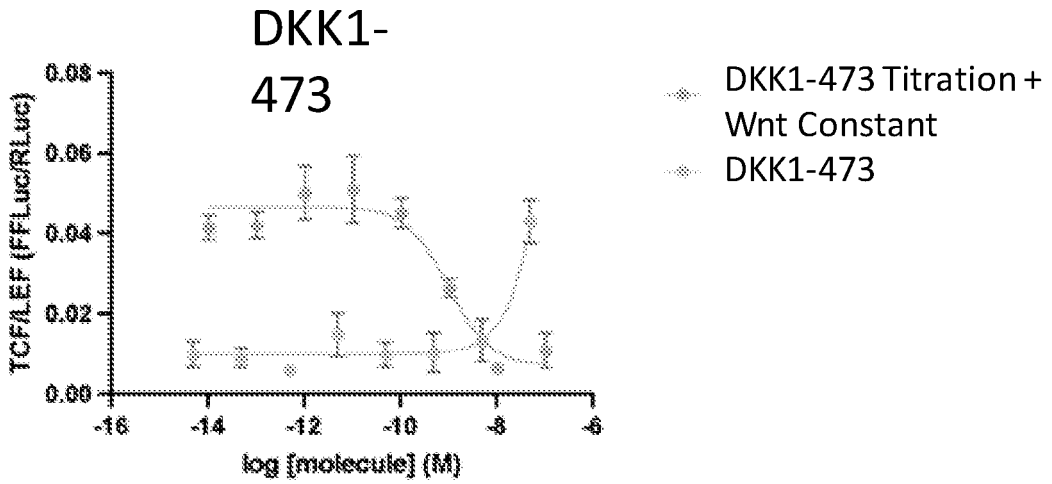


FIG. 28A

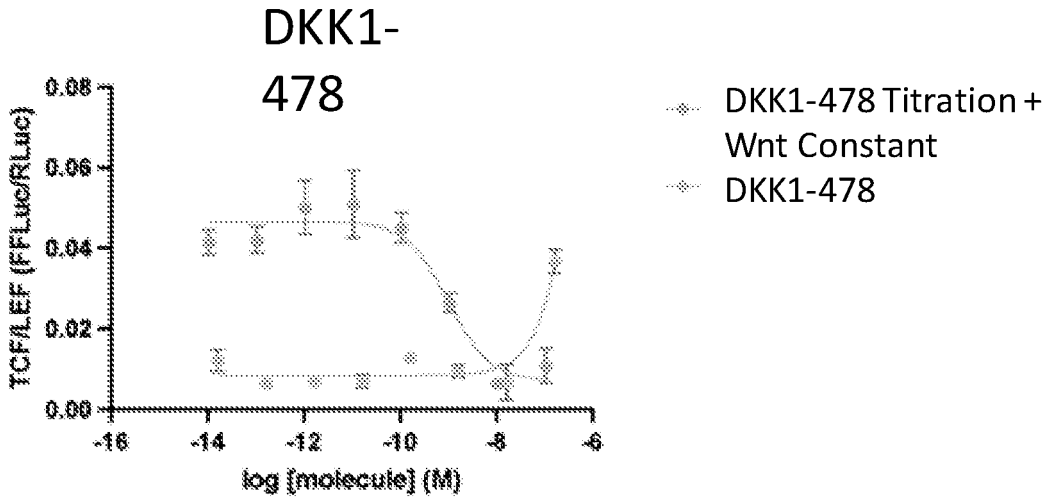


FIG. 28B

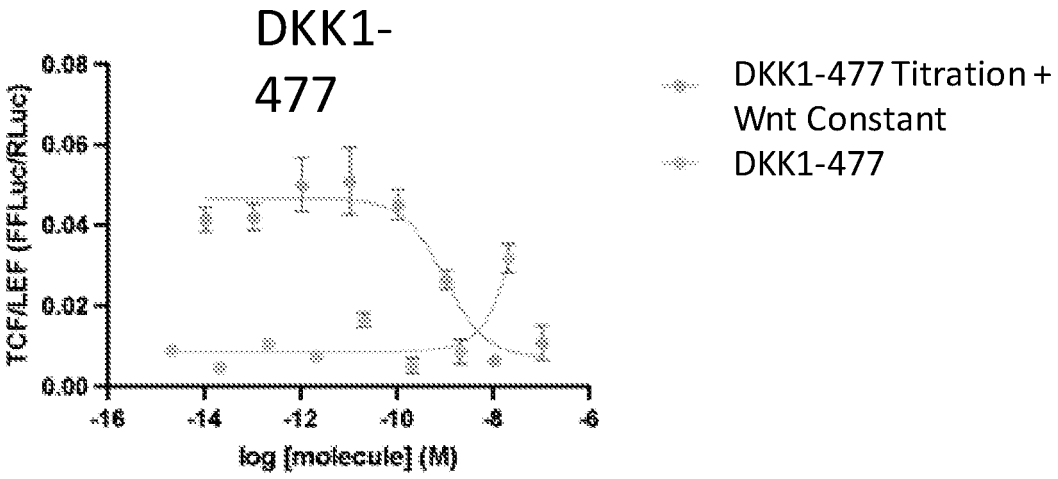


FIG. 28C

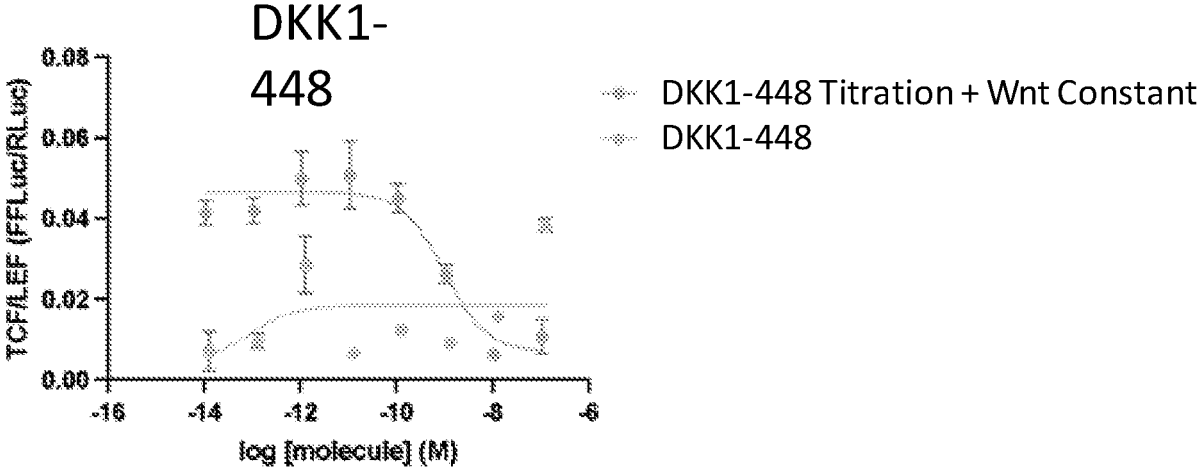


FIG. 28D

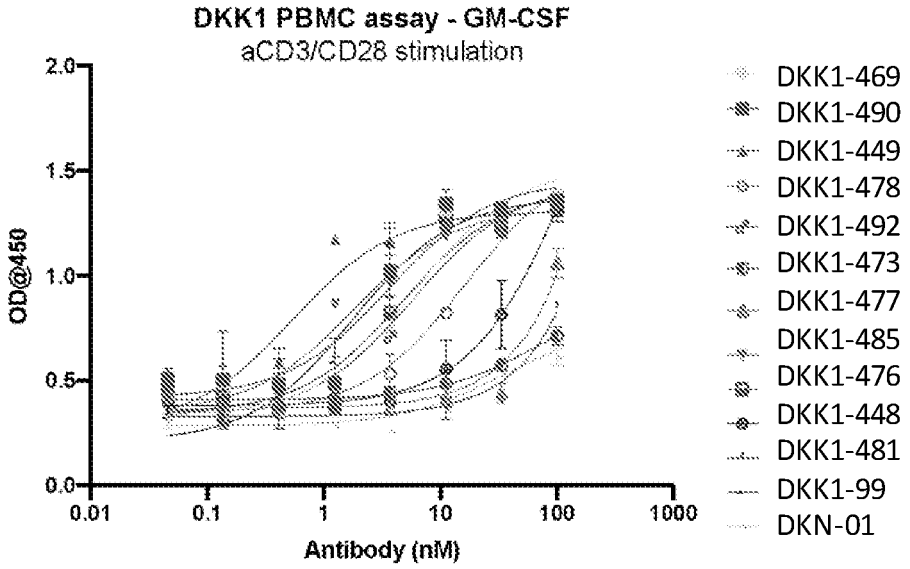


FIG. 29A

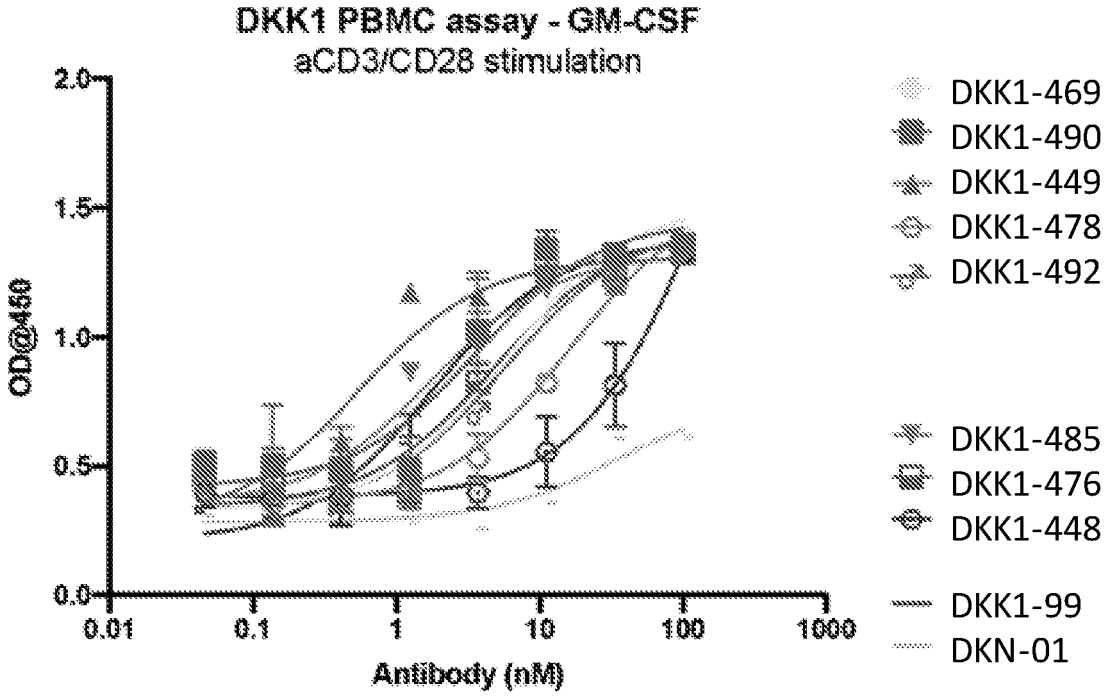


FIG. 29B

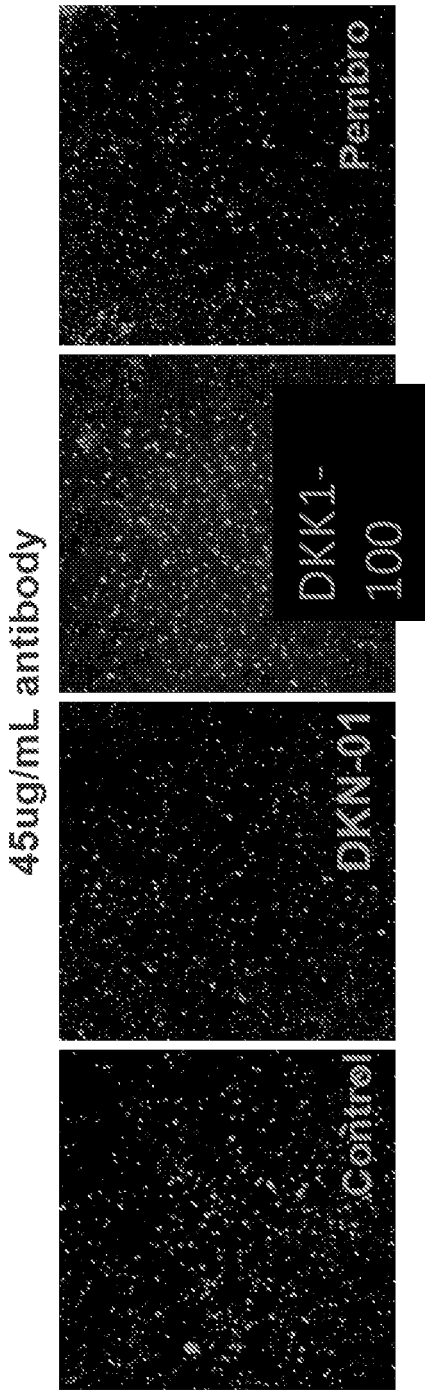


FIG. 30